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THE INHERITANCE AND GENETIC EXPRESSION
OF LOW MOLECULAR WEIGHT GLUTENIN SUBUNITS
IN SOUTH AFRICAN WHEAT CULTIVARS

by

Hilke Maartens

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Supervisor: Prof. M.T. Labuschagne

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Chapter 1

Bread wheat

1.1 Introduction

"The basis of modern crop production is the variety. That scarcely needs emphasising, for it is well known that the difference between growing one variety and another may be the difference between a profit and a loss. In consequence, it is essential for the buyer to get the variety he ask for and not something else. And I may also add that quite apart from any question of profit and loss, the buyer is still entitled to receive what he orders (Carson, 1957)."

Wheat is grown all around the world and more land is devoted to the production of wheat than to any other commercial crop (Briggle and Curtis, 1987; Cook and Veseth, 1991). This makes the need for variety identification probably far greater.

An advantage for the scientist who identifies food grains, is the many methods available to discriminate between varieties. It can however, also be frustrating to know which of these techniques will be the most appropriate for a particular task of identification. Visual identification of grain samples is the traditional approach and is based on the distinguishing characteristics of the grain (Wrigley and Batey, 1995).

Breeders have to recognise specific features of a variety that makes it attractive and desirable to the consumer (Cooke, 1984). In traditional breeding programmes, breeders had to be able to observe differences in plants of the same species that might have economical importance. This was however, unreliable and other methods to recognise specific characteristics are needed (Maunder, 1992). With the introduction of Plant Breeders' Rights, it became even more important for exact methods to identify genotypes and to prove distinctness between cultivars. Plant Breeders' Rights reward breeders financially for their efforts and offer protection for their varieties, but in turn require that new varieties are distinct from others and also uniform and stable in the expression of their characteristics (Cooke, 1995).

Electrophoresis is the most commonly used laboratory method to distinguish between food grains (Wrigley and Batey, 1995). Gel electrophoresis has been used for the identification or verification of varieties at all stages from breeding to variety release, pure seed propagation and sowing at harvest and into marketing and processing of the harvested grain. Gel electrophoresis is faster, costs less and also requires less space and fewer personnel than traditional techniques. Gel electrophoresis obtains information of the identity of a grain from plant proteins. It uses a potential difference (voltage) to separate proteins in a polymer matrix on the basis of their apparent size, charge and pH (Lookhart and Wrigley, 1995).

It should be possible to read the information about the identity and genetic history of a grain sample from its grain-protein composition. Proteins are direct products of gene transcription and translation and it contains a wealth of information, ready to be read off, given the appropriate techniques. Examination of storage proteins is a reasonable compromise between the direct study of the genotype and ease of accessibility to chemical constituents. Analysis of protein composition would thus be expected to provide a better basis for varietal identification than the study of pigmentation or even morphology (Wrigley, 1992; Lookhart and Wrigley, 1995).

The endosperm is the largest tissue in the grain and it contains the majority of proteins (Shewry and Mifflin, 1985). There are five classes of proteins, namely the albumins, globulins, gliadins, glutenins and an insoluble residue (Eliasson and Larsson, 1993). The gliadins and the glutenins are the most important proteins.

The gliadins are the best and most often used for varietal identification. They are readily extracted and fractionated and the genetic control of their synthesis is well understood (Wrigley and Shepherd, 1973). The glutenins constitute 40 to 50 percent of the total protein content in wheat flour (Eliasson and Larsson, 1993). The high molecular weight (HMW) glutenin subunits are not reliable for variety identification as many cultivars have the same composition. This was also found for South African wheat cultivars (Labuschagne *et al*, 1998). It is however, reliable and very easy to use to determine seed purity, that is to see if a specific sample consists of more than one variety. Research on LMW subunits has been limited, because they do not fractionate adequately by SDS-PAGE and on one-dimensional SDS-PAGE gels, many LMW

subunits overlap with gliadins (Zhen and Mares, 1991). A simplified technique for the extraction of LMW glutenins was introduced by Singh *et al* (1991) and it allows for the identification of LMW subunits in a gliadin-free background. This technique was used in this thesis.

The aim of this study was to determine:

1. The HMW glutenin subunits of the South African bread wheat cultivars. The HMW glutenins of South African wheat cultivars were tested previously by Randall *et al* (1992) and Randall *et al* (1993). It was re-tested in this study.
2. The effectiveness of the LMW glutenins for variety identification.
3. The different groups of LMW glutenins in bread wheat cultivars.
4. The band intensities of the different groups.
5. The correlations between the different groups.
6. The genetic distances between different cultivars.

1.2 Literature review

1.2.1. The wheat industry in South Africa

Wheat (*Triticum aestivum* L.) is grown all around the world and more land is devoted to the production of wheat than to any other commercial crop (Briggle and Curtis, 1987; Cook and Veseth, 1991). All wheats belong to the genus *Triticum*. This genus along with *Hordeum*, *Secale*, *Aegilops*, *Bromus* and *Agropyron* are the most important groups in the grass family *Gramineae* (*Poaceae*) (Cook and Veseth, 1991). In 1753 Linnaeus proposed the first classification of wheats based on morphological and physiological differences (Bozzini, 1988). In 1918, Sakamura showed that wheat falls into three categories (Knott, 1987; Bozzini, 1988; Cook and Veseth, 1991). According to Orth and Shellenberger (1988) four species of the genus *Triticum* are relevant, namely *T. monococcum* (diploid), *T. turgidum* (tetraploid), *T. timopheevi* (tetraploid) and *T. aestivum* (hexaploid).

T. turgidum (the durum or macaroni wheats) and *T. aestivum* (the common or bread wheats) are the most important and are, furthermore, the most widely grown. Bread and durum wheats are allopolyploids. Bread wheat is hexaploid ($2n=6x=42$) and has three genomes (AABBDD). Durum wheat is tetraploid ($2n=4x=24$) and has two genomes (AABB) (Baenziger *et al*, 1994).

Common winter and spring bread wheats have a close cytogenetic relationship with durum wheat as they originated from a cross between the tetraploid emmer wheats (genome AABB) and *A. squarrosa* L. (genome DD) (McFadden and Sears, 1946). As the A, B, and D genomes derived from related diploid species, they have genes encoded related but not identical proteins. The interactions of proteins encoded by the different genomes are important when one wants to determine the precise physical and technological properties of doughs that are produce from bread and durum wheats (Tatham *et al*, 1990).

There are also subclassifications of the species of wheat. Hard red winter and hard red spring (according to when planted) are used for leavened bread production. Soft red winter and common white wheat classes are mainly used for pastries, crackers and cookies. Durum wheat is used for pasta products, like spaghetti and macaroni (Jackel,

1995). All parties in international trade must understand that the specifications have very real meanings.

Wheat is not indigenous in Southern and Central Africa. It was introduced into the Cape area of South Africa in the late seventeenth century, but it was only in the mid eighteenth century that production increased and larger quantities of wheat were produced (Anon, 1990). The average size of the annual wheat crop of about 2.2 million metric tons has varied between 1.2 and 3.5 million metric tons over the past ten years. It is largely determined by the climate and rainfall patterns in the summer rainfall areas of the Orange Free State and Western Cape provinces. The breeding and release of new varieties adapted to the different conditions will ensure the future of wheat production in South Africa (Randall *et al*, 1995).

Wheat is at the present the second biggest type of grain in South Africa, after maize. There was a slight decrease in the production of wheat over the last two years (SAGIS, 1999). See Table 1.1. for an indication of the production of wheat over the past years in South Africa.

Table 1.1 The production of wheat in South Africa from 1996 to 1999 (SAGIS, 1999).

Wheat		
	Ton	Ha
1996/1997	2700	1294
1997/1998	2284	1382
1998/1999	1531	748

The world production of wheat increases at a significant rate. Wheat is consumed in many forms, but bread has established itself as a convenient and delicious food (Jackel,

1995). Cereal proteins form 70 to 90 percent of the total protein consumption in many developing countries and in most countries around the world, the area contributed to cereals is the highest among cultivated plants (Lasztity, 1986).

1.2.2. The identification of varieties

Wheat is one of the world's most important crops and the need for variety identification is probably far greater than for any other cereal grain. Breeders have to recognise specific features of a variety that makes it attractive and desirable to the consumer (Cooke, 1984). In traditional breeding programmes, breeders had to be able to observe differences in plants of the same species that might have economical value. This criterion was, however, unreliable and alternative selection methods and criteria were needed (Maunder, 1992).

With the introduction of Plant Breeders' Rights it became even more important to have exact methods to identify genotypes and prove distinctness between cultivars. Plant Breeders' Rights (PBR) have been in place in South Africa since 1976 under the Plant breeders' Rights Act No. 15, as amended in 1996. The main benefits of the PBR have been worldwide access to new varieties, the use of such varieties for food production, plant breeding and development and the proper protection against the alienation of such varieties. It is important to recognise that none of the major staple food crops originated in South Africa and South Africa is therefore, dependent on access to international germplasm and technology. Legislation should ensure that free exchange is not limited. Biodiversity policies and legislation are still in early stages and need considerable refinement (Van der Walt, 1997).

If information about the identity, or even genetic history, of a grain sample is sought, it should be possible to read this information from the grain-protein composition. Proteins contain a wealth of genetic information, ready for reading, given the appropriate techniques. Semantides (sense-carrying molecules, such as DNA, RNA and proteins) provide reliable information about genotype. This is not so for episemantic molecules (the products of enzymes) or for asemantic molecules (not specifically produced by the organism), since in these latter cases, environmental or extraneous influences might be expected to predominate. The most reliable information about identity will thus be provided by primary or secondary semantides (DNA or RNA). Examination of proteins

(classed as tertiary semantides) is a reasonable compromise between the direct study of the genotype and ease of accessibility to chemical constituents. Analysis of protein composition would thus be expected to provide a better basis for varietal identification than the study of pigmentation or even morphology (Wrigley, 1992; Lookhart and Wrigley, 1995).

Prolamin allelic blocks are phenotypical markers of polygenic *loci* at molecular level. It gives information on the characteristics of genotypes, thus serving as markers of gene clusters or non recombinant parts of chromosomes that play an important role in the determination of some characters like quality of grain, temperature tolerance and disease resistance (Sozinov and Popereleya, 1980).

1.2.3. The composition of wheat proteins

The endosperm is the largest tissue in the grain. It contains the majority of proteins (Shewry and Mifflin, 1985), for instance the storage proteins (gliadin and glutenin), proteins and enzymes that have survived from the metabolically active endosperm of the developing grain and also structural proteins (like those in membranes) (Payne *et al*, 1985).

The proteins of cereal grains can be divided into three groups based on their morphology, namely starchy endosperm proteins, proteins of the aleurone layer and proteins of the embryo (Lasztity, 1986). The different possibilities of this classification are summarised in Table 1.2.

Table 1.2 Differences in the classification of cereal proteins (Lasztity, 1984).

On the basis of morphology	On the basis of biological function	According to solubility (Osborne)	On the basis of chemical composition
Endosperm proteins	Metabolically active/	Albumins	Simple proteins
Proteins of the aleurone layer	cytoplasmic proteins	Globulins	Complex proteins
Proteins of the embryo	Enzymes	Prolamins	Lipoproteins
	Membrane proteins	glutenins	Glycoproteins
	Proteins of ribosomes		Nucleoproteins
	Regulatory proteins		etc.
	Other proteins		
	Storage proteins		
	Low molecular weight proteins		
	High molecular weight proteins		

The understanding by scientists of the role of the wheat proteins in baking is still incomplete, mainly because of the complexity of their composition and their physical properties. There are five classes of proteins: albumins (soluble in water), globulins (soluble in salt solutions), gliadins (soluble in aqueous ethanol), glutenins (soluble, or rather dispersible, in dilute acid or alkali) and an insoluble residue (Eliasson and Larsson, 1993).

The gliadins and glutenins are the most important proteins of these different classes. It seems to be a common opinion that the composition of albumins and globulins does not vary between wheat varieties, and there is no correlation between the amount of albumins and globulins and baking performance (MacRitchie, 1984). It is thus not possible to use the albumins and globulins to identify varieties or to discriminate between varieties differing in baking performance. There are results that indicate that

more soluble proteins might be extracted from a good variety of wheat than from a poor variety (Eliasson and Larsson, 1993).

Gluten proteins have been divided into two main classes based on their solubility in 70 percent ethanol. The alcohol-soluble class is considered to be gliadin and the residue glutenin, a part of which can be solubilised in 0.1M acetic acid. The distinction between solubility classes is not too clear, because the components overlap. Consequently, there has been a tendency to define these classes on the basis of molecular size. Proteins larger than 100 kDa were considered to be mainly glutenin, those between 100 and 25 kDa mainly gliadin, and proteins smaller than 25 kDa were classed as albumins and globulins. This definition minimised the overlap of components, but did not eliminate it completely. Bietz and Wall (1972) showed that some albumins and/or globulins are considerably larger than 25 kDa. Furthermore, dimers of some low molecular weight (LMW) glutenin subunits (30-50 kDa) have molecular weights similar to those of ω -gliadins (Bietz and Wall, 1972) and minor triplet band proteins (globulin) form oligomers of 150-160 kDa and larger size (Singh and Shepherd, 1985). Clearly the classification based on molecular size also has limitations, and recently all gluten proteins, apart from minor globulin components, have been classified as prolamins. Their subdivision into gliadin and glutenin is based on functional properties. Glutenins are aggregating or polymeric and gliadins are non-aggregating or monomeric (Singh *et al*, 1990b). Prolamins are very important for processing wheat into food products. When flour is mixed with water, it forms a dough and it becomes both extensible and elastic. These properties are conferred primarily by protein (Wall, 1979). It is important in food science to breed and grow wheat varieties in which the protein component is optimum for the ultimate product (Lasztity, 1986).

The gliadin-glutenin classification is still widely used, because of its convenience and its technological significance. There is however, also an alternative classification based on primary structure relationships rather than subunit interactions, as is the case with the gliadin-glutenin classification. Three groups are recognised in this approach, namely the sulphur-rich (S-rich), sulphur-poor (S-poor) and HMW prolamins. (See Figure 1.1). The S-poor and HMW prolamins respond to the ω -gliadins and the HMW glutenin subunits, while the LMW glutenin subunits, α -type gliadins and γ -type gliadins are all S-rich (Tatham *et al*, 1990).

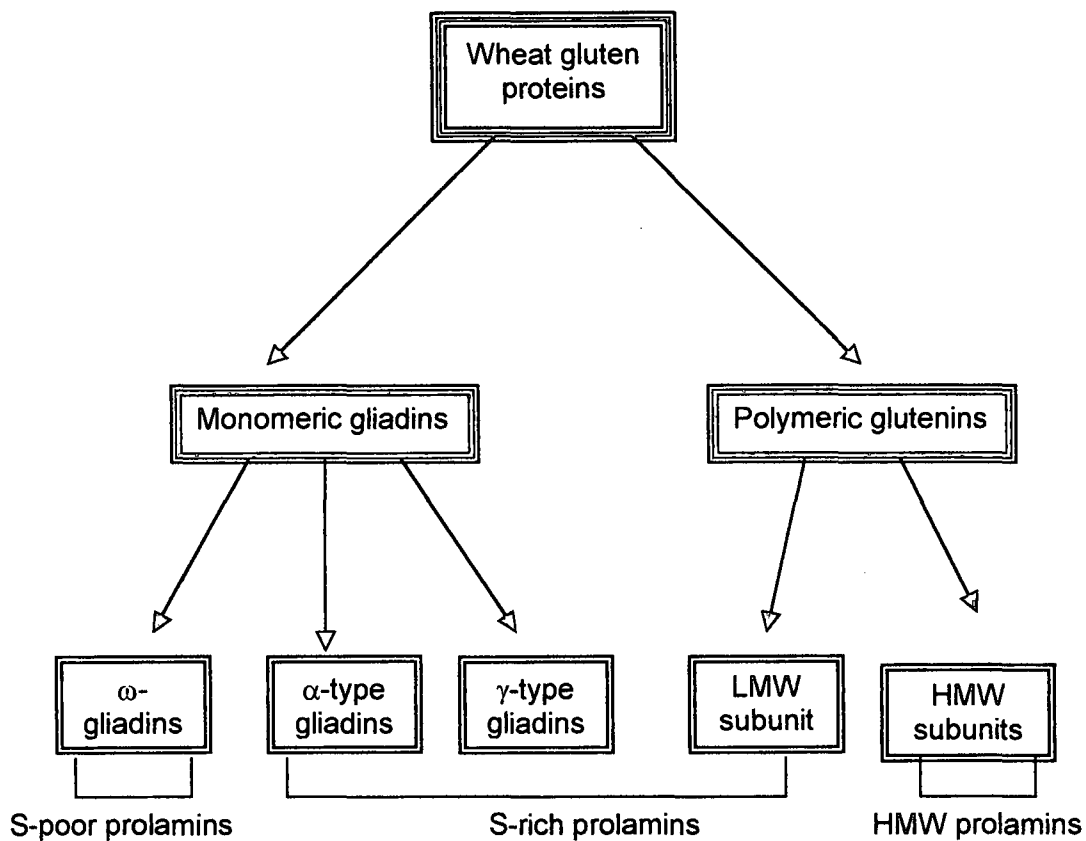


Figure 1.1. The classification of wheat gluten proteins (After Shewry and Mifflin, 1985).

The fractionation is based on extraction procedures and there are no clear-cut limits between the classes. The composition of each class will depend on the exact conditions during the extraction, such as temperature and solvent/flour ratio. For complete extraction of the wheat proteins, many different solvent systems have been tried. If surfactants (for example sodium dodecyl sulphate (SDS) or cetyltrimethyl ammonium bromide (CTAB) or soaps) are included, 90 to 95 percent of the proteins are claimed to be extracted. It has been suggested that the extractability in certain solvents reflects the baking performance of the wheat flour; for example, less detergent is needed to extract

the proteins from a poor variety. On the other hand, the extractability in SDS is related to the protein content but not to the protein quality (Eliasson and Larsson, 1993).

One important concern of chemistry is to understand the relationship between the chemical structure of a compound and its functionality. The unique position of wheat depends on its ability to form gluten. Even cereals like rye and barley, which are close phylogenetic relatives, do not have this ability (Belitz *et al*, 1986). Wheat flour has the important property that when it is moistened and worked by mechanical action, it forms an elastic dough (Potter and Hotchkiss, 1995).

Whereas the metabolic proteins are found among the soluble proteins, the gluten proteins constitute the main storage protein in the wheat endosperm. This has important applications for the composition of the gluten protein. They are rich in glutamine and proline, but poor in lysine and arginine. With time many mutations have occurred in the storage protein complex without detrimental effects on their function, which is to be digested once the seed germinates. Gluten could perhaps be viewed as a protein mixture with a continuous molecular weight distribution from about 30 000 to perhaps 20 million Da. Attempts are made to divide this complex mixture into less complex subgroups in order to understand their behaviour better. The most common separation is into gliadins and glutenins (Eliasson and Larsson, 1993).

Important chemical and physical differences exist between the gliadin and glutenin proteins that are relevant to their functional characteristics. The gliadin fraction comprises monomeric proteins and where present, disulphide bonds are intra-chain. The glutenin fraction, on the other hand, comprises polymeric proteins, whose component subunits are almost certainly linked by inter-chain disulphide bonds since they cannot dissociate in strongly dissociating solvents but are readily dissociated on addition of reducing agents. The glutenin proteins are also extremely polydisperse with respect to molecular size.

As many as 50 different polypeptides may compose the gliadin fraction and as many as 20 the glutenin fraction as determined by two-dimensional electrophoretic techniques. The polypeptides present in each fraction are quite distinct, as shown by high-resolution two-dimensional electrophoresis. The two fractions also have quite different physical

properties when hydrated, the gliadin fraction behaving as a viscous liquid and the glutenin fraction as a cohesive elastic solid (Schofield, 1986).

A major problem in working with gluten proteins has been the difficulty of solubilising the total protein. Gluten has strong aggregation tendencies generally assumed to result from the hydrogen bonding potential of the unusually large numbers of glutamine side chains. Also of importance is the large potential for apolar bonding of the many nonpolar side chains and gluten's low ionic character. To completely solubilise the gluten proteins, workers have resorted to breaking the glutenin polymers into smaller molecules.

The gluten from poor-quality flour has higher solubility than gluten from good-quality flour. The differences in protein solubilisation between different quality flours suggest that the proteins in poor-quality flour might have smaller molecular weights or possess less of a tendency to interact with themselves. The surface of the starch granule is presumed to be more hydrophilic. This means that the poor-quality gluten, which has a greater tendency to interact with starch, is more hydrophilic than is the good-quality gluten. Therefore, the good-quality gluten is more difficult to solubilise (He and Hosney, 1990).

1.2.3.1 The gliadins

Gliadins are defined as the wheat proteins soluble in aqueous ethanol in the classic Osborne extraction procedure. As mentioned earlier, gliadins are monomeric proteins. The disulphide bonds present are thus all intramolecular. The gliadin conformations are stabilised by hydrogen bonding and hydrophobic interactions. They constitute about 30 to 35 percent of the total protein when they are extracted in 70 percent ethanol. The gliadin group is heterogeneous, and the mobility in aluminium lactate starch gel electrophoresis has been used to divide the gliadins into four groups: the α -, β -, γ - and ω - gliadins. α - Gliadins are the fastest moving, and ω -gliadins the slowest moving (Eliasson and Larsson, 1993). The majority of the gliadin proteins of wheat endosperm are simple polypeptides without subunit structure under normal conditions of extractions (Payne *et al*, 1984b).

The proportion of the total protein content has been estimated for different gliadins from their electrophoretic patterns. The ω -gliadins constitute about eight to 13 percent of the

protein, whereas the sum of the α -, β - and γ -gliadins constitute about 34 to 38 percent of the protein. The ω -gliadins are found in the smallest amount, followed by the α -gliadins, β -gliadins and γ -gliadins, respectively, in increasing amounts. The amount of one individual gliadin component is in the range 0.06 to 3.00g/100g storage protein. The molecular weight of most gliadins is in the range 30 000 to 40 000 Da, but the ω -gliadins have a molecular weight around 60 000 to 80 000 Da.

The amino acid composition of the gliadins is characterised by a high level of glutamine and proline. It has been suggested that the gliadins could be classified according to their content of sulphur-containing amino acids. The ω -gliadins would then belong to the sulphur-poor prolamins, whereas α -, β - and γ -gliadins would belong to the sulphur-rich prolamins. The content of ionic amino acid residues is very low, whereas the content of the hydrophobic residues is high. This results in a very low water solubility of the proteins. Among the gliadins, γ -gliadins exhibit the highest surface hydrophobicity. The number of hydrophobic sites was not affected by folding of the gliadin molecule, and it was concluded that hydrophobic interactions are not of great importance for the gliadin structure. However, when the gliadins aggregated, the number of hydrophobic bonding sites decreased considerably.

The high level of proline will affect the secondary structure of gliadins in that the proline residues disrupt α -helices. The ω -gliadins differ from the other gliadins in that they do not contain α -helix or β -sheet structures. Instead, the ω -gliadins contain β -turns. This structure is stabilised by hydrophobic interactions between aromatic amino acid residues and by hydrogen bonding involving glutamine residues. As the cystine content is very low, disulphide bonds are not important for the conformation of the ω -gliadins. The α -helix structure of the other gliadins is very stable. The disulphide bonds may help in stabilising the structure, but the main stabilising forces are attributed to the very high number of hydrogen bonds (Eliasson and Larsson, 1993).

The flour of related cereals that do not have α -gliadins (for example rye) as a rule results in very weak gluten. In relatives that lack the ω -gliadin (for example oats) or where the α - and β -prolamin are predominant (for example barley) the gluten is not formed or is not elastic. Normal gluten may be obtained from barley and rye flour mixture at the expense

of mutual compensation in respect of α - and ω -gliadins. High quality gluten in wheat and triticale is also the result of compensation, but in this case the compensation is carried out by biological ways that is due to the combination of corresponding genomes in evolution or breeding of allopolyploid genotypes (Konarev, 1982).

The gliadin composition is characteristic of the wheat variety. It does not change over the years, but improved electrophoretic techniques might affect the pattern so that a greater number of bands may be detected. The gliadin pattern is not affected by growth conditions, by total protein content, or by sprouting. Gliadins can thus be used as a possible means of identification of wheat varieties. The number of gliadins is high — in one single variety there are 20 to 25 different gliadins — but the total number of different gliadins is even higher (Eliasson and Larsson, 1993). Tatham *et al* (1990) found that more than 30 components can be separated by two-dimensional electrophoretic techniques.

As will be discussed later, the glutenin HMW subunits are found in pairs. Some gliadins are also found together, but the presence of certain gliadins seem not to be linked to the presence of certain HMW glutenin subunits (Payne *et al*, 1984b). However, gliadins can be used as markers for LMW glutenins, because of the linkage between *Gli-1* and *Glu-3*. Cultivars carrying the same allele at one *Gli-1* locus are expected to show identical LMW glutenin patterns at the corresponding *Glu-3* locus (Singh and Shepherd, 1988).

All the ω -gliadins, most of the γ -gliadins and a few of the β -gliadins are now known to be coded by genes on the short arms of chromosomes 1A, 1B and 1D (as will be discussed later). Gliadin proteins were shown to be inherited as several blocks, but in some crosses, a small amount of recombination occurred within a block between ω - and γ -gliadins, thought to be coded by chromosome 1B. It is not clear whether each of the short arms of the homologous group 1 chromosomes have a single, complex locus coding for the classical gliadins or two or more *loci* (Payne *et al*, 1984b). Another major group of storage proteins in wheat, the LMW subunits of glutenin were also shown to be located on the short arms of the homoeologous group 1 chromosomes (Jackson *et al*, 1983).

1.2.3.2 The glutenin subunits

Glutenins are the proteins remaining after the albumins, globulins and gliadins have been extracted, according to the classification of Osborne (1907). They constitute 40 to 50 percent of the total protein present in wheat flour. Glutenins are soluble, or rather dispersible, in dilute acid or alkali, in denaturants such as urea, and in surfactants. The low solubility of glutenins is mainly because of their high molecular weight. Molecular weights up to 20 million Da have been reported. It is difficult to measure the molecular weight distribution of native, nonreduced glutenin, because of the insolubility of the proteins (Eliasson and Larsson, 1993).

The glutenin subunits are usually divided into two groups, HMW subunits and LMW subunits. The HMW subunits have a molecular weight in the range 90 000 to 150 000 Da, whereas the LMW subunits have molecular weights in the range 30 000 to 51 000 Da. The average molecular weight of the LMW glutenins (40 kDa) is about half the average of the HMW glutenin subunits (average 85 kDa). There are thus about six molecules of LMW glutenin subunits for every HMW glutenin molecule. The molar ratio is 6:1. With characters such as formation of large polymers and dough strength, the HMW glutenins have a greater influence than the LMW glutenin subunits and it can be calculated that the effect of one HMW subunit molecule is four times that of one LMW subunit molecule (Gupta *et al*, 1995).

The high molecular weight glutenin subunits

The conformation of the HMW glutenin is similar to that of the ω -gliadins. The conformation is characterised by a large proportion of β -turns in the central domain. The terminal domains contain some α -helix structure. The existence of β -turns has been suggested as one of the reasons for the elasticity of glutenins (Tatham *et al*, 1985). The other reason is the number and distribution of cross-links formed between cysteine residues, which are predominantly located in the N-terminal and C-terminal domains (Buonocore *et al*, 1996).

The HMW subunits constitute only about one percent of the dry matter content of the endosperm. The total number of different HMW subunits is around 20. A single variety usually contains three to five different subunits. The glutenin subunits are linked together by disulphide bonds to the huge polymeric glutenin molecules. This is consistent with the

location of the disulphide bonds in the terminal domains of each subunit, as is evident from the cysteine residues located there (Eliasson and Larsson, 1993). The disulphide bonds are very important. Cleavage of disulphide bonds causes a decrease in viscosity, because the polymers break into smaller pieces (Bietz and Lookhart, 1996).

Each HMW subunit has been assigned a number, and the presence of certain combinations of these subunits is related to different quality aspects (Payne *et al*, 1981). The HMW subunits 5+10 are said to be present in varieties of good baking performance, whereas 2+12 are present in varieties of poor performance (Campbell *et al*, 1987; Cressey *et al*, 1987). The presence of subunits 5+10 is also associated with a high sedimentation volume in the SDS sedimentation test, whereas the presence of subunits 2+12 is associated with a low sedimentation volume (Payne *et al*, 1981). On the basis of these results, quality scores are assigned to each of the HMW subunits, and by adding these scores for the different HMW subunits present, a quality score, called the *Glu-1* score, is obtained for each wheat variety. The highest score is obtained for the subunits 5+10. The *Glu-1* score is positively correlated with baking performance in the case of bread, and 47 to 60 percent of the variation in breadmaking qualities could be accounted for by the variation in HMW subunits. The quality score is negatively correlated with the baking performance in the case of biscuits (Payne *et al*, 1987a), which is in accordance with what is expected. The correlation between subunits 5+10 and baking quality is lower in some countries. For Australian wheats a somewhat weaker relation was observed, perhaps related to the presence of subunits 17+18 (Campbell *et al*, 1987). The HMW glutenins seem not to influence loaf volume during fermentation or proofing (Singh *et al*, 1990b). Lines with poor combinations of HMW glutenin subunits generally were poor in quality. The presence of favourable combinations of HMW glutenin subunits did not however, guarantee acceptable quality (Primard *et al*, 1991).

It is significant that subunits 5+10 and subunits 2+12 are coded by genes on the D-genome. This is the genome that distinguishes bread wheats from durums. This probably explains why HMW glutenin subunits have not been found to be associated in any way with dough properties in durum wheats. The differential effects of the HMW subunits of glutenin appear to be strongest for those coded by chromosome 1D, followed closely by chromosome 1A with the 1B chromosomes the least effective (Payne *et al*, 1981).

Among allelic HMW subunits controlled by the *Glu-A1* locus on chromosome 1A, bands 1 and 2* have an equal positive effect over the null allele, suggesting a quantitative effect. Similarly, among several alleles at the *Glu-B1* locus on chromosome 1B, those producing double bands or intensely staining bands (for example subunits 7+8, 13+16 and 17+18) are associated with superior bread-making quality compared with those with single or faint bands (for example subunits 7, 20 and 6+8) (Singh *et al*, 1990b).

It is evident that the HMW glutenin subunits are important to baking performance. However, it is not known if the presence of a specific HMW subunit is directly responsible for the quality observed or if the presence of the subunit coincides with other properties that are the direct cause. It has been argued that it is the amount of glutenin and not its composition that is most important. The presence of subunits 5+10 could also be related to a higher proportion of glutenin, and a high amount of glutenin is beneficial (Campbell *et al*, 1987; Singh *et al*, 1990a). The loaf volume is related directly to the proportion of HMW subunits determined by SDS-PAGE, a further indication that the amount might be more important than the type of glutenin.

Randall *et al* (1993) found that bands 13+16 and 17+18 were much more prevalent in South African wheats than researchers had published for American (Khan *et al*, 1989), British (Payne *et al*, 1987a) and Canadian (Lukow *et al*, 1989) wheats. Figure 2.2 shows the frequency of alleles for HMW glutenin subunits in South African wheats.

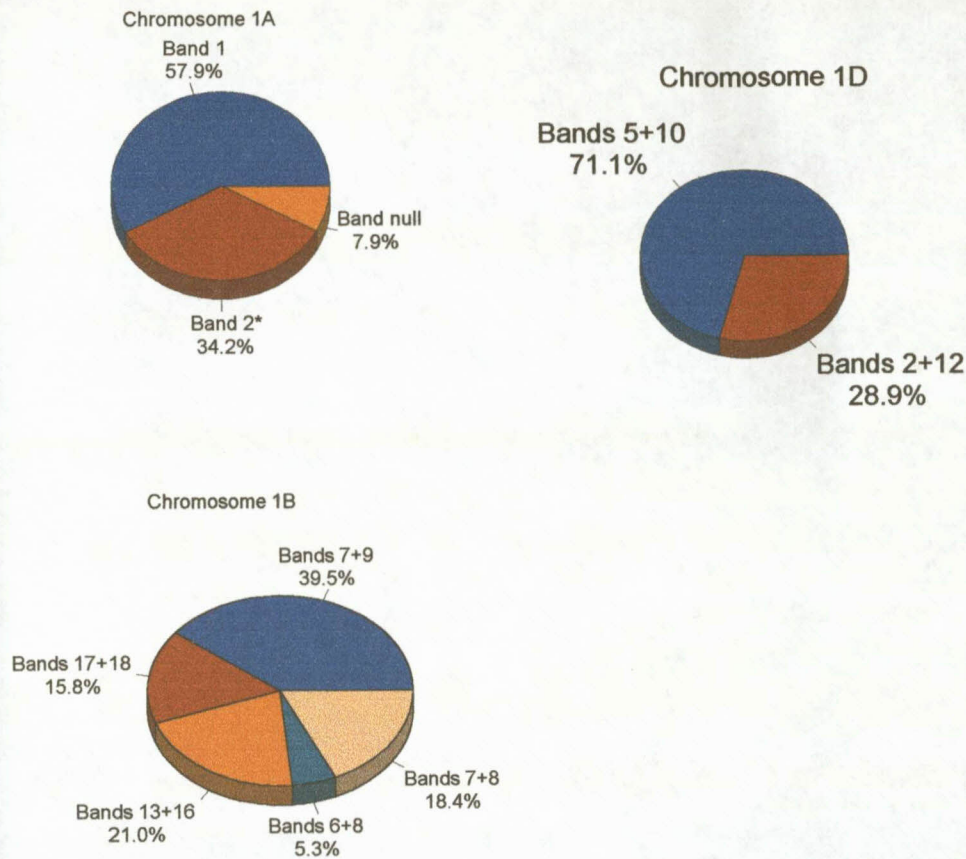


Figure 1.2 The HMW glutenin subunit composition of South African wheat cultivars (Randall *et al*, 1992).

The structure of the high molecular weight subunits

Wheat gluten proteins, and prolamins from related species, are complex mixtures of structurally-related components, making the purification and characterisation of individual proteins difficult (Brett *et al*, 1999). The detailed structure of gluten proteins have become known in the last 20 years, mainly because of two types of studies. Molecular cloning technology led to the isolation of cloned cDNAs and genes for all the major groups of gluten proteins, except the ω -gliadins. The complete amino acid sequences of the proteins encoded by these cDNAs were deduced and a basis was provided with direct information on the structures and interactions of the different types of gluten proteins.

Molecular and biophysical studies have been combined to give a detailed picture of the HMW subunit structure. A total of nine different genes have been isolated and it gave the amino acid sequences of the encoded proteins (Shewry *et al*, 1992; Reddy and Appels, 1993). Individual subunits consist of between 627 and 827 amino acid residues, with M_r values of about 67 500 to 88 000. The proteins have similar structures, each consisting of a central repetitive domain, flanked by non-repetitive domains at the N- and C-termini. The N-terminal domain has a length of 81 to 104 residues, while the C-terminal domain have 42 residues. The repetitive domain has a length of 480 to 680 residues and it is mainly responsible for the differences in the sizes of whole proteins. The repetitive sequences may provide a mechanism for generating variation in the HMW subunit size, by unequal crossing over resulting from mispairing of the genes during meiosis (Shewry *et al*, 1997).

The repetitive domains also appear to form an unusual supersecondary structure, a loose spiral based on regularly repeated β -reverse turns. Miles *et al* (1991) used scanning probe microscopy and showed that the protein molecules had a diameter of about 19.5Å with spiral striations of pitch about 14.9Å. The β -spiral structure also confers an extended rod-like conformation to the whole molecule (Field *et al*, 1987).

The role of the HMW subunits in gluten elasticity relates to their presence in high M_r glutenin polymers. These polymers are stabilised by the formation of inter-chain disulphide bonds between cysteine residues. The number and distribution of these bonds will have an influence on their size and biophysical properties. The amino acid sequences of the HMW subunits show the presence of four to seven cysteine residues. One cysteine residue is present in the C-terminal domains of all the HMW subunits. In the N-terminal domain three cysteine residues (in the x-type subunits) or five (in the y-type subunits) are present. The 1By and 1Dy subunits contain single cysteine residues towards the C-terminal ends of their repetitive domains. Subunit 1Dx5 has an additional cysteine residue at the N-terminal end of this domain. The latter subunit is part of the quality-related subunit pair 1Dx5 and 1Dy10. The additional cysteine residue is not present in the poor quality related subunit 1Dx2 (Shewry *et al*, 1997).

One of the features of HMW subunits is that they contain large amounts of glutamine (35 mol%), glycine (20 mol%) and proline (10 mol%). HMW glutenins are linear proteins,

which consist of C and N terminal domains, that are largely alpha helical, separated by long domains of repeat sequences. The C and N termini consist of cysteine residues that are able to form disulphide links with residue on other subunits. The repeat domains have hexapeptide and nonapeptide repeats in the y-type subunits (PGQGQQ and GYYPTSLQQ) and hexa-nona and tripeptide repeats in the x-type subunits (PGQGQQ GYYPTSPQQ and GQQ) (Tatham *et al*, 1990).

HMW subunits are characterised by high levels of mobility in the presence of water and they consist of β -turns and β -sheets in proportions that vary with water content. Evidence obtained from spectroscopic results has lead to the suggestion that hydrogen bonding between the repeat regions of the HMW subunits is responsible for the elasticity of gluten (Belton, 1994; Belton *et al* 1994).

The essence of elasticity is that, following extension, a restoring force exists which tends to return the material to its original dimensions. The hypothesis of the existence of some crosslinking mechanism in dough may explain the resistance of dough to extension, but will not in itself explain elasticity.

As discussed earlier, HMW glutenins contain a very high level of glutamine. In subunits 1Dx5 (Shewry *et al*, 1994), the ratio of glutamine to other amino acids is about 1:1:1. The glutamines occur 102 times as pairs of residues, 90 times separated by a single amino acid, 69 times separated by two amino acids and 19 times separated by seven amino acids. The repeat sequences are thus very hydrophilic along their whole length and they will have a very high capacity to form both intra- and inter-molecular hydrogen bonds, because of the structure of glutamine.

HMW subunits may be represented as a long chain that becomes sticky by the high density of polar hydrogen bonding groups. The globular ends contain cysteine residues. In the absence of water the chains will tend to hydrogen bond to each other to form a dense mass. As water is added, there will be an increase in the number of water-protein hydrogen bonds formed, but the number of interchain hydrogen bonds will ensure that it is very unlikely that all the interchain hydrogen bonds will break simultaneously. There will always be a balance between the residues involved in interchain hydrogen bonds and those that are hydrated. A similar situation occurs in the absorption of polymers on

surfaces. Although the interactions of each individual residue may be weak, it is highly unlikely that the number of surface polymer interactions will terminate simultaneously. This effect leads to the formation of "loops and trains", that is regions with polymer surface interactions and regions with polymer solvent interactions (Belton, 1999).

The low molecular weight glutenin subunits

Previous work has demonstrated that the *Glu-1* score (HMW glutenin subunits) accounts for a substantial proportion (50 to 70 percent) of the variation in bread-making quality for wheats from many countries. The results for Australian wheats, however, gave contrasting results, showing that the *Glu-1* score accounted for very little of the variation in bread-making resistance (*R*_{max}) (19 percent). Alleles at the *Glu-D1* locus showed no relationship to *R*_{max} or extensibility (*Ext*), despite their predictive value for many other sets of wheat. The *Glu-D1d* allele (representing HMW subunits 5+10) is associated with greater dough strength than its counterpart (*Glu-D1a* representing subunits 2+12) in several studies of wheat genetic lines and in many analyses of sets of varieties (Campbell *et al*, 1987). This generally claimed superiority of subunits 5+10 to subunits 2+12 was not seen in the set of Australian wheats studied by Gupta *et al* (1991). Part of the explanation for the difficulties in assessing the relevance of *Glu-1* composition for Australian wheats having a relatively high average *Glu-1* score, lies in their *Glu-3* composition (LMW glutenin subunits). The *Glu-3* LMW subunits of glutenin accounted for a higher proportion of variation (42 percent) than did the *Glu-1* score in the set of 48 Australian wheats. Several of the Australian wheat cultivars, which have very high *Glu-1* scores, were found to carry the *Glu-3* alleles of low ranks. These cultivars have low to average *R*_{max} and *Ext*. These data thus emphasise the previously little recognised importance of LMW subunits of glutenin as significant components to the assessment of the bread-making potential of wheat flour (Gupta *et al*, 1991).

The gliadins and HMW subunits of glutenin are easily resolved by one-dimensional SDS-PAGE and exhibit extensive pattern variation among different cultivars. The availability of several sets of intervarietal substitution lines, in which individual chromosome pairs of a recipient variety are substituted by the homologous chromosome pairs from another variety, has enabled the genes controlling pattern variation in gliadins and HMW subunits (*A* subunits) of glutenin to be assigned to particular chromosomes in several cultivars (Gupta and Shepherd, 1990a). The HMW subunits of glutenin have been

shown to be controlled by genes (*Glu-1*) located on the long arms of group one chromosomes, whereas gliadins are controlled by genes (*Gli-1*, *Gli-2*) located on the short arms of both group 1 and group 6 chromosomes (Shepherd, 1988).

Research on LMW subunits has been limited, because they do not fractionate adequately by SDS-PAGE, or by other one-dimensional systems such as isoelectric focusing (IEF) or electrophoresis in aluminium lactate buffer at pH 3.1. On one-dimensional SDS-PAGE gels many LMW glutenin subunits overlap with gliadins (Zhen and Mares, 1991) and until recently, solubility fractionation methods for wheat flour proteins did not yield these subunits free of appreciable contamination with other gluten proteins (Skerritt and Robson, 1990).

Studies to date suggest that the LMW glutenin subunits share similarities with both gliadins and HMW glutenin subunits. Certain glutenin subunits have been noted to be soluble in aqueous ethanol (Bietz and Wall, 1973), whereas size-exclusion chromatographic experiments have identified high molecular weight, aggregating gliadins (Bietz and Wall, 1980). Genes for LMW glutenin subunits on the short arms of homoeologous group 1 chromosomes have been found to be closely linked to the group 1 gliadin genes (Singh and Shepherd, 1988).

The majority of aggregated storage protein (glutenin) is insoluble in neutral aqueous ethanol, in contrast to gliadin, but a small proportion of it, respectively described as HMW gliadin, LMW glutenin and glutenin III is freely soluble. This fraction consists of subunits that migrate like LMW glutenin subunits in SDS-PAGE, and they lack HMW glutenin subunits (Jackson *et al*, 1983).

It is conceivable that some polypeptides are common to both classical gliadin and glutenin, as considered by Bietz and Rothfus (1970), since α -, β -, γ -gliadins and LMW glutenin subunits have similar electrophoretic mobilities and are both soluble in aqueous ethanol. In such a scheme, any one polypeptide in the developing endosperm could either become aggregated, *via* disulphide bonds, with other species of LMW and with HMW glutenin subunits to form glutenin, or form intramolecular disulphide bonds and become part of the classical gliadin fraction. The results of Jackson *et al* (1983) showed that this is not the case since all the 14 major LMW glutenin subunits have different

positions to the α -, β -, γ - and ω -gliadins on the composite two-dimensional map and their conclusion was that they are different and distinctive proteins.

It is clear from the above discussions that the current definitions of gliadin and glutenin are different from the original definitions of Osborne (1907) which are based entirely on solubility properties in different solvents. A fraction of the gliadin in the definition of Osborne is apparently really glutenin if the latter is defined as aggregated storage protein. When reducing agents are used for extraction, or when ethanol is acidified, or replaced by an alcohol such as n-propanol, or when the temperature is raised somewhat, then much of the "glutenin" becomes "gliadin". Evolutionary relationships between LMW glutenin subunits and gliadin polypeptides need to be understood more fully. This will come from amino acid sequencing of purified components from each group and from genetic analysis (Jackson *et al*, 1983).

The LMW glutenins have relatively large amounts of cysteine and their disulphide bonds are highly reactive. Thioldisulphide interchange reactions are thought to play an important role in gluten protein breakdown during mixing and gluten protein re-polymerisation during proving. It raises the possibility of a functional role for the LMW glutenins in relation to dough properties and bread-making performance (Weegels *et al*, 1995).

The structure of low molecular weight glutenin subunits

Triticum durum cv. Lira is particularly suitable for studying the mechanism involved in quality differences, because its two biotypes differ only in the electrophoretic patterns of 1B-coded γ -gliadins, ω -gliadins and LMW glutenin subunits. Of particular interest is the presence of the group of LMW glutenin subunits designated LMW-1 in one biotype and the group designated LMW-2 in the other, which correlate with poor quality for the former and good quality for the latter (Masci *et al*, 1995).

It is generally accepted that LMW glutenin subunits are primarily responsible for the determination of pasta-making properties (Payne *et al*, 1984a) and that the difference in quality between cultivars with LMW glutenin subunits type 1 and type 2 results mainly from considerably greater amount of LMW glutenin subunits in the good quality type 2 cultivars (Autran and Galterio, 1989; Dachkevitch and Autran, 1989). Masci *et al* (1995)

have found that the additional insoluble protein of the type 2 line consists largely of LMW-s type subunits although LMW-s was the predominant type in the glutenin of both lines. The LMW-m type was present in much lower amounts according to their sequencing-based analysis of proportions, but still contributed significantly to the glutenin of the good type, Lira 45. (See Table 1.3.) Please note that the designations LMW-s and LMW-m are based on the nomenclature of Lew *et al* (1992) and m and s refer to methionine and serine, the first N-terminal amino acid of the respective sequences (Vensel *et al*, 1997).

Table 1.3 Overall percentages of the main sequence types (Masci *et al*, 1995).

	Quality	LMW-s	LMW-m	α	γ
Lira 42	Poor	36	20	26	17
Lira 45	Good	53	27	13	7

It is likely that both LMW-s and LMW-m type subunits act as chain extenders in glutenin polymerisation (Lew *et al*, 1992). This means that there are at least two cysteine residues in the primary structure that tend to form intermolecular rather than intramolecular disulphide bonds. It is somewhat surprising that LMW-s should be a chain extender when its N-terminal sequence, which is all that is available for this type of subunit, is compared with the sequence of a LMW-m type subunit from durum wheat, for which the complete sequence is available (based on the DNA sequence).

Lew *et al* (1992) have also suggested that there are two likely cysteines that might be involved in intermolecular disulphide bond formation in a LMW-m type subunit: one is the cysteine at position 5, and the other at position 210 in the B11-33 sequence. Although there is some homology between the LMW-s and LMW-m type sequences, the LMW-s type of sequences has no cysteine at position 5, nor any through at least 30 cycles of sequencing. If the two types of subunits are largely similar through the rest of the sequence, then LMW-s would be likely to have only one cysteine available for intermolecular disulphide bond formation (the one at position 210) and would thereby be a chain terminator, which would favour shorter glutenin polymers (that is a lower molecular weight distribution).

The apparent conflict would be resolved if it turned out that the C^b cysteine present in the LMW glutenin subunit and which is involved in intermolecular disulphide linkages were present in the LMW-s type subunit. This cysteine is likely to be found somewhere in the repeating sequence region near the N-terminal, but beyond the first 30 residues. It might also be present in the LMW-m type, although it was not present according to the DNA sequences for this type of subunit. The DNA sequences should not be considered definite at this time. All clones reported so far indicate a cysteine at position 5, whereas the actual sequencing results of Lew *et al* (1992) demonstrate that there are variations of the LMW-m type sequence in which either arginine or histidine is substituted for the cysteine at position 5. Furthermore, no DNA clone has yielded a sequence that begins with Ser-His-Ile-, which is in fact the beginning sequence of the major LMW glutenin subunit type. The presence of the C^b cysteine and the C^x cysteine would make the LMW-s subunit a chain extender despite the absence of the cysteine at position 5.

In addition to the LMW-s and LMW-m type of subunits, Masci *et al* (1995) found a significant amount of subunits with N-terminal sequences similar to those with α -type and γ -type gliadins. They have encountered some reluctance among cereal chemists to accept these gliadin-like components found in glutenin as true glutenin subunits. If the definition of glutenin components is that they are proteins linked by intermolecular disulphide bonds and the definition of gliadins is that they are monomeric proteins consisting of a single polypeptide chain, then these gliadin-like components of glutenin should be considered as glutenin subunits even though they are almost certainly coded at the *Gli-1* and *Gli-2 loci* rather than the *Glu-3 loci*.

In support of this contention, they have defined a disulphide-linked pair of peptides from a glutenin digest in which one peptide of the pair is derived from a γ -gliadin and the other from a LMW glutenin subunit (as defined by the DNA sequences corresponding to LMW-m type subunits). The cysteine of the γ -type sequence had not been defined by DNA sequences of γ -gliadins, but it was presumably an extra cysteine that had resulted from mutation of a codon for phenylalanine into one for cysteine. Furthermore, α - and γ -type sequences found in highly purified glutenin preparations by Lew *et al* (1992) had a marker sequence different from those of normal gliadins that defined them as gliadin mutants with, in each case, a single extra cysteine. This would make them glutenin

subunits, and furthermore, likely chain terminators of growing glutenin polymers. Masci *et al* (1993) has shown that D glutenin subunits are in fact mutated ω -gliadins that have acquired at least one cysteine residue.

If the two main groups of sequences found, namely the sequences peculiar to LMW glutenin subunits (LMW-s and LMW-m) and the gliadin type sequences (α -type and γ -type), are considered, it is noteworthy that there are 43 percent of the gliadin type in Lira 42, but only 20 percent of the gliadin type in Lira 45. The large amount of these likely chain terminators in the Lira 42 (type 1) glutenin is likely to be a factor in determining the poorer quality of the type 1 line, contributing to a lower size range of glutenin polymers in Lira 42. Since α -type gliadins are most probably coded at the *Gli-2 loci*, not linked to the *Gli-1/Glu-3 loci*, the particular situation described here could not be common to the other LMW glutenin subunit type 1 and type 2 durum wheats and could reflect a different degree of expression of these α -type genes between the two biotypes. However, in the case of cultivar Lira, the presence of a rather high amount of α - and γ -type sequences would exchange the effect of lesser amounts of the key chain-extending subunits, LMW-s and LMW-m, in decreasing the molecular weight distribution of the glutenin polymers in Lira 42 (Masci *et al*, 1995).

1.2.4. Extraction and separation of LMW glutenin subunits

The development of gel filtration materials for chromatography has contributed greatly to the separation of wheat flour proteins on the basis of size, and to the estimation of their molecular weight. Initial studies with Sephadex G-100 and G-200 allowed separation of proteins with molecular weights of up to 200 000 Da, and not only permitted distinction between glutenin and gliadins, but also the separation of a high molecular weight gliadin (Beckwith *et al*, 1966). Polyacrylamide gel filtration was used to separate glutenins, but no distinct fractionation was achieved. The use of Sepharose columns GHCL solvent appears to yield the first successful fractionation of high molecular weight glutenin. Unfortunately, the recovery of pure proteins was hampered by the solubility of Sepharose solvent (Huebner and Wall, 1976).

There have been a few attempts to purify LMW glutenin subunits, but this presented considerable difficulties, because of the heterogeneous and insoluble nature of LMW glutenin subunits and their strong tendency to aggregate (Melas *et al*, 1994).

Shepherd (1988) stressed the importance of achieving genetic separations between products of genes encoding LMW glutenin subunits, and those controlling the production of linked gliadin subunits, as a means of ascertaining the quality effects of LMW subunits. Genetic separation requires the identification of recombinants within the complex *loci* on group 1 chromosomes encoding these proteins. Application of the procedure for glutenin purification, coupled with simultaneous analysis of both glutenin subunits and gliadins on one-dimensional SDS gels will be a useful tool in achieving this goal. The one step, one-dimensional system allows the analysis of LMW glutenin subunit variation in larger numbers of lines than currently possible using two step, one-dimensional or two-dimensional electrophoretic systems (Graybosch and Morris, 1990).

Application of one-dimensional SDS-PAGE separation of glutenin subunits in the prediction of end-use quality has limitations. Since the assignment of proteins to discreet classes was based on migration distances, proteins with similar molecular size but different amino acid composition (or quality effects) could have been included in the same molecular weight class. This could alter correlations between protein subunits and quality parameters. However, appropriate statistical tests in genetic studies necessitate the objective analysis of a large number of lines. The experiments reported were designed to test the usefulness of a potential technology. Two-dimensional protein separation obviously would, with better resolution, allow the identification of quality-related proteins. However, the time and labour required for such analyses would limit their utility in breeding programs (Primard *et al*, 1991).

Previous studies by Jackson *et al* (1983) used two-dimensional electrophoresis and they located the genes controlling most of the LMW subunits on the short arms of group 1 chromosomes in Chinese Spring wheat. Payne *et al* (1984b) using one-dimensional SDS-PAGE, were able to map the genes controlling some easily recognisable B subunits at the *Gli-1 loci*. These separation techniques, however, lacked general application for studying the variability in B and C subunits and their inheritance, because the two-dimensional systems could analyse only one or two samples per gel, and furthermore, these subunits could not be directly distinguished from gliadins. Consequently, only a few B subunit differences have been detected in both durum and bread wheats (Payne *et al* 1984a; 1984b).

The introduction of a two-step, one-dimensional SDS-PAGE procedure by Singh and Shepherd (1988) provided a rapid method for analysing a large number of samples in a single gel in a gliadin-free background. Using this method, they were able to map the genes controlling some of these subunits at the *Glu-3 loci*, and further investigations revealed extensive variation for these subunits in durum and bread wheats (Gupta and Shepherd, 1988). This two-step method also separated some globulins and albumins with similar mobility to the B and C subunits of glutenin. The procedure has now been modified to allow the latter subunits to be analysed in a background free from globulins and albumins (Gupta and Shepherd, 1990a). Despite its proven advantages over two-dimensional methods, the two-step procedure has not been adopted widely in other laboratories, probably because it requires a high level of experience to obtain clear separation routinely (Singh *et al*, 1991).

When proteins extracted in TRIS-HCl buffer (pH 6.8) containing SDS were separated by two-step SDS-PAGE, they were resolved into three groups of bands with different electrophoretic mobility (slow, medium and fast) in the second step of separation. The slowest moving bands correspond to the A subunits of glutenin, and the majority of the fast-moving bands corresponds to B and C subunits of glutenin. However, when these patterns were compared with those obtained in hot ethanol extracts, it became evident that all the bands with medium mobility and some of the fastest moving bands are non-prolamins, and these have been arbitrarily divided into HMW and LMW components, respectively. Some of these non-prolamin bands have similar mobilities to the B and C subunits and they obscure the resolution of these bands, particularly the C subunits, and thus only the B subunit was described in the previous report (Gupta and Shepherd, 1988). The absence of these non-prolamin bands in the ethanol extracts has greatly improved the resolution of the LMW glutenin subunits into two clear groups representing B and C subunits (Gupta and Shepherd, 1990b).

Acidic polyacrylamide gel electrophoresis (A-PAGE) or high performance liquid chromatography (HPLC) analyses of gliadins can uncover more variation than one-dimensional SDS-PAGE, largely because they can detect biochemical changes (amino acid substitutions) that occur in the absence of molecular weight alterations. However, SDS-PAGE may provide molecular weight estimations. Knowledge of the molecular weight of various endosperm storage proteins will facilitate the identification of both the

proteins and the gene sequences responsible for their production. Molecular weight estimations also provide information regarding relationships between the proteins of different classes (Graybosch and Morris, 1990).

Morel (1994) used A-PAGE and SDS-PAGE. He found that the survey of wheat cultivars revealed extensive variation in both the A-PAGE and the SDS-PAGE patterns of slow and fast moving bands. A-PAGE patterns of glutenin subunits generally contained more bands than did the SDS-PAGE patterns, but they were less clearly separated.

The SDS-PAGE results show that previous researchers used somewhat different glutenin preparations for essentially the same purpose, namely, to elucidate the structure to function relationship of glutenin in bread making. Those researchers concerned with the function of glutenin in bread making (Orth and Bushuk 1972) used "crude" glutenin preparations from the Osborne or similar solubility fractionation procedures. On the other hand, those researchers concerned with fundamental physico-chemical studies (Bietz and Wall, 1975; Orth and Bushuk, 1973) used more or less "purified" glutenins. In most of the fundamental studies, the aim of purification was to remove the low molecular weight contaminants, which, because of their similarity in electrophoretic mobility to albumin, globulin and gliadin proteins, were assumed to be the latter proteins.

Gliadins are typically studied through the use of either A-PAGE or HPLC. It would be advantageous to analyse simultaneously both LMW glutenin subunits and gliadins by one dimensional SDS-PAGE in order to understand the relationships between these classes of proteins (Graybosch and Morris, 1990).

The protein fractionation and gel electrophoresis results of the study of Chakraborty and Khan (1988) showed that variations in the procedures used to isolate the different wheat protein fractions such as albumins, globulins, gliadins and glutenins can result in compositional differences in these protein classes. Variation in protein fractions could have resulted from the type of solvent used, the starting material (such as flour or dough), and the type of stirrer used to solubilise the gluten proteins.

Singh *et al* (1991) developed a simplified procedure for one-dimensional separation of glutenin subunits, suitable for the rapid screening of a large number of samples. It gives an improved resolution for both HMW and LMW subunits of glutenin, and it has been tested on a large number of bread and durum wheat cultivars and wild tetraploid wheats. This method provides a much simpler alternative, to those available in the past, for screening both HMW and LMW glutenin subunits in a single gel, although the positive identification of individual alleles of LMW subunits controlled by the *Glu-3* homoeoloci on chromosomes 1A, 1B and 1D remains difficult. Their identification is facilitated by analysing the same sample for gliadin patterns also, especially for ω -gliadins, which are coded by very tightly linked *Gli-1* genes. This approach is particularly useful for identifying the *Glu-B3* alleles and some of the *Glu-D3* alleles. The *Glu-A3* alleles are easily identified without any help from gliadin patterns, although its null allele (*Glu-A3e*) is linked with a prominent ω -gliadin band.

Since a number of LMW glutenin subunits and gliadin bands are controlled by a cluster of very tightly linked genes, for practical screening purposes any protein band of a specific gene cluster (or 'block') should give an indication of the LMW subunit allele present. The inherent danger with this approach is that a low level of recombination can occur within some gliadin/LMW subunit blocks. Consequently, the gliadin bands can only be used as an indicator rather than confirmatory evidence for the presence of specific LMW subunit alleles, especially when dealing with cultivars or lines of unknown origin, where rare recombinants may have been fixed. This approach is very convenient for analysing segregating progenies from crosses between cultivars of known LMW subunits/gliadin patterns, because the level of recombination is extremely low (Singh *et al*, 1991).

1.2.5 Gene location

Over the last few years, the chromosomal locations of genes controlling the synthesis of wheat storage proteins became known. This knowledge is important when strategies are considered to manipulate protein components to target specific end use requirements (Gao *et al*, 1992).

The HMW subunits of glutenin are encoded by three *loci*, *Glu-A1*, *Glu-B1* and *Glu-D1*, located on the long arms of chromosomes 1A, 1B and 1D, respectively. The ω - and γ -

gliadins are encoded by the *loci*, *Gli-A1*, *Gli-B1* and *Gli-D1*, located on the short arms of chromosomes 1A, 1B and 1D, respectively. The α - and β -gliadins are encoded by the *loci*, *Gli-A2*, *Gli-B2* and *Gli-D2*, located on the short arms of chromosomes 6A, 6B and 6D, respectively. Each of the *Gli-1 loci* is furthermore, closely linked to a locus coding for LMW glutenin subunits (*Glu-3*). There are several alleles at each of the *Glu-3* (located on chromosome 1), *Gli-1* (located on chromosome 1) and *Gli-2* (located on chromosome 6), *loci* and the potential number of permutations are enormous (Rogers *et al*, 1989).

All the *loci* encoding storage protein polypeptides are composed of tightly linked genes which rarely recombine, thus called complex *loci* (Galili and Feldman, 1983; Maghaub and Odenbach, 1988; Mosleth and Uhlen, 1990). The genes are co-dominant and products of each gene are present in the grain endosperm (Day *et al*, 1986; Payne, 1987; MacRitchie *et al*, 1990). A hexaploid wheat cultivar contains six HMW glutenin genes, but most cultivars synthesise only three to five subunits, because of gene inactivation (Forde *et al*, 1985; Haberd *et al*, 1987; Anderson *et al*, 1988).

There are two further series of homoeo*loci* coding for endosperm proteins on the short arms of group 1 chromosomes: *Gli-A3* and *Gli-B3*, coding for the ω -type gliadins and the D subunits of LMW glutenin respectively (Payne *et al*, 1988) and *Tri-1*, coding for proteins (triticins) more closely alike globulins than prolamins (Rogers *et al*, 1989).

The genes controlling the synthesis of the major, basic structures of LMW glutenin are located on the short arms of chromosomes 1A, 1B and 1D, like the genes for the ω -gliadins and the majority of the γ -gliadins. The only genes of LMW glutenin subunits not located to chromosomes are the minor components which migrate to similar positions on IEF x SDS-PAGE gels as the group 6 α - and β -gliadins (Jackson *et al*, 1983).

1.3 Materials and Methods

1.3.1 Materials

One hundred and forty-seven South African bread wheat cultivars or cultivars currently used as germplasm in some breeding programmes in South Africa and some near isogenic lines were screened for their LMW glutenin subunit composition. Of these cultivars, 105 were screened for their HMW glutenin subunit composition. Many researchers have looked at the HMW glutenin composition of South African cultivars and for the sake of this study, some of these cultivars were re-tested and some new ones were tested for the first time. A summary of the cultivars used, their classification and origin are given in Table 1.3.

Table 1.3 Summary of the cultivars used for HMW and LMW glutenin subunit composition screening.

Cultivars	Classification	Origin
1 Adam Tas	HRS	RSA
2 Australian hard white	HWS	Australia
3 Barta	HRI	RSA
4 Belinda	HRW	USA
5 Bella	SRS	Mexico
6 Betana	HRI	RSA
7 Betta	HRI	Argentina
8 Betta DN	HRW	RSA
9 Bona	HRI	RSA
10 Caledon	HRW	RSA
11 Canna	HRW	USA
12 Carolus	HRW	Germany
13 Corella	SWS	Australia
14 Dirkwin	SWS	Australia
15 Eland	HRS	RSA
16 Elize	HRS	RSA
17 Elina	HRS	RSA
18 Flameks	HRS	RSA

Table 1.3 (Continued)

Cultivars	Classification	Origin
19 Flamink	HRI	RSA
20 Gamka	HRS	RSA
21 Gamtoos	HRS	RSA
22 Gamtoos DN	HRS	RSA
23 Gandum I Fasai	unknown	
24 Gariep	HRS	RSA
25 Gariep DN	HRW	RSA
26 Gourits	HRS	RSA
27 Harts	HRS	RSA
28 Hugenoot	HRW	RSA
29 Inia	HRS	RSA
30 Jager	HRW	Kansas
31 K29-1	HRI	RSA
32 K29-2	HRI	RSA
33 K29-3	HRI	RSA
34 K29-4	HRI	RSA
35 K29-5	HRI	RSA
36 K29-6	HRI	RSA
37 K29-7	HRI	RSA
38 K29-8	HRI	RSA
39 K29-9	HRI	RSA
40 K29-10	HRI	RSA
41 K34-1	HRI	RSA
42 K34-2	HRI	RSA
43 K34-3	HRI	RSA
44 K34-4	HRI	RSA
45 K34-6	HRI	RSA
46 K34-7	HRI	RSA
47 K34-8	HRI	RSA
48 K34-9	HRI	RSA
49 K34-10	HRI	RSA
50 K35-2	HRI	RSA

Table 1.3 (Continued)

Cultivars	Classification	Origin
51. K35-3	HRI	RSA
52. K35-4	HRI	RSA
53. K35-5	HRI	RSA
54. K35-6	HRI	RSA
55. K35-7	HRI	RSA
56. K35-8	HRI	RSA
57. K35-9	HRI	RSA
58. K35-10	HRI	RSA
59. K37-1	HRI	RSA
60. K37-2	HRI	RSA
61. K37-3	HRI	RSA
62. K37-4	HRI	RSA
63. K37-5	HRI	RSA
64. K37-6	HRI	RSA
65. K37-7	HRI	RSA
66. K37-8	HRI	RSA
67. K37-9	HRI	RSA
68. K37-10	HRI	RSA
69. Karee	HRI	RSA
70. Kanega	HRS	RSA
71. Katyil	HRS	Russia
72. Kavkaz	HRW	Russia
73. Limpopo	HRS	RSA
74. Limpopo DN	HRW	RSA
75. M29519	SWS	Mexico
76. M29568	SRS	Mexico
77. Marico	HRS	RSA
78. Molen	HRW	RSA
79. Molopo	HRW	RSA
80. Nantes	HRS	RSA
81. Norstar	HRW	NE
82. Oom Charl	HRW	RSA

Table 1.3 (Continued)

Cultivars	Classification	Origin
83 Oranje	HRS	RSA
84 Oubaard	HRS	RSA
85 Owens	SRS	Australia
86 Palala	HRS	RSA
87 Palmiet	HRS	RSA
88 Palmiet DN	HRS	RSA
89 Palmiet kort	HRS	RSA
90 PAN 3211	SRI	RSA
91 PAN 3232	HRW	RSA
92 PAN 3235	HRW	RSA
93 PAN 3349	HRI	RSA
94 PAN 3364	HRW	RSA
95 PAN 3377	HRI	RSA
96 PAN 9303	HRW	RSA
97 PAN 9316	HRI	RSA
98 PAN 9409	HRI	RSA
99 PAN 9413	HRW	RSA
100 PAN 9414	HRI	RSA
101 PAN 9416	HRI	RSA
102 PAN 9417	HRI	RSA
103 PAN 9418	HRW	RSA
104 PAN 9419	HRS	RSA
105 PAN 9711	HRW	RSA
106 PAN 9712	HRW	RSA
107 PAN 9713	HRW	RSA
108 PAN LE 4	HRS	RSA
109 PAN LE 7	HRS	RSA
110 PAN LE 9	HRS	RSA
111 PAN LE 10	HRS	RSA
112 PAN LE 12	HRS	RSA
113 Red Victory	HRW	USA
114 Riemland	HRW	RSA

Table 1.3 (Continued)

Cultivars		Classification	Origin
115.	SA 1684	Unknown	
116.	SA 463	Unknown	
117.	Sch 69	SRI	RSA
118.	Snack	SWS	RSA
119.	Sonop	HRS	RSA
120.	SST 3	SRS	RSA
121.	SST 16	SRS	RSA
122.	SST 23	SRS	RSA
123.	SST 33	SRS	RSA
124.	SST 44	SRS	RSA
125.	SST 55	HRS	RSA
126.	SST 66	SRS	RSA
127.	SST 101	HRW	RSA
128.	SST 102	HRW	RSA
129.	SST 107	HRW	RSA
130.	SST 124	HRW	RSA
131.	SST 333	HRI	RSA
132.	SST 363	HRI	RSA
133.	SST 367	HRW	RSA
134.	SST 822	HRS	RSA
135.	SST 825	HRS	RSA
136.	SST 936	HRW	RSA
137.	SST 966	HRW	RSA
138.	SST 972	HRW	RSA
139.	Stirling	HRS	RSA
140.	T4	HRS	RSA
141.	Tugela	HRW	RSA
142.	Tugela DN	HRW	RSA
143.	Tugela f-g	HRW	RSA
144.	Tugela nuut	HRI	RSA
145.	Turpin 7	HRS	RSA
146.	Turtsikum	Unknown	

Table 1.3 (Continued)

Cultivars	Classification	Origin
147 Verbeterde Kenia	SRS	RSA

HRW = hard, red winter wheat

HRI = hard, red intermediary wheat

HRS = hard, red spring wheat

SWS = soft, white spring wheat

SRS = soft, red spring wheat

Two control cultivars, Gabo and Chinese Spring were used. Gabo originates from Australia, and Chinese Spring from China. Their LMW glutenin subunits are known and this was used to compare the LMW compositions of the South African cultivars tested.

1.3.2 Methods

1.3.2.1 Extraction of glutenins

An adapted method of Singh *et al* (1991) was used. The advantage of this technique is that the HMW and LMW glutenin subunits can be read from the same gel. All the protein extractions were done in a waterbath at 60°C. Half a kernel was crushed to a fine powder. The gliadins were removed with 70% ethanol for one hour as they overlapped with the LMW glutenins. After the removal of the gliadins, the glutenins were washed with 1-propanol, twice for half an hour each time. During the washing procedure, the eppendorf tubes were vortexed for 30 seconds every 10 minutes. The eppendorf tubes were then centrifuged for 2 minutes at 10 rpm's. The 1-propanol and all of the remaining supernatant were removed and 75µl extraction buffer [80mM tris-HCl (pH 8.0)] containing 1.25% dithiothreitol was added. The tubes were again vortexed to loosen the seed material. After an hour, 75µl extraction buffer containing 16.8µl/ml vinylpyridine was added, the tubes were vortexed and left for an hour in the waterbath. After the extraction of the glutenins, the seeds were centrifuged for 2 minutes at 10 rpm. Of supernatant, 110µl were transfer to a new eppendorf tube containing 100µl sample buffer [80mM tris-HCl (ph 8.0), 40 g glycerol, 2 g SDS, 0.02 g bromophenol blue]. After

15 minutes in the waterbath, the samples were ready for loading (20 μ l or more as required).

1.3.2.2. Sodium dodecyl sulphate gel electrophoresis (SDS-PAGE)

A 10% uniform separating gel was used. It consisted of 14ml separating buffer (45.412 g Tris in 460 ml H₂O, titrate to pH 8.88, add 1.0 g SDS), 9.4ml separating acrylamide [(30% Ac/1% crosslinker), 75g acrylamide, 0.75g bisacrylamide, 181ml H₂O] and 4.7 ml water. Temed (55 μ l) and 65 μ l 10% ammonium persulphate (APS) were used as catalysts.

The stacking gel consisted of 5 ml stacking buffer (6.06 g Tris in 190 ml H₂O, titrate to pH 6.8, add 0.4 g SDS), 1.3 ml stacking acrylamide [(35% Ac/ 1.5% crosslinker), 87.5 g acrylamide, 1.32 g Bis, 181 ml H₂O] and 3.7 ml water. Temed (20 μ l) and 50 μ l 10% APS were used as catalysts.

The gel was run at 66 mA at a constant temperature of 15°C for approximately 3 hours. The cathode buffer consisted of 30.28 g Tris, 144 g glycine and 10 g SDS made up to 1 l with dH₂O. The anode buffer consisted of 30.28 g Tris and 800 ml dH₂O, titrated to pH 8.4. The cathode and anode were diluted 10x before use.

1.3.2.3. Staining of the gel

The staining method of Wrigley (1992) was used. The gel is immersed in a fixing solution (400 ml methanol, 100ml glacial acetic acid, 500 ml dH₂O) for one hour. It was then stained overnight in a staining solution (30 g trichloroacetic acid made up to 200 ml with water and 0.1g Coomassie Blue made up to 10 ml in methanol). The stained gel was rinsed in distilled water for a few hours before examination and photography.

1.3.2.4. Gel analysis

The "Molecular Analyst Fingerprinting" software of Biorad was used to analyse the gels. The gels were scanned with the Gel Doc 1000 using an UV-gel camera and VGA graphics in 256 colours as recommended. The analysing procedure consisted of three steps, namely a) the conversion of the gel, b) the normalisation of the tracks and c) the analysis of the tracks.

Using the conversion programme a rectangle was drawn around the LMW glutenin subunits on the gel. The identification process was easier as only the LMW glutenin subunits were screened and not the HMW glutenin subunits and albumins and globulins.

The normalisation settings were as follow: the resolution was set at 200 points and a smoothing factor of three was chosen (this implied that one point at either side of a data point would be averaged with the data point). To subtract the background, the rolling disk method was chosen. The principle of the rolling disk mechanism is that a disk is rolled on the inside across the curve. Every area of the curve below the imaginary trace left behind the disk will be subtracted as background. This method gives very stable and reliable background subtraction. The intensity of the background subtraction was set at ten (typical settings for SDS-PAGE protein patterns are between eight and 12). The clearest Gabo pattern (replication one) was used as the standard reference pattern and all the other Gabo reference patterns were aligned to the standard reference. Normalisation of a gel is achieved by aligning the bands of all reference patterns on the gel to the corresponding ones of the standard. Non-reference tracks are interpolated gradually according to both surrounding references. At least three references were loaded on each gel for the best normalisation results.

After normalisation the gels were analysed using the main program of the "Molecular Analyst Fingerprinting" software. A densitometric curve of every replication of every cultivar was drawn and from this the migration distances were determined. The program gave the migration distance of each peak and the intensity of the band. Five classes of intensity were assigned with 1 being a very light band and 5 a very dark band. Peak positions with repeatability of more than 67 percent in the replications were accepted as representative of a specific cultivar. Repeatability was calculated as the percentage of the occurrence of a band in the replications. An average of the band positions (the migration distance of the bands on the gel) of the six replications of each cultivar were calculated. These values were used to compare the cultivars with each other.

1.3.2.5. Determination of the molecular weights

A low range (14 to 97.4 kDa) SDS-PAGE molecular marker of Biorad was used to determine the molecular weights of the LMW glutenin groups. It consisted of the following:

	Molecular weight (kDa)
Phosphorylase b	97.4
Serum albumin	66.2
Ovalbumin	45.0
Carbonic anhydrase	31.0
Trypsin inhibitor	21.5
Lysozyme	14.4

It was possible to determine the molecular weights of the LMW glutenin subunits. The migration distance of each band was calculated as a molecular weight in kDa. Eighteen replications of the molecular marker were loaded on different gels and each one was analysed using the Gel Doc software.

1.3.2.6. Grouping of the LMW bands

The standard deviations of the 40 most important cultivars were calculated and using this information, the possible overlapping of bands was determined. The possible different groups of LMW banding patterns with different class intervals were determined. According to Mason, Gunst and Hess (1989) it is possible to estimate the population standard deviation using the standard deviation of the sample. It is thus possible to determine the standard deviation of all the possible bands, using the standard deviations of each individual cultivar, or in other words, it is possible to determine the grouping and possible overlapping of the bands. According to Groeneveld (1988) boxplots are useful in giving information about the spread of observations in a data set. With this technique the observations are ordered and displayed horizontally. Using the boxplots of the forty most important cultivars, it was possible to determine the overlapping of the different bands. Only 40 cultivars were used, because they were the most important and all had different banding patterns. It was assumed that their boxplots would gave enough differences and similarities between them to make it possible to group the different LMW bands.

1.3.2.7. Correlation between the different LMW bands

The correlation between the different LMW bands was determined using the Spearman-rank correlation matrices of the NCSS 2000 program. The Spearman-rank calculates the

correlation by applying the Pearson correlation formulas to the ranks of the data rather than to the actual data values themselves, thus reducing many of the distortions that affect the Pearson correlation. Pair-wise removal of missing values were chosen, because missing values occurring in other variables do not have an influence on the calculations.

1.3.2.8. The band intensities of the different LMW glutenin groups

All the LMW glutenin bands of the cultivars were divided into five classes of very light (1) to very dark bands (5). In the replications of some cultivars, the intensity of the bands varied from one to five and it was therefore, impossible to put it in a discrete class of intensity. In these cases, a class of six was given to the bands, and it only means that it does not have a definite intensity.

1.3.2.9. Calculation of genetic distance

The index for genetic similarity (F) is suitable to calculate the pairwise distance matrixes from SDS-PAGE data. The formula for F is:

$$F = 2n_{xy} / (n_x + n_y)$$

Where F is the ratio of shared bands between two individuals x and y, $2n_{xy}$ is the number of shared bands and n_x and n_y are the numbers of bands observed in cultivars x and y respectively (Nei and Li, 1979).

The F-ratio resembles the coefficient of similarity between two cultivars. This is used to determine the genetic distance (D) for a pairwise combination. The formula for D is:

$$D = -\ln (F)$$

Using the NCSS 2000 program the genetic distances of forty-five South African cultivars were determined. Three seed companies are important in South Africa in wheat production, namely the Small Grain Institute in Bethlehem, Sensako and PANNAR. Cultivars that were developed by these companies were chosen. The SST cultivars were developed by Sensako, the PAN cultivars and lines were developed by PANNAR and

cultivars like Eland and Karioga were developed by the Small Grain Institute. The genetic distances of the near isogenic lines were calculated separately.

Hierarchical clustering were done on the data. With hierarchical clustering each object (or in this case cultivar) is placed in the beginning in a separate cluster. At each step, the two clusters that are the most similar are joined into a single new cluster. Eight methods of defining the similarity between clusters are available in this program, and the single linkage (or nearest neighbour clustering) was chosen. This is the oldest and most famous of the hierarchical techniques. The distance between two groups is defined as the distance between their two closest members. It can produce clusters in which individuals are added sequentially to a single group. The coefficients of the distance equation are:

$$\alpha_i = \alpha_j = 0.5, \beta = 0 \text{ and } \gamma = 0.5.$$

The two distance methods that are available, are Euclidean (can be defined as a straight- line distance or as the crow flies) and Manhattan (can be defined as city-block distance as it is analogous to walking along an imaginary sidewalk to get from point A to B). The Euclidean distance was used (Hintze, 1998).

1.4 Results and discussion

The HMW glutenin subunits

Only hundred and two South African cultivars and the near isogenic lines of K29, K34, K35 and K37 were tested for their HMW glutenin subunit composition. The HMW glutenin subunits were already tested extensively in South Africa (Randall *et al*, 1992, 1993). Some of the cultivars they tested were re-tested and some new cultivars were also tested. Only South African cultivars were tested. The near isogenic lines of K29, K34, K35 and K37 were developed through the backcrossing technique using Karee as the recurrent parent. The leaf rust resistance genes (*Lr29*, *Lr34*, *Lr35* and *Lr37*) were transferred to Karee. Two standards were used to compare the banding patterns. Zaragosa (pattern 2*; 17+18; 2+12) was used in the studies of Labuschagne (1993) and Karee (pattern 1; 7+9; 5+10) are commonly used in our laboratory for electrophoresis tests. The results of the HMW glutenin subunits are given in Table 1.4.

Table 1.4 The HMW glutenins of the South African bread wheat cultivars tested.

Cultivars	A genome	B genome	D genome
1. Adam Tas	1	7+8	5+10
2. Barta	1	6+8	5+10
3. Belinda	2*	7+9	5+10
4. Bella	0/2*	7	2+12
5. Betana	1	7+9	5+10
6. Betta	1	7+9	5+10
7. Betta DN	1	7+9	5+10
8. Bona	0	7+9	5+10
9. Elize	1	13+16	5+10
10. Elrina	1	7+9	5+10
11. Flameks	2*	17+18	5+10
12. Flamink	1	7+9	5+10
13. Gamka	1	6+8	5+10
14. Gamtoos	1	7+9	5+10
15. Gamtoos DN	1	7+9	5+10
16. Gariep	1	7+9	5+10
17. Gariep DN	1	7+9	5+10

Table 1.4 (Continued)

Cultivars	A genome	B genome	D genome
18. Harts	0	7+9	5+10
19. Hugenoot	2*	7+9	5+10
20. Inia	1	13+16	5+10
21. K29-1	1	7+9	5+10
22. K29-2	1	7+9	5+10
23. K29-3	1	7+9	5+10
24. K29-4	1	7+9	5+10
25. K29-5	1	7+9	5+10
26. K29-6	1	7+9	5+10
27. K29-7	1	7+9	5+10
28. K29-8	1	7+9	5+10
29. K29-9	1	7+9	5+10
30. K29-10	1	7+9	5+10
31. K34-1	1	7+9	5+10
32. K34-2	1	7+9	5+10
33. K34-3	1	7+9	5+10
34. K34-4	2*	7+9	5+10
35. K34-6	1	7+9	5+10
36. K34-7	1	7+9	5+10
37. K34-8	2*	7+9	5+10
38. K34-9	1	7+9	5+10
39. K34-10	2*	13+16	5+10
40. K35-2	1	7+9	5+10
41. K35-3	1	7+9	5+10
42. K35-4	1	7+9	5+10
43. K35-5	1	7+9	5+10
44. K35-6	1	7+9	5+10
45. K35-7	1	7+9	5+10
46. K35-8	1	7+9	5+10
47. K35-9	1	7+9	5+10
48. K35-10	1	7+9	5+10
49. K37-1	1	7+9	5+10

Table 1.4 (Continued)

Cultivars	A genome	B genome	D genome
50 K37-2	1	7+9	5+10
51 K37-3	1	7+9	5+10
52 K37-4	1	7+9	5+10
53 K37-5	1	7+9	5+10
54 K37-6	1	7+9	5+10
55 K37-7	1	7+9	5+10
56 K37-8	1	7+9	5+10
57 K37-9	1	7+9	5+10
58 K37-10	1	7+9	5+10
59 Karee	1	7+9	5+10
60 Kariega	2*	17+18	5+10
61 Limpopo	2*	7+8	5+10
62 Limpopo DN	2*	7+8	5+10
63 Marico	0/2*	7+8	2+12
64 Molen	2*	7+9	2+12
65 Molopo	1	7+9	5+10
66 Nantes	1	7+8	2+12
67 Oom Charl	1	7+8	5+10
68 Oubaard	2*	7+8	2+12
69 Palmiet	2*	13+16	5+10
70 Palmiet DN	2*	13+16	5+10
71 Palmiet kort*	2*	13+16	5+10
72 PAN 3211	2*	7+8	5+10
73 PAN 3232	2*	7+9	5+10
74 PAN 3235	2*	7+8	5+10
75 PAN 3349	2*	7+8	5+10
76 PAN 9419	0/2*	7+8	2+12
77 Red Victory	1	7+9	2+12
78 Riemland	2*	7+9	5+10
79 Sch 69	0/2*	17+18	2+12
80 Snack	0/2*	17+18	2+12
81 SST 3	0/2*	13+16	2+12

Table 1.4 (Continued)

Cultivars	A genome	B genome	D genome
82. SST 16	1	13+16	5+10
83. SST 23	1	13+16	5+10
84. SST 33	0	13+16	5+10
85. SST 44	0/2*	7+8	2+12
86. SST 55	1	13+16	2+12
87. SST 57	1	1+8	5+10
88. SST 66	1	7+8	2+12
89. SST 86	1	13+16	5+10
90. SST 101	1	7+9	5+10
91. SST 102	1	7+9	5+10
93. SST 107	2*	7+9	5+10
94. SST 124	1	7+9	5+10
95. SST 972	2*	7+9	5+10
96. T4	0/2*	7+8	2+12
97. Tugela	2*	7+8	5+10
98. Tugela DN	2*	7+8	5+10
99. Tugela f-g	2*	7+8	5+10
100. Tugela nuut	2*	7+8	5+10
101. Turpin 7	0/2*	13+16	2+12
102. Verbeterde Kenia	1	17+18	2+12

In the A genome most of the cultivars (64 out of the 102 cultivars tested) had band 1, that is 63 percent of the cultivars. Twenty-three of the cultivars had band 2*, that is 23 percent. It was not possible to clearly distinguish between band 2* and the null band in cultivars that had subunits 2+12. According to Payne *et al* (1987) subunits 2 and 2* appear as a single band in resolving gels that are normally used to resolve most of the other HMW subunits. Two different resolving gels (10% and 5%) are needed to separate subunits 2 and 2* to see if a genotype contains these subunits. Two different gel systems take longer and are more expensive. It is also difficult to determine quantitatively, the relative staining intensities of the two subunits in the two different gels compared to a one-gel system (Huang and Khan, 1998). For this reason the combination 0/2* was taken into account and 11 of the cultivars had this

combination. In only three cultivars (3%) the A band was absent. This was in accordance with the findings of Randall *et al* (1992) who also tested the HMW glutenins of the South African wheat cultivars and found that band 1 was the most abundant.

In the B genome the combination of 7+9 was most prevalent. This was also in accordance with the findings of Randall *et al* (1992). The second most abundant combination was 7+8. Eighteen of the cultivars had these bands, that is 18 percent. It was followed by 13+16 (12 percent), 17+18 (5 percent) and band 7 (1 percent). Bands 6+8 were present only in two cultivars. In the cultivars that Randall *et al* (1992) tested more cultivars had the combination 13+16 (21 percent) than 7+8 (18.4 percent). Sixteen percent of the cultivars they tested had the combination 17+18 and five percent of the cultivars they tested had the bands 6+8. None of their cultivars had the band 7 alone.

In the D genome 83 percent of the cultivars had the 5+10 bands. Seventeen percent of the cultivars had the 2+12 bands. Randall *et al* (1992) also found that bands 5+10 are more abundant in South African bread wheat cultivars.

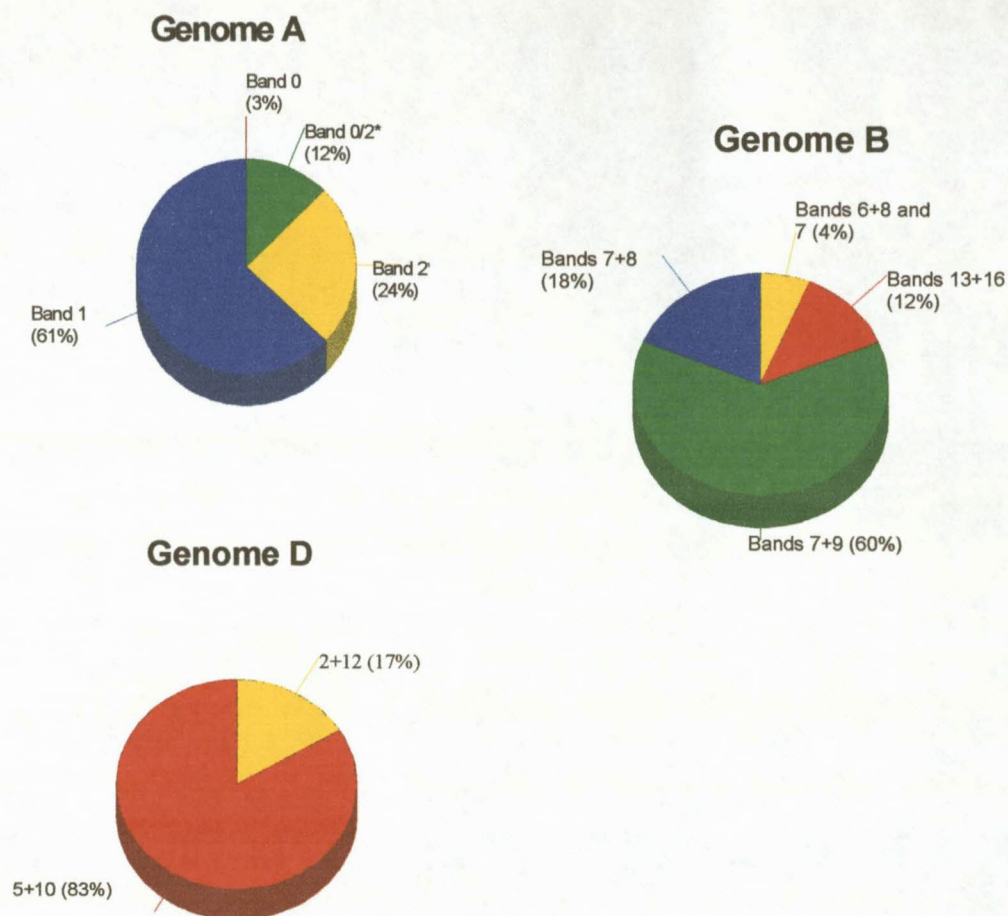


Figure 1.4. The HMW glutenin subunits composition of South African wheat cultivars.

The LMW glutenin bands

The results of the migration distances of the LMW bands of all the cultivars are given in Appendix A. Please note that a minimum of five replications of each cultivar was tested. The replications were also done on different gels. The average migration distance and intensity of each band are also shown. A summary of the results is given in Table 1.5. The different banding patterns of each cultivar are given with, in brackets, the intensity of the band in classes from one (very light) to five (very dark).

Please note that a class of six means that some replications of the same band had dark bands while others were light. It was thus impossible to give an exact intensity class. Chinese Spring was used as a standard cultivar on all the gels. Please refer to Chapter 3, Figure 3.1 to see the banding pattern of Chinese Spring as given by Gupta and Shepherd (1990). Table 1, Appendix C also gives the banding combinations of Chinese Spring.

Table 1.5 A summary of the different LMW glutenin bands of the cultivars tested. The intensity of the bands are in brackets.

Adam T	Aus hard	Barta	Belinda	Bella	Betana	Betta	Betta DN
9 (1)	43 (2)	15 (1)	15 (1)	9 (1)	13 (1)	24 (1)	26 (1)
16 (1)	67 (5)	23 (1)	43 (3)	18 (1)	21 (1)	36 (1)	49 (4)
23 (4)	81 (1)	38 (4)	64 (3)	26 (1)	35 (1)	51 (3)	52 (4)
45 (2)	90 (2)	54 (3)	77 (5)	37 (6)	61 (2)	55 (3)	64 (1)
53 (1)	102 (4)	85 (5)	96 (4)	55 (2)	82 (5)	68 (2)	79 (5)
74 (5)	110 (1)	96 (2)	113 (2)	87 (5)	103 (2)	83 (5)	86 (3)
94 (6)	120 (1)	108 (2)	143 (5)	111 (2)	110 (2)	93 (3)	92 (3)
101 (1)	132 (1)	124 (4)	159 (3)	123 (4)	117 (3)	103 (2)	100 (3)
121 (2)	136 (2)	140 (4)	184 (1)	141 (4)	134 (4)	107 (2)	112 (1)
133 (6)	147 (1)	156 (2)	191 (1)	157 (1)	152 (1)	118 (1)	132 (4)
153 (3)	162 (1)	172 (3)		174 (2)	166 (2)	124 (1)	147 (4)
174 (4)	168 (1)	181 (1)		185 (1)	177 (1)	136 (5)	166 (2)
184 (1)					186 (1)	148 (5)	
192 (1)						153 (4)	
						172 (2)	

Table 1.5 (Continued)

Bona	Galedon	Garina	Carolus	Corella	Dirkwin	Eland	Elize
13 (1)	38 (1)	8 (1)	8 (1)	10 (1)	7 (1)	8 (1)	8 (1)
23 (1)	68 (5)	15 (1)	14 (1)	25 (1)	12 (1)	15 (1)	20 (2)
45 (3)	76 (2)	22 (1)	33 (1)	33 (2)	17 (1)	22 (1)	31 (6)
62 (6)	94 (3)	34 (1)	65 (6)	44 (1)	27 (1)	35 (1)	48 (1)
83 (5)	105 (3)	44 (1)	74 (2)	56 (1)	46 (1)	50 (1)	64 (3)
106 (3)	115 (2)	61 (5)	84 (4)	71 (1)	73 (5)	81 (5)	74 (3)
118 (4)	123 (1)	76 (6)	96 (5)	95 (5)	86 (5)	112 (6)	87 (4)
135 (6)	139 (2)	95 (5)	108 (1)	108 (1)	98 (3)	125 (4)	94 (5)
151 (1)	149 (1)	104 (5)	125 (6)	119 (2)	117 (3)	138 (2)	106 (2)
167 (1)	167 (2)	116 (4)	156 (6)	125 (2)	124 (3)	152 (1)	116 (2)
184 (1)		134 (6)	168 (1)	136 (2)	145 (1)	163 (1)	127 (3)
191 (1)		157 (2)	186 (1)	144 (2)	176 (1)	181 (1)	136 (4)
		165 (1)		162 (1)	182 (1)	192 (1)	144 (2)
		181 (1)		175 (2)	186 (1)		155 (2)
		193 (1)		184 (1)	192 (1)		167 (1)
				193 (1)			174 (1)
							187 (1)

Table 1.5 (Continued)

Elina	Flameks	Flamink	Camka	Camtoos	Camtoos DN	Gandum Jasa
12 (2)	6 (1)	15 (1)	16 (3)	12 (1)	25 (5)	26 (2)
25 (1)	17 (1)	21 (1)	48 (5)	27 (5)	45 (5)	36 (1)
34 (1)	35 (3)	45 (5)	56 (5)	47 (5)	56 (2)	47 (3)
52 (4)	51 (3)	58 (5)	72 (1)	59 (2)	80 (1)	62 (5)
64 (6)	64 (5)	73 (1)	83 (1)	74 (1)	89 (1)	70 (5)
88 (5)	81 (1)	81 (1)	94 (1)	86 (1)	107 (3)	78 (3)
95 (5)	94 (1)	91 (2)	109 (4)	94 (2)	126 (3)	91 (3)
106 (6)	103 (2)	108 (3)	128 (2)	121 (3)	156 (2)	95 (3)
123 (3)	114 (3)	111 (2)	153 (1)	164 (6)	162 (6)	103 (5)
136 (3)	134 (1)	129 (3)	165 (1)	174 (1)	173 (1)	108 (4)
152 (5)	157 (2)	147 (1)	174 (2)	185 (1)	183 (2)	123 (1)
166 (1)	167 (1)	161 (2)	185 (1)		194 (1)	127 (1)
175 (1)	174 (1)	171 (1)	192 (1)			134 (1)
185 (2)	186 (1)	178 (1)				144 (1)
192 (1)	195 (1)	185 (6)				152 (1)
		193 (1)				167 (1)
						173 (1)
						176 (1)

Table 1.5 (Continued)

Carlep	Carlep DN	Gourits	Harts	Hugenoot	Inia	Jager	K29-1
63 (4)	45 (1)	15 (1)	16 (1)	45 (1)	16 (3)	7 (1)	9 (1)
73 (5)	69 (5)	30 (1)	25 (1)	63 (5)	24 (3)	14 (1)	30 (1)
97 (2)	78 (2)	48 (5)	45 (5)	68 (5)	36 (5)	25 (1)	42 (2)
107 (3)	95 (3)	61 (5)	60 (5)	79 (2)	52 (5)	36 (1)	52 (3)
116 (5)	103 (4)	73 (6)	75 (1)	86 (1)	62 (4)	57 (5)	74 (4)
124 (1)	106 (4)	94 (6)	83 (1)	91 (2)	86 (2)	67 (6)	91 (5)
136 (1)	117 (1)	100 (4)	90 (1)	95 (2)	100 (4)	78 (3)	102 (1)
145 (1)	125 (1)	112 (4)	102 (2)	103 (2)	105 (3)	88 (4)	110 (1)
153 (1)	138 (1)	133 (6)	117 (3)	116 (2)	116 (4)	103 (6)	125 (6)
166 (1)	144 (2)	145 (1)	126 (3)	127 (1)	123 (3)	115 (2)	146 (5)
174 (1)	151 (1)	159 (6)	136 (2)	135 (1)	139 (1)	147 (4)	167 (2)
	168 (2)	183 (6)	169 (2)	144 (2)	158 (6)	161 (6)	174 (2)
		193 (1)	177 (2)	151 (2)	166 (5)	170 (3)	183 (1)
			187 (1)	163 (1)	181 (1)	181 (2)	
			193 (1)	173 (1)	188 (1)	192 (1)	

Table 1.5 (Continue)

K29-2	K29-3	K29-4	K29-5	K29-6	K29-7	K29-8	K29-9
15 (1)	27 (2)	24 (6)	26 (5)	29 (5)	22 (1)	25 (1)	16 (1)
24 (2)	38 (2)	44 (2)	47 (2)	42 (1)	35 (5)	38 (2)	37 (2)
37 (2)	49 (4)	65 (4)	61 (6)	49 (1)	58 (1)	53 (1)	48 (2)
47 (6)	73 (5)	75 (4)	74 (2)	67 (4)	66 (2)	68 (5)	62 (4)
65 (6)	92 (5)	84 (6)	85 (4)	83 (2)	78 (3)	84 (3)	83 (2)
86 (6)	122 (5)	96 (2)	101 (5)	89 (4)	89 (3)	107 (4)	87 (4)
97 (2)	147 (5)	107 (1)	114 (1)	106 (5)	109 (4)	117 (1)	103 (1)
106 (1)	163 (3)	114 (6)	138 (3)	117 (1)	122 (1)	123 (1)	113 (1)
119 (6)	176 (1)	125 (2)	146 (4)	129 (1)	128 (1)	142 (5)	118 (1)
129 (3)	185 (1)	141 (5)	162 (2)	137 (2)	146 (3)	169 (4)	126 (6)
143 (5)	192 (1)	163 (4)	171 (2)	147 (4)	156 (3)	188 (1)	137 (5)
164 (2)		178 (1)	191 (1)	171 (4)	169 (2)		142 (5)
176 (1)		186 (1)		186 (1)	183 (1)		162 (2)
185 (1)		192 (1)		192 (1)	192 (2)		167 (2)
							183 (1)

Table 1.5 (Continued)

K29-10	K34-1	K34-2	K34-3	K34-4	K34-5	K34-7	K34-8
25 (4)	48 (5)	26 (1)	14 (1)	17 (2)	16 (1)	34 (2)	38 (2)
34 (1)	77 (5)	37 (3)	17 (1)	37 (5)	26 (2)	47 (3)	51 (6)
47 (4)	88 (1)	48 (4)	37 (4)	53 (5)	40 (6)	66 (5)	72 (4)
69 (5)	106 (1)	61 (2)	47 (4)	62 (3)	68 (4)	82 (5)	85 (6)
78 (3)	123 (1)	72 (5)	57 (1)	77 (4)	84 (4)	99 (1)	125 (4)
90 (4)	133 (2)	86 (4)	73 (4)	87 (1)	99 (1)	116 (4)	138 (5)
103 (1)	148 (2)	103 (1)	89 (3)	94 (3)	114 (6)	135 (4)	165 (1)
117 (2)	161 (3)	116 (5)	98 (1)	103 (1)	133 (5)	159 (2)	191 (1)
143 (6)	180 (3)	123 (4)	103 (1)	108 (1)	154 (4)	188 (1)	
157 (2)		132 (4)	106 (1)	132 (5)	164 (1)		
175 (3)		158 (1)	116 (3)	146 (4)	174 (1)		
194 (1)		177 (1)	124 (5)	161 (1)	192 (1)		
		182 (2)	138 (5)	168 (1)			
		187 (1)	146 (4)	172 (1)			
			158 (1)	187 (1)			
			163 (1)				
			172 (1)				
			179 (1)				
			189 (1)				

Table 1.5 (Continued)

K34-9	K34-10	K35-2	K35-3	K35-4	K35-5	K35-6	K35-7
27 (6)	41 (2)	13 (1)	27 (1)	24 (2)	15 (2)	18 (1)	18 (1)
43 (2)	58 (4)	23 (1)	43 (3)	45 (3)	26 (1)	31 (3)	28 (6)
51 (4)	79 (4)	61 (3)	52 (2)	64 (3)	39 (3)	47 (4)	45 (2)
76 (4)	93 (5)	82 (4)	64 (3)	79 (4)	56 (3)	66 (5)	52 (6)
96 (6)	125 (5)	90 (3)	84 (4)	110 (6)	73 (5)	93 (4)	63 (5)
122 (4)	147 (5)	125 (4)	113 (6)	133 (5)	106 (5)	113 (5)	77 (6)
141 (5)	167 (2)	148 (5)	135 (5)	149 (5)	127 (5)	135 (6)	94 (5)
165 (2)	173 (1)	165 (2)	151 (5)	158 (2)	149 (2)	148 (2)	123 (4)
185 (1)		173 (2)	164 (1)	168 (1)	189 (1)	179 (1)	141 (6)
			192 (1)	187 (1)		194 (1)	158 (3)
							177 (1)
							188 (1)

Table 1.5 (Continued)

K35-8	K35-9	K35-10	K37-1	K37-2	K37-3	K37-4	K37-5
15 (1)	22 (1)	46 (2)	9 (1)	12 (1)	15 (1)	25 (2)	17 (1)
25 (1)	32 (3)	60 (3)	16 (1)	25 (1)	26 (2)	32 (1)	23 (1)
43 (3)	46 (2)	82 (4)	25 (1)	38 (2)	45 (4)	45 (3)	34 (1)
64 (4)	55 (2)	94 (5)	31 (2)	46 (2)	68 (4)	68 (5)	44 (6)
82 (3)	69 (3)	124 (4)	42 (3)	72 (5)	79 (2)	82 (2)	64 (6)
96 (5)	87 (6)	145 (5)	52 (6)	88 (5)	88 (4)	85 (2)	74 (2)
124 (5)	102 (6)	158 (3)	72 (5)	103 (1)	102 (6)	99 (6)	92 (6)
134 (3)	127 (4)	166 (2)	85 (5)	119 (3)	127 (6)	114 (4)	98 (1)
143 (6)	147 (5)	192 (2)	92 (5)	127 (4)	144 (5)	123 (6)	105 (1)
159 (3)	164 (6)		105 (1)	143 (5)	153 (5)	145 (5)	143 (5)
169 (2)	185 (1)		125 (3)	152 (5)	167 (1)	165 (6)	162 (3)
176 (1)			135 (3)	168 (2)	183 (1)	187 (1)	187 (1)
192 (1)			143 (5)	185 (3)	191 (1)	194 (1)	192 (1)
			153 (5)	190 (6)			
			173 (1)				
			181 (1)				
			192 (1)				

Table 1.5 (Continued)

K37-6	K37-7	K37-8	K37-9	K37-10	Karee	Karaga	Katyl
16 (1)	17 (1)	17 (1)	13 (1)	25 (2)	7 (1)	15 (1)	16 (1)
25 (1)	28 (2)	26 (2)	25 (4)	33 (1)	14 (1)	33 (1)	21 (1)
34 (1)	40 (6)	37 (6)	37 (2)	47 (3)	34 (3)	43 (1)	62 (5)
46 (6)	54 (1)	48 (2)	47 (3)	61 (6)	54 (4)	57 (3)	69 (5)
57 (2)	65 (2)	60 (2)	73 (5)	71 (4)	73 (2)	68 (4)	90 (1)
77 (3)	88 (3)	74 (4)	83 (6)	80 (1)	79 (4)	81 (5)	105 (2)
98 (3)	94 (3)	85 (4)	93 (6)	84 (2)	88 (5)	91 (6)	124 (4)
111 (6)	104 (1)	91 (4)	104 (1)	100 (1)	96 (6)	98 (1)	137 (1)
117 (1)	112 (1)	105 (1)	124 (4)	106 (1)	105 (1)	104 (1)	150 (1)
136 (4)	118 (1)	132 (5)	132 (5)	125 (4)	115 (3)	117 (3)	166 (2)
142 (5)	142 (6)	143 (5)	148 (5)	145 (5)	147 (5)	145 (5)	178 (1)
154 (5)	152 (5)	153 (5)	164 (1)	177 (1)	165 (4)	157 (2)	188 (1)
163 (5)	168 (6)	173 (2)	173 (1)	187 (1)	185 (1)	165 (2)	
182 (1)	176 (1)	191 (1)	183 (1)			173 (2)	
	187 (1)		189 (1)			191 (1)	

Table 1.5 (Continued)

Kavkaz	Limpopo	Limpopo DN	M29519	M29568	Marico	Molen	Molopo
13 (1)	32 (2)	63 (5)	15 (1)	7 (1)	8 (1)	53 (3)	45 (1)
21 (1)	46 (2)	72 (5)	43 (5)	13 (1)	24 (2)	65 (5)	73 (5)
28 (1)	58 (4)	94 (2)	64 (4)	25 (3)	43 (3)	72 (5)	81 (2)
54 (5)	68 (5)	98 (3)	70 (5)	37 (1)	66 (5)	90 (3)	99 (4)
76 (2)	88 (2)	106 (4)	90 (1)	63 (5)	84 (5)	101 (4)	110 (5)
91 (4)	97 (4)	115 (1)	96 (1)	78 (5)	102 (6)	107 (3)	121 (1)
102 (1)	104 (6)	117 (1)	103 (1)	107 (5)	113 (5)	114 (2)	128 (1)
121 (6)	111 (1)	133 (1)	115 (4)	116 (3)	135 (1)	123 (1)	138 (1)
132 (1)	117 (1)	139 (1)	135 (6)	127 (1)	144 (2)	134 (1)	144 (2)
155 (4)	129 (2)	162 (1)	156 (1)	140 (4)	154 (1)	141 (2)	152 (1)
168 (2)	137 (2)	169 (1)	175 (1)	173 (1)	163 (1)	149 (1)	161 (1)
174 (1)	147 (1)		185 (1)	186 (1)	174 (1)	156 (1)	171 (2)
194 (1)	156 (1)		194 (1)	192 (1)	183 (1)	162 (1)	
	165 (1)				195 (1)	172 (1)	

Table 1.5 (Continued)

Nantes	Norstar	Oom Charl	Oranje	Oubaard	Owens	Palala	Palmiet
12 (1)	17 (1)	9 (1)	14 (1)	11 (2)	15 (1)	14 (2)	48 (3)
45 (1)	44 (1)	15 (1)	21 (1)	21 (1)	22 (1)	29 (1)	57 (3)
62 (5)	63 (3)	25 (1)	34 (1)	27 (2)	29 (1)	45 (1)	62 (4)
76 (6)	75 (2)	37 (1)	44 (6)	45 (5)	56 (6)	62 (6)	69 (5)
86 (6)	93 (5)	43 (1)	54 (1)	63 (6)	69 (6)	81 (6)	91 (3)
104 (2)	105 (6)	67 (5)	64 (1)	73 (3)	88 (6)	93 (1)	103 (4)
113 (2)	134 (2)	87 (1)	73 (1)	94 (3)	106 (1)	99 (1)	114 (2)
125 (2)	150 (2)	104 (1)	85 (2)	105 (4)	114 (1)	114 (3)	139 (2)
141 (6)	162 (4)	123 (4)	102 (5)	121 (6)	124 (1)	128 (1)	164 (2)
174 (1)	175 (2)	134 (4)	127 (1)	133 (6)	131 (1)	148 (1)	
182 (1)	185 (1)	148 (1)	143 (2)	151 (6)	152 (1)	166 (2)	
194 (1)	192 (1)	176 (2)	166 (1)	166 (1)	156 (1)	175 (1)	
		185 (1)	184 (1)	178 (2)	171 (1)	182 (1)	
		193 (1)	193 (1)	187 (1)	185 (1)	188 (1)	
				194 (1)		194 (1)	

Table 1.5 (Continued)

Palmet DN	Palmet short	PAN321	PAN323	PAN 325	PAN334	PAN336
38 (2)	36 (2)	37 (1)	18 (1)	14 (1)	36 (2)	11 (1)
53 (2)	58 (4)	53 (5)	25 (1)	26 (1)	43 (2)	15 (1)
63 (4)	68 (5)	65 (5)	36 (1)	35 (1)	51 (4)	21 (1)
71 (5)	89 (3)	72 (4)	55 (1)	45 (1)	61 (2)	32 (1)
94 (3)	103 (4)	96 (3)	76 (5)	58 (1)	71 (3)	49 (5)
104 (4)	117 (1)	109 (5)	92 (4)	73 (5)	93 (2)	64 (3)
117 (1)	137 (2)	127 (2)	107 (4)	89 (5)	106 (5)	73 (4)
121 (1)	145 (1)	143 (2)	117 (1)	103 (1)	124 (1)	84 (2)
125 (1)	152 (1)	154 (1)	125 (1)	123 (2)	138 (3)	95 (1)
135 (4)	162 (1)	159 (1)	135 (2)	132 (2)	148 (1)	101 (1)
141 (2)	167 (1)	172 (2)	144 (3)	157 (6)	157 (1)	115 (3)
154 (1)	175 (1)		157 (3)	175 (1)	170 (2)	143 (5)
166 (1)			177 (1)	184 (1)	182 (1)	163 (5)
			185 (1)			183 (1)
						192 (1)

Table 1.5 (Continued)

PAN337	PAN930	PAN931	PAN940	PAN941	PAN941	PAN941	PAN941
9 (1)	11 (1)	12 (1)	6 (1)	14 (1)	15 (1)	10 (1)	7 (1)
32 (5)	33 (5)	16 (1)	11 (1)	23 (3)	26 (1)	15 (1)	15 (1)
48 (4)	47 (2)	27 (1)	18 (1)	35 (1)	35 (1)	34 (1)	24 (1)
65 (1)	59 (3)	41 (5)	22 (1)	47 (1)	46 (1)	45 (5)	31 (1)
96 (3)	73 (1)	52 (3)	45 (4)	63 (2)	68 (5)	57 (1)	49 (5)
106 (3)	86 (1)	67 (6)	64 (4)	75 (5)	76 (5)	78 (3)	66 (5)
118 (6)	97 (3)	78 (1)	74 (3)	93 (6)	104 (4)	88 (1)	77 (1)
136 (1)	104 (2)	84 (1)	83 (1)	95 (1)	114 (5)	115 (5)	91 (2)
153 (1)	122 (6)	90 (1)	90 (1)	103 (3)	126 (3)	119 (6)	112 (5)
166 (1)	136 (1)	96 (4)	97 (4)	113 (3)	142 (1)	133 (6)	123 (5)
172 (1)	153 (2)	104 (5)	107 (5)	122 (2)	152 (1)	146 (1)	135 (1)
176 (1)	161 (1)	118 (4)	119 (5)	132 (1)	165 (1)	154 (1)	149 (2)
181 (1)	166 (1)	124 (1)	132 (1)	146 (1)	175 (1)	162 (1)	156 (1)
188 (1)	174 (1)	133 (1)	146 (2)	152 (1)	184 (1)	173 (1)	163 (2)
195 (1)	185 (1)	143 (1)	162 (2)	164 (2)	187 (1)	182 (1)	172 (1)
	194 (1)	156 (1)	175 (1)	176 (1)	193 (1)	192 (1)	181 (1)
		170 (1)	185 (1)	181 (1)			188 (1)
		175 (1)	189 (1)	187 (1)			193 (1)
		181 (1)	195 (1)	191 (1)			
		186 (1)					
		193 (1)					

Table 1.5 (Continued)

PAN941	PAN971	PAN971	PAN971	PAN LE	PAN LE	PAN LE	PAN LE
				4	7	9	10
7 (1)	50 (5)	36 (1)	33 (1)	8 (1)	6 (1)	9 (1)	13 (1)
21 (4)	60 (5)	52 (5)	50 (5)	23 (4)	14 (1)	14 (1)	22 (1)
35 (1)	79 (1)	62 (5)	61 (5)	33 (1)	22 (6)	23 (1)	49 (5)
48 (2)	91 (3)	78 (1)	75 (1)	37 (1)	30 (1)	33 (1)	63 (1)
66 (3)	102 (5)	83 (1)	90 (3)	43 (1)	40 (1)	47 (3)	79 (4)
84 (5)	114 (2)	92 (3)	102 (5)	57 (1)	46 (1)	60 (6)	93 (1)
94 (3)	124 (1)	104 (5)	112 (2)	64 (1)	62 (1)	74 (4)	97 (1)
102 (2)	135 (2)	113 (2)	117 (1)	77 (5)	73 (5)	83 (2)	117 (1)
121 (5)	145 (1)	124 (1)	134 (2)	87 (5)	85 (5)	93 (1)	134 (5)
134 (6)	158 (2)	142 (2)	147 (1)	98 (1)	97 (1)	98 (1)	143 (4)
146 (1)	167 (3)	157 (1)	152 (1)	106 (2)	104 (1)	116 (4)	152 (6)
154 (1)	178 (1)	163 (1)	158 (1)	123 (5)	121 (4)	126 (3)	168 (1)
166 (1)		169 (2)	163 (1)	133 (6)	133 (4)	135 (4)	176 (1)
174 (1)		177 (1)	167 (1)	146 (1)	153 (2)	161 (1)	188 (1)
182 (1)			172 (1)	157 (2)	164 (2)	172 (1)	191 (1)
187 (1)				167 (2)	174 (2)	181 (1)	
194 (1)				184 (1)	184 (1)	186 (1)	
				190 (1)	193 (1)	191 (1)	
				193 (1)		196 (1)	

Table 1.5 (Continued)

PAN LE 12	Red Victory	Riemland	SA 1684	SA 468	Sch 69	Snack	Sonop
9 (1)	7 (1)	8 (1)	48 (2)	42 (1)	29 (1)	13 (1)	9 (1)
15 (1)	13 (1)	13 (1)	67 (5)	68 (5)	36 (1)	26 (1)	14 (1)
24 (4)	19 (1)	18 (1)	76 (2)	74 (3)	55 (4)	43 (1)	23 (1)
32 (1)	24 (1)	24 (1)	92 (2)	90 (2)	65 (4)	53 (2)	41 (5)
42 (1)	29 (1)	31 (1)	103 (4)	105 (4)	72 (4)	64 (3)	50 (4)
56 (1)	43 (5)	38 (1)	114 (2)	113 (1)	87 (1)	74 (5)	68 (3)
77 (5)	62 (1)	54 (1)	136 (2)	120 (1)	95 (3)	86 (4)	77 (2)
83 (5)	76 (4)	63 (1)	142 (2)	140 (2)	109 (5)	96 (1)	85 (1)
103 (1)	93 (1)	76 (5)	149 (1)	145 (1)	117 (3)	102 (1)	96 (3)
109 (1)	98 (1)	92 (1)	164 (1)	167 (1)	125 (1)	114 (2)	103 (6)
130 (5)	104 (1)	99 (1)	168 (1)		140 (3)	134 (2)	113 (2)
147 (2)	111 (1)	112 (6)			153 (1)	145 (3)	124 (6)
163 (1)	117 (1)	118 (2)			167 (2)	163 (3)	142 (1)
174 (1)	124 (2)	132 (3)			178 (1)	173 (1)	150 (1)
187 (1)	135 (5)	140 (1)				185 (1)	163 (1)
193 (1)	157 (1)	152 (1)					168 (1)
	162 (1)	163 (2)					175 (1)
	172 (1)	174 (2)					184 (1)
	177 (2)	183 (1)					192 (1)
	184 (1)	192 (1)					
	191 (1)						
	195 (1)						

Table 1.5 (Continued)

SST 3	SST 16	SST 23	SST 33	SST 44	SST 55	SST 66	SST101
16 (1)	9 (1)	13 (1)	13 (1)	15 (1)	13 (1)	14 (1)	12 (1)
24 (1)	16 (1)	20 (1)	30 (3)	26 (1)	26 (6)	27 (2)	22 (1)
32 (1)	27 (1)	33 (1)	47 (1)	37 (1)	41 (6)	49 (1)	34 (1)
57 (5)	37 (1)	46 (4)	57 (1)	49 (1)	47 (6)	63 (3)	47 (6)
66 (2)	46 (2)	63 (3)	64 (1)	62 (1)	62 (1)	75 (5)	76 (1)
74 (1)	57 (1)	76 (3)	84 (5)	66 (1)	74 (2)	85 (4)	83 (1)
83 (5)	67 (1)	93 (3)	99 (1)	74 (1)	82 (5)	106 (1)	93 (1)
103 (1)	77 (1)	104 (6)	131 (5)	82 (2)	93 (6)	115 (2)	110 (3)
112 (2)	83 (1)	132 (5)	154 (1)	94 (2)	112 (1)	123 (2)	123 (1)
123 (3)	91 (1)	153 (6)	168 (1)	104 (1)	134 (1)	155 (3)	133 (1)
132 (2)	107 (5)	162 (1)	173 (1)	116 (1)	145 (1)	175 (1)	139 (1)
145 (3)	124 (1)	174 (1)	182 (1)	128 (6)	153 (1)	188 (1)	149 (1)
154 (2)	132 (1)	183 (1)	187 (1)	136 (1)	176 (1)		163 (2)
174 (1)	153 (3)	189 (1)	192 (1)	149 (1)	184 (1)		174 (1)
182 (1)	164 (1)	193 (1)		157 (1)	190 (1)		182 (1)
192 (1)	176 (1)			165 (1)			189 (1)
195 (1)	182 (1)			173 (1)			192 (1)
	187 (1)			178 (1)			
	194 (1)			182 (1)			
				192 (1)			

Table 1.5 (Continued)

SST102	SST107	SST124	SST333	SST363	SST367	SST322	SST325
36 (1)	8 (1)	33 (1)	43 (3)	27 (1)	69 (5)	14 (1)	12 (1)
45 (1)	14 (1)	44 (3)	62 (5)	45 (3)	80 (2)	23 (1)	17 (1)
50 (1)	29 (6)	67 (5)	67 (5)	72 (5)	91 (1)	32 (1)	27 (1)
74 (5)	46 (2)	84 (1)	76 (1)	83 (1)	103 (3)	43 (2)	32 (1)
93 (2)	76 (1)	91 (2)	83 (1)	92 (2)	110 (2)	55 (4)	55 (5)
105 (4)	91 (1)	101 (3)	90 (2)	96 (2)	114 (1)	87 (6)	67 (3)
116 (1)	103 (1)	108 (3)	100 (3)	105 (4)	127 (1)	97 (2)	85 (2)
122 (1)	116 (4)	116 (1)	107 (3)	116 (1)	138 (1)	105 (1)	94 (6)
132 (1)	127 (1)	142 (2)	114 (2)	122 (1)	152 (1)	122 (3)	104 (2)
137 (1)	141 (1)	150 (1)	123 (1)	136 (1)	164 (1)	132 (3)	114 (2)
142 (1)	152 (1)	165 (1)	128 (1)	145 (1)	172 (1)	147 (2)	133 (3)
156 (1)	159 (1)	175 (1)	141 (2)	163 (1)		175 (1)	161 (4)
168 (1)	171 (2)		148 (1)	172 (1)		186 (1)	182 (1)
182 (1)	187 (1)		165 (1)				
	192 (1)						

Table 1.5 (Continued)

SST 936	SST 936	SST 972	Stirling	T4	Tugela	Tugela DN	Tugela fg
26 (1)	26 (1)	13 (1)	9 (1)	9 (1)	27 (1)	27 (1)	28 (1)
33 (1)	34 (1)	24 (5)	24 (5)	16 (1)	43 (3)	37 (2)	36 (1)
37 (1)	51 (5)	39 (1)	35 (1)	32 (4)	52 (5)	46 (4)	53 (5)
49 (5)	66 (5)	57 (3)	51 (1)	42 (1)	64 (4)	53 (4)	65 (4)
63 (5)	73 (5)	77 (1)	73 (1)	52 (1)	77 (5)	60 (4)	74 (4)
72 (5)	94 (3)	82 (1)	81 (1)	65 (5)	94 (3)	72 (5)	77 (3)
94 (3)	109 (5)	102 (2)	98 (1)	83 (1)	103 (4)	92 (3)	93 (3)
107 (5)	117 (3)	115 (5)	102 (1)	97 (2)	108 (5)	96 (3)	108 (5)
132 (1)	126 (1)	141 (1)	116 (5)	106 (2)	118 (4)	103 (5)	116 (3)
140 (1)	147 (1)	150 (1)	126 (1)	113 (3)	128 (1)	113 (1)	139 (1)
148 (2)	153 (1)	162 (1)	137 (1)	126 (5)	142 (2)	123 (2)	146 (2)
156 (2)	166 (1)	172 (1)	155 (1)	144 (1)	148 (3)	126 (2)	158 (1)
162 (1)		181 (1)	162 (1)	163 (1)	172 (1)	142 (1)	165 (1)
167 (1)		192 (1)	171 (1)	173 (1)		148 (1)	
			180 (1)	186 (1)		155 (1)	
			194 (1)	195 (1)		165 (1)	
						172 (1)	

Table 1.5 (Continued)

Tugela new	Turpin 7	Turistikum	Verbatende Kenia
28 (1)	14 (1)	28 (1)	7 (1)
45 (3)	37 (5)	34 (1)	14 (1)
53 (5)	53 (1)	47 (3)	21 (1)
66 (4)	74 (5)	68 (5)	32 (1)
78 (5)	92 (1)	78 (2)	39 (1)
94 (3)	102 (1)	92 (3)	48 (1)
103 (5)	109 (1)	100 (3)	59 (1)
108 (5)	119 (2)	108 (3)	76 (4)
115 (3)	129 (3)	114 (3)	88 (1)
123 (1)	154 (1)	129 (1)	104 (1)
144 (2)	167 (1)	139 (2)	107 (1)
154 (1)	182 (1)	147 (1)	116 (2)
167 (1)	193 (1)	167 (1)	128 (3)
			137 (5)
			157 (1)
			164 (1)
			176 (1)
			182 (2)
			186 (2)
			192 (1)

The number of bands differed from a minimum of eight bands to a maximum of 22 bands. The cultivar with the least bands was the near isogenic line K34-8 (eight bands) and the cultivar with the highest amount of bands was Red Victory (22 bands). The average amount of bands per bread wheat cultivar was 13,8. Gupta and Shepherd (1988) found that cultivars usually possess from two to nine (usually three or more) B subunits and Denery-Papini *et al* (1995) found that as many as 16 LMW glutenin subunits might be expressed in a single cultivar. The South African cultivars with the highest amount of bands, therefore had a higher amount than reported in literature.

The class intervals of the bands were determined using the NCSS 2000 program and the standard deviations of 40 cultivars. Box plots were drawn to determine the possible overlapping of bands. Figure 1.5 shows the standard deviations of the 40 cultivars tested.

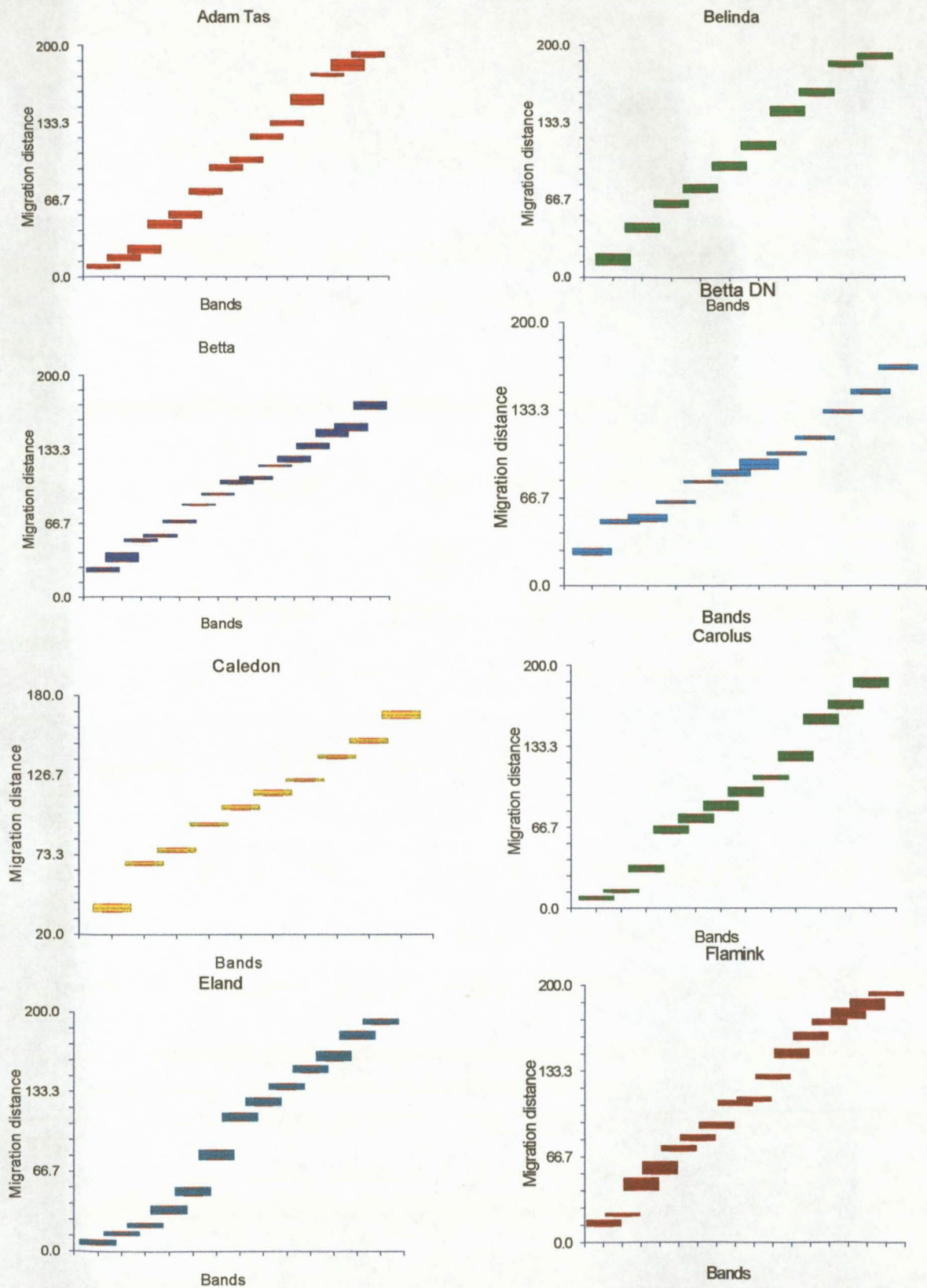


Figure 1.5. The standard deviations of the cultivars to indicate the possible overlapping of bands. The vertical axes gives the migration distance of the bands and the horizontal axes gives the different bands starting from one.

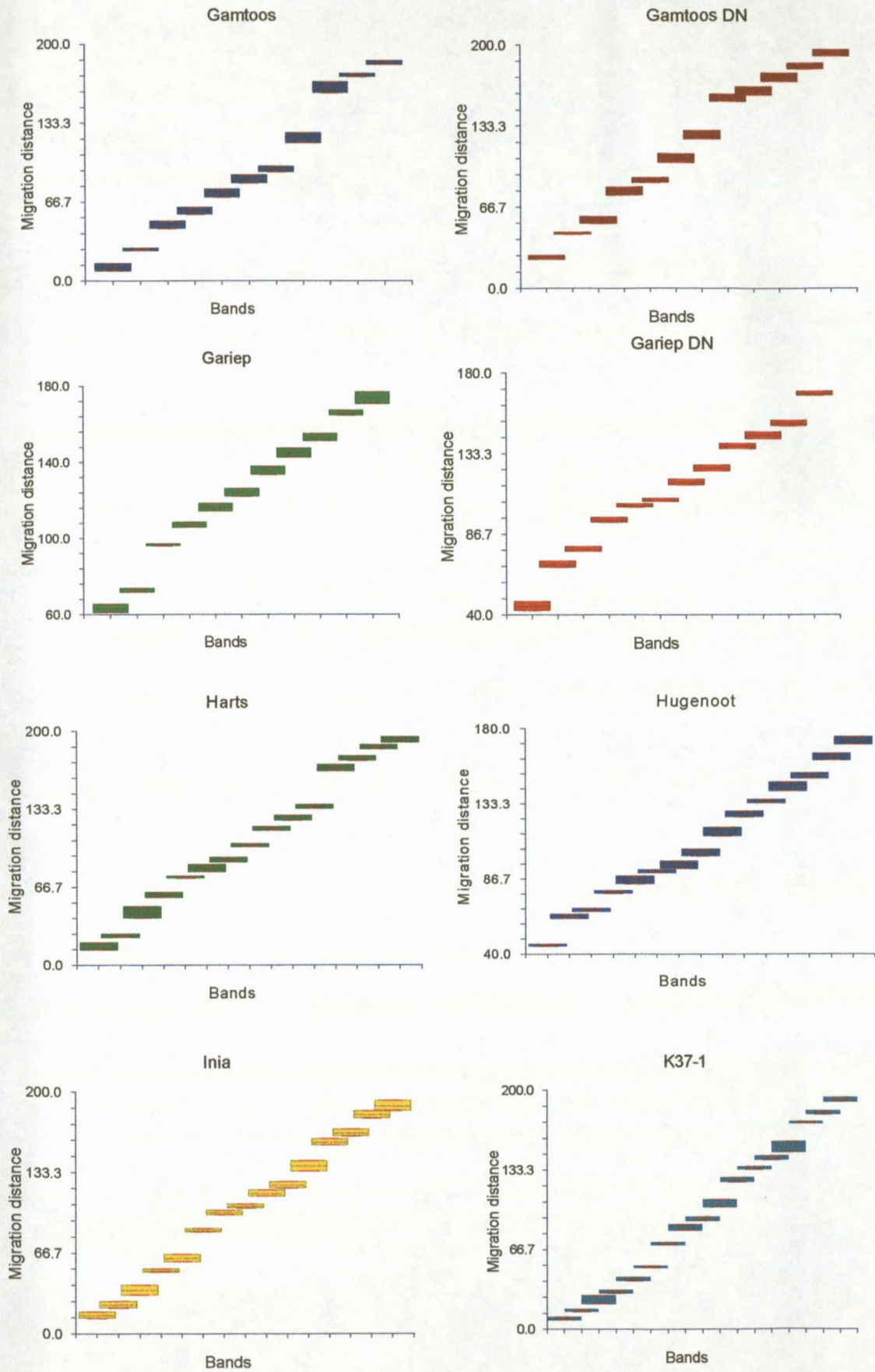


Figure 1.5. (Continued)

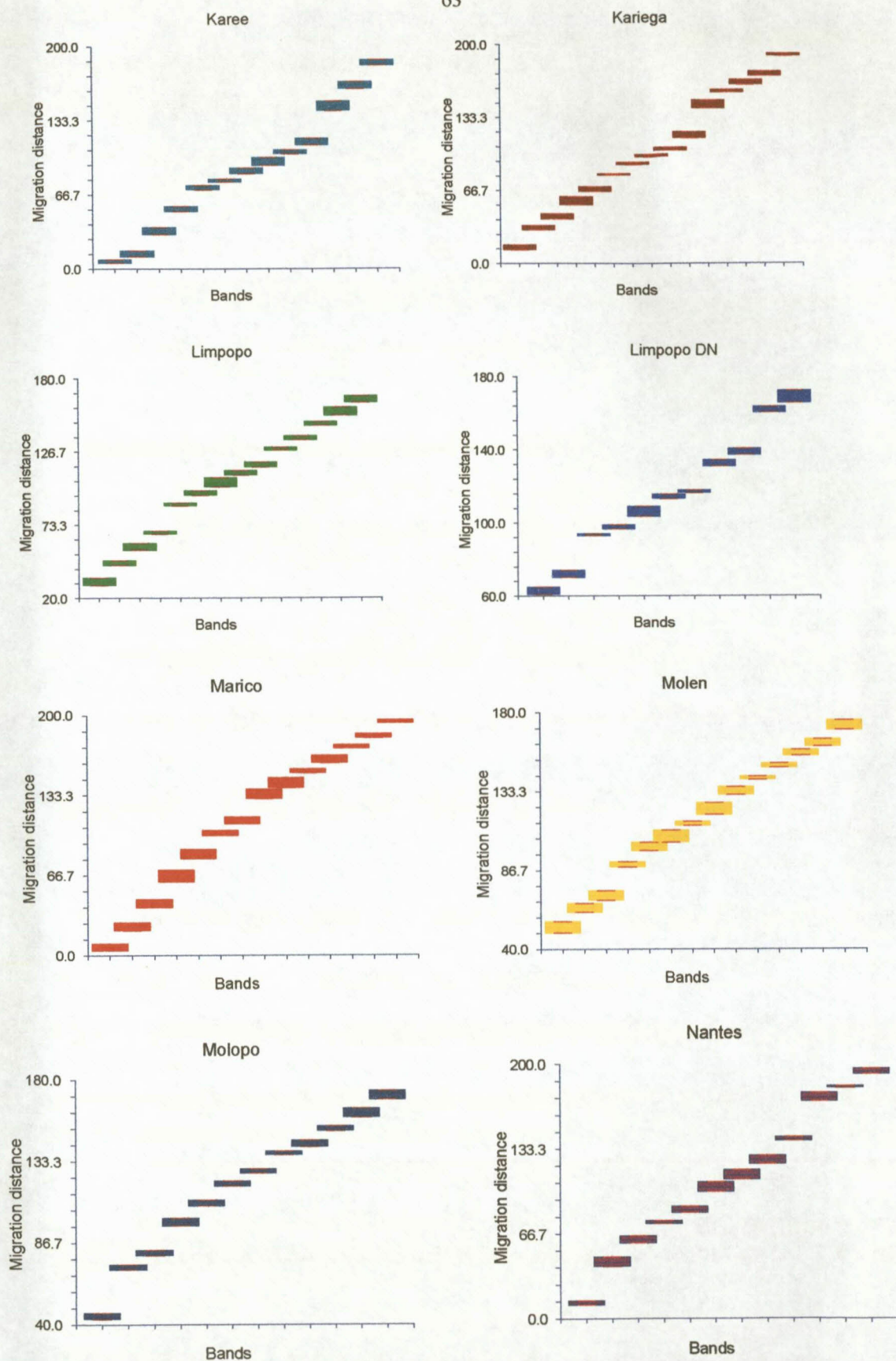


Figure 1.5. (Continued)

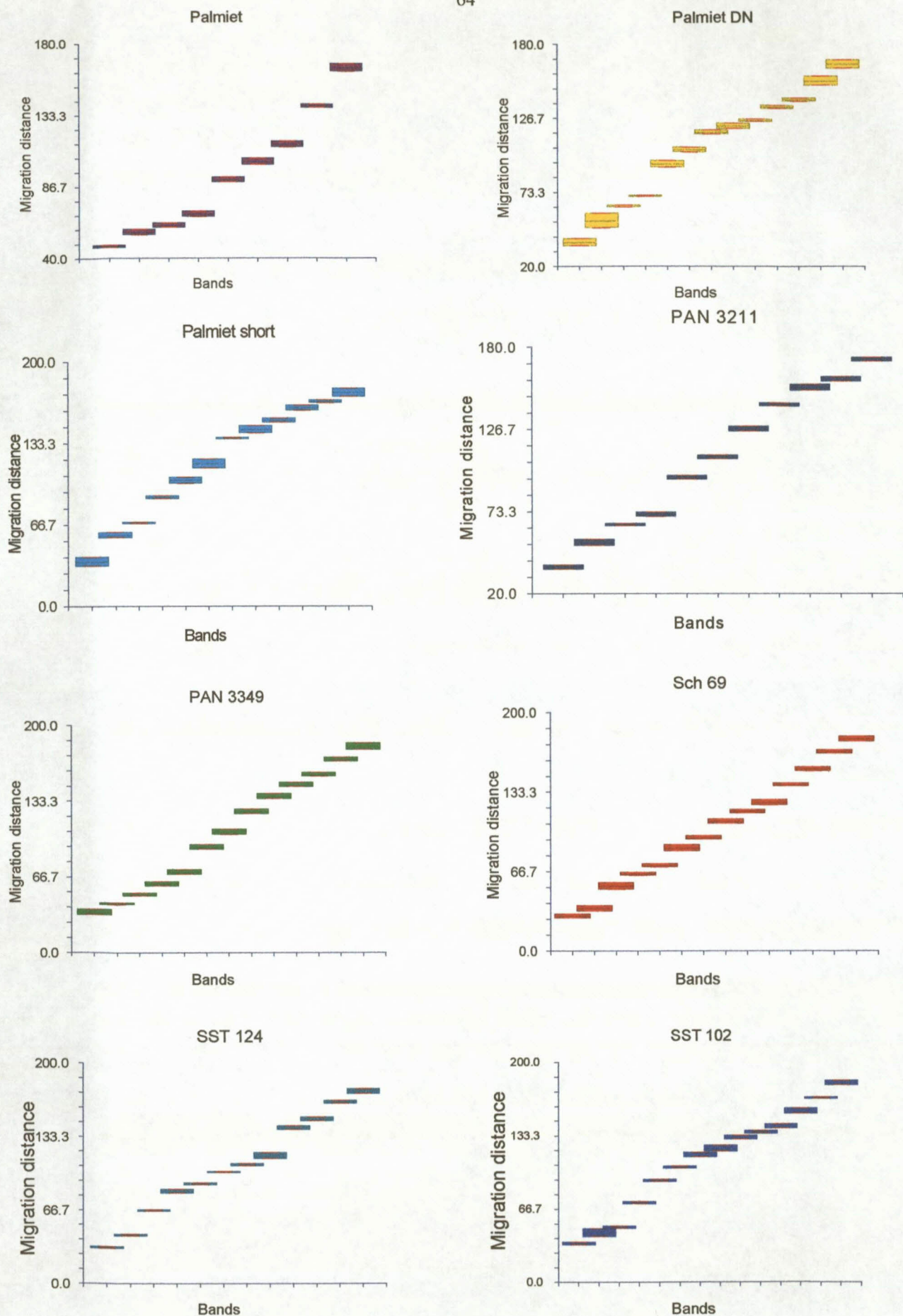


Figure 1.5. (Continued)

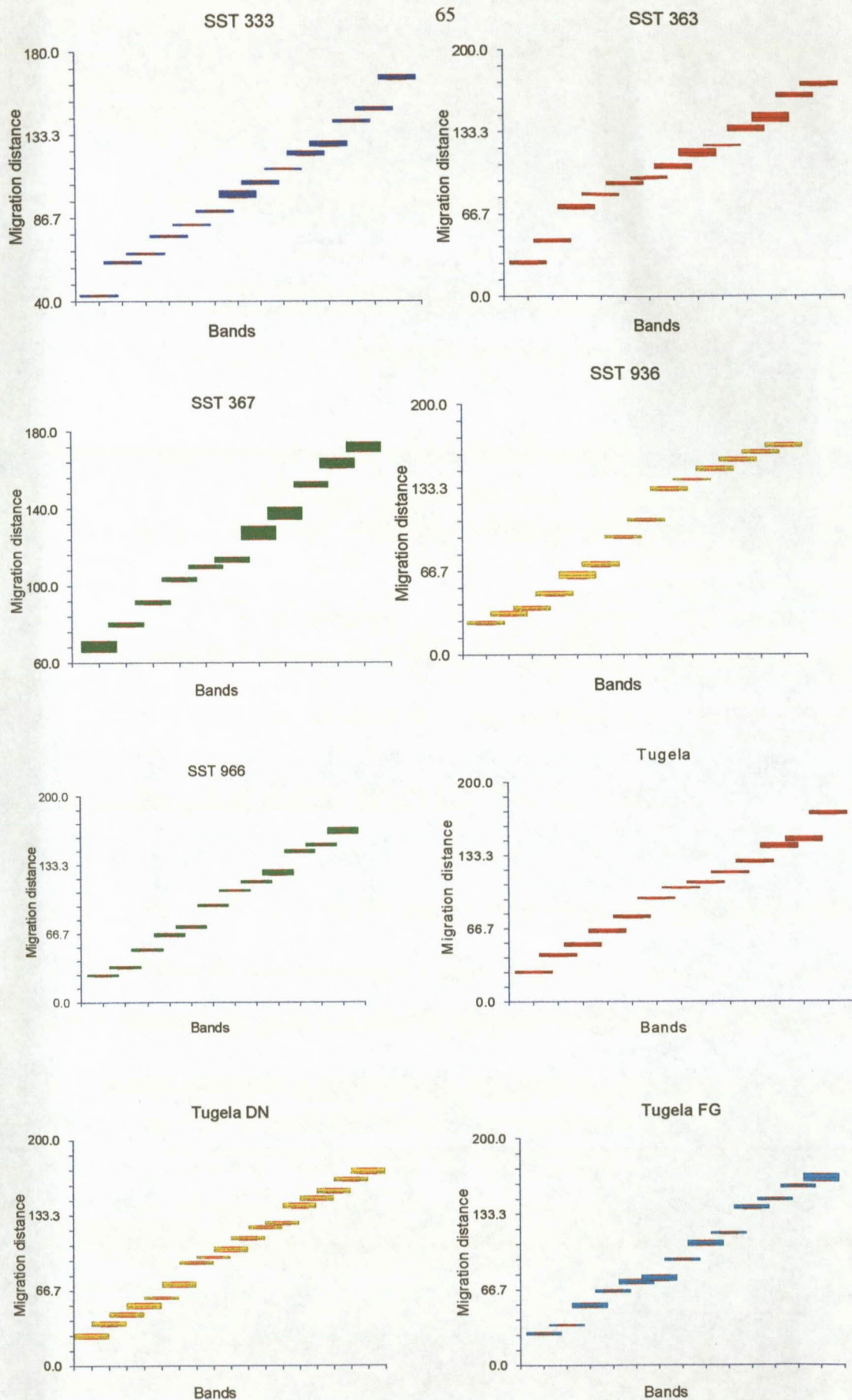


Figure 1.5. (Continued)

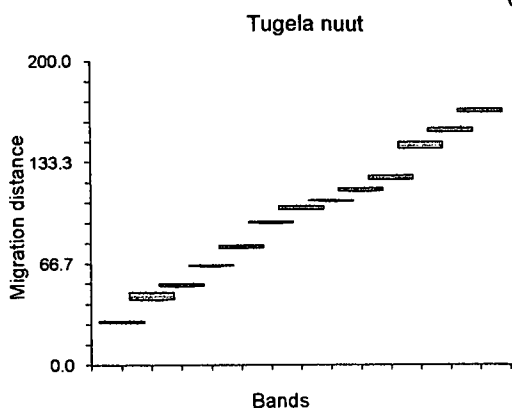


Figure 1.5. (Continued)

The bands that overlap according to the standard deviations were:

1. Bands with migration distance 16 and 23 and 45 and 53 in Adam Tas.
2. Bands with migration distance 51 and 55, 103 and 107, and 148 and 153 in the cultivar Betta.
3. Bands with migration distance 49 and 51, and 86 and 92 in Betta DN.
4. Bands with migration distance 8 and 14, and 65 and 74 in Carolus.
5. Bands with migration distance 15 and 22 in Eland.
6. Bands with migration distance 15 and 21, 108 and 111, 171 and 178 and 185 and 193 in Flamink.
7. Bands with migration distance 86 and 94 in Gamtoos.
8. Bands with migration distance 156 and 162 in Gamtoos DN.
9. Bands with migration distance 103 and 106 and 146 and 151 in Gariep DN.
10. Bands with migration distance 186 and 193 in Harts.
11. Bands with migration distance 63 and 67, 86 and 91, and 95 and 103 in Hugenoot.
12. Bands with migration distance 16 and 24, 100 and 105, 116 and 123 and 181 and 188 in Inia.
13. Bands with migration distance 25 and 31 and 85 and 92 in K37-1.
14. Bands with migration distance 7 and 14, 73 and 79 and 88 and 96 in Karee.
15. Bands 91, 98 and 104 in Kariëga and also bands 165 and 173.
16. Bands with migration distance 97 and 104 and 111 and 117 in Limpopo.
17. Bands with migration distance 94 and 98, 114 and 117, 133 and 139 and 162 and 169 in Limpopo DN.
18. Bands with migration distance 135 and 144 in Marico.

19. Bands with migration distance 65 and 72, 101 and 107 and 156 and 162 in Molen.
20. Bands with migration distance 138 and 144 in Molopo.
21. Bands with migration distance 104 and 113 in Nantes.
22. Bands with migration distance 57 and 62 in Palmiet.
23. Bands with migration distance 117, 121 and 125, and 135 and 141 in Palmiet DN.
24. Bands with migration distance 145 and 152 and 162 and 167 in Palmiet short.
25. Bands with migration distance 154 and 159 in PAN 3211.
26. Bands with migration distance 36 and 43 in PAN 3349.
27. Bands with migration distance 29 and 36, 65 and 65 and 72 in Sch 69.
28. Bands with migration distance 45 and 50, 116 and 122 and 132, 137 and 142 in SST 102.
29. Bands with migration distance 123 and 128 in SST 333.
30. Bands with migration distance 92 and 96 and 116 and 122 in SST 363.
31. Bands with migration distance 110 and 115 in SST 367.
32. Bands with migration distance 33 and 37 and 152, 162 and 167 in SST 936.
33. Bands with migration distance 66 and 73 and 147 and 153 in SST 966.
34. Bands with migration distance 103 and 108 and 142 and 148 in Tugela.
35. Bands with migration distance 46 and 53, 92, 96 and 103, 123 and 126, 142 and 148 and 165 and 172 in Tugela DN.
36. Bands with migration distance 74 and 77 and 158 and 165 in Tugela f-g.
37. Bands with migration distance 45 and 53 and 103 and 108 in Tugela new.

Taking all the possible double bands into account it was decided that bands within a molecular distance of 5 units apart could be seen as one. That means that bands with a molecular distance of 5 and 9 can be seen as the same band. Table 1.6 gives all the cultivars with their bands. In the first column are the class intervals that were chosen.

Table 1.6. The LMW glutenin bands of the cultivars tested

	Adam T	Aus Hard	Barta	Belinda	Bella	Betana	Betta
5-9	—				—	—	
10-14							
15-19	—		—	—	—	—	—
20-24	—		—		—	—	—
25-29					—		
30-34							
35-39			—		—	—	—
40-44		—		—			
45-49	—						
50-54	—		—				—
55-59					—		—
60-64				—		—	
65-69		—			—		—
70-74	—						
75-79				—			
80-84		—			—	—	—
85-89			—		—		
90-94	—	—	—	—			—
95-99			—	—			
100-104	—	—	—			—	—
105-109			—			—	—
110-114		—		—	—	—	—
115-119					—	—	—
120-124	—	—	—		—		
125-129							
130-134	—	—			—	—	—
135-139		—	—	—			—
140-144			—	—	—		—
145-149		—				—	—
150-154	—				—	—	—
155-159			—	—	—		
160-164		—				—	
165-169		—			—	—	
170-174	—		—		—		—
175-179					—	—	
180-184	—		—	—	—	—	
185-189				—			
190-194	—			—			
195-200							

Table 1.6 (Continued)

	Betta DN	Bona	Caledon	Carina	Carolus	Corella	Dirkwin
5-9							
10-14		—		—	—	—	—
15-19		—		—			—
20-24				—			
25-29	—					—	—
30-34				—	—	—	
35-39			—	—			
40-44				—		—	
45-49	—	—					—
50-54	—						
55-59		—		—		—	
60-64	—	—		—			
65-69			—		—		
70-74			—	—	—	—	—
75-79	—		—	—			
80-84		—			—		
85-89	—				—		—
90-94	—		—				
95-99				—	—	—	—
100-104	—			—			
105-109	—	—	—	—	—	—	
110-114							
115-119		—	—	—		—	—
120-124			—			—	—
125-129					—	—	
130-134	—			—		—	
135-139		—	—			—	
140-144			—			—	
145-149	—		—				—
150-154		—		—	—		
155-159				—			
160-164						—	
165-169	—	—	—	—	—		
170-174							
175-179		—		—		—	—
180-184				—		—	—
185-189		—		—	—	—	—
190-194							—
195-200							

Table 1.6 (Continued)

	Eland	Elize	Elrina	Flamink	Gamka	Gamtoos	Gamtoos DN
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 1.6 (Continued)

	Gandum I Fasai	Gariep	Gariep DN	Courits	Harts	Hugenoot	Infa
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 1.6 (Continued)

	K29-8	K29-9	K29-10	K34-1	K34-2	K34-3	K34-4	K34-6
5-9								
10-14								
15-19								
20-24								
25-29								
30-34								
35-39								
40-44								
45-49								
50-54								
55-59								
60-64								
65-69								
70-74								
75-79								
80-84								
85-89								
90-94								
95-99								
100-104								
105-109								
110-114								
115-119								
120-124								
125-129								
130-134								
135-139								
140-144								
145-149								
150-154								
155-159								
160-164								
165-169								
170-174								
175-179								
180-184								
185-189								
190-194								
195-200								

Table 1.6 (Continued)

	K34-7	K34-8	K34-9	K34-10	K35-2	K35-3	K35-4	K35-5
5-9								
10-14								
15-19								
20-24								
25-29								
30-34								
35-39								
40-44								
45-49								
50-54								
55-59								
60-64								
65-69								
70-74								
75-79								
80-84								
85-89								
90-94								
95-99								
100-104								
105-109								
110-114								
115-119								
120-124								
125-129								
130-134								
135-139								
140-144								
145-149								
150-154								
155-159								
160-164								
165-169								
170-174								
175-179								
180-184								
185-189								
190-194								
195-200								

Table 1.6 (Continued)

	K35-6	K35-7	K35-8	K35-9	K35-10	K37-1	K37-2	K37-3
5-9								
10-14								
15-19	—	—	—			—	—	—
20-24				—		—		
25-29	—	—	—	—		—	—	—
30-34	—			—		—		
35-39						—	—	
40-44			—			—		
45-49	—	—		—	—	—	—	—
50-54		—		—		—		
55-59				—				
60-64	—	—	—	—	—			
65-69	—			—				—
70-74		—				—	—	—
75-79								—
80-84			—		—			—
85-89				—		—	—	—
90-94	—	—	—		—	—		
95-99			—	—			—	—
100-104								
105-109	—					—		
110-114								
115-119		—	—		—		—	
120-124			—	—			—	—
125-129				—		—	—	—
130-134			—					
135-139	—		—			—	—	—
140-144	—	—	—	—	—	—	—	—
145-149	—			—	—			
150-154		—	—		—	—	—	—
155-159			—		—			
160-164				—	—		—	—
165-169			—		—		—	—
170-174			—			—		
175-179	—	—	—			—		
180-184						—		—
185-189		—		—		—	—	—
190-194	—		—		—	—	—	—
195-200								

Table 1.6 (Continued)

	K37-4	K37-5	K37-6	K37-7	K37-8	K37-9	K37-10	Karee
5-9								
10-14								
15-19								
20-24								
25-29								
30-34								
35-39								
40-44								
45-49								
50-54								
55-59								
60-64								
65-69								
70-74								
75-79								
80-84								
85-89								
90-94								
95-99								
100-104								
105-109								
110-114								
115-119								
120-124								
125-129								
130-134								
135-139								
140-144								
145-149								
150-154								
155-159								
160-164								
165-169								
170-174								
175-179								
180-184								
185-189								
190-194								
195-200								

Table 1.6 (Continued)

	Kariega	Katyi	Kavkaz	Limpopo	Limpopo DN	M29519	M29568
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 1.6 (Continued)

	Marico	Molen	Molopo	Nantes	Norstar	Oom Charl	Oranje
5-9	—					—	
10-14				—			—
15-19							
20-24	—				—	—	—
25-29						—	
30-34						—	—
35-39						—	
40-44	—				—	—	—
45-49			—	—	—	—	—
50-54		—					—
55-59		—					—
60-64		—		—	—	—	—
65-69	—	—				—	—
70-74		—	—			—	—
75-79				—	—		
80-84	—		—	—		—	—
85-89				—		—	—
90-94		—			—		
95-99			—				
100-104	—	—		—		—	—
105-109		—			—		
110-114	—	—	—	—			
115-119		—				—	
120-124		—	—	—			—
125-129		—	—	—		—	—
130-134		—			—	—	
135-139	—	—	—	—		—	—
140-144	—	—	—	—			—
145-149	—	—				—	
150-154	—	—	—		—		
155-159	—	—	—		—		
160-164	—	—	—		—		
165-169							—
170-174	—	—	—	—		—	
175-179				—	—	—	
180-184	—			—			—
185-189					—	—	
190-194	—			—	—	—	—
195-200	—						

Table 1.6 (Continued)

	Oubaard	Owens	Palala	Palmiet	Palmiet DN	Palmiet short	PAN3211
5-9							
10-14	—		—				
15-19		—					
20-24	—	—	—				
25-29	—	—	—				
30-34							
35-39					—	—	—
40-44							
45-49	—		—	—			
50-54					—		—
55-59		—	—	—	—	—	—
60-64	—		—	—	—		—
65-69		—				—	—
70-74	—				—		—
75-79							
80-84			—				
85-89		—	—		—	—	
90-94	—		—	—	—		—
95-99			—				
100-104				—	—	—	—
105-109	—	—		—			—
110-114		—	—	—			
115-119						—	
120-124	—	—	—		—		—
125-129			—		—		—
130-134	—	—					
135-139		—		—	—	—	—
140-144					—		—
145-149			—			—	
150-154	—	—			—	—	—
155-159		—		—		—	—
160-164				—		—	
165-169	—		—		—		
170-174		—					—
175-179	—		—			—	
180-184			—				
185-189	—	—	—				
190-194	—		—				
195-200							

Table 1.6 (Continued)

	PAN3232	PAN3235	PAN3349	PAN3364	PAN3377	PAN9303	PAN9316
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 1.6 (Continued)

	PAN9409	PAN9413	PAN9414	PAN9416	PAN9417	PAN9418	PAN9419
5-9	—	—	—	—	—	—	—
10-14	—	—	—	—	—	—	—
15-19	—	—	—	—	—	—	—
20-24	—	—	—	—	—	—	—
25-29	—	—	—	—	—	—	—
30-34	—	—	—	—	—	—	—
35-39	—	—	—	—	—	—	—
40-44	—	—	—	—	—	—	—
45-49	—	—	—	—	—	—	—
50-54	—	—	—	—	—	—	—
55-59	—	—	—	—	—	—	—
60-64	—	—	—	—	—	—	—
65-69	—	—	—	—	—	—	—
70-74	—	—	—	—	—	—	—
75-79	—	—	—	—	—	—	—
80-84	—	—	—	—	—	—	—
85-89	—	—	—	—	—	—	—
90-94	—	—	—	—	—	—	—
95-99	—	—	—	—	—	—	—
100-104	—	—	—	—	—	—	—
105-109	—	—	—	—	—	—	—
110-114	—	—	—	—	—	—	—
115-119	—	—	—	—	—	—	—
120-124	—	—	—	—	—	—	—
125-129	—	—	—	—	—	—	—
130-134	—	—	—	—	—	—	—
135-139	—	—	—	—	—	—	—
140-144	—	—	—	—	—	—	—
145-149	—	—	—	—	—	—	—
150-154	—	—	—	—	—	—	—
155-159	—	—	—	—	—	—	—
160-164	—	—	—	—	—	—	—
165-169	—	—	—	—	—	—	—
170-174	—	—	—	—	—	—	—
175-179	—	—	—	—	—	—	—
180-184	—	—	—	—	—	—	—
185-189	—	—	—	—	—	—	—
190-194	—	—	—	—	—	—	—
195-200	—	—	—	—	—	—	—

Table 1.6 (Continued)

	PAN9711	PAN9712	PAN9713	PAN LE 4	PAN LE 7	PAN LE 9	PAN LE 10
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 1.6 (Continued)

	PAN LE 12	Red Victory	Riemland	SA 1684	SA 463	Sch 69	Snack
5-9	—	—	—				
10-14	—	—	—				—
15-19	—	—	—				
20-24	—	—	—				
25-29		—				—	—
30-34	—		—				
35-39			—			—	
40-44	—	—			—		—
45-49				—			—
50-54			—				—
55-59	—	—	—			—	—
60-64		—	—				—
65-69				—	—	—	
70-74					—	—	
75-79	—	—	—	—			—
80-84	—						—
85-89							—
90-94		—	—	—	—	—	—
95-99		—	—			—	—
100-104	—	—		—			—
105-109	—	—			—	—	—
110-114		—	—	—	—	—	—
115-119		—	—		—	—	—
120-124		—			—	—	
125-129						—	
130-134	—		—				—
135-139		—	—	—			—
140-144			—	—		—	—
145-149	—			—	—	—	—
150-154			—			—	
155-159		—	—				
160-164	—	—	—	—			—
165-169				—	—	—	—
170-174	—	—	—			—	—
175-179		—				—	
180-184		—	—				
185-189	—		—				—
190-194	—	—	—				
195-200		—					

Table 1.6 (Continued)

	Sonop	SST 3	SST 16	SST 44	SST 55	SST 66	SST101
5-9	—	—	—				
10-14	—	—	—		—	—	—
15-19	—	—	—	—			—
20-24		—	—	—	—	—	—
25-29		—	—	—			
30-34		—	—	—			—
35-39			—	—			
40-44	—	—	—	—			
45-49	—		—	—	—	—	—
50-54	—						
55-59		—	—		—	—	
60-64	—	—	—	—	—	—	
65-69	—	—	—	—			
70-74	—	—		—	—	—	
75-79	—	—	—	—		—	
80-84	—	—	—	—	—	—	—
85-89	—		—			—	—
90-94			—	—	—		—
95-99	—	—		—			
100-104	—	—	—	—			
105-109	—		—			—	
110-114	—				—		—
115-119	—	—		—		—	—
120-124	—	—	—			—	—
125-129		—	—	—	—		
130-134		—	—	—			
135-139				—			—
140-144	—	—		—	—		—
145-149	—	—	—	—	—		—
150-154	—		—	—	—		
155-159				—		—	
160-164	—	—	—	—			—
165-169	—	—		—			—
170-174				—			—
175-179	—	—	—	—	—	—	—
180-184	—	—	—	—	—	—	—
185-189	—	—	—	—		—	—
190-194	—		—	—	—		—
195-200		—					

Table 1.6 (Continued)

	SST102	SST107	SST124	SST333	SST363	SST367	SST325
5-9		==					
10-14		==					
15-19							==
20-24							
25-29		==					==
30-34			==		==		==
35-39	==						
40-44		==	==	==	==		
45-49	==						
50-54	==						
55-59							==
60-64				==			
65-69			==	==		==	
70-74	==				==		
75-79		==		==			==
80-84			==	==	==	==	
85-89							==
90-94	==	==	==	==	==	==	==
95-99					==		
100-104		==	==			==	==
105-109	==		==	==		==	
110-114				==		==	==
115-119	==	==			==		
120-124	==	==	==	==	==		
125-129		==		==		==	
130-134	==						==
135-139	==				==	==	
140-144		==	==	==			
145-149				==	==		
150-154		==	==			==	
155-159	==	==	==		==		==
160-164					==	==	
165-169	==		==	==			
170-174		==			==	==	
175-179			==				
180-184	==						==
185-189		==					
190-194		==					
195-200							

Table 1.6 (Continued)

	SST822	SST936	SST966	SST972	Stirling	T4	Tugela
5-9							
10-14	—			—			
15-19	—			—		—	
20-24	—			—			
25-29			—	—	—		—
30-34	—	—	—	—		—	
35-39	—	—		—	—		
40-44	—			—		—	—
45-49		—					
50-54			—	—	—	—	—
55-59	—			—			—
60-64		—					—
65-69		—	—		—	—	
70-74		—	—		—		
75-79				—			—
80-84				—	—	—	
85-89	—						
90-94		—	—				—
95-99	—				—	—	—
100-104				—	—		—
105-109	—	—	—			—	—
110-114						—	—
115-119			—	—	—		—
120-124	—		—		—	—	—
125-129			—		—		—
130-134	—	—			—	—	—
135-139					—		
140-144		—		—		—	—
145-149	—	—	—				—
150-154			—	—			
155-159		—		—	—	—	
160-164		—		—	—		
165-169		—	—			—	
170-174				—	—	—	—
175-179	—			—			
180-184				—	—		
185-189	—			—		—	
190-194				—	—		
195-200					—	—	

Table 1.6 (Continued)

	Tugela DN	Tugela f-g	Tugela new	Turpin7	Turtsikum	Verbeterde Kenia
5-9						
10-14						
15-19						
20-24						
25-29						
30-34						
35-39						
40-44						
45-49						
50-54						
55-59						
60-64						
65-69						
70-74						
75-79						
80-84						
85-89						
90-94						
95-99						
100-104						
105-109						
110-114						
115-119						
120-124						
125-129						
130-134						
135-139						
140-144						
145-149						
150-154						
155-159						
160-164						
165-169						
170-174						
175-179						
180-184						
185-189						
190-194						
195-200						

Variation between cultivars

There were clear differences between the cultivars. None of the cultivars were identical. It was also possible to distinguish between the near isogenic lines of K29, K34, K35 and K37. Cultivars with a close genetic background could also be distinguished. Examples of these cultivars are Tugela, Tugela DN, Tugela fast-growing and Tugela new and also Gariep and Gariep DN, Gamtoos and Gamtoos DN and Limpopo and Limpopo DN. This makes LMW glutenins very suitable for cultivar identification. It was not possible to distinguish between these cultivars using the HMW glutenin subunits. Lasztity (1986) found that the gliadins are more often used for variety identification, as they are more effective than using the glutenins. This study shows that the LMW glutenins are quite effective for variety identification, but it is however, a complex technique.

The occurrence of bands in the different groups

Table 1.7 gives a summary of the different class intervals (hereafter called groups), the migration distance of the group, the occurrence of bands in the groups and the percentage of occurrence.

Table 1.7 The occurrence of bands in the different groups of LMW glutenins in the South African bread wheat cultivars studied.

Group	Migration distance	Occurrence	Percentage (%)
1	5-9	33	23
2	10-14	46	31
3	15-19	50	34
4	20-24	42	29
5	25-29	58	40
6	30-34	42	29
7	35-39	47	32
8	40-44	41	28
9	45-49	71	48
10	50-54	42	29
11	55-59	35	24
12	60-64	60	41
13	65-69	48	33

Table 1.7 (Continued)

Group	Migration distance	Occurrence	Percentage (%)
14	70-74	54	37
15	75-79	56	38
16	80-84	49	33
17	85-89	47	32
18	90-94	76	52
19	95-99	50	34
20	100-104	72	49
21	105-109	63	43
22	110-114	49	33
23	115-119	61	42
24	120-124	56	38
25	125-129	52	35
26	130-134	46	31
27	135-139	50	34
28	140-144	50	34
29	145-149	62	42
30	150-154	51	35
31	155-159	47	32
32	160-164	58	40
33	165-169	69	47
34	170-174	59	40
35	175-179	47	32
36	180-184	55	37
37	185-189	65	44
38	190-194	71	48
39	195-200	9	6

The most frequent were groups 18, molecular distance 90-94 (in 52 percent of the cultivars tested), and group 20, molecular distance 100-104 (49 percent of the cultivars tested). Group 1 was only present in 23 percent of the cultivars tested and group 39 was only present in six percent of the cultivars tested. None of the groups occurred in more

than 60 percent of the cultivars, which also shows the variation of LMW glutenins between cultivars.

The intensities of the bands in the different groups

The different groups had specific intensities. Table 1.8 gives a summary of the different groups and the intensities of the bands in classes from one (very light) to five (very dark). Class six has no specific intensity, that means in some of the replications it appeared as a very dark band, while in other replications it had a very light to medium intensity.

Table 1.8 The intensities of the bands in the different groups.

Group	Occur	Class1	Class2	Class3	Class4	Class5	Class6
1	33	33	0	0	0	0	0
2	46	42	4	0	0	0	0
3	50	45	2	3	0	0	0
4	42	28	5	2	3	2	2
5	58	37	10	1	2	4	4
6	42	30	4	4	1	2	1
7	47	25	11	3	2	4	2
8	41	16	7	8	0	5	5
9	71	17	14	12	11	13	4
10	42	10	3	6	7	12	4
11	35	11	5	7	6	5	1
12	60	9	5	12	10	16	8
13	48	2	3	3	8	27	5
14	54	10	5	5	10	23	1
15	56	12	9	9	9	14	3
16	49	20	8	2	5	11	3
17	47	10	6	5	10	10	6
18	76	18	14	23	5	8	8
19	50	18	8	11	5	5	3
20	72	27	10	6	11	10	8
21	63	18	9	10	11	13	2

Table 1.8 (Continued)

Group	Occur	Class1	Class2	Class3	Class4	Class5	Class6
22	49	14	15	6	2	5	7
23	61	19	10	13	9	8	2
24	56	23	6	5	10	7	5
25	52	20	7	10	6	3	6
26	46	15	5	4	5	10	7
27	50	18	13	4	4	7	3
28	50	12	17	1	4	13	4
29	62	29	9	4	6	12	2
30	51	31	5	2	2	8	3
31	47	24	10	7	1	1	4
32	58	33	12	4	3	2	4
33	69	41	22	1	2	2	1
34	59	42	14	2	1	0	0
35	47	40	6	1	0	0	0
36	55	49	4	1	0	0	1
37	62	58	2	1	0	0	1
38	71	68	2	0	0	0	1
39	9	9	0	0	0	0	0

Group 1

In all 33 cultivars that contained group 1, it was always expressed as a very light band (intensity class 1).

Group 2

All of the bands in this group was light to very light.

Group 3

Only three of the 50 bands in this group were of medium intensity (intensity class 3), the others were light to very light.

Group 4

Thirty-three of the bands in this group were expressed as light to very light bands. Two were of medium intensity, three were dark (intensity class 4), two were very dark (intensity class 5) and two could not be assigned to any specific intensity class (intensity class 6).

Group 5

Most of the bands in this group were light to very light. Six bands were dark to very dark, one was of medium intensity and four could not be assigned to any specific intensity class.

Group 6

Most of the bands in this group were light to very light. Four bands were of medium intensity, three were dark to very dark and only one could not be assigned to any specific intensity class.

Group 7

Most of the bands in this group were expressed as light to very light bands. Three were of medium intensity, six were dark to very dark and two could not be assigned to any specific intensity class.

Group 8

Twenty-three of the bands in this group were light to very light, eight were of medium intensity and five were very dark. Five could not be assigned to any specific intensity class.

Group 9

Thirty-one of the bands in this group were expressed as light to very light bands, 12 of the bands were of medium intensity, 24 were dark to very dark and four could not be assigned to any specific intensity class.

Group 10

Thirteen of the bands were expressed as light to very light bands, six were of medium intensity, 19 were dark to very dark and four could not be assigned to any specific intensity class.

Group 11

Sixteen of the bands were expressed as light to very light bands, seven was of medium intensity, 11 were dark to very dark and one could not be assigned to any specific intensity class.

Group 12

Fourteen of the bands were light to very light, 12 were of medium intensity, 26 were dark to very dark and eight could not be assigned to any specific intensity class.

Group 13

Five of the bands were light to very light, three were of medium intensity, 35 were dark to very dark and five could not be assigned to any specific intensity class.

Group 14

Fifteen of the bands were light to very light, five were of medium intensity, 33 were dark to very dark and one could not be assigned to any specific intensity class.

Group 15

Twenty-one of the bands were light to very light, nine were of medium intensity, 23 were dark to very dark and three could not be assigned to any specific intensity class.

Group 16

Twenty-eight of the bands were expressed as light to very light bands, two were of medium intensity, 16 were dark to very dark and three could not be assigned to any specific intensity class.

Group 17

Sixteen of the bands were light to very light, five were of medium intensity, 20 were dark to very dark and six could not be assigned to any specific intensity class.

Group 18

Thirty-two of the bands were expressed as light to very light, 23 were of medium intensity, 13 were dark to very dark and eight could not be assigned to any specific intensity class.

Group 19

Twenty-six of the bands were expressed as light to very light bands, 11 were of medium intensity, 10 were dark to very dark and three could not be assigned to any specific intensity class.

Group 20

Thirty-seven of the bands were light to very light, six were of medium intensity, 21 were dark to very dark and eight could not be assigned to any specific intensity class.

Group 21

Twenty-seven of the bands were light to very light, 10 were of medium intensity, 24 were dark to very dark and two could not be assigned to any specific intensity class.

Group 22

Twenty-nine of the bands were light to very light, six were of medium intensity, seven were dark to very dark and seven could not be assigned to any specific intensity class.

Group 23

Twenty-nine of the bands were light to very light, 13 were of medium intensity, 17 were dark to very dark and two could not be assigned to any specific intensity class.

Group 24

Twenty-seven of the bands were light to very light, five were of medium intensity, 17 were dark to very dark and five could not be assigned to any specific intensity class.

Group 25

Twenty-seven of the bands were light to very light, 10 were of medium intensity, nine were dark to very dark and six could not be assigned to any specific intensity class.

Group 26

Twenty of the bands were light to very light, four were of medium intensity, 15 were dark to very dark and seven could not be assigned to any specific intensity class.

Group 27

Thirty-one of the bands were light to very light, four were of medium intensity, 11 were dark to very dark and three could not be assigned to any specific intensity class.

Group 28

Twenty-nine of the bands were light to very light, one was of medium intensity, 17 were dark to very dark and four could not be assigned to any specific intensity class.

Group 29

Thirty-eight of the bands were light to very light, four were of medium intensity, 18 were dark to very dark and two could not be assigned to any specific intensity class.

Group 30

Thirty-six of the bands were light to very light, two were of medium intensity, 10 were dark to very dark and three could not be assigned to any specific intensity class.

Group 31

Thirty-four of the bands were light to very light, seven were of medium intensity, two were dark to very dark and four could not be assigned to any specific intensity class.

Group 32

Forty-five of the bands were light to very light, four were of medium intensity, five were dark to very dark and four could not be assigned to any specific intensity class.

Group 33

Sixty-three of the bands were light to very light, one was of medium intensity, four were dark to very dark and one could not be assigned to any specific intensity class.

Group 34

Fifty-six of the bands were light to very light, two were of medium intensity and one was dark.

Group 35

Forty-six of the bands were light to very light and one was of medium intensity.

Group 36

One of the bands was of medium intensity and one could not be assigned to any specific intensity class. All the other bands were light to very light.

Group 37

Most of the bands were light to very light. Only one was of medium intensity and one could not be assigned to any specific intensity class.

Group 38

Most of the bands were light to very light. Only one could not be assigned to any specific intensity class.

Group 39

All of the bands were expressed as very light bands.

The bands in some groups were expressed as light or medium or dark bands. The bands in the following groups were mostly expressed as light to very light bands: group one to seven, and groups 30 to 39. Group 18 was mostly expressed as very light to medium bands. Groups 12 to 14 were mostly dark to very dark bands. Gupta and Shepherd (1990b) also found differences in the intensities of the bands they tested. In Chapter 3, this will further be investigated to see if the different genomes have an influence on the intensity of the bands.

Correlations between the LMW groups of bands

The following significant correlations were observed between the LMW groups of bands ($p < 0.05$):

1. Group 1 was positively correlated with group 2 ($r=0.19$), group 3 ($r=0.18$), group 4 ($r=0.92$), group 6 ($r=0.27$), group 34 ($r=0.21$), group 36 ($r=0.36$), group 37 ($r=0.18$), group 38 ($r=0.26$) and with group 39 ($r=0.45$). It was, however, negatively correlated with group 21 ($r= -0.19$) and group 33 ($r= -0.16$).
2. Group 2 was positively correlated with group 4 ($r=0.22$), group 36 ($r=0.29$), group 37 ($r=0.18$), group 38 ($r=0.3$) and with group 39 ($r=0.17$). It was negatively correlated with group 13 ($r= -0.34$) and with group 27 ($r= -0.21$).
3. Group 3 was positively correlated with group 35 ($r=0.19$), group 36 ($r=0.19$), group 37 ($r=0.18$) and with group 38 ($r=0.25$). It was negatively correlated with group 33 ($r= -0.26$).
4. Group 4 was positively correlated with group 26 ($r=0.18$), group 32 ($r=0.18$), group 36 ($r=0.26$), group 37 ($r=0.17$) and with group 38 ($r=0.26$). It was negatively correlated with group 5 ($r= -0.39$).
5. Group 5 was positively correlated with group 35 ($r=0.24$) and negatively correlated with group 27 ($r= -0.19$) and with group 32 ($r= -0.2$).
6. Group 6 was positively correlated with group 19 ($r=0.18$) and negatively correlated with group 7 ($r= -0.29$) and with group 24 ($r= -0.24$).
7. Group 7 was negatively correlated with group 8 ($r= -0.27$) and with group 22 ($r= -0.2$).
8. Group 8 was positively correlated with group 19 ($r=0.16$) and group 38 ($r=0.17$) and negatively correlated with group 9 ($r= -0.48$).
9. Group 9 was negatively correlated with group 10 ($r= -0.41$).
10. Group 10 was positively correlated with group 28 ($r=0.17$). It was negatively correlated with group 11 ($r= -0.27$), group 35 ($r= -0.2$) and with group 37 ($r= -0.2$).
11. Group 11 was positively correlated with group 17 ($r=0.31$). It was negatively correlated with group 12 ($r= -0.38$), group 18 ($r= -0.21$), group 28 ($r= -0.17$) and with group 33 ($r= -0.19$).
12. Group 12 was positively correlated with group 18 ($r=0.19$) and group 26 ($r=0.2$) and negatively correlated with group 13 ($r= -0.42$).

13. Group 13 was negatively correlated with group 14 ($r = -0.3$), group 26 ($r = -0.21$) and with group 36 ($r = -0.19$).
14. Group 14 was negatively correlated with group 15 ($r = -0.52$) and with group 22 ($r = -0.24$).
15. Group 15 was positively correlated with group 28 ($r = 0.18$) and negatively correlated with group 16 ($r = -0.24$) and group 27 ($r = -0.16$).
16. Group 16 was positively correlated with group 32 ($r = 0.19$) and group 39 ($r = 0.22$) and negatively correlated with group 17 ($r = -0.33$).
17. Group 17 was negatively correlated with group 18 ($r = -0.48$) and with group 39 ($r = -0.17$).
18. Group 18 was positively correlated with group 29 ($r = 0.17$) and negatively correlated with group 19 ($r = -0.27$) and group 36 ($r = -0.17$).
19. Group 19 was negatively correlated with group 20 ($r = -0.17$).
20. Group 20 was negatively correlated with group 21 ($r = -0.35$) and group 37 ($r = -0.2$).
21. Group 21 was negatively correlated with group 22 ($r = -0.33$), group 36 ($r = -0.23$) and group 38 ($r = -0.26$).
22. Group 22 was positively correlated with group 32 ($r = 0.24$) and negatively correlated with group 23 ($r = -0.34$) and group 37 ($r = -0.17$).
23. Group 23 was positively correlated with group 27 ($r = 0.25$) and negatively correlated with group 24 ($r = -0.22$) and group 26 ($r = -0.2$).
24. Group 24 was positively correlated with group 26 ($r = 0.18$) and group 31 ($r = 0.17$) and negatively correlated with group 25 ($r = -0.42$).
25. Group 25 was positively correlated with group 28 ($r = 0.18$) and negatively correlated with group 26 ($r = -0.44$).
26. Group 26 was positively correlated with group 32 ($r = 0.17$) and negatively correlated with group 27 ($r = -0.37$) and group 28 ($r = -0.2$).
27. Group 27 was negatively correlated with group 37 ($r = -0.18$).
28. Group 28 was negatively correlated with group 29 ($r = -0.43$).
29. Group 29 was negatively correlated with group 30 ($r = -0.32$).
30. Group 30 was negatively correlated with group 31 ($r = -0.35$).
31. Group 31 was negatively correlated with group 32 ($r = -0.21$).
32. Group 32 was positively correlated with group 39 ($r = 0.18$) and negatively correlated with group 33 ($r = -0.39$).

33. Group 33 was negatively correlated with group 34 ($r = -0.33$), group 36 ($r = -0.18$) and group 38 ($r = -0.2$).
34. Group 34 was positively correlated with group 39 ($r = 0.18$) and negatively correlated with group 35 ($r = -0.32$).
35. Group 35 was positively correlated with group 37 ($r = 0.32$).
36. Group 36 was positively correlated with group 38 ($r = 0.35$) and group 39 ($r = 0.2$).

The correlations reveal that some groups do not occur together in the same line. This is in accordance with Gupta and Shepherd (1988) who found that some combinations occur as alternatives to each other. This will be investigated further in Chapter 3.

The apparent molecular weight of the different groups

Gupta *et al* (1995) found that the molecular weight of the LMW glutenins varied from 30 to 51 kDa. In this study the molecular weight of the different LMW groups varied from 29 to 51 kDa. Table 1.9 gives the different LMW groups with the apparent molecular weight of the specific group.

Table 1.9 The apparent molecular weight in kDa of the different LMW groups.

Group	Molecular weight	Group	Molecular weight
1	51	2	50.5
3	50	4	49.5
5	49	6	48
7	47.5	8	47
9	46.5	10	46
11	45	12	44.5
13	44	14	43.5
15	43	16	42.5
17	41.5	18	41
19	40.5	20	40
21	39	22	38.5
23	38	24	38
25	37	26	36
27	35.5	28	35

Table 1.9 (Continued)

Group	Molecular weight	Group	Molecular weight
29	34.5	30	34
31	33.5	32	33
33	32	34	31.5
35	31	36	30.5
37	30	38	29.5
39	29		

Genetic distances

Cultivars

Figure 1.6 shows a dendrogram that was drawn from the data of 45 of the cultivars. Only some of the most important cultivars of the three seed companies in South Africa were chosen. The dendrogram also has a space restriction.

The following cultivars are closely related ($D < 0.10$, that is 10 percent). In brackets are the actual differences between them.

1. Adam Tas and PAN 3235 (0.07)
2. Betta DN and Sch 69 (0.1)
3. Betta DN and Tugela fast-growing (0.09)
4. Caledon and Molopo (0.09)
5. Caledon and Palmiet short (0.09)
6. Flamink and Inia (0.09)
7. Flamink and Kariëga (0.09)
8. Gamka and Nantes (0.09)
9. Gariep and SST 367 (0.09)
10. Gariep DN and Molen (0.08)
11. Inia and Kariëga (0.09)
12. Limpopo and Tugela new (0.09)
13. Limpopo DN and SST 367 (0.09)
14. Oom Charl and PAN 3235 (0.1)
15. Palmiet and PAN 3211 (0.1)

16. Palmiet short and PAN 3211 (0.1)
17. Pan 3235 and SST 822 (0.09)
18. Sch 69 and Tugela (0.07)
19. Sch 69 and Tugela fast growing (0.07)
20. Sch 69 and Tugea new (0.07)
21. Tugela and Tugela new (0.04)

The highest amount of dissimilarity ($D > 0.70$, that is 70 percent) were between the following cultivars:

1. Adam Tas and Gariep (0.72)
2. Belinda and PAN 3364 (0.77)
3. Caledon and PAN 3364 (0.73)
4. Gariep and PAN 3364 (0.88)
5. Gariep and SST 825 (0.79)
6. Gariep and T4 (0.79)
7. Limpopo DN and PAN 3364 (0.77)
8. Molopo and PAN 3364 (0.73)
9. Oom Charl and PAN 3235 (0.72)
10. Palmiet short and PAN 3364 (0.71)
11. PAN 3364 and SST 367 (0.83)
12. SST 367 and SST 825 (0.75)
13. SST 367 and T4 (0.75)

Although there was some genetic diversity in South African wheat, it is alarming how closely related some cultivars are. De Swardt (1998) who tested the gliadins in South African wheat cultivars, also found that the level of genetic variation between cultivars was very low. In Table 1.10 is a summary of the genetic distances between the different cultivars tested.

Near isogenic lines

Figure 1.7 shows the dendrogram that was drawn from the near isogenic lines of Karee. The following near isogenic lines were very similar ($D < 0.10$). In brackets are the actual differences between them.

1. K29-1 and K37-2 (0.08)
2. K29-2 and K37-2 (0.09)
3. K29-2 and K37-6 (0.09)
4. K29-2 and K37-7 (0.09)
5. K29-2 and K37-8 (0.09)
6. K29-2 and K37-9 (0.04)
7. K29-3 and K34-9 (0.05)
8. K29-3 and K35-3 (0.09)
9. K29-6 and K29-7 (0.09)
10. K29-6 and K34-2 (0.08)
11. K29-7 and K34-2 (0.09)
12. K29-10 and K35-9 (0.09)
14. K29-10 and K37-4 (0.09)
15. K34-2 and K37-4 (0.1)
16. K34-10 and K35-10 (0.07)
17. K35-7 and K35-9 (0.07)
18. K37-2 and K37-9 (0.09)
19. K37-6 and K37-8 (0.1)
20. K37-7 and K37-9 (0.09)

The highest amount of dissimilarity ($D > 0.80$) were between the following near isogenic lines:

1. K34-1 and K37-1 (0.92)
2. K34-8 and K37-1 (0.85)
3. K34-10 and K37-1 (0.88)
4. K35-10 and K37-1 (0.9)

The genetic distances confirm the high degree of genetic similarity between the near isogenic lines. The only exception was K37-1 that differed highly from some of the other lines. In Table 1.11 is a summary of the genetic distances between the different near isogenic lines tested.

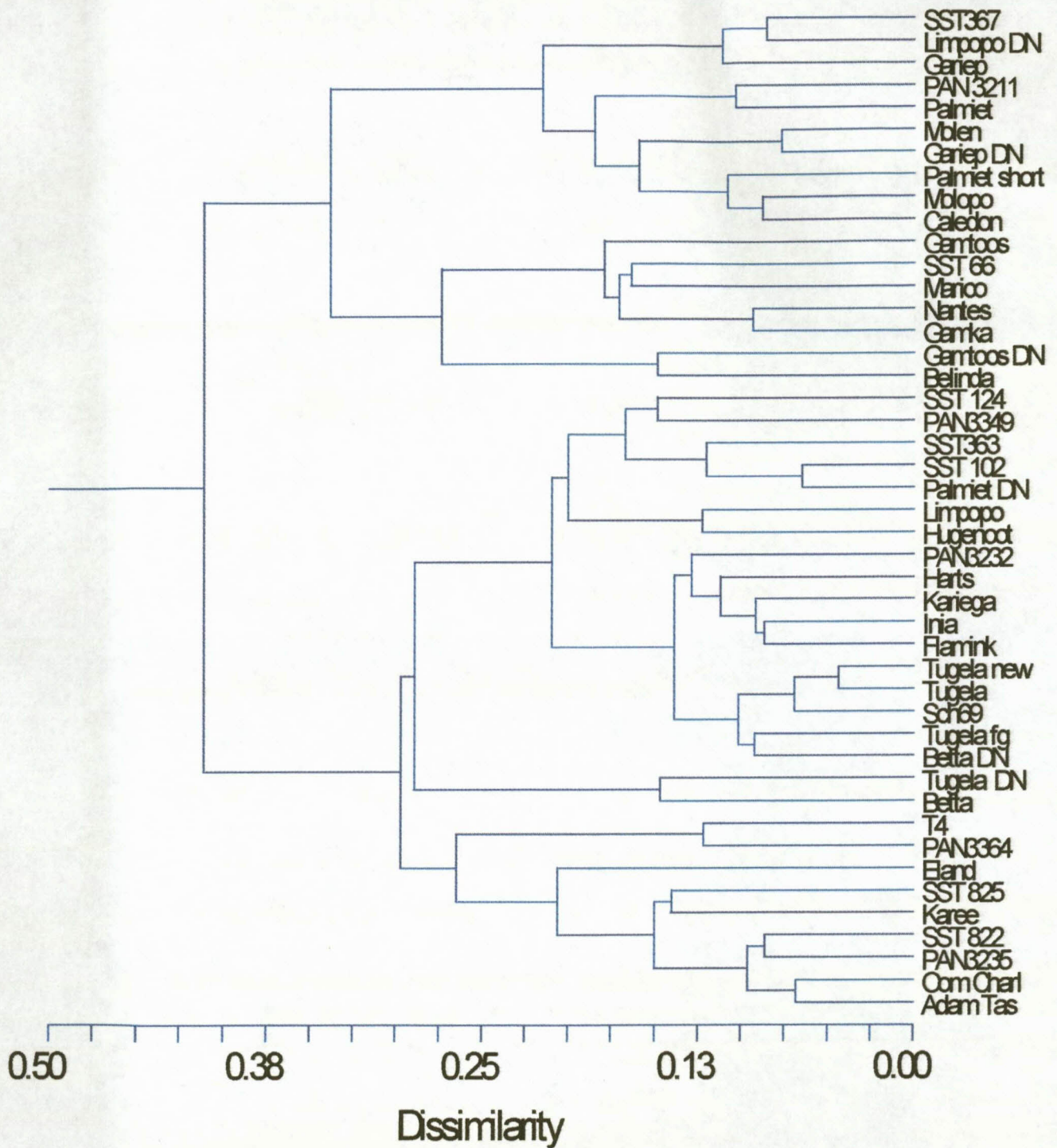


Figure 1.6 A dedrogram of some of the South African bread wheat cultivars.

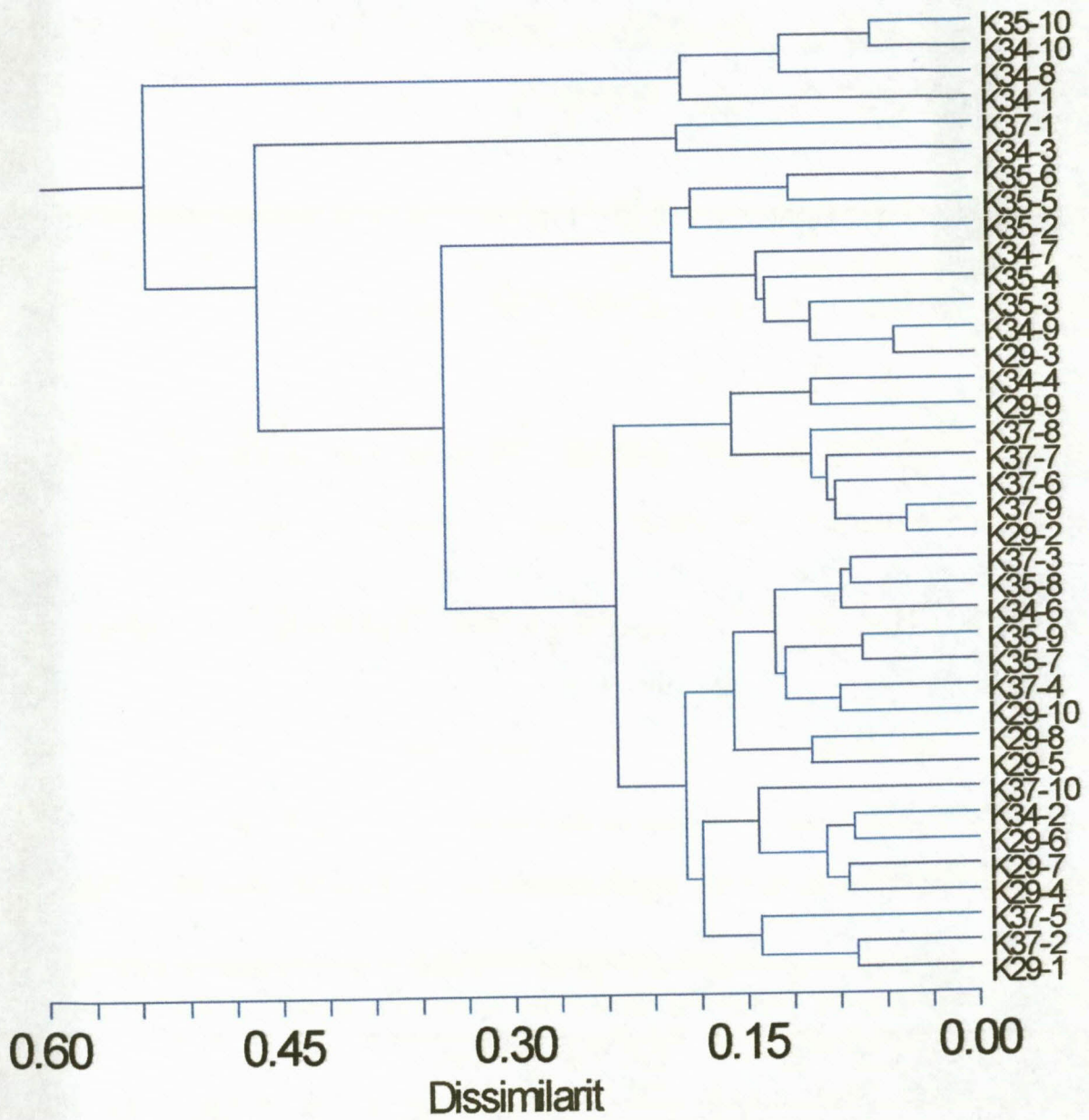


Figure 1.7. A dendrogram of the near isogenic lines of Karee.

Table 1.10 The genetic distances between the cultivars tested.

	A. Tas	Belinda	Betta	Betta DN	Caledon	Eland	Flamink	Gamka	Gamtoos	Gamtoos DN
A. Tas	0	0.59	0.39	0.24	0.58	0.17	0.17	0.33	0.3	0.47
Belinda	0.59	0	0.55	0.51	0.27	0.48	0.53	0.28	0.36	0.15
Betta	0.39	0.55	0	0.19	0.46	0.43	0.26	0.46	0.39	0.52
Betta DN	0.24	0.51	0.19	0	0.39	0.32	0.14	0.26	0.31	0.4
Caledon	0.58	0.27	0.46	0.39	0	0.55	0.47	0.25	0.4	0.2
Eland	0.17	0.48	0.43	0.32	0.55	0	0.27	0.28	0.25	0.38
Flamink	0.17	0.53	0.26	0.14	0.47	0.27	0	0.31	0.29	0.43
Gamka	0.33	0.28	0.46	0.26	0.25	0.28	0.31	0	0.16	0.17
Gamtoos	0.3	0.36	0.39	0.31	0.4	0.25	0.29	0.16	0	0.27
Gamtoos DN	0.47	0.15	0.52	0.4	0.2	0.38	0.43	0.17	0.27	0
Gariep	0.72	0.39	0.62	0.53	0.19	0.68	0.61	0.41	0.55	0.34
Gariep DN	0.5	0.37	0.4	0.3	0.13	0.5	0.39	0.27	0.42	0.31
Harts	0.16	0.52	0.32	0.13	0.46	0.28	0.1	0.31	0.32	0.44
Hugenoot	0.44	0.51	0.2	0.18	0.32	0.5	0.3	0.41	0.42	0.46
Inia	0.17	0.53	0.25	0.17	0.49	0.27	0.09	0.35	0.32	0.45
Karee	0.13	0.61	0.29	0.21	0.57	0.26	0.12	0.36	0.35	0.5
Kariega	0.21	0.57	0.23	0.13	0.5	0.32	0.09	0.36	0.34	0.47
Limpopo	0.37	0.44	0.17	0.14	0.31	0.41	0.21	0.35	0.35	0.4
Limpopo DN	0.63	0.41	0.52	0.42	0.16	0.61	0.51	0.35	0.48	0.32
Manco	0.27	0.3	0.45	0.27	0.34	0.23	0.25	0.16	0.19	0.23
Molen	0.48	0.4	0.36	0.28	0.16	0.5	0.35	0.33	0.42	0.34
Molopo	0.57	0.34	0.5	0.39	0.09	0.55	0.48	0.31	0.46	0.28
Nantes	0.38	0.27	0.45	0.31	0.24	0.33	0.34	0.09	0.19	0.16
Oom Charl	0.07	0.62	0.41	0.28	0.62	0.18	0.22	0.37	0.33	0.51
Palmiet	0.5	0.27	0.37	0.33	0.19	0.46	0.4	0.2	0.31	0.18
Palmiet DN	0.38	0.37	0.27	0.2	0.22	0.41	0.26	0.3	0.36	0.34
Palmiet short	0.52	0.22	0.49	0.38	0.09	0.47	0.44	0.24	0.38	0.18
PAN 3211	0.47	0.22	0.43	0.34	0.14	0.41	0.4	0.18	0.31	0.13
PAN 3232	0.18	0.44	0.3	0.17	0.41	0.23	0.12	0.27	0.27	0.37
PAN 3235	0.07	0.56	0.32	0.19	0.53	0.18	0.14	0.29	0.27	0.44
PAN 3349	0.26	0.37	0.32	0.17	0.31	0.26	0.21	0.17	0.23	0.27
PAN 3364	0.28	0.77	0.32	0.36	0.73	0.43	0.27	0.57	0.53	0.7
Sch 69	0.25	0.49	0.21	0.1	0.4	0.34	0.11	0.32	0.32	0.42
SST 66	0.22	0.41	0.35	0.22	0.39	0.21	0.21	0.16	0.17	0.28
SST 102	0.34	0.35	0.31	0.2	0.24	0.37	0.23	0.27	0.33	0.32
SST 124	0.37	0.34	0.35	0.2	0.21	0.36	0.28	0.15	0.26	0.23
SST 363	0.34	0.41	0.28	0.16	0.26	0.39	0.21	0.25	0.33	0.34
SST 367	0.68	0.41	0.58	0.49	0.19	0.65	0.58	0.39	0.52	0.34
SST 822	0.08	0.53	0.31	0.2	0.52	0.16	0.15	0.29	0.29	0.43
SST 825	0.14	0.68	0.29	0.27	0.65	0.28	0.19	0.44	0.42	0.58
T4	0.24	0.67	0.24	0.29	0.64	0.36	0.18	0.48	0.43	0.61
Tugela	0.27	0.46	0.19	0.11	0.35	0.36	0.15	0.3	0.32	0.4
Tugela DN	0.43	0.61	0.15	0.24	0.52	0.48	0.43	0.52	0.43	0.59
Tugela fg	0.23	0.5	0.18	0.09	0.41	0.32	0.11	0.3	0.29	0.4
Tugela new	0.27	0.47	0.18	0.09	0.36	0.35	0.15	0.3	0.33	0.4

Table 1.10 (Continued)

Cultivar	Gariep	Gariep DN	Harts	Hugenoot	Inia	Karee	Kariega	Limpopo	Limpopo DN	Marico
Altas	0.72	0.5	0.16	0.44	0.17	0.13	0.21	0.37	0.63	0.27
Belinda	0.39	0.37	0.52	0.51	0.53	0.61	0.57	0.44	0.41	0.3
Betta	0.62	0.4	0.32	0.2	0.25	0.29	0.23	0.17	0.52	0.45
Betta DN	0.53	0.3	0.13	0.18	0.17	0.21	0.13	0.14	0.42	0.27
Caledon	0.19	0.13	0.46	0.32	0.49	0.57	0.5	0.31	0.16	0.34
Eland	0.68	0.5	0.28	0.5	0.27	0.26	0.32	0.41	0.61	0.23
Flamink	0.61	0.39	0.1	0.3	0.09	0.12	0.09	0.21	0.51	0.25
Gamka	0.41	0.27	0.31	0.41	0.35	0.36	0.36	0.35	0.35	0.16
Gamtoos	0.55	0.42	0.32	0.42	0.32	0.35	0.34	0.35	0.48	0.19
Gamtoos DN	0.34	0.31	0.44	0.46	0.45	0.5	0.47	0.4	0.32	0.23
Gariep	0	0.24	0.61	0.45	0.64	0.7	0.64	0.46	0.13	0.49
Gariep DN	0.24	0	0.38	0.23	0.41	0.47	0.4	0.25	0.16	0.34
Harts	0.61	0.38	0	0.34	0.11	0.12	0.13	0.24	0.52	0.24
Hugenoot	0.45	0.23	0.34	0	0.31	0.39	0.28	0.12	0.33	0.43
Inia	0.64	0.41	0.11	0.31	0	0.16	0.09	0.22	0.55	0.27
Karee	0.7	0.47	0.12	0.39	0.16	0	0.15	0.31	0.61	0.29
Kariega	0.64	0.4	0.13	0.28	0.09	0.15	0	0.18	0.54	0.31
Limpopo	0.46	0.25	0.24	0.12	0.22	0.31	0.19	0	0.37	0.34
Limpopo DN	0.13	0.16	0.52	0.33	0.55	0.61	0.64	0.37	0	0.44
Marico	0.49	0.34	0.24	0.43	0.27	0.29	0.31	0.34	0.44	0
Molen	0.26	0.08	0.36	0.19	0.36	0.45	0.35	0.2	0.17	0.36
Molopo	0.15	0.16	0.47	0.34	0.5	0.55	0.49	0.34	0.13	0.37
Nantes	0.4	0.3	0.35	0.4	0.37	0.4	0.38	0.34	0.34	0.19
Oom Charl	0.76	0.54	0.2	0.48	0.21	0.18	0.25	0.41	0.67	0.31
Palmiet	0.33	0.2	0.39	0.27	0.4	0.49	0.42	0.25	0.26	0.3
Palmiet DN	0.37	0.17	0.26	0.18	0.27	0.35	0.27	0.11	0.29	0.27
Palmiet short	0.21	0.18	0.44	0.37	0.46	0.52	0.47	0.34	0.21	0.29
PAN 3211	0.28	0.2	0.41	0.34	0.41	0.48	0.43	0.29	0.24	0.24
PAN 3232	0.56	0.36	0.12	0.32	0.11	0.18	0.17	0.22	0.48	0.18
PAN 3235	0.67	0.45	0.15	0.39	0.17	0.14	0.18	0.32	0.57	0.26
PAN 3349	0.44	0.26	0.21	0.29	0.23	0.28	0.25	0.23	0.36	0.18
PAN 3364	0.88	0.63	0.27	0.44	0.23	0.26	0.24	0.39	0.77	0.48
Sch 69	0.54	0.31	0.13	0.21	0.12	0.21	0.11	0.14	0.44	0.28
SST 66	0.53	0.36	0.22	0.37	0.24	0.25	0.25	0.29	0.45	0.16
SST 102	0.39	0.19	0.23	0.23	0.23	0.33	0.25	0.16	0.32	0.23
SST 124	0.35	0.17	0.28	0.25	0.31	0.35	0.31	0.21	0.26	0.2
SST 363	0.41	0.18	0.21	0.2	0.25	0.3	0.23	0.14	0.31	0.24
SST 367	0.09	0.2	0.58	0.39	0.6	0.67	0.6	0.43	0.09	0.49
SST 822	0.66	0.44	0.14	0.39	0.15	0.14	0.18	0.31	0.57	0.24
SST 825	0.79	0.55	0.19	0.42	0.18	0.14	0.19	0.35	0.69	0.38
T4	0.79	0.55	0.22	0.37	0.16	0.21	0.16	0.31	0.69	0.41
Tugela	0.5	0.29	0.15	0.19	0.15	0.23	0.14	0.11	0.41	0.25
Tugela DN	0.67	0.46	0.43	0.28	0.37	0.34	0.35	0.25	0.57	0.52
Tugela fg	0.55	0.32	0.13	0.21	0.14	0.22	0.12	0.15	0.44	0.27
Tugela new	0.5	0.27	0.16	0.18	0.15	0.24	0.14	0.09	0.4	0.26

Table 1.10 (Continued)

Cultivar	Molen	Molopo	Nantes	O. Chari	Palmiet	Palmiet DN	Palmiet Short	PAN 3211	PAN 3232	PAN 3235
A-Tas	0.48	0.57	0.38	0.07	0.5	0.38	0.52	0.47	0.18	0.07
Belinda	0.4	0.34	0.27	0.62	0.27	0.37	0.22	0.22	0.44	0.56
Betta	0.36	0.5	0.45	0.41	0.37	0.27	0.49	0.43	0.3	0.32
Betta DN	0.28	0.39	0.31	0.28	0.33	0.2	0.38	0.34	0.17	0.19
Caledon	0.18	0.09	0.24	0.62	0.19	0.22	0.09	0.14	0.41	0.53
Eland	0.5	0.55	0.33	0.18	0.46	0.41	0.47	0.41	0.23	0.18
Flamink	0.35	0.48	0.34	0.22	0.4	0.26	0.44	0.4	0.12	0.14
Gamka	0.33	0.31	0.09	0.37	0.2	0.3	0.24	0.18	0.27	0.29
Gamtoos	0.42	0.46	0.19	0.33	0.31	0.36	0.38	0.31	0.27	0.27
Gamtoos DN	0.34	0.28	0.16	0.51	0.18	0.34	0.18	0.13	0.37	0.44
Gariep	0.26	0.15	0.4	0.76	0.33	0.37	0.21	0.28	0.56	0.67
Gariep DN	0.08	0.16	0.3	0.54	0.2	0.17	0.18	0.2	0.36	0.45
Harts	0.36	0.47	0.35	0.2	0.39	0.26	0.44	0.41	0.12	0.15
Hugenoot	0.19	0.34	0.4	0.48	0.27	0.18	0.37	0.34	0.32	0.39
Inia	0.36	0.5	0.37	0.21	0.4	0.27	0.46	0.41	0.11	0.17
Karoo	0.45	0.55	0.4	0.18	0.49	0.35	0.52	0.48	0.18	0.14
Kariega	0.35	0.49	0.38	0.25	0.42	0.27	0.47	0.43	0.17	0.18
Limpopo	0.2	0.34	0.34	0.41	0.25	0.11	0.34	0.29	0.22	0.32
Limpopo DN	0.17	0.13	0.34	0.67	0.26	0.29	0.21	0.24	0.48	0.57
Manico	0.36	0.37	0.19	0.31	0.3	0.27	0.29	0.24	0.18	0.26
Molen	0	0.16	0.33	0.52	0.18	0.13	0.21	0.21	0.33	0.44
Molopo	0.16	0	0.31	0.62	0.24	0.25	0.12	0.19	0.43	0.53
Nantes	0.33	0.31	0	0.43	0.23	0.31	0.24	0.18	0.31	0.35
Oom Chari	0.52	0.62	0.43	0	0.54	0.43	0.57	0.52	0.23	0.1
Palmiet	0.18	0.24	0.23	0.64	0	0.18	0.19	0.1	0.33	0.44
Palmiet DN	0.13	0.25	0.31	0.43	0.18	0	0.25	0.21	0.22	0.35
Palmiet short	0.21	0.12	0.24	0.57	0.19	0.25	0	0.1	0.38	0.49
PAN 3211	0.21	0.19	0.18	0.52	0.1	0.21	0.1	0	0.33	0.43
PAN 3232	0.33	0.43	0.31	0.23	0.33	0.22	0.38	0.33	0	0.18
PAN 3235	0.44	0.53	0.35	0.1	0.44	0.35	0.49	0.43	0.18	0
PAN 3349	0.26	0.32	0.23	0.3	0.2	0.19	0.28	0.21	0.16	0.22
PAN 3364	0.56	0.73	0.62	0.28	0.63	0.48	0.71	0.66	0.33	0.31
Sch 69	0.27	0.41	0.35	0.29	0.31	0.18	0.4	0.35	0.14	0.22
SST 66	0.37	0.41	0.18	0.27	0.34	0.3	0.35	0.29	0.21	0.19
SST 102	0.16	0.26	0.29	0.39	0.18	0.06	0.24	0.21	0.18	0.32
SST 124	0.19	0.23	0.17	0.41	0.19	0.17	0.2	0.17	0.25	0.32
SST 363	0.18	0.27	0.27	0.38	0.25	0.11	0.28	0.26	0.21	0.3
SST 367	0.22	0.15	0.39	0.72	0.29	0.34	0.22	0.27	0.54	0.83
SST 822	0.43	0.51	0.34	0.12	0.43	0.33	0.47	0.42	0.15	0.09
SST 825	0.52	0.64	0.5	0.14	0.55	0.41	0.61	0.56	0.24	0.16
T4	0.49	0.65	0.52	0.24	0.55	0.4	0.62	0.57	0.26	0.24
Tugela	0.25	0.37	0.33	0.31	0.28	0.14	0.36	0.31	0.13	0.24
Tugela DN	0.43	0.58	0.52	0.45	0.43	0.34	0.55	0.48	0.37	0.36
Tugela-fg	0.29	0.42	0.32	0.27	0.34	0.21	0.4	0.35	0.16	0.2
Tugela new	0.24	0.36	0.32	0.32	0.28	0.14	0.35	0.31	0.15	0.24

Table 1.10 (Continued)

Cultivar	PAN 3349	PAN 3364	Sch 69	SST 66	SST 102	SST 124	SST 363	SST 367	SST 822	SST 825
A-Tas	0.26	0.28	0.25	0.22	0.34	0.37	0.34	0.68	0.08	0.14
Belinda	0.37	0.77	0.49	0.41	0.35	0.34	0.41	0.41	0.53	0.68
Betta	0.32	0.32	0.21	0.35	0.31	0.35	0.28	0.58	0.31	0.29
Betta DN	0.17	0.36	0.1	0.22	0.2	0.2	0.16	0.49	0.2	0.27
Caledon	0.31	0.73	0.4	0.39	0.24	0.21	0.26	0.19	0.52	0.65
Eland	0.26	0.43	0.34	0.21	0.37	0.36	0.39	0.65	0.16	0.28
Flamink	0.21	0.27	0.11	0.21	0.23	0.28	0.21	0.58	0.15	0.19
Gamka	0.17	0.57	0.32	0.16	0.27	0.15	0.25	0.39	0.29	0.44
Gamtoos	0.23	0.53	0.32	0.17	0.33	0.26	0.33	0.62	0.29	0.42
Gamtoos DN	0.27	0.7	0.42	0.28	0.32	0.23	0.34	0.34	0.43	0.58
Ganep	0.44	0.88	0.54	0.53	0.39	0.35	0.41	0.09	0.68	0.79
Ganep DN	0.26	0.63	0.31	0.36	0.19	0.17	0.18	0.2	0.44	0.55
Harts	0.21	0.27	0.13	0.22	0.23	0.28	0.21	0.58	0.14	0.19
Hugenoot	0.29	0.44	0.21	0.37	0.23	0.25	0.2	0.39	0.39	0.42
Inia	0.23	0.23	0.12	0.24	0.23	0.31	0.25	0.6	0.15	0.18
Karee	0.28	0.26	0.21	0.25	0.33	0.35	0.3	0.67	0.14	0.14
Kanega	0.25	0.24	0.11	0.25	0.25	0.31	0.23	0.6	0.18	0.19
Limpopo	0.23	0.39	0.14	0.29	0.16	0.21	0.14	0.43	0.31	0.35
Limpopo DN	0.36	0.77	0.44	0.45	0.32	0.26	0.31	0.09	0.57	0.69
Marico	0.18	0.48	0.28	0.16	0.23	0.2	0.24	0.49	0.24	0.38
Molen	0.26	0.56	0.27	0.37	0.18	0.19	0.18	0.22	0.43	0.52
Molopo	0.32	0.73	0.41	0.41	0.26	0.23	0.27	0.15	0.51	0.64
Nantes	0.23	0.62	0.35	0.18	0.29	0.17	0.27	0.39	0.34	0.5
Oom Charl	0.3	0.28	0.29	0.27	0.39	0.41	0.38	0.72	0.12	0.14
Palmiet	0.2	0.63	0.31	0.34	0.18	0.19	0.25	0.29	0.43	0.55
Palmiet DN	0.19	0.48	0.18	0.3	0.06	0.17	0.11	0.34	0.33	0.41
Palmiet short	0.28	0.71	0.4	0.35	0.24	0.2	0.28	0.22	0.47	0.61
PAN 3211	0.21	0.66	0.35	0.29	0.21	0.17	0.26	0.27	0.42	0.56
PAN 3232	0.16	0.33	0.14	0.21	0.18	0.25	0.21	0.54	0.15	0.24
PAN 3235	0.22	0.31	0.22	0.19	0.32	0.32	0.3	0.63	0.09	0.16
PAN 3349	0	0.45	0.18	0.18	0.17	0.15	0.18	0.41	0.21	0.34
PAN 3364	0.45	0	0.31	0.47	0.45	0.55	0.46	0.83	0.31	0.17
Sch 69	0.18	0.31	0	0.25	0.17	0.24	0.15	0.5	0.21	0.26
SST 66	0.18	0.47	0.25	0	0.28	0.21	0.25	0.5	0.2	0.34
SST 102	0.17	0.45	0.17	0.28	0	0.16	0.13	0.37	0.3	0.39
SST 124	0.15	0.55	0.24	0.21	0.16	0	0.14	0.32	0.32	0.45
SST 363	0.18	0.46	0.15	0.25	0.13	0.14	0	0.38	0.3	0.38
SST 367	0.41	0.83	0.5	0.5	0.37	0.32	0.38	0	0.62	0.75
SST 822	0.21	0.31	0.21	0.2	0.3	0.32	0.3	0.62	0	0.17
SST 825	0.34	0.17	0.26	0.34	0.39	0.45	0.38	0.75	0.17	0
T4	0.37	0.12	0.23	0.38	0.38	0.46	0.38	0.75	0.25	0.14
Tugela	0.17	0.35	0.07	0.26	0.14	0.22	0.14	0.47	0.23	0.28
Tugela DN	0.39	0.39	0.28	0.4	0.39	0.41	0.35	0.63	0.37	0.31
Tugela fg	0.18	0.32	0.08	0.21	0.2	0.23	0.17	0.5	0.22	0.26
Tugela new	0.17	0.36	0.07	0.25	0.14	0.21	0.13	0.46	0.23	0.29

Table 1.10 (Continued)

Cultivar	T4	Tugela	Tugela DN	Tugela fg	Tugela new
A. Tas	0.24	0.27	0.43	0.23	0.27
Belinda	0.67	0.46	0.61	0.5	0.47
Betta	0.24	0.19	0.15	0.18	0.74
Betta DN	0.29	0.11	0.24	0.09	0.09
Caledon	0.64	0.35	0.52	0.41	0.36
Eland	0.36	0.36	0.48	0.32	0.35
Flamink	0.18	0.15	0.43	0.11	0.15
Gamka	0.48	0.3	0.52	0.3	0.3
Gamtoos	0.43	0.32	0.43	0.29	0.33
Gamtoos DN	0.61	0.4	0.59	0.4	0.4
Gariép	0.79	0.5	0.67	0.55	0.5
Gariép DN	0.55	0.29	0.46	0.32	0.27
Harts	0.22	0.15	0.43	0.13	0.16
Hugenoot	0.37	0.19	0.28	0.21	0.18
Inia	0.16	0.15	0.37	0.14	0.15
Karee	0.21	0.23	0.34	0.22	0.24
Kariega	0.16	0.14	0.35	0.12	0.14
Limpopo	0.31	0.11	0.25	0.15	0.09
Limpopo DN	0.69	0.41	0.57	0.44	0.4
Marico	0.41	0.25	0.52	0.27	0.26
Molen	0.49	0.25	0.43	0.29	0.24
Molopo	0.65	0.37	0.56	0.42	0.36
Nantes	0.52	0.33	0.52	0.32	0.32
Oom Charl	0.24	0.31	0.45	0.27	0.32
Palmiet	0.55	0.28	0.43	0.34	0.28
Palmiet DN	0.4	0.14	0.34	0.21	0.14
Palmiet short	0.62	0.36	0.55	0.4	0.35
PAN 3211	0.57	0.31	0.48	0.35	0.31
PAN 3232	0.26	0.13	0.37	0.16	0.15
PAN 3235	0.24	0.24	0.36	0.2	0.24
PAN 3349	0.37	0.17	0.39	0.18	0.17
PAN 3364	0.12	0.35	0.39	0.32	0.36
Sch 69	0.23	0.07	0.28	0.08	0.07
SST 66	0.38	0.26	0.4	0.21	0.25
SST 102	0.38	0.14	0.39	0.2	0.14
SST 124	0.46	0.22	0.41	0.23	0.21
SST 363	0.38	0.14	0.35	0.17	0.13
SST 367	0.75	0.47	0.63	0.5	0.46
SST 822	0.25	0.23	0.37	0.22	0.23
SST 825	0.14	0.28	0.31	0.26	0.29
T4	0	0.28	0.4	0.24	
Tugela	0.28	0	0.26	0.12	0.04
Tugela DN	0.4	0.26	0	0.24	0.25
Tugela fg	0.24	0.12	0.24	0	0.11
Tugela new	0.28	0.04	0.25	0.11	0

Table 1.11 The genetic distances between the near isogenic lines of Karee.

	K29-1	K29-2	K29-3	K29-4	K29-5	K29-6	K29-7	K29-8	K29-9	K29-10
K29-1	0	0.14	0.37	0.19	0.24	0.19	0.14	0.21	0.22	0.18
K29-2	0.14	0	0.45	0.23	0.32	0.19	0.17	0.31	0.19	0.25
K29-3	0.37	0.45	0	0.33	0.22	0.36	0.32	0.2	0.42	0.27
K29-4	0.19	0.23	0.33	0	0.13	0.11	0.09	0.17	0.28	0.15
K29-5	0.24	0.32	0.22	0.13	0	0.19	0.16	0.11	0.31	0.12
K29-6	0.19	0.19	0.36	0.11	0.19	0	0.09	0.22	0.24	0.17
K29-7	0.14	0.17	0.32	0.09	0.16	0.09	0	0.17	0.24	0.15
K29-8	0.21	0.31	0.2	0.17	0.11	0.22	0.17	0	0.28	0.11
K29-9	0.22	0.19	0.42	0.28	0.31	0.24	0.24	0.28	0	0.3
K29-10	0.18	0.25	0.27	0.15	0.12	0.17	0.15	0.11	0.3	0
K34-1	0.66	0.7	0.4	0.48	0.41	0.51	0.53	0.47	0.59	0.53
K34-2	0.15	0.15	0.37	0.12	0.19	0.08	0.09	0.21	0.23	0.14
K34-3	0.4	0.36	0.6	0.52	0.5	0.48	0.47	0.45	0.33	0.46
K34-4	0.17	0.15	0.43	0.21	0.27	0.19	0.18	0.27	0.11	0.23
K34-6	0.18	0.27	0.23	0.21	0.16	0.23	0.19	0.14	0.31	0.11
K34-7	0.43	0.47	0.14	0.3	0.21	0.31	0.32	0.25	0.38	0.3
K34-8	0.59	0.62	0.27	0.43	0.37	0.46	0.46	0.41	0.52	0.49
K34-9	0.39	0.43	0.05	0.31	0.21	0.3	0.3	0.23	0.36	0.29
K34-10	0.62	0.66	0.32	0.45	0.39	0.48	0.49	0.43	0.55	0.51
K35-2	0.36	0.41	0.16	0.33	0.26	0.35	0.31	0.26	0.35	0.31
K35-3	0.33	0.38	0.09	0.28	0.16	0.28	0.26	0.15	0.34	0.23
K35-4	0.41	0.48	0.12	0.33	0.23	0.35	0.33	0.24	0.41	0.32
K35-5	0.27	0.3	0.2	0.33	0.26	0.3	0.27	0.23	0.3	0.24
K35-6	0.32	0.39	0.12	0.32	0.22	0.32	0.29	0.19	0.36	0.25
K35-7	0.14	0.21	0.33	0.21	0.2	0.22	0.17	0.19	0.29	0.12
K35-8	0.14	0.23	0.25	0.19	0.18	0.19	0.14	0.15	0.28	0.14
K35-9	0.16	0.25	0.27	0.2	0.17	0.21	0.17	0.12	0.26	0.09
K35-10	0.63	0.67	0.33	0.47	0.4	0.49	0.51	0.44	0.57	0.51
K37-1	0.4	0.34	0.69	0.53	0.56	0.49	0.49	0.53	0.31	0.49
K37-2	0.08	0.09	0.39	0.21	0.27	0.17	0.14	0.26	0.24	0.21
K37-3	0.12	0.21	0.3	0.16	0.17	0.17	0.13	0.17	0.28	0.11
K37-4	0.15	0.21	0.34	0.13	0.17	0.12	0.12	0.17	0.28	0.09
K37-5	0.14	0.16	0.46	0.25	0.31	0.22	0.21	0.29	0.29	0.21
K37-6	0.19	0.09	0.46	0.28	0.34	0.23	0.22	0.32	0.17	0.28
K37-7	0.19	0.09	0.47	0.26	0.34	0.22	0.21	0.32	0.12	0.29
K37-8	0.19	0.09	0.51	0.27	0.37	0.22	0.21	0.34	0.21	0.29
K37-9	0.12	0.05	0.44	0.23	0.31	0.19	0.18	0.29	0.18	0.24
K37-10	0.18	0.14	0.47	0.18	0.28	0.13	0.16	0.3	0.22	0.22

Table 1.11 (Continued)

	K34-1	K34-2	K34-3	K34-4	K34-6	K34-7	K34-8	K34-9	K34-10
K29-1	0.66	0.15	0.4	0.17	0.18	0.43	0.59	0.39	0.62
K29-2	0.7	0.15	0.36	0.15	0.27	0.47	0.62	0.43	0.66
K29-3	0.4	0.37	0.6	0.43	0.23	0.14	0.27	0.05	0.32
K29-4	0.48	0.12	0.52	0.21	0.21	0.3	0.43	0.31	0.45
K29-5	0.41	0.19	0.5	0.27	0.16	0.21	0.37	0.21	0.39
K29-6	0.51	0.08	0.48	0.19	0.23	0.31	0.46	0.3	0.48
K29-7	0.53	0.09	0.47	0.18	0.19	0.32	0.46	0.3	0.49
K29-8	0.47	0.21	0.45	0.27	0.14	0.25	0.41	0.23	0.43
K29-9	0.59	0.23	0.33	0.11	0.31	0.38	0.52	0.36	0.55
K29-10	0.53	0.14	0.46	0.23	0.11	0.3	0.49	0.29	0.51
K34-1	0	0.56	0.77	0.61	0.56	0.29	0.25	0.37	0.18
K34-2	0.56	0	0.45	0.16	0.21	0.36	0.5	0.34	0.53
K34-3	0.77	0.45	0	0.27	0.42	0.55	0.41	0.57	0.4
K34-4	0.61	0.16	0.32	0	0.3	0.47	0.25	0.52	0.23
K34-6	0.56	0.21	0.47	0.27	0	0.22	0.11	0.24	0.24
K34-7	0.29	0.36	0.55	0.42	0.3	0	0.25	0.1	0.34
K34-8	0.25	0.5	0.69	0.55	0.47	0.22	0	0.3	0.18
K34-9	0.37	0.34	0.51	0.41	0.25	0.11	0.25	0	0.39
K34-10	0.18	0.53	0.75	0.57	0.52	0.24	0.1	0.3	0
K35-2	0.48	0.36	0.48	0.4	0.23	0.24	0.34	0.18	0.39
K35-3	0.42	0.31	0.5	0.36	0.2	0.16	0.32	0.12	0.36
K35-4	0.33	0.4	0.59	0.43	0.29	0.14	0.2	0.12	0.23
K35-5	0.58	0.29	0.38	0.35	0.15	0.3	0.47	0.22	0.52
K35-6	0.48	0.35	0.5	0.39	0.17	0.21	0.37	0.13	0.42
K35-7	0.64	0.16	0.42	0.23	0.15	0.4	0.58	0.37	0.62
K35-8	0.57	0.18	0.48	0.25	0.09	0.32	0.47	0.26	0.51
K35-9	0.58	0.18	0.39	0.24	0.12	0.33	0.52	0.3	0.56
K35-10	0.13	0.55	0.75	0.61	0.52	0.23	0.15	0.3	0.07
K37-1	0.92	0.45	0.39	0.34	0.51	0.69	0.85	0.66	0.88
K37-2	0.68	0.14	0.43	0.19	0.2	0.43	0.59	0.39	0.63
K37-3	0.59	0.15	0.47	0.22	0.09	0.34	0.52	0.3	0.56
K37-4	0.57	0.1	0.47	0.21	0.16	0.36	0.5	0.34	0.53
K37-5	0.74	0.17	0.42	0.22	0.25	0.52	0.66	0.49	0.7
K37-6	0.72	0.19	0.3	0.15	0.29	0.49	0.64	0.44	0.68
K37-7	0.68	0.18	0.36	0.1	0.31	0.46	0.6	0.42	0.63
K37-8	0.74	0.19	0.36	0.17	0.33	0.53	0.68	0.5	0.71
K37-9	0.7	0.15	0.43	0.13	0.25	0.47	0.63	0.42	0.66
K37-10	0.64	0.11	0.37	0.14	0.28	0.45	0.58	0.44	0.61

Table 1.11 (Continued)

	K35-2	K35-3	K35-4	K35-5	K35-6	K35-7	K35-8	K35-9	K35-10
K29-1	0.36	0.33	0.41	0.27	0.32	0.14	0.14	0.16	0.63
K29-2	0.41	0.38	0.48	0.3	0.39	0.21	0.23	0.25	0.67
K29-3	0.16	0.09	0.12	0.2	0.12	0.33	0.25	0.27	0.33
K29-4	0.33	0.28	0.33	0.33	0.32	0.21	0.19	0.2	0.47
K29-5	0.26	0.16	0.23	0.26	0.22	0.2	0.18	0.17	0.4
K29-6	0.35	0.28	0.35	0.3	0.32	0.22	0.19	0.21	0.49
K29-7	0.31	0.26	0.33	0.27	0.29	0.17	0.14	0.17	0.51
K29-8	0.26	0.15	0.24	0.23	0.19	0.19	0.15	0.12	0.44
K29-9	0.35	0.34	0.41	0.3	0.36	0.29	0.28	0.26	0.57
K29-10	0.31	0.23	0.32	0.24	0.25	0.12	0.14	0.09	0.51
K34-1	0.48	0.42	0.33	0.58	0.48	0.64	0.57	0.58	0.13
K34-2	0.36	0.31	0.4	0.29	0.35	0.16	0.18	0.18	0.55
K34-3	0.48	0.5	0.59	0.38	0.5	0.42	0.48	0.39	0.75
K34-4	0.4	0.36	0.43	0.35	0.39	0.23	0.25	0.24	0.61
K34-6	0.23	0.2	0.29	0.15	0.17	0.15	0.09	0.12	0.52
K34-7	0.24	0.16	0.14	0.3	0.21	0.4	0.32	0.33	0.23
K34-8	0.34	0.32	0.2	0.47	0.37	0.58	0.47	0.52	0.15
K34-9	0.18	0.12	0.12	0.22	0.13	0.37	0.26	0.3	0.3
K34-10	0.39	0.36	0.23	0.52	0.42	0.62	0.51	0.56	0.07
K35-2	0	0.21	0.18	0.22	0.15	0.36	0.23	0.32	0.41
K35-3	0.21	0	0.16	0.19	0.12	0.29	0.21	0.22	0.37
K35-4	0.18	0.16	0	0.3	0.18	0.4	0.29	0.34	0.26
K35-5	0.22	0.19	0.3	0	0.12	0.24	0.17	0.21	0.51
K35-6	0.15	0.12	0.18	0.12	0	0.29	0.2	0.24	0.42
K35-7	0.36	0.29	0.4	0.24	0.29	0	0.15	0.07	0.61
K35-8	0.23	0.21	0.29	0.17	0.2	0.15	0	0.14	0.53
K35-9	0.32	0.22	0.34	0.21	0.24	0.07	0.14	0	0.55
K35-10	0.41	0.37	0.26	0.51	0.42	0.61	0.53	0.55	0
K37-1	0.63	0.61	0.72	0.51	0.62	0.43	0.51	0.45	0.9
K37-2	0.36	0.33	0.42	0.26	0.32	0.16	0.15	0.19	0.64
K37-3	0.28	0.26	0.34	0.21	0.25	0.11	0.08	0.12	0.56
K37-4	0.36	0.29	0.38	0.3	0.32	0.14	0.15	0.15	0.55
K37-5	0.48	0.41	0.51	0.37	0.42	0.16	0.22	0.22	0.72
K37-6	0.43	0.38	0.49	0.32	0.39	0.23	0.27	0.24	0.69
K37-7	0.41	0.41	0.49	0.32	0.42	0.26	0.28	0.27	0.66
K37-8	0.49	0.44	0.54	0.39	0.45	0.26	0.29	0.28	0.73
K37-9	0.41	0.38	0.47	0.3	0.38	0.2	0.22	0.23	0.67
K37-10	0.45	0.4	0.48	0.38	0.43	0.22	0.25	0.26	0.63

Table 1.11 (Continued)

	K37-1	K37-2	K37-3	K37-4	K37-5	K37-6	K37-7	K37-8	K37-9	K37-10
K29-1	0.4	0.08	0.12	0.15	0.14	0.19	0.19	0.19	0.12	0.18
K29-2	0.34	0.09	0.21	0.21	0.16	0.09	0.09	0.09	0.05	0.14
K29-3	0.69	0.39	0.3	0.34	0.46	0.46	0.47	0.51	0.44	0.47
K29-4	0.56	0.27	0.17	0.17	0.31	0.34	0.34	0.37	0.31	0.28
K29-5	0.56	0.27	0.17	0.17	0.31	0.34	0.34	0.37	0.31	0.28
K29-6	0.49	0.17	0.17	0.12	0.22	0.23	0.22	0.22	0.19	0.13
K29-7	0.49	0.14	0.13	0.12	0.21	0.22	0.21	0.21	0.18	0.16
K29-8	0.53	0.26	0.17	0.17	0.29	0.32	0.32	0.34	0.29	0.3
K29-9	0.31	0.24	0.28	0.28	0.29	0.17	0.12	0.21	0.18	0.22
K29-10	0.49	0.21	0.11	0.09	0.21	0.28	0.29	0.29	0.24	0.22
K34-1	0.92	0.68	0.59	0.57	0.74	0.72	0.68	0.74	0.7	0.64
K34-2	0.45	0.14	0.15	0.1	0.17	0.19	0.18	0.19	0.15	0.11
K34-3	0.39	0.43	0.47	0.47	0.42	0.3	0.36	0.36	0.43	0.37
K34-4	0.34	0.19	0.22	0.21	0.22	0.15	0.1	0.17	0.13	0.14
K34-6	0.51	0.2	0.09	0.16	0.25	0.29	0.31	0.33	0.25	0.28
K34-7	0.69	0.43	0.34	0.36	0.52	0.49	0.46	0.53	0.47	0.45
K34-8	0.85	0.59	0.52	0.5	0.66	0.64	0.6	0.68	0.63	0.58
K34-9	0.66	0.39	0.3	0.34	0.49	0.44	0.42	0.5	0.42	0.44
K34-10	0.88	0.63	0.56	0.53	0.7	0.68	0.63	0.71	0.66	0.61
K35-2	0.63	0.36	0.28	0.36	0.48	0.43	0.41	0.49	0.41	0.45
K35-3	0.61	0.33	0.26	0.29	0.41	0.38	0.41	0.44	0.38	0.4
K35-4	0.72	0.42	0.34	0.38	0.51	0.49	0.49	0.54	0.47	0.48
K35-5	0.51	0.26	0.21	0.3	0.37	0.32	0.32	0.39	0.3	0.38
K35-6	0.62	0.32	0.25	0.32	0.42	0.39	0.42	0.45	0.38	0.43
K35-7	0.43	0.16	0.11	0.14	0.16	0.23	0.26	0.26	0.2	0.22
K35-8	0.51	0.15	0.08	0.15	0.22	0.27	0.28	0.29	0.22	0.25
K35-9	0.45	0.19	0.12	0.15	0.22	0.24	0.27	0.28	0.23	0.26
K35-10	0.9	0.64	0.56	0.55	0.72	0.69	0.66	0.73	0.67	0.63
K37-1	0	0.42	0.49	0.48	0.4	0.29	0.3	0.33	0.35	0.38
K37-2	0.42	0	0.14	0.17	0.14	0.15	0.17	0.16	0.09	0.17
K37-3	0.49	0.14	0	0.11	0.19	0.26	0.26	0.26	0.2	0.2
K37-4	0.48	0.17	0.11	0	0.16	0.27	0.25	0.25	0.21	0.14
K37-5	0.4	0.14	0.19	0.16	0	0.22	0.22	0.19	0.16	0.15
K37-6	0.29	0.15	0.26	0.27	0.22	0	0.09	0.1	0.09	0.2
K37-7	0.3	0.17	0.26	0.25	0.22	0.09	0	0.12	0.1	0.16
K37-8	0.33	0.16	0.26	0.25	0.19	0.1	0.12	0	0.11	0.16
K37-9	0.35	0.09	0.2	0.21	0.16	0.09	0.1	0.11	0	0.16
K37-10	0.38	0.17	0.2	0.14	0.15	0.2	0.16	0.16	0.16	0

1.5 Conclusions

HMW glutenin subunits

The HMW glutenin subunits are used in South Africa to distinguish between cultivars. This study showed that the HMW glutenins are however, not reliable to distinguish between all the cultivars. It is however, very reliable to determine seed purity. The different banding combinations are easy to read with the use of the nomenclature of Payne and Lawrence (1983).

In some countries, the HMW glutenins are believed to explain up to 60 percent of the bread-making variation between cultivars. The HMW glutenin subunits accounts for only 20 to 25 percent of the variation in bread-making quality in South African wheat cultivars (Randall, 1998; personal communication). It is therefore not very effective to use as genetic markers in breeding programmes for bread-making quality in South Africa.

LMW glutenin subunits

Thirty-nine different groups of LMW glutenin subunits were found in South African bread wheat cultivars. The different bands were divided into class intervals. These classes were called groups and their molecular weights were determined using a low range SDS molecular marker.

All the cultivars had different banding patterns. It was also possible to distinguish between the near isogenic lines of K29, K34, K35 and K37. It was also possible to distinguish between cultivars that have a close genetic relationship, like Tugela, Tugela DN, Tugela new and Tugela fast growing. When the genetic distances were determined, it was found that Tugela and Tugela new are closely related with only four percent dissimilarity. This only proves that LMW glutenin subunits are indeed very effective in variety identification. The reading of the bands is complex, but with computer software it is possible to clearly distinguish between different bands.

Significant correlations between certain groups were found. This could help to identify the influence of the different chromosomes on the inheritance and expression of the different groups. This will be investigated in Chapter 3.

It was also possible to assign different band intensities to certain groups. Some classes were always expressed as a dark band, while others were expressed as light bands. In some classes different intensities were observed and it is possible that these bands are inherited by different genomes.

Genetic distance

This study proves like the study of De Swardt (1998) that there are bread wheat cultivars that are closely related in South Africa. New germplasm must be introduced to breeding programmes or in the near future some problems will be encountered.

The genetic distances between the near isogenic lines of Karee confirm their high degree of similarity. The only exception was K37-1 that had a high degree of dissimilarity to some of the other lines.

Chapter 2

Durum wheat

2.1 Introduction

Durum wheat is the eighth most important cereal in the world based on the area grown. It is better adapted to drought, but have a lower yield and fitness for bread-making than bread wheat (Bozzini, 1988).

Evidence supports the conclusion that protein quantity and quality are involved in determining cooked pasta characteristics, like firmness, surface condition and stickiness after cooking and overcooking. The ability of proteins to form an insoluble network that entraps the swollen starch granules, avoid the disruption of the spaghetti surface and the leaching of carbohydrates and proteins by the boiling water is probably the basis of good quality in durum wheat.

A high protein content is favourable for good quality, because there are more polypeptide chains and the possible interactions of proteins and the forming of a resistant network is higher (Feillet, 1988).

Protein quality, however, is more complex. A relationship between γ -gliadin 45 and gluten strength and γ -gliadin 42 and gluten weakness was proposed. Nowadays, it looks as though this relationship is more likely due to the LMW glutenin subunits than the γ -gliadins (Payne *et al*, 1984c).

As grain quality is known to be modified by genetic factors other than protein composition, it is over simplistic to suggest that quality differences can be explained merely in terms of quality-associated protein components. However, evidence is accumulating to support the view that this approach can indicate the existence of major genes that can simplify breeding for grain quality by conventional means (Campbell *et al*, 1987).

Today, because of their important roles in determining the functional properties of wheat flour, both LMW and HMW glutenin subunits are being used as genetic markers in breeding programmes to improve flour properties (Gupta, 1990).

Many wheat breeders are taking HMW glutenins into account in their selection programmes, but this approach will become more useful if the effects of gliadins, triticins, HMW albumins and LMW glutenins are also known. It is therefore important to try and separate the LMW glutenins from the closely linked gliadins to measure their separate effects on quality parameters as achieved by Pogna *et al* (1988) in durum wheats (Shepherd, 1988).

The LMW glutenin subunits can serve as additional genetic markers. Allelic differences in the LMW glutenins have been shown to be significantly related to flour qualities in bread (Payne *et al*, 1987b; Gupta and Shepherd, 1988; Gupta *et al*, 1989) and durum wheats (Autran *et al*, 1989). More information is however, required on the relationships between the different LMW glutenin subunits and the technological qualities of wheat flour. Eventually it may be possible to select for improved quality on the basis of the LMW glutenin subunits (Gupta and Shepherd, 1990).

The durum wheat industry is currently very small in South Africa. It is dominated by Fatti's and Moni's and most of the durum wheats are imported (Randall *et al*, 1995). No research has been done so far on the gluten proteins.

The aim of this study was to determine:

1. The different HMW glutenins of South African durum wheat,
2. The different LMW glutenin groups in durum wheat,
3. If the LMW glutenins can be used for cultivar identification,
4. The genetic distances between the South Africa lines.

2.1 Literature review

2.2.1 History of durum wheat

As discussed in Chapter 1, *T. turgidum* (the durum or macaroni wheats) and *T. aestivum* (the common or bread wheats) are the most important and widely grown species of the genus *Triticum*. Bread wheat is hexaploid ($2n=6x=42$) and has three genomes (AABBDD). Durum wheat is tetraploid ($2n=4x=24$) and has two genomes (AABB) (Baenziger *et al*, 1994). There is a close genetic relationship between durum and bread wheat (Garcia-Olmedo *et al*, 1982).

The area of adaptation of durum wheat could nearly overlap the area for bread wheat, but it ranks only eighth among all cereals based on the area grown. There are several reasons for the lower distribution of durum wheats to bread wheats, namely

- 1) it has a lower fitness for bread-making
- 2) it has a lower resistance to cold and long winters
- 3) it has a lower yield, and less effort is made towards breeding for higher yield.

However, durum wheats are better adapted to drought and they are also more productive in marginal areas. In the past twenty years, breeding efforts were initiated both nationally and internationally that will certainly contribute to the improvement of durum yield (Bozzini, 1988).

2.2.2. Major uses of durum wheat

European and American countries use durum wheat mostly for pasta products, whereas the Middle East and North African countries use durum for bread-making, pasta, couscous and other uses (Bozzini, 1988).

Durum flours usually produce a smaller loaf volume than bread wheats, but it has a yellowish colour, a characteristic taste and smell, a fine and uniform crumb structure and a prolonged shelf-life that appeal to some customers (Liu *et al*, 1996). It has been reported that durum bread is less toxic for people who suffer from intolerance to wheat gluten (celiac disease) (Troncone and Auricchio, 1991).

South Africa produces up to 29 000 ton durum wheat per annum. The pasta industry is dominated by Fatti's and Moni's, which is part of the Tiger Milling group (Randall *et al*, 1995).

2.2.3 Protein composition of durum wheat

Durum wheat is typically very vitreous and much harder than bread wheat, with usually a higher protein content that varies from nine to 18 percent. It is thus a good source of protein (Feillet, 1988). It is well recognised that the vitreousness of the kernel is positively correlated with the protein content, but it also appears to have a slight negative influence on semolina yield (Matsuo and Dexter, 1980). The extreme hardness is required to give a coarse, granular, regular-sized particle flour called semolina which is free from bran and fine flour particles. Semolina is mixed with water to form a stiff dough which is extruded at high pressure to ensure a translucent product with no air bubbles. Other characteristics required by durum wheat include low α -amylase activity and a high content of β -carotene, which gives pasta its characteristic yellow colour. A strong gluten maintains the stiffness of the dough, preventing its disintegration and after cooking, adds retention to the shape and firmness of the product (Blackman and Payne, 1987). The relaxed gluten of durum wheat may be more porous than the gluten of bread wheat (Dronzek *et al*, 1980).

There are no clear differences between bread and durum wheat in the proportions of their soluble proteins, gliadins and glutenins (Feillet, 1988).

Electrophoretic and genetic studies were used to compare the gliadins of bread and durum wheats. The following results were obtained:

- 1) The less mobile gliadin components are absent in durum wheats (Autran, 1975).
- 2) The inheritance of gliadins in bread and durum wheats is codominant and it is accomplished by groups of components or blocks (Akhmedov *et al*, 1981).
- 3) The F_1 seeds contain all the components of the parents. The intensity of the components is determined by a gene dosage effect (Bebyakin and Kunakov, 1981).
- 4) Gliadins could be used for variety identification in bread and durum wheats (Wrigley *et al*, 1982).

- 5) The gliadins are more often used for variety identification, as it is more effective than using the glutenins (Lasztity, 1986).

The properties of durum wheat glutenins are poorly characterised. Orth *et al* (1973) showed with electron microscopy that the glutenins of durum wheats are composed of ribbons in random orientation. The glutenins of bread wheats are composed of parallel fibrils grouped in aggregates.

SDS-PAGE of reduced glutenins revealed varietal differences in the molecular weight distribution and concentrations of the six largest subunits. These differences appeared to be related to the spaghetti-making quality of durum wheat varieties (Wasik and Bushuk, 1975). Branlard and Le Blanc (1985) observed fourteen different HMW glutenin subunits in 38 French durum wheat cultivars.

2.2.4 Relationship between pasta quality and protein composition

The cooking quality of pasta depends on the firmness of cooked pasta and the surface condition of pasta after cooking. A consistent relationship between the protein and gluten content of wheat and semolina and the cooking quality of pasta was shown. A protein content higher than 13 percent was reported to yield a satisfactory final product, whereas a protein content lower than 11 percent resulted in a poor product. Gluten properties were also identified as an essential factor for cooking quality (Sheu *et al*, 1967; Matsou and Irvine, 1970). Wheat protein content appears to account for 30 to 40 percent of the variability of cooking quality (Dexter *et al*, 1980).

Pasta cooking quality has been shown to depend on two main parameters, namely rheological characteristics (related to gluten elasticity or strength) and surface condition, especially absence of such surface deteriorations as stickiness and clumping or mushiness. These two parameters do not seem to be directly correlated, but it rather looks as though they are relatively independent (Autran *et al*, 1986). These two parameters must therefore, be estimated separately in quality breeding.

The surface state of cooked pasta has been correlated positively with the amount of S-H plus S-S groups in glutenin of various durum wheat cultivars. Two major low molecular protein fractions have been reported, namely DGS-1 and DGS-2 (durum-wheat sulfur-

rich glutenin fractions), that were likely to be involved in the cooking quality of durum wheat semolina (Feillet *et al*, 1989). It also looked as though nonpolar lipids have an influence on the surface stickiness of cooked spaghetti (Matsou *et al*, 1986).

Viscoelasticity of cooked pasta correlates to the γ -gliadin electrophoretic type. Durum wheat varieties with the γ -gliadin 45 component generally have a higher firmness and viscoelasticity than varieties with the γ -gliadin 42 component (Carillo *et al*, 1990).

A major objective in breeding durum wheats for manufacturing in pasta products is the development of varieties with strong elastic gluten. A strong gluten is essential to maintain the integrity of the pasta cooking so that a firm, resilient product is obtained. There is an association between the presence of γ -gliadin 45 and gluten strength and γ -gliadin 42 and gluten weakness.

In bread wheat, the locus *Gli-B1* occurs distally on the short arm of chromosome 1B and it contains the three families of genes coding for ω -gliadins, γ -gliadins and the LMW glutenin subunits (Payne *et al*, 1984a). It is very likely that the same arrangement of storage protein genes occurs in durum wheats, because of the close genetic relationship between bread and durum wheat. In bread wheats Jackson *et al* (1983) did not observe recombination between genes at *Gli-B1* in several hundred progeny, although recombination can occur very rarely at a frequency of one in several thousands. It is therefore not surprising that durum wheats which contain γ -gliadin 45 all contain the same group of LMW glutenin subunits coded by chromosome 1B (LMW-2). Varieties with γ -gliadin 42 all contain LMW-1 (Carillo *et al*, 1990). This raises the question as to whether strong gluten properties, which are necessary to make acceptable pasta products, and which are associated with γ -gliadin 45 are actually caused by this protein or are due to closely-linked genes coding for ω -gliadin 35 or for LMW-2 (Payne *et al*, 1984a). Pogna *et al* (1988) found that the ω -gliadin 35 made up a minor amount of fractions that have no apparent functional properties.

Strong clues as to which of these proteins are the actual causal agents can be obtained from studying the methods used to test the pasta cooking quality in γ -gliadin 45 associations. Two of the methods require the prior preparations of gluten. In the French

procedure (Damidaux *et al*, 1980) gluten is moulded in a cell, heat-treated, cooked, rested briefly and then analysed using a viscoelastograph. A constant load compresses the gluten disc and the extent of recoil is measured up to 20 seconds after the removal of the load. The greater the recoil, the better the cooking quality. In the other gluten test (Matsuo, 1978) the moulded, compressed gluten is stretched after a resting period and the force required for it to break into two pieces is measured. For the two tests, the presence of γ -gliadin 45 is associated with good recoil and strong resistance to stretching and these are the measures of gluten strength (that is elasticity).

The mixograph has also been used to assess pasta-cooking quality. A dough is made and mixed at a set speed. The force required to maintain dough mixing at this speed is monitored continuously. Mixing curves of good quality doughs usually have long times to peak development height, a high peak and a large curve area. The procedure is primarily measuring the resistance to stretching, though in a more sophisticated and more informative way than the stretching test (Matsuo, 1978).

Of the two major proteins comprising gluten, glutenin imparts strength to a dough for it has the property of viscoelasticity. Gliadin, on the other hand, becomes a viscous mass when hydrated and has no apparent elasticity. Thus, of the three groups of genetically linked proteins coded at the *Gli-B1* locus, the LMW glutenins seem the most likely candidates for the casual proteins from this evidence.

The large differences in gluten strength can much more easily be explained in terms of biochemical differences between glutenin subunits LMW-1 and LMW-2, than between γ -gliadin 42 and 45. LMW-1 and LMW-2 have different molecular weights and isoelectric points and LMW-2 is also expressed in much larger amounts. The corresponding properties and the dosage of γ -gliadin 42 and 45 are very similar to each other. They also have very similar amino-acid compositions.

Thus, it can be concluded that the LMW glutenin subunits linked to γ -gliadin 45 are probably causing the associations with gluten strength rather than the γ -gliadin 45 itself. However, allelic variation at other loci coding for other glutenin subunits, namely *Gli-A1*, *Glu-A1* and *Glu-B1*, probably also affect pasta quality, but to a much lesser extent than *Glu-B3* (Payne *et al*, 1984a).

The evidence that the pasta-making quality depends on the preferential accumulation of specific glutenins and that high grain protein contents are essential for the quality to be expressed, imply that in breeding for high quality durum wheats, gene pools must be obtained which promote the high protein content in the grain and direct the preferential accumulation of glutenins. Quality stability would in turn, require an abundant accumulation of glutenins under different environmental conditions. These regulatory genes must be sought and considered by breeders in their effort to improve pasta quality of durum wheat (Galterio *et al*, 1993).

The HMW glutenins have been shown to be correlated to some extent with the strength of durum doughs, but the relationship in durums seems to be much less pronounced than with the bread wheats (Liu *et al*, 1996). The study of Carillo *et al* (1990) has shown that the HMW glutenin subunits are poor indicators of pasta quality in durum wheats, although cultivars with band 20 were slightly poorer than others. γ -Gliadins could be markers for selecting lines in a breeding programme of durum wheat quality, but it is safer to use LMW glutenin patterns, because the same γ -gliadin can be associated with two different patterns of LMW glutenin. HMW subunits 7+8 are associated with large SDS sedimentation volumes and high elastic recoveries compared with subunits 6+8 and 20. Subunits 7+8 are also strongly correlated with bread-making quality of durum wheat cultivars. Allelic variation at *Glu-B1* had a smaller effect on gluten quality than the variation at *Glu-B3* allele. The effects at each locus were additive and genotypes containing HMW 7+8 and LMW-2 had the best gluten properties (Pogna *et al*, 1990).

2.3 Materials and Methods

2.3.1 Materials

Twenty-nine durum wheats were used to determine their HMW and LMW glutenin subunit compositions. A summary of the cultivars used, is given in Table 2.1. Please note that the USD types are from the University of Stellenbosch and they are all pure breeding lines.

Table 2.1. The names and origin of the durum cultivars used in this study.

Cultivar	Origin
1. Aconchi	Mexico
2. Altar	Mexico
3. Fargo	RSA
4. Goeie Hoop	RSA
5. Kronos	Australia
6. Mexicale 75	Mexico
7. Moni	RSA
8. Nordum	RSA
9. Orania	RSA
10. USD 9302	RSA
11. USD 9503	RSA
12. USD 9509	RSA
13. USD 9511	RSA
14. USD 9607	RSA
15. USD 9608	RSA
16. USD 9609	RSA
17. USD 9610	RSA
18. USD 9612	RSA
19. USD 9614	RSA
20. USD 9701	RSA
21. USD 9702	RSA
22. USD 9703	RSA

Table 2.1 (Continued)

Cultivar	Origin
23. USD 9704	RSA
24. USD 9705	RSA
25. USD 9706	RSA
26. USD 9707	RSA
27. USD 9708	RSA
28. USD 9709	RSA
29. USD 9710	RSA

2.3.2 Methods

2.3.2.1 Extraction of glutenins

The same method (Singh *et al*, 1991) as in Chapter 1 was used to extract the glutenin proteins. Please refer to Chapter 1 for a detailed discussion. Six replications of each cultivar were evaluated.

2.3.2.2 Sodium dodecyl sulphate gel electrophoresis (SDS-PAGE)

The same gel concentrations as in Chapter 1 were used. The gels were also run at 66 mA at a temperature of 15°C. Please refer to Chapter 1 for a detailed discussion.

2.3.2.3 Staining of the gel

The staining method of Wrigley (1992) was used as in Chapter 1.

2.3.2.4 Gel analysis

The "Molecular Analyst Fingerprinting" software was also used. All the settings used were exactly the same as was done with the bread wheats in Chapter 1.

2.3.2.4 Determination of the HMW glutenins

The different HMW glutenin subunits were determined using the nomenclature of Payne and Lawrence (1983).

2.3.2.6 Grouping of the LMW glutenins

The differences in the banding patterns of the cultivars were used to group them into 39 possible groups. Using the NCSS 2000 program, the standard deviations of all the cultivars were calculated and possible double bands were looked at. This helped to identify the different groups. Please refer to Chapter 1 for the reasons for using the standard deviations of the cultivars.

2.3.2.7 Band intensity and LMW glutenin groups

As with the bread wheats in Chapter 1, the LMW glutenin bands were also divided into five classes according to their band intensities with class1 being a faintly stained band and class 5 a very dark band. Class 6 had no definite intensity, as was the case in Chapter 1. It was determined which of the groups had specific band intensities and whether some groups could have light and dark bands.

2.3.2.8 Correlation between the different LMW bands

The correlation between the different LMW bands was determined using the Spearman-rank correlation matrices of the NCSS 2000 program. The Spearman-rank calculates the correlation by applying the Pearson correlation formulas to the ranks of the data rather than to the actual data values themselves, thus reducing many of the distortions that affect the Pearson correlation. Pair-wise removal of missing values were chosen, because missing values occurring in other variables do not have an influence on the calculations.

2.3.2.9 The molecular weight of the different groups

The same low range SDS-marker of Biorad was used to determine the molecular weights of the different groups.

2.3.2.10 Calculation of genetic distance

The genetic distance between the different durum cultivars was calculated using the hierarchical clustering method as in Chapter 1. Please refer to Chapter 1 for a detailed discussion and interpretation of this method.

2.4 Results and Discussion

HMW glutenins

In Table 2.2 is a summary of all the HMW glutenin subunits that were present in the durum wheats.

Table 2.2. The HMW glutenin subunits present in the durum wheat cultivars tested.

Cultivar	Genome A	Genome B
1. Aconchi	0	7+8
2. Altar	0	7+8
3. Fargo	0	6+8
4. Goeie Hoop	0	20
5. Kronos	0	6+8
6. Mexicale 75	0	7+8
7. Moni	0	13+16
8. Nordum	0	6+8
9. Orania	0	13+16
10. USD 9302	0	20
11. USD 9503	0	6+8
12. USD 9509	0	20
13. USD 9511	0	6+8
14. USD 9607	0	7+8
15. USD 9608	0	7+8
16. USD 9609	0	6+8
17. USD 9610	0	13+16
18. USD 9612	0	6+8
19. USD 9614	0	7+8
20. USD 9701	0	6+8
21. USD 9702	0	20
22. USD 9703	0	7+8
23. USD 9704	0	6+8
24. USD 9705	0	7+8
25. USD 9706	0	7+8

Table 2.2 (Continue)

Cultivar	Genome A	Genome B
26. USD 9707	0	7+8
27. USD 9708	0	20
28. USD 9709	0	6+8
29. USD 9710	0	13+16

In the A genome no bands occurred in any of the cultivars, thus the 0 banding pattern according to Payne and Lawrence (1983) was evident. Branlard *et al* (1989) found that 83 percent of the durum cultivars they tested carried the null allele. In the B genome 10 cultivars had the 7+8 banding patterns, 10 had the 6+8 pattern, five had the 20 banding pattern and four had the 13+16 pattern. In the research of Branlard *et al* (1989) they analysed 502 durum cultivars and they did not found subunit 17 or 21 in any of the durum cultivars. In this study, these subunits were also not found. They also found alleles that were previously not identified by Payne and Lawrence (1983). All the alleles found in this study was however identified by these two authors. Branlard *et al* (1989) found that banding patterns 20, 6+8 and 7+8 occurred more frequently than other banding patterns. The latter two occurred more frequently in South African cultivars. Figure 2.1 shows the occurrence of the different patterns.

B genome

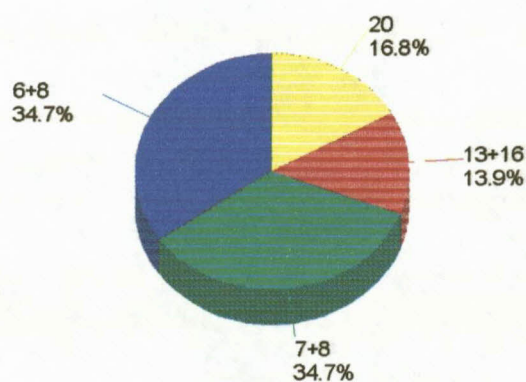


Figure 2.1. The occurrence of the HMW glutenin bands in the B genome of the durum wheats tested.

The grouping of the LMW glutenin bands

Please refer to Appendix B for the tables with all the replications of the cultivars and the intensities of the different bands.

Table 2.3 is a summary of the averages of the migration distances of the different bands of all the cultivars. The intensities of the bands are in brackets. An intensity of one was a very light band, while an intensity of five was a very dark band. An intensity of six means that some bands in the replications were very light, while others were very dark. It was thus impossible to put it into a specific class.

Table 2.3. The migration distances of the different bands of the durum cultivars tested. Band intensities are given in brackets.

Aconchi	Altar	Fargo	G. Hoop	Kronos	Mexicale	Moni	Nordum
16 (1)	25 (1)	32 (3)	19 (1)	22 (1)	14 (1)	15 (3)	15 (1)
28 (6)	44 (4)	43 (6)	34 (4)	34 (5)	29 (4)	37 (4)	34 (4)
45 (4)	57 (5)	57 (5)	54 (5)	48 (5)	39 (5)	47 (5)	46 (2)
58 (4)	70 (4)	68 (4)	65 (5)	60 (4)	53 (5)	61 (5)	64 (5)
72 (5)	85 (5)	81 (6)	77 (6)	73 (6)	72 (5)	77 (5)	75 (5)
92 (6)	94 (1)	95 (6)	90 (4)	82 (3)	81 (1)	97 (4)	86 (4)
101 (2)	103 (2)	106 (3)	104 (3)	98 (3)	95 (6)	110 (3)	102 (4)
113 (3)	109 (2)	117 (3)	114 (4)	109 (4)	108 (2)	122 (4)	117 (4)
127 (3)	120 (3)	123 (3)	126 (4)	120 (4)	123 (2)	134 (3)	129 (4)
146 (6)	131 (3)	135 (3)	136 (3)	134 (4)	136 (2)	143 (3)	143 (4)
159 (3)	143 (2)	144 (2)	142 (2)	146 (1)	157 (2)	170 (2)	173 (2)
171 (1)	156 (1)	156 (1)	164 (1)	167 (2)	168 (2)	186 (2)	189 (2)
192 (1)	176 (2)	179 (2)	186 (1)	184 (1)	179 (1)		
	193 (1)	195 (1)		193 (1)	188 (1)		

Table 2.3 (Continued)

Orania	USD9302	USD9503	USD9509	USD9511	USD9607	USD9608
36 (4)	18 (1)	14 (1)	11 (1)	13 (2)	9 (1)	29 (2)
48 (5)	37 (5)	34 (5)	33 (4)	34 (4)	30 (3)	48 (5)
64 (4)	47 (5)	46 (5)	47 (5)	45 (5)	45 (5)	62 (5)
75 (6)	65 (5)	60 (4)	62 (4)	63 (5)	60 (5)	73 (4)
89 (4)	76 (5)	78 (5)	76 (6)	78 (5)	74 (5)	86 (5)
107 (3)	87 (5)	87 (1)	89 (2)	95 (6)	93 (4)	103 (4)
122 (4)	97 (4)	100 (3)	105 (3)	107 (2)	103 (1)	113 (3)
136 (3)	115 (4)	116 (2)	119 (3)	123 (2)	115 (3)	128 (3)
149 (3)	124 (5)	135 (3)	129 (3)	134 (4)	132 (3)	139 (3)
157 (2)	136 (4)	148 (6)	145 (3)	153 (4)	144 (3)	151 (4)
166 (1)	148 (4)	156 (1)	158 (2)	178 (1)	168 (1)	163 (1)
180 (1)	158 (2)	174 (1)	176 (1)	192 (1)	182 (1)	181 (1)
	186 (2)		187 (2)		192 (1)	192 (1)
			193 (1)			

Table 2.3 (Continued)

USD9609	USD9610	USD9612	USD9614	USD9701	USD9702	USD9703
17 (2)	18 (2)	27 (3)	17 (1)	24 (3)	9 (1)	10 (1)
49 (5)	39 (4)	45 (4)	32 (4)	33 (6)	29 (3)	29 (2)
70 (4)	53 (5)	63 (5)	47 (4)	50 (4)	49 (5)	46 (5)
86 (5)	69 (4)	84 (4)	64 (5)	55 (5)	59 (5)	59 (5)
99 (1)	85 (6)	99 (2)	76 (4)	69 (5)	74 (5)	75 (5)
112 (3)	105 (4)	109 (4)	89 (4)	88 (5)	85 (5)	96 (2)
121 (2)	115 (4)	116 (1)	116 (4)	99 (1)	98 (2)	105 (6)
136 (4)	123 (6)	132 (5)	135 (3)	106 (3)	107 (1)	124 (3)
156 (1)	132 (3)	141 (1)	153 (6)	118 (3)	125 (3)	133 (1)
164 (1)	141 (4)	149 (6)	163 (1)	124 (3)	133 (3)	147 (6)
178 (1)	163 (1)	162 (1)	173 (1)	146 (3)	148 (4)	165 (1)
188 (2)	174 (1)	176 (1)	184 (1)	165 (1)	158 (1)	179 (1)
	186 (1)	194 (1)	194 (1)	185 (1)	174 (1)	192 (2)
	193 (1)			194 (1)	189 (1)	

Table 2.3 (Continued)

USD9704	USD9705	USD9706	USD9707	USD9708	USD9709	USD9710
13 (1)	10 (1)	13 (1)	16 (1)	14 (1)	13 (1)	8 (1)
27 (2)	23 (1)	22 (1)	34 (6)	34 (2)	26 (6)	24 (6)
43 (5)	42 (4)	54 (5)	46 (4)	47 (6)	44 (6)	37 (6)
56 (5)	54 (5)	72 (4)	61 (4)	61 (4)	59 (5)	52 (5)
68 (4)	67 (4)	85 (5)	78 (5)	81 (5)	78 (5)	59 (4)
83 (5)	82 (5)	94 (2)	86 (1)	92 (6)	93 (3)	72 (5)
97 (3)	93 (2)	108 (3)	102 (5)	107 (5)	105 (5)	88 (4)
104 (3)	104 (3)	122 (5)	116 (4)	117 (3)	115 (2)	102 (4)
113 (1)	119 (3)	137 (3)	132 (3)	135 (3)	124 (4)	113 (3)
124 (3)	133 (3)	147 (3)	146 (3)	148 (2)	133 (3)	127 (4)
133 (2)	144 (3)	163 (1)	158 (2)	157 (3)	148 (3)	143 (4)
146 (2)	155 (1)	184 (2)	168 (2)	185 (3)	162 (3)	162 (3)
167 (1)	169 (1)	192 (1)	181 (2)	192 (1)	170 (1)	177 (2)
177 (2)	176 (1)		193 (1)		185 (2)	187 (2)
188 (1)	183 (1)				191 (1)	192 (1)
194 (2)	192 (1)				197 (1)	

The LMW band number differed from a minimum of 12 to a maximum of 16. The cultivars with the highest number of LMW bands were USD 9704 (16 bands), USD 9705 (16 bands), USD 9709 (16 bands) and USD 9710 (15 bands). The cultivars with the lowest amount of bands, that is 12 bands, were Moni, Nordum, Orania, USD 9503, USD 9511 and USD 9609. The average amount of bands for the durum wheats tested were thus, 13,48 bands per cultivar. This is in accordance with literature, as Gupta and Shepherd (1988) found that cultivars usually possess from two to nine (usually three or more) B subunits and Denery-Papini *et al* (1995) found that as many as 16 LMW glutenin subunits may be expressed in a single cultivar.

The standard deviations of all the cultivars were tested and using the NCSS 2000 program, box plots were drawn to see if there was any overlapping of bands. Figure 2.3 gives all the cultivars with the standard deviations of the different bands.

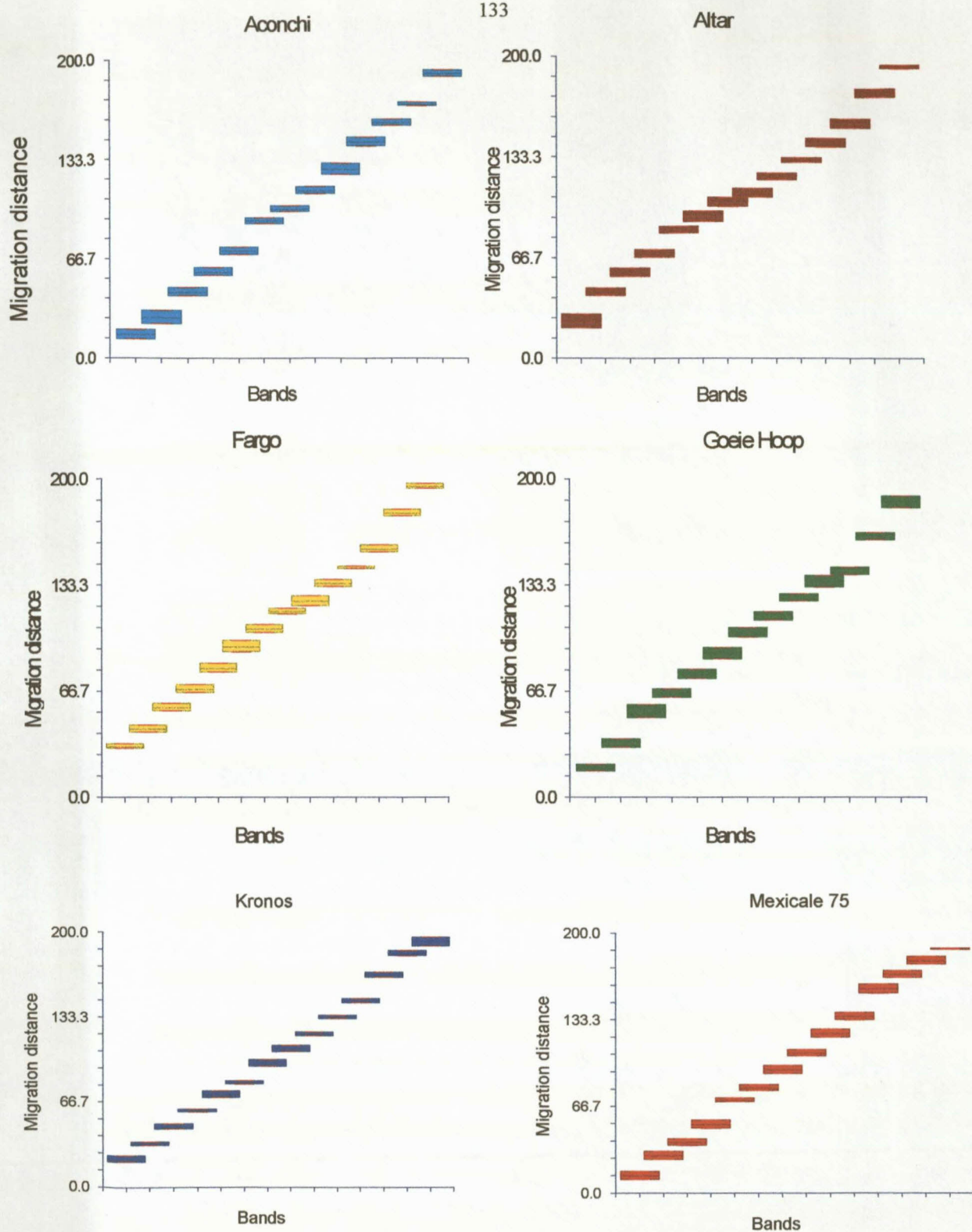


Figure 2.3. The standard deviations of the cultivars to indicate the possible overlapping of bands. The vertical axes gives the migration distance of the bands and the horizontal axes gives the different bands starting from one.

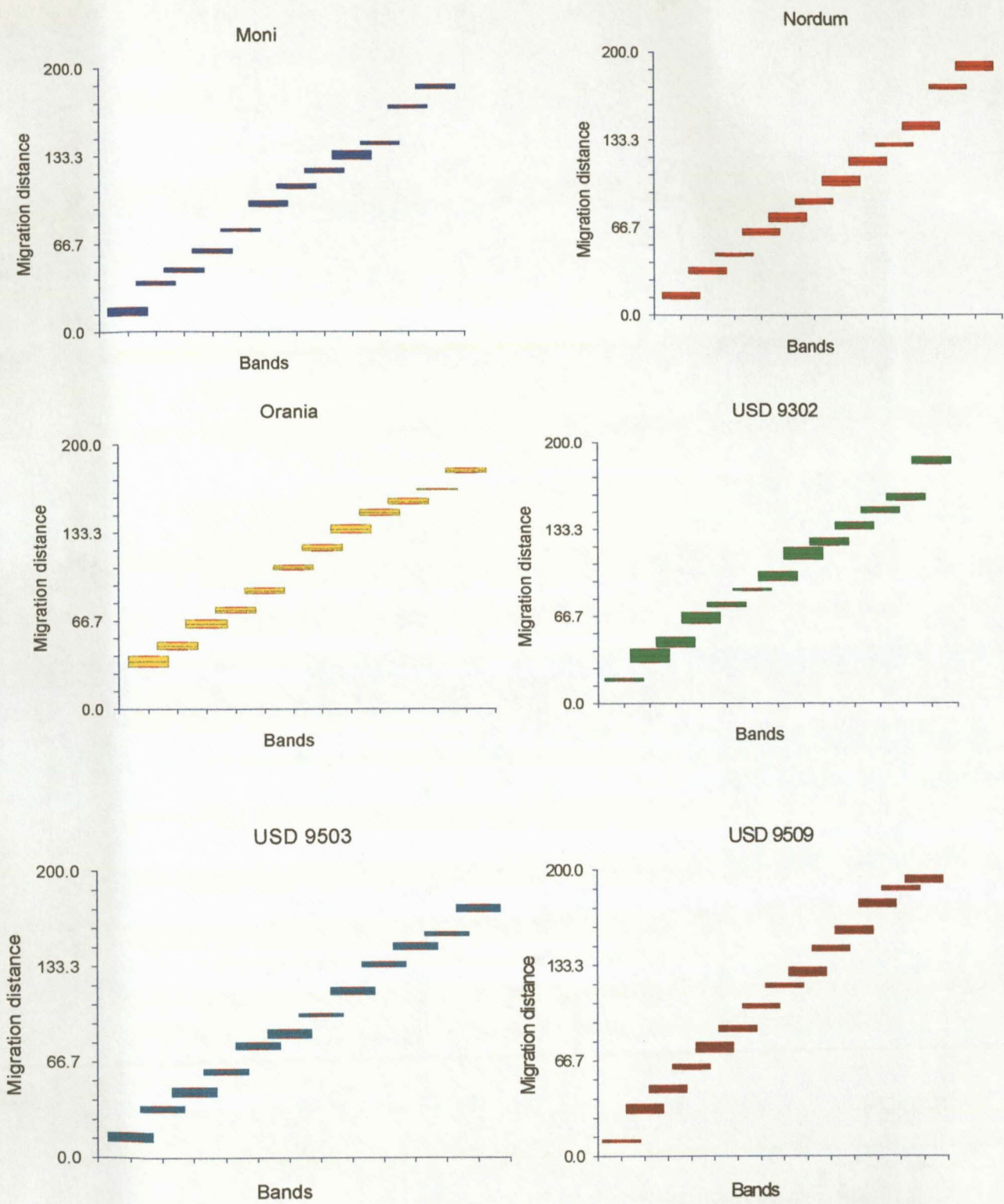


Figure 2.3 (Continued)

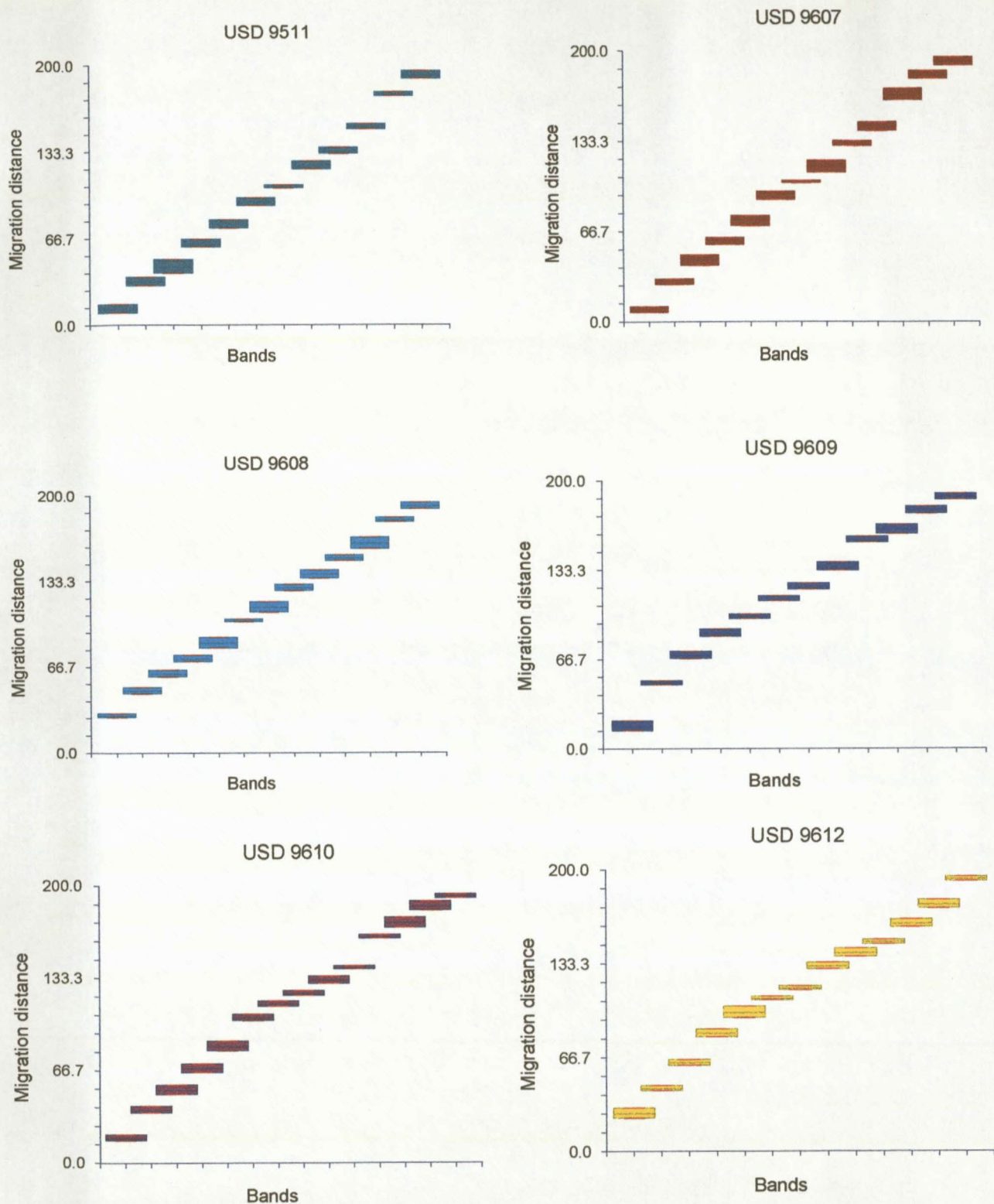


Figure 2.3 (Continued)

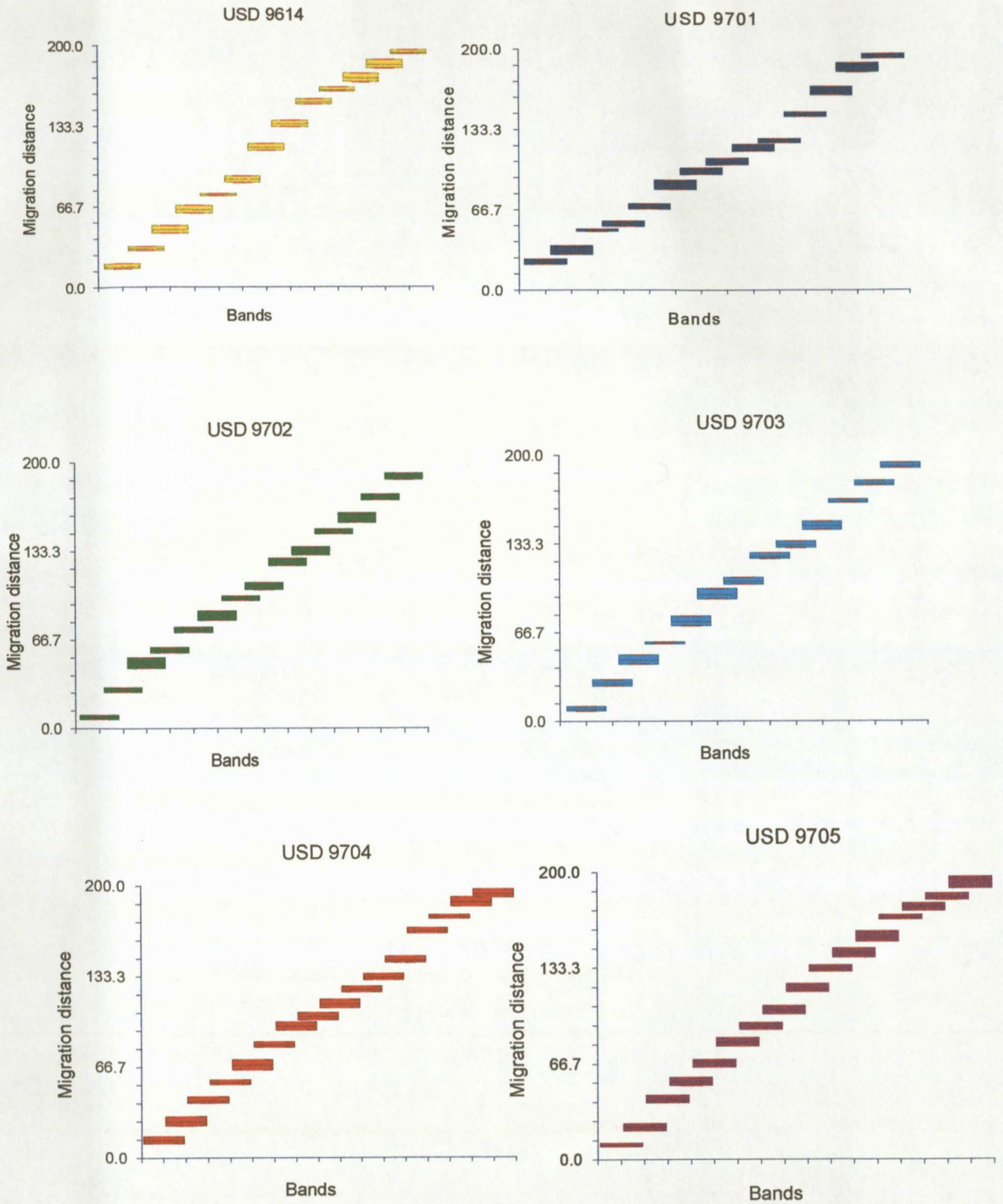
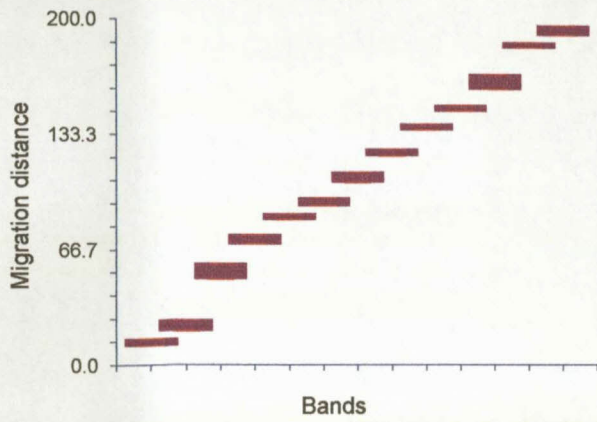
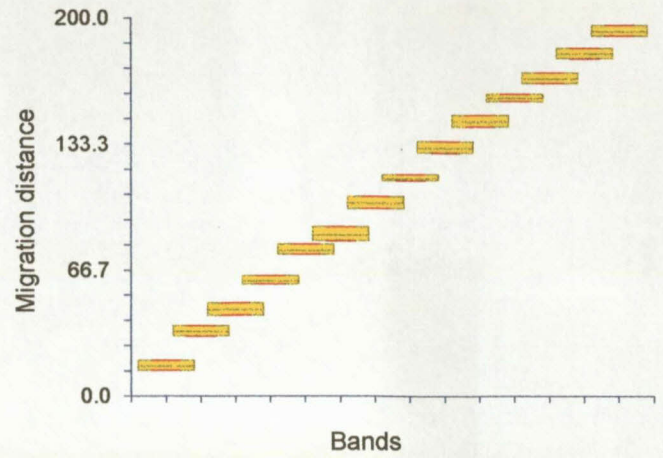


Figure 2.3 (Continued)

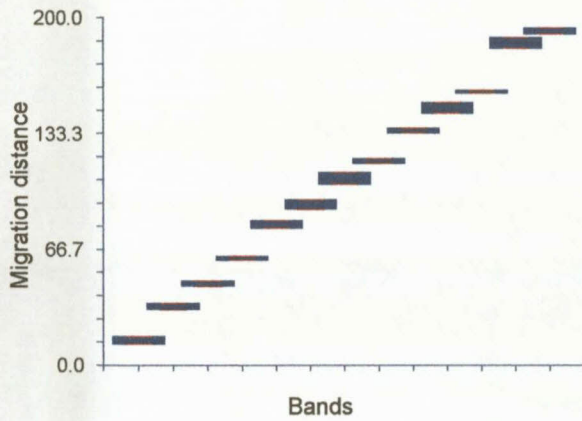
USD 9706



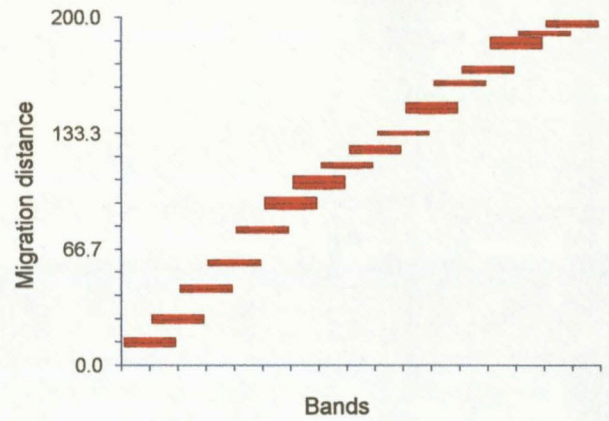
USD 9707



USD 9708



USD 9709



USD 9710

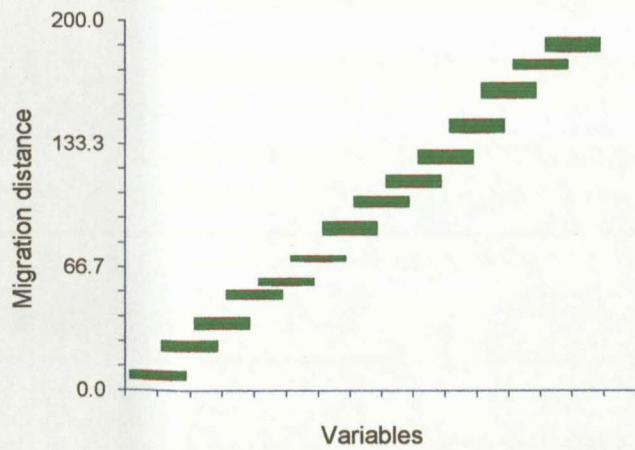


Figure 2.3 (Continued)

The bands that definitely overlap according to the standard deviations were taken into account to determine the class intervals. They were:

- 1) Bands five and six, molecular distance 85 and 94 and bands seven and eight, molecular distance 103 and 110 of the cultivar Altar.
- 2) Bands eight and nine, molecular distance 117 and 123 of the cultivar Fargo.
- 3) Bands 10 and 11, molecular distance 136 and 142 of the cultivar Goeie Hoop.
- 4) Bands two and three, molecular distance 37 and 47 and bands eight and nine, molecular distance 115 and 124 of the cultivar USD 9302.
- 5) The last two bands of USD 9509 with molecular distances of 187 and 193.
- 6) Bands nine and 10 of USD 9609 with molecular distances of 156 and 164.
- 7) The last two bands of USD 9610 with molecular distances of 186 and 193.
- 8) Bands nine and ten, molecular distance 141 and 149 of USD 9612.
- 9) Bands three and four, molecular distance 50 and 55, bands seven and eight, molecular distance 99 and 106 and bands nine and 10, molecular distance 118 and 124 of USD 9701.
- 10) Bands nine and 10, molecular distance 125 and 133 of USD 9702.
- 11) Bands six and seven, molecular distance 96 and 105 of USD 9703.
- 12) Bands seven and eight, molecular distance 97 and 104 and the last two bands with molecular distances of 188 and 194 of USD 9704.
- 13) Bands 14 and 15, molecular distance 176 and 183 of USD 9705.
- 14) Bands five and six, molecular distance 78 and 86 of USD 9707.
- 15) The last two bands of USD 9708 with molecular distance of 185 and 192.
- 16) Bands 14 and 15, molecular distance 185 and 191 of USD 9709.
- 17) Bands four and five, molecular distance 52 and 59 and the last two bands, molecular distance 187 and 192 of USD 9710.

All the different bands of all the cultivars were drawn on graph paper and the possible double bands were taken into account (thus the overlapping of bands) and it was decided that bands that are five molecular distance units apart will be considered as the same band. That means that bands with molecular distances of five and nine will be considered as the same band. In Table 2.4 all the different cultivars with their banding patterns are shown. The first column shows the different class intervals. Please note that bands that are in two following class intervals are considered as double bands. For

example in the cultivar Altar, the bands with molecular distances 85 to 89 and 90 to 94 are considered as a double band.

In all the cultivars tested there were 22 possible double bands. This will be discussed further in Chapter 3 to see if these double bands are inherited through genome A and B and if only one genome is responsible for the expression of double bands.

This distribution of bands resulted in 39 different LMW groups, which is in accordance with Gupta and Shepherd (1990) who found 40 different B and C subunits in the cultivars they tested.

Table 2.4 The different class intervals with the LMW bands of the cultivars.

	Aconchi	Altar	Fargo	G. Hoop	Kronos	Mexicale	Moni
5-9							
10-14						=====	
15-19	=====			=====			=====
20-24					=====		
25-29	=====	=====				=====	
30-34			=====	=====	=====		
35-39						=====	=====
40-44		=====	=====				
45-49	=====				=====		=====
50-54				=====		=====	
55-59	=====	=====	=====				
60-64					=====		=====
65-69			=====	=====			
70-74	=====	=====			=====	=====	
75-79				=====			=====
80-84			=====		=====	=====	
85-89		=====		=====			
90-94	=====	=====					
95-99			=====		=====	=====	=====
100-104	=====	=====		=====			
105-109		=====	=====		=====	=====	
110-114	=====			=====			=====
115-119			=====				
120-124		=====	=====		=====	=====	=====
125-129	=====			=====			
130-134		=====			=====		=====
135-139			=====	=====		=====	
140-144		=====	=====	=====			=====
145-149	=====				=====		
150-154							
155-159	=====	=====	=====			=====	
160-164				=====			
165-169					=====	=====	
170-174	=====						=====
175-179		=====	=====			=====	
180-184					=====		
185-189				=====		=====	=====
190-194	=====	=====			=====		
195-200			=====				

Table 2.4 (Continued)

	Nordum	Orania	USD9302	USD9303	USD9309	USD9311	USD9307
5-9							
10-14							
15-19							
20-24							
25-29							
30-34							
35-39							
40-44							
45-49							
50-54							
55-59							
60-64							
65-69							
70-74							
75-79							
80-84							
85-89							
90-94							
95-99							
100-104							
105-109							
110-114							
115-119							
120-124							
125-129							
130-134							
135-139							
140-144							
145-149							
150-154							
155-159							
160-164							
165-169							
170-174							
175-179							
180-184							
185-189							
190-194							
195-200							

Table 2.4 (Continued)

	USD9608	USD9609	USD9610	USD9612	USD9614	USD9701	USD9702
5-9							—
10-14							
15-19		—	—		—		
20-24						—	
25-29	—			—			—
30-34					—	—	
35-39			—				
40-44							
45-49	—	—		—	—		—
50-54			—			—	
55-59						—	—
60-64	—			—	—		
65-69			—			—	
70-74	—	—					—
75-79					—		
80-84				—			
85-89	—	—	—		—	—	—
90-94							
95-99		—		—		—	—
100-104	—						
105-109			—	—		—	—
110-114	—	—					
115-119			—	—	—	—	
120-124		—	—			—	
125-129	—						—
130-134			—	—			—
135-139	—	—			—		
140-144			—	—			
145-149				—		—	—
150-154	—				—		
155-159		—					—
160-164	—	—	—	—	—		
165-169						—	
170-174			—		—		—
175-179		—		—			
180-184	—				—		
185-189		—	—			—	—
190-194	—		—	—	—	—	
195-200							—

Table 2.4 (Continued)

	USD9703	USD9704	USD9705	USD9706	USD9707	USD9708	USD9709	USD9710
5-9								
10-14								
15-19								
20-24								
25-29								
30-34								
35-39								
40-44								
45-49								
50-54								
55-59								
60-64								
65-69								
70-74								
75-79								
80-84								
85-89								
90-94								
95-99								
100-104								
105-109								
110-114								
115-119								
120-124								
125-129								
130-134								
135-139								
140-144								
145-149								
150-154								
155-159								
160-164								
165-169								
170-174								
175-179								
180-184								
185-189								
190-194								
195-200								

Variation between cultivars

There were clear differences between the cultivars. None of the cultivars were identical. This makes LMW glutenins very suitable for cultivar identification. The assignment of proteins into discreet classes was based on migration distances and proteins with similar molecular size, but different amino acid composition (or quality effects) could have been included in the same molecular weight class. This could have an effect on protein subunits and quality parameters (Primard *et al*, 1991).

The occurrence of bands in the different groups

Table 2.5 gives a summary of the different class intervals (hereafter called groups), the migration distance of the group, the occurrence of bands in the group and the percentage of occurrence.

Table 2.5. The occurrence of bands in the different groups of LMW glutenins in the 29 South African durum cultivars studied.

Group	Migration distance	Occurrence	Percentage (%)
1	5-9	3	10
2	10-14	10	35
3	15-19	9	31
4	20-24	5	17
5	25-29	9	31
6	30-34	12	41
7	35-39	6	21
8	40-44	5	17
9	45-49	18	62
10	50-54	7	24
11	55-59	9	31
12	60-64	13	45
13	65-69	7	24
14	70-74	11	38
15	75-79	11	38

Table 2.5 (Continued)

Group	Migration distance	Occurrence	Percentage (%)
16	80-84	7	24
17	85-89	16	55
18	90-94	7	24
19	95-99	12	41
20	100-104	11	38
21	105-109	15	52
22	110-114	7	24
23	115-119	14	48
24	120-124	15	52
25	125-129	7	24
26	130-134	13	45
27	135-139	11	38
28	140-144	10	35
29	145-149	15	52
30	150-154	3	10
31	155-159	13	45
32	160-164	9	31
33	165-169	9	31
34	170-174	7	24
35	175-179	12	41
36	180-184	7	24
37	185-189	14	48
38	190-194	20	69
39	195-200	2	7

The groups that were present the most, were group 9, molecular distance 45-49 (in 62 percent of the cultivars tested) and group 38, molecular distance 190-194 (in 69 percent of the cultivars tested). Group 1 and 30 were only present in three cultivars and group 39 was only present in two cultivars.

The intensities of the bands in the different groups

The different groups had specific intensities. Table 2.6 gives a summary of the different groups and the intensities in classes from one (very light) to five (very dark). Class six has no specific intensity.

Table 2.6. The intensities of the bands in the different groups.

Group	Occur	Class1	Class2	Class3	Class4	Class5	Class6
1	3	3	0	0	0	0	0
2	10	9	1	0	0	0	0
3	9	6	2	1	0	0	0
4	5	3	0	1	0	0	1
5	9	1	3	2	1	0	2
6	12	0	1	2	5	2	2
7	6	0	0	0	3	2	1
8	5	0	0	0	2	1	2
9	18	0	1	0	4	12	1
10	7	0	0	0	1	6	0
11	9	0	0	0	2	7	0
12	13	0	0	0	6	7	0
13	7	0	0	0	4	3	0
14	11	0	0	0	4	6	1
15	11	0	0	0	1	7	3
16	7	1	0	1	1	3	1
17	16	2	1	0	5	7	1
18	7	1	2	1	1	0	2
19	12	2	3	2	2	0	3
20	11	1	2	4	3	1	0
21	15	1	3	5	3	2	1
22	7	1	0	5	1	0	0
23	14	1	2	6	5	0	0
24	15	0	3	5	4	2	1
25	7	0	0	4	3	0	0

Table 2.6 (Continued)

Group	Occur	Class1	Class2	Class3	Class4	Class5	Class6
26	13	1	1	8	2	1	0
27	11	0	1	8	2	0	0
28	10	1	3	3	3	0	0
29	15	1	2	6	2	0	4
30	3	0	0	0	2	0	1
31	13	6	5	2	0	0	0
32	9	7	0	2	0	0	0
33	9	6	3	0	0	0	0
34	7	6	1	0	0	0	0
35	12	7	5	0	0	0	0
36	7	5	2	0	0	0	0
37	14	7	6	1	0	0	0
38	20	17	3	0	0	0	0
39	2	2	0	0	0	0	0

Group 1

In the three cultivars that contained group 1, this band was always expressed as a very light band (intensity class 1).

Group 2

Nine of the 10 bands in this group were very light (class 1) and one was light (class 2).

Group 3

Six bands in this group were very light (class 1), two were light (class 2) and one band was of medium intensity (class 3).

Group 4

Three bands in group 4 were expressed as very light bands, one was of medium intensity and one could not be assigned to any specific intensity class (class 6).

Group 5

One band in this group was very light, three were light, two were of medium intensity, one was dark and two were in class 6.

Group 6

One band was light, two were of medium intensity, five were dark, two were very dark and two were in class 6.

Group 7

Five of the six bands were dark to very dark and only one band could not be assigned to any intensity class.

Group 8

Three of the five bands were dark to very dark and two could not be assigned to any specific intensity class.

Group 9

Sixteen of the 18 bands were dark to very dark, while one was light. One band could not be assigned to any specific intensity class.

Group 10

All seven bands were dark to very dark.

Group 11

All nine bands were dark to very dark.

Group 12

The 13 bands were all expressed as dark to very dark.

Group 13

All seven bands were dark to very dark.

Group 14

Ten of the 11 bands were dark to very dark and only one could not be assigned to any intensity class.

Group 15

Eight bands were dark to very dark and three bands could not be assigned to any intensity class.

Group 16

One band in this group was very light, one was of medium intensity, one was dark, three were very dark and one could not be assigned to any intensity class.

Group 17

Twelve of the 16 bands were dark to very dark, three were light to very light and one could not be assigned to any intensity class.

Group 18

Three of the bands were light to very light, one was of medium intensity, one was dark and two could not be assigned to any intensity class.

Group 19

Five of the bands were light to very light, two were of medium intensity, two were dark and three could not be assigned to any intensity class.

Group 20

Three of the bands were light to very light, while four of the bands were dark to very dark. Four of the bands were of medium intensity.

Group 21

Four of the bands were light to very light, while five of the bands were dark to very dark. Five of the bands were of medium intensity and one could not be assigned to any specific intensity class.

Group 22

Five of the seven bands were of medium intensity, one band was very light and one band was dark.

Group 23

Six of the bands were of medium intensity, five were very dark and three bands were light to very light.

Group 24

Three of the bands light, five were of medium intensity, six were dark to very dark and one could not be assigned to any specific intensity class.

Group 25

Four of the bands were of medium intensity and three were expressed as dark bands.

Group 26

Eight of the bands were of medium intensity, two of the bands were light to very light and three of the bands were dark to very dark.

Group 27

Eight of the bands were of medium intensity, one band was light and two bands were dark.

Group 28

Four of the bands were light to very light, three were of medium intensity and three were dark bands.

Group 29

Three of the bands were light to very light, six were of medium intensity, two were dark and four could not be assigned to any intensity class.

Group 30

Two of the three bands were dark and one could not be assigned to any group.

Group 31

Eleven of the 13 bands were light to very light and two were of medium intensity.

Group 32

Seven of the bands were very light and two were of medium intensity.

Group 33

All nine bands were light to very light.

Group 34

All the bands were light to very light.

Group 35

All the bands were light to very light.

Group 36

All the bands were light to very light.

Group 37

Thirteen of the bands were light to very light and one of the bands was of medium intensity.

Group 38

All the bands were light to very light.

Group 39

Both bands were very light.

It is clear that if one looks at this data that the bands in some groups were expressed as light or medium or dark bands. The following groups were mostly expressed as light to very light bands: groups one to three and groups 31 to 39. Groups seven to 15 and group 17 were mostly expressed as dark to very dark bands. Group 22, 26 and 27 were mostly of medium intensity. In the other groups the intensities of the bands vary. Gupta and Shepherd (1990) also found different intensity bands.

Correlation between the LMW groups of bands

The following significant correlations were observed between the LMW groups of bands ($p < 0.05$):

1. Group 1 was positively correlated with group 14 ($r = 0.44$).
2. Group 2 was negatively correlated with group 3 ($r = -0.49$) and group 28 ($r = -0.37$).
3. Group 3 was negatively correlated with group 16 ($r = -0.38$) and also with group 21 ($r = -0.55$).
4. Group 4 was negatively correlated with group 9 ($r = -0.4$) and positively correlated with group 10 ($r = 0.6$).
5. Group 5 was negatively correlated with group 6 ($r = -0.56$) and positively correlated with group 11 ($r = 0.52$).
6. Group 6 was negatively correlated with group 7 ($r = -0.43$) and positively correlated with group 12 ($r = 0.51$) and group 23 ($r = 0.45$).
7. Group 7 was negatively correlated with group 38 ($r = -0.39$).
8. Group 8 was negatively correlated with group 9 ($r = -0.58$) and group 12 ($r = -0.41$). It was positively correlated with group 11 ($r = 0.48$), group 13 ($r = 0.38$), group 16 ($r = 0.38$), group 18 ($r = 0.38$) and with group 39 ($r = 0.6$).
9. Group 9 was negatively correlated with group 10 ($r = -0.72$), group 11 ($r = -0.4$), group 13 ($r = -0.56$) and with group 37 ($r = -0.38$). It was positively correlated with group 12 ($r = 0.71$).
10. Group 10 was negatively correlated with group 12 ($r = -0.51$) and positively correlated with group 13 ($r = 0.44$) and group 37 ($r = 0.42$).
11. Group 11 was negatively correlated with group 12 ($r = -0.61$), group 27 ($r = -0.37$) and with group 36 ($r = -0.38$). It was positively correlated with group 39 ($r = 0.41$).
12. Group 12 was negatively correlated with group 13 ($r = -0.51$), group 24 ($r = -0.38$) and with group 37 ($r = -0.46$). It was positively correlated with group 30 ($r = 0.38$) and group 37 ($r = -0.46$).
13. Group 13 was negatively correlated with group 14 ($r = -0.44$) and positively correlated with group 37 ($r = 0.42$).
14. Group 14 was negatively correlated with group 15 ($r = -0.61$) and 23 ($r = -0.47$) and positively correlated with group 25 ($r = 0.39$).
15. Group 15 was negatively correlated with group 16 ($r = -0.44$).
16. Group 16 was negatively correlated with group 17 ($r = -0.63$).

17. Group 17 was negatively correlated with group 19 ($r = -0.37$) and group 26 ($r = -0.44$).
18. Group 18 was negatively correlated with group 19 ($r = -0.47$) and positively correlated with group 38 ($r = 0.38$).
19. Group 19 was negatively correlated with group 20 ($r = -0.51$) and positively correlated with group 24 ($r = 0.53$).
20. Group 20 was negatively correlated with group 21 ($r = -0.67$) and with group 24 ($r = -0.52$). It was positively correlated group 22 ($r = 0.39$) and group 25 ($r = 0.39$).
21. Group 21 was negatively correlated with group 22 ($r = -0.58$) and positively correlated with group 24 ($r = 0.45$).
22. Group 22 was negatively correlated with group 23 ($r = -0.55$) and positively correlated with group 25 ($r = 0.44$).
23. Group 24 was negatively correlated with group 25 ($r = -0.58$).
24. Group 25 was negatively correlated with group 33 ($r = -0.38$).
25. Group 26 was negatively correlated with group 27 ($r = -0.71$).
26. Group 27 was negatively correlated with group 38 ($r = -0.55$).
27. Group 28 was negatively correlated with group 29 ($r = -0.61$).
28. Group 31 was negatively correlated with group 32 ($r = -0.46$) and group 38 ($r = -0.45$).
29. Group 32 was negatively correlated with group 33 ($r = -0.45$).
30. Group 33 was negatively correlated with group 34 ($r = -0.38$).
31. Group 34 was negatively correlated with group 35 ($r = -0.47$).
32. Group 36 was negatively correlated with group 37 ($r = -0.55$).

The correlations reveals that some LMW glutenin bands are not present together in the same cultivar, that is the combinations occur as alternatives to each other. This was also found by Gupta and Shepherd (1988). The correlations of the different groups will be further investigated in Chapter 3.

The apparent molecular weight of the different groups

The apparent molecular weights of the different groups were determined. Literature reports the molecular weights of LMW glutenins in the range of 30 to 51 kDa (Gupta *et al*, 1995). In this study the molecular range varied from 29 kDa in group 1 to 51 kDa in group 39. Table 2.7 is a summary of all the groups together with the apparent molecular weight of the group.

Table 2.7 The groups of LMW glutenin subunits with their molecular weights

Group	Molecular weight	Group	Molecular weight
1	51	2	50.5
3	50	4	49.5
5	49	6	48
7	47.5	8	47
9	46.5	10	46
11	45	12	44.5
13	44	14	43.5
15	43	16	42.5
17	41.5	18	41
19	40.5	20	40
21	39	22	38.5
23	38	24	37.5
25	37	26	36
27	35.5	28	35
29	34.5	30	34
31	33.5	32	33
33	32	34	33
35	31	36	31.5
37	30	38	30.5
39	29		29.5

Genetic distances

Figure 2.4 shows a dendrogram that was drawn from the data. It is clear from the dendrogram that some cultivars are closely related to each other. The following cultivars are closely related ($D < 0.15$, that is 15 percent) (in brackets are the actual differences between them):

1. USD 9608 and Orania (0.15)
2. USD 9704 and USD 9705 (0.14)

3. USD 9702 and USD 9709 (0.14)
4. Kronos and USD 9701 (0.11)
5. Goeie Hoop and USD 9302 (0.08)
6. Altar and Fargo (0.11)
7. Moni and USD 9511 (0.12)
8. USD 9603 and USD 9707 (0.09)
9. USD 9503 and USD 9707 (0.06)

Aconchi, USD 9614 and USD 9609 are not closely related to any other cultivar. The highest amount of dissimilarity ($D > 60$, that is 60 percent) were between the following cultivars:

1. Acconchi and USD 9609 (0.603)
2. Kronos and USD 9609 (0.67)
3. Mexicale and Orania (0.63)
4. Orania and USD 9702 (0.62)
5. Orania and USD 9704 (0.73)
6. Orania and USD 9705 (0.73)
7. USD 9609 and USD 9701 (0.72)
8. USD 9609 and USD 9702 (0.69)
9. USD 9609 and USD 9704 (0.84)
10. USD 9609 and USD 9705 (0.81)
11. USD 9609 and USD 9709 (0.65)
12. USD 9609 and USD 9710 (0.897)
13. USD 9612 and USD 9704 (0.69)
14. USD 9612 and USD 9705 (0.68)
15. USD 9612 and USD 9710 (0.74)
16. USD 9614 and USD 9704 (0.65)
17. USD 9614 and USD 9710 (0.62)

There was thus genetic diversity in South African durum wheat. The genetic differences between the cultivars are given in Table 2.8.

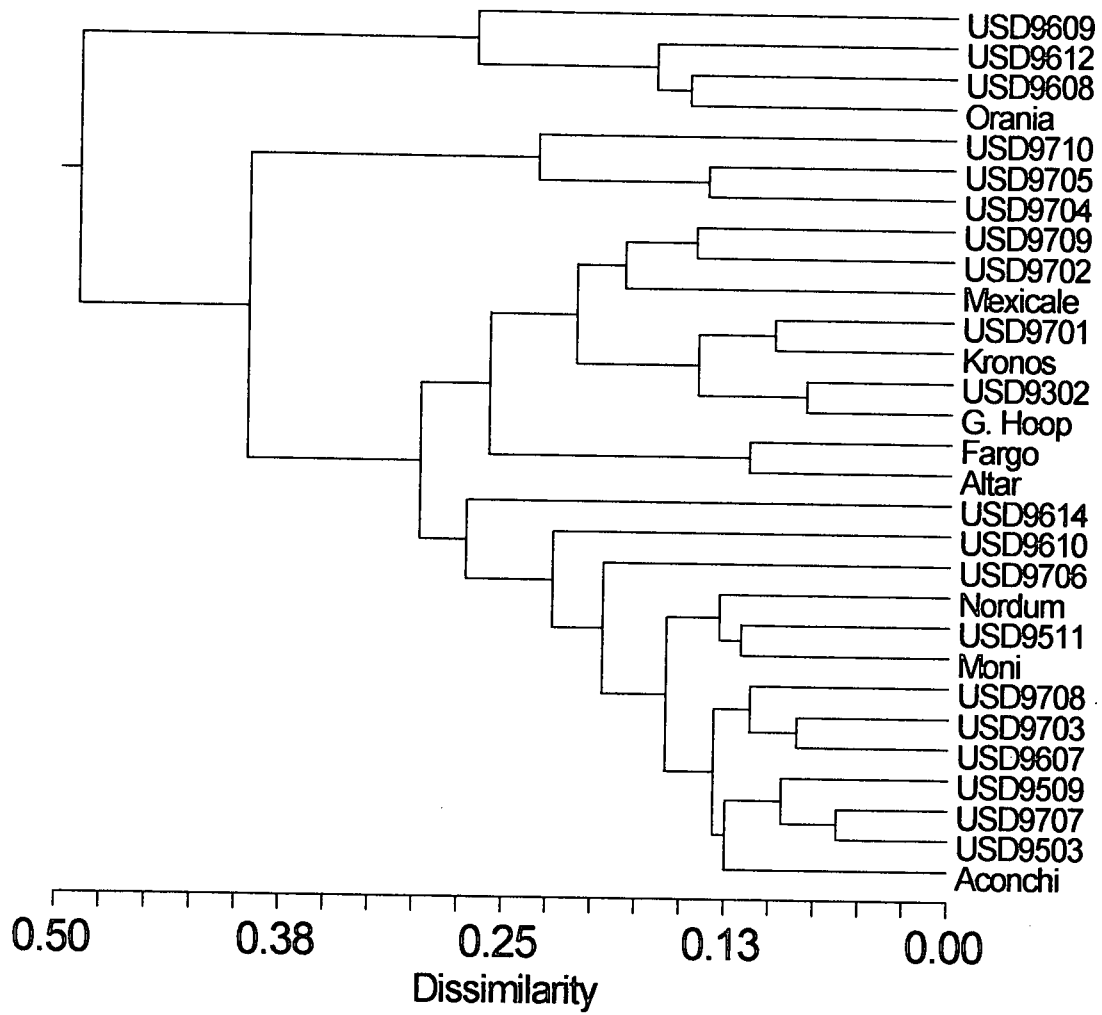


Figure 2.4. A dendrogram of all the durum cultivars tested to show the genetic distance between the cultivars.

Table 2.8 The genetic distances between the cultivars tested.

	Aconchi	Altar	Fargo	G. Hoop	Kronos	Mexicale	Moni	Nordum	Orania	USD9302	USD9503
Aconchi	0	0.34	0.32	0.18	0.18	0.17	0.2	0.18	0.52	0.17	0.12
Altar	0.34	0	0.11	0.19	0.22	0.34	0.36	0.37	0.47	0.2	0.31
Fargo	0.32	0.11	0	0.19	0.23	0.36	0.34	0.37	0.41	0.21	0.32
G. Hoop	0.18	0.19	0.19	0	0.13	0.24	0.26	0.26	0.48	0.08	0.18
Kronos	0.18	0.22	0.23	0.13	0	0.16	0.3	0.26	0.56	0.11	0.2
Mexicale	0.17	0.34	0.36	0.24	0.16	0	0.29	0.23	0.63	0.21	0.19
Moni	0.2	0.36	0.34	0.26	0.3	0.29	0	0.13	0.4	0.28	0.18
Nordum	0.18	0.37	0.37	0.26	0.26	0.23	0.13	0	0.48	0.26	0.16
Orania	0.52	0.47	0.41	0.48	0.56	0.63	0.4	0.48	0	0.51	0.49
USD9302	0.17	0.2	0.21	0.08	0.11	0.21	0.28	0.26	0.51	0	0.18
USD9503	0.12	0.31	0.32	0.18	0.2	0.19	0.18	0.16	0.49	0.18	0
USD9509	0.13	0.32	0.32	0.19	0.21	0.22	0.14	0.13	0.48	0.19	0.08
USD9511	0.23	0.44	0.43	0.33	0.36	0.32	0.12	0.13	0.44	0.34	0.21
USD9607	0.12	0.4	0.39	0.25	0.26	0.23	0.14	0.11	0.51	0.25	0.13
USD9608	0.38	0.37	0.3	0.34	0.41	0.49	0.29	0.35	0.15	0.36	0.36
USD9609	0.6	0.59	0.56	0.58	0.67	0.72	0.46	0.53	0.25	0.61	0.55
USD9610	0.26	0.27	0.25	0.22	0.3	0.35	0.16	0.25	0.31	0.25	0.25
USD9612	0.45	0.41	0.37	0.39	0.49	0.57	0.35	0.43	0.18	0.42	0.43
USD9614	0.33	0.52	0.47	0.39	0.45	0.45	0.24	0.29	0.36	0.41	0.3
USD9701	0.22	0.24	0.25	0.17	0.1	0.2	0.34	0.32	0.6	0.17	0.27
USD9702	0.25	0.27	0.32	0.21	0.18	0.17	0.33	0.29	0.62	0.2	0.2
USD9703	0.15	0.4	0.38	0.24	0.29	0.27	0.12	0.15	0.46	0.25	0.13
USD9704	0.38	0.39	0.44	0.32	0.33	0.31	0.47	0.44	0.73	0.3	0.35
USD9705	0.32	0.44	0.48	0.32	0.34	0.26	0.42	0.37	0.73	0.3	0.29
USD9706	0.22	0.4	0.39	0.26	0.33	0.34	0.2	0.21	0.44	0.29	0.21
USD9707	0.13	0.26	0.26	0.15	0.16	0.18	0.17	0.16	0.47	0.15	0.06
USD9708	0.15	0.35	0.34	0.21	0.26	0.27	0.12	0.14	0.43	0.23	0.1
USD9709	0.24	0.29	0.32	0.21	0.23	0.2	0.27	0.27	0.56	0.21	0.19
USD9710	0.34	0.44	0.47	0.36	0.27	0.19	0.48	0.42	0.81	0.33	0.36

Table 2.8 (Continued)

	USD9509	USD9511	USD9607	USD9608	USD9609	USD9610	USD9612	USD9614	USD9701	USD9702	USD9703
Aconchi	0.13	0.23	0.12	0.38	0.6	0.26	0.45	0.33	0.22	0.25	0.15
Altar	0.32	0.44	0.4	0.37	0.59	0.27	0.41	0.52	0.24	0.27	0.4
Fargo	0.32	0.43	0.39	0.3	0.56	0.25	0.37	0.47	0.25	0.32	0.38
G. Hoop	0.19	0.33	0.25	0.34	0.58	0.22	0.39	0.39	0.17	0.21	0.24
Kronos	0.21	0.36	0.26	0.41	0.67	0.3	0.49	0.45	0.1	0.18	0.29
Mexicale	0.22	0.32	0.23	0.49	0.72	0.35	0.57	0.45	0.2	0.17	0.27
Moni	0.14	0.12	0.14	0.29	0.46	0.16	0.35	0.24	0.34	0.33	0.12
Nordum	0.13	0.13	0.11	0.35	0.53	0.25	0.43	0.29	0.32	0.29	0.15
Orania	0.48	0.44	0.51	0.15	0.25	0.31	0.18	0.36	0.6	0.62	0.46
USD9302	0.19	0.34	0.25	0.36	0.61	0.25	0.42	0.41	0.17	0.2	0.25
USD9503	0.08	0.21	0.13	0.36	0.55	0.25	0.43	0.3	0.27	0.2	0.13
USD9509	0	0.17	0.1	0.34	0.53	0.2	0.4	0.28	0.27	0.25	0.1
USD9511	0.17	0	0.14	0.35	0.46	0.24	0.4	0.22	0.41	0.37	0.13
USD9607	0.1	0.14	0	0.38	0.55	0.25	0.43	0.28	0.3	0.31	0.09
USD9608	0.34	0.35	0.38	0	0.31	0.2	0.16	0.31	0.45	0.51	0.34
USD9609	0.53	0.46	0.55	0.31	0	0.4	0.24	0.4	0.72	0.69	0.51
USD9610	0.2	0.24	0.25	0.2	0.4	0	0.24	0.29	0.33	0.35	0.22
USD9612	0.4	0.4	0.43	0.16	0.24	0.24	0	0.36	0.53	0.56	0.39
USD9614	0.28	0.22	0.28	0.31	0.4	0.29	0.36	0	0.5	0.51	0.23
USD9701	0.27	0.41	0.3	0.45	0.72	0.33	0.53	0.5	0	0.22	0.33
USD9702	0.25	0.37	0.31	0.51	0.69	0.35	0.56	0.51	0.22	0	0.34
USD9703	0.1	0.13	0.09	0.34	0.51	0.22	0.39	0.23	0.33	0.34	0
USD9704	0.45	0.52	0.46	0.63	0.84	0.52	0.69	0.65	0.34	0.25	0.48
USD9705	0.42	0.45	0.39	0.62	0.81	0.51	0.68	0.59	0.36	0.24	0.42
USD9706	0.18	0.2	0.18	0.33	0.46	0.23	0.34	0.24	0.38	0.37	0.16
USD9707	0.1	0.22	0.17	0.34	0.55	0.21	0.41	0.32	0.23	0.21	0.18
USD9708	0.1	0.15	0.12	0.3	0.49	0.19	0.35	0.24	0.31	0.33	0.11
USD9709	0.26	0.32	0.3	0.47	0.65	0.31	0.52	0.46	0.26	0.14	0.3
USD9710	0.38	0.51	0.4	0.67	0.9	0.52	0.74	0.62	0.28	0.22	0.44

Table 2.8 (Continued)

	USD9704	USD9705	USD9706	USD9707	USD9708	USD9709	USD9710
Aconchi	0.38	0.32	0.22	0.13	0.15	0.24	0.34
Altar	0.39	0.44	0.4	0.26	0.35	0.29	0.44
Fargo	0.44	0.48	0.39	0.26	0.34	0.32	0.47
G. Hoop	0.32	0.32	0.26	0.15	0.21	0.21	0.36
Kronos	0.33	0.34	0.33	0.16	0.26	0.23	0.27
Mexicale	0.31	0.26	0.34	0.18	0.27	0.2	0.19
Moni	0.47	0.42	0.2	0.17	0.12	0.27	0.48
Nordum	0.44	0.37	0.21	0.16	0.14	0.27	0.42
Orania	0.73	0.73	0.44	0.47	0.43	0.56	0.81
USD9302	0.3	0.3	0.29	0.15	0.23	0.21	0.33
USD9503	0.35	0.29	0.21	0.06	0.1	0.19	0.36
USD9509	0.45	0.42	0.18	0.1	0.1	0.26	0.38
USD9511	0.52	0.45	0.2	0.22	0.15	0.32	0.51
USD9607	0.46	0.39	0.18	0.17	0.12	0.3	0.4
USD9608	0.63	0.62	0.33	0.34	0.3	0.47	0.67
USD9609	0.84	0.81	0.46	0.55	0.49	0.65	0.9
USD9610	0.52	0.51	0.23	0.21	0.19	0.31	0.52
USD9612	0.69	0.68	0.34	0.41	0.35	0.52	0.74
USD9614	0.65	0.59	0.24	0.32	0.24	0.46	0.62
USD9701	0.34	0.36	0.38	0.23	0.31	0.26	0.28
USD9702	0.25	0.24	0.37	0.21	0.33	0.14	0.22
USD9703	0.48	0.42	0.16	0.18	0.11	0.3	0.44
USD9704	0	0.14	0.52	0.41	0.47	0.24	0.25
USD9705	0.14	0	0.46	0.38	0.42	0.23	0.5
USD9706	0.52	0.46	0	0.24	0.15	0.34	0.5
USD9707	0.41	0.38	0.24	0	0.15	0.22	0.35
USD9708	0.47	0.42	0.15	0.15	0	0.3	0.45
USD9709	0.24	0.23	0.34	0.22	0.3	0	0.29
USD9710	0.25	0.22	0.5	0.35	0.45	0.29	0

2.5 Conclusions

HMW glutenin subunits

Accurate identification of breeding material is very important to the plant breeder. HMW glutenin subunits are currently used in South Africa to distinguish between cultivars. According to Hemmingway (1993) the South African Wheat Board's laboratories have been doing electrophoresis since 1960. From the mid 1980's SDS-PAGE was used to investigate the HMW glutenin subunits and their influence on baking quality were determined. Currently, this technique is used to screen early generation lines (F3 and F4). It is also used for cultivar identification and purity determination.

This study showed that HMW glutenin could not distinguish between all the cultivars tested. It was, however, easy to read and interpret the different banding combinations. It can be used for initial cultivar identification and if there is no differences between the cultivars, one can look at the LMW glutenin subunits. This was also the finding of Labuschagne, Maartens and Oberholster (1998) who compared HMW and LMW glutenins and RAPD fingerprinting for cultivar identification.

LMW glutenin subunits

Thirty-nine different LMW glutenin bands were found in South African durum wheat cultivars. The different bands were divided into certain class intervals or groups that will be investigated further.

The 29 durum cultivars tested all had different LMW banding patterns. This makes LMW glutenins very suitable for cultivar identification. It is however, a more complex technique and computer software helps with the identification of the different bands. This computer software is expensive and not available to everyone.

The correlation between certain LMW bands will help to identify nomenclature that can be used for the identification of genetic markers. This will be further investigated in Chapter 3.

The bands in certain classes have specific intensities. Some classes did not have a specific intensity and it is possible that these bands are inherited by different genomes.

Genetic distances

The data obtained by the hierarchical clustering proves that there are enough differences between the LMW banding patterns of durum to be able to distinguish between them. There is also genetic variation between cultivars. However, the dissimilarity between some cultivars is very low and they probably came from the same genetic background.

Chapter 3

Nomenclature system

3.1 Introduction

Previous work has demonstrated that the *Glu-1* score, that is the HMW glutenin subunits account for a substantial proportion (50 to 70 percent) of the variation of bread-making quality for wheats from many countries. The results for Australian wheats, however, gave contrasting results, showing that the *Glu-1* score accounted for very little of the variation in bread-making resistance (only 19 percent). The generally claimed superiority of subunits 5+10 to subunits 2+12 was also not seen by Gupta *et al* (1991). The difficulties in accessing the relevance of the *Glu-1* composition can be explained by the *Glu-3* (LMW glutenin) composition. The *Glu-3* composition accounted for a higher proportion of variation (42 percent) than did the *Glu-1* score for a set of 48 Australian wheats. These data thus emphasise the previously little recognised importance of the LMW glutenin as significant components to the assessment of the bread-making potential of wheat flour (Gupta *et al*, 1991).

It is clear that the LMW glutenins can be used as genetic markers for bread-making quality. In Chapter 1 it was seen that the LMW glutenins could also be used for variety identification as it is very effective to distinguish between cultivars. To be of use as genetic markers or for the identification of varieties a nomenclature system must be used.

Gupta and Shepherd (1990) developed a nomenclature system for the LMW glutenin subunits. It will be discussed in detail in this chapter. The aim of this study is to see if this nomenclature system is sufficient for South African cultivars and if another system is needed that would be more effective.

3.2 Literature review

3.2.1 Gene location

The HMW subunits of glutenin are encoded by three *loci*, *Glu-A1*, *Glu-B1* and *Glu-D1*, located on the long arms of chromosomes 1A, 1B and 1D, respectively. The ω - and γ -gliadins are encoded by the *loci*, *Gli-A1*, *Gli-B1* and *Gli-D1*, located on the short arms of chromosomes 1A, 1B and 1D, respectively. The α - and β -gliadins are encoded by the *loci*, *Gli-A2*, *Gli-B2* and *Gli-D2*, located on the short arms of chromosomes 6A, 6B and 6D, respectively. Each of the *Gli-1 loci* is furthermore, closely linked to a locus coding for LMW glutenin subunits (*Glu-3*). There are several alleles at each of the *Glu-3* (located on chromosome 1), *Gli-1* (located on chromosome 1) and *Gli-2* (located on chromosome 6) *loci* and the potential number of permutations are enormous (Rogers *et al*, 1989).

There are two further series of homoeo*loci* coding for endosperm proteins on the short arms of group 1 chromosomes. *Gli-A3* and *Gli-B3* are coding for the ω -type gliadins and the D subunits of LMW glutenin respectively (Payne *et al*, 1988) and *Tri-1*, are coding for proteins (triticins) more closely related to globulins than prolamins (Rogers *et al*, 1989). See Table 3.1 for a summary of the chromosomal location of the storage proteins.

The genes controlling the synthesis of the major, basic structures of LMW glutenin are located on the short arms of chromosomes 1A, 1B and 1D, like the genes for the ω -gliadins and the majority of the γ -gliadins. The only genes of LMW glutenin subunits not located to chromosomes are the minor components which migrate to similar positions on IEF x SDS-PAGE gels as the group 6 α - and β -gliadins (Jackson *et al*, 1983).

The ω - and γ -gliadins genes on the short arms of chromosomes 1A, 1B and 1D are tightly linked and occur at the same complex *loci*. Since the LMW glutenin subunits are also coded by genes on the short arms of chromosomes 1A, 1B and 1D they could either be:

- 1) related to the γ -gliadins
- 2) related to the ω -gliadins
- 3) not related either to the ω -gliadins or to the γ -gliadins.

Possibility (2) above is unlikely, because the sulphur content, amino acid composition (Bietz and Wall, 1973) and electrophoretic mobility at pH 3.1 after reduction and alkylation of the major LMW glutenin subunits and ω -gliadins are different. These three properties of LMW subunits are similar to those of the γ -gliadins and it is thus supporting possibility (1). However, the resemblance may only be superficial, which make possibility (3) most likely (Jackson *et al*, 1983). Clearly, evolutionary relationships between LMW and gliadins must be investigated.

Table 3.1 Chromosomal location of the storage-protein genes of the wheat endosperm (Blackman and Payne, 1987).

Gene locus of alleles	Approx. no.	Chromosome Arm	Position	Storage proteins coded for
Glu-A1	6	1A	Long Close to centromere	HMW glutenin subunits
Glu-B1	11	1B	Long Close to centromere	
Glu-D1	6	1D	Long Close to centromere	
Gli-A1	7	1A	Short Towards the end	ω -gliadins, γ - gliadins, and LMW glutenin
Gli-B1	7	1B	Short Towards the end*	
Gli-D1	3	1D	Short Towards the end	
Gli-A2	3	6A	Short Towards the end	α -gliadins and β -gliadins
Gli-B2	4	6B	Short Towards the end*	
Gli-D2	3	6D	Short Towards the end	

*The genes on these chromosomes are located on the short-arm satellites (the terminal part of the chromosome 1Arm beyond the nucleolar organising region). The three homoeologous sets of *loci* are called collectively *Glu-1*, *Gli-1* and *Gli-2*.

The *Gli-1 loci* and the *Glu-3 loci* are linked tightly on the short arms of group 1 chromosomes. It was found that the *Glu-B3* locus was 1.8 to 2.0 cM from the *Gli-B1* locus. So far, no recombination has been found between the *Gli-1* and *Glu-3 loci* on chromosomes 1A and 1D. *Gli-3*-encoded gliadins can therefore, be considered as reliable markers of LMW glutenin subunits (Redaelli *et al*, 1995).

3.2.2 The need for a nomenclature system

Nomenclature is the language that researchers used to communicate their work. The system of naming must be uniform and agreed otherwise there will be confusion in the literature, as well as poor interaction between research groups. Nomenclature combines concepts and methods (Wrigley *et al*, 1996).

The nomenclature of LMW subunits is based on their apparent sizes on a SDS-PAGE gel as well as the complementary evidence provided by the locations of genes coding for them on the short arms of the group 1 chromosomes. There are more individual LMW subunits compared to the HMW subunits and the region of their mobility in a SDS-PAGE gel has been divided into the B and C regions. The B region corresponds to subunits with a molecular weight of 40 000 to 50 000 Daltons and the C region to subunits with a molecular weight of 30 000 to 40 000 Daltons (Vensel *et al*, 1997). The use of numbers to specify band mobility has not been generally successful. So far, there is not yet a classification system or description in terms of banding patterns that has been universally accepted (Jackson *et al*, 1996).

The ideal nomenclature system would be based on information of amino acid and nucleotide sequences, but this kind of data is not so widely available as to permit a systematic application (Wrigley *et al*, 1996).

3.2.3 Banding combinations of LMW glutenin subunits

Each cultivar possesses from two to nine (usually three or more) B subunits (Gupta and Shepherd, 1988), but as many as 16 LMW glutenin subunits may be expressed in a single cultivar (Denery- Papini *et al*, 1995). Examination of the banding combinations of some cultivars revealed that some LMW bands, or band combinations, were not present together in the same cultivar; the combinations occurred as alternatives to each other. Based on their mutual exclusiveness and the available expression data (Gupta and Shepherd, 1988) these subunit bands were assigned to three groups (Figure 3.1).

The chromosomal control of these combinations was determined by analysing the intervarietal substitution lines, and the results obtained clearly indicated that combinations within each group were controlled by genes on the same chromosome. Six

combinations were assigned to group 1. Pattern 'a' and 'b' correspond to Chinese Spring and Gabo bands, respectively, and are controlled by genes on chromosome 1Arm 1AS (Gupta and Shepherd, 1988).

Tests have shown that pattern 'd' in cultivar Orca is controlled by genes on chromosome 1AS. Many cultivars did not have any of the bands known to be controlled by chromosome 1A, and thus they were classified as null phenotypes (pattern 'e'). It should be noted that the faster moving band in pattern 'a' usually overlaps with a band controlled by 1DS in Chinese Spring and it is therefore not completely absent in these substitution lines (Gupta and Shepherd, 1990b).

Nine different combinations have been assigned to group two and each pattern had two or more B subunit bands (Figure 2.3). Combinations 'a' and 'b' were controlled by chromosome 1Arms 1BS in Chinese Spring and Gabo, respectively.

The five different combinations allocated to group 3 were associated with chromosome 1D. Combinations 'a' and 'b' corresponding to the bands in Chinese Spring and Gabo, respectively, were controlled by genes on the short arms of chromosomes 1D (Gupta and Shepherd, 1988).

They have also analysed 222 cultivars and detected 20 LMW subunit band combinations. Genetic evidence has indicated that 6, 9 and 5 of these combinations were controlled by allelic genes at *Glu-A3*, *Glu-B3* and *Glu-D3 loci* on the chromosome 1Arms 1AS, 1BS and 1DS, respectively.

In the analysis of the LMW subunit combinations of these cultivars some difficulties were encountered. The *Glu-B3* bands (group 2, Figure 2.3) represented a wide range of mobilities, and some of them overlapped with *Glu-A3* and *Glu-D3* bands (group 1 and 3, Figure 2.3). For example, the four slowest moving bands in combinations 'd', 'h', and 'i' often separated as two distinctly different darker bands, and the faster one has similar mobility to a *Glu-A3* band in combinations 'a' and 'c'. Similarly, the slowest *Glu-B3* band in pattern 'b' (group 2) often coincided with that of pattern *Glu-A3a* (group 1), but the former was usually paler and thinner, which helped to distinguish between them. Many cultivars had the darkest B subunit band (shown by * in Figure 2.3), but this did not show

mutual exclusiveness with any other bands. Further studies have revealed that this band represented two subunits in cultivars Gabo and Chinese Spring, one controlled by 1BS and the other by 1DS, and hence, this could not be assigned to any group. Based on this information, it was assumed for simplicity that this band in other cultivars was also controlled by 1BS + 1DS (although this may not be true for all cultivars) and, hence, one band of similar mobility to this has been included group 2 (*Glu-B3*) and 3 (*Glu-D3*) combinations respectively of all the cultivars exhibiting it. This composite band sometimes joined the adjacent faster moving B subunit in pattern *Glu-D3b* and formed an even thicker band. This composite band was, however, missing from most of the cultivars having *Glu-D3* combinations 'c', 'd', and 'e' and in some cases only a faint band was present in the background.

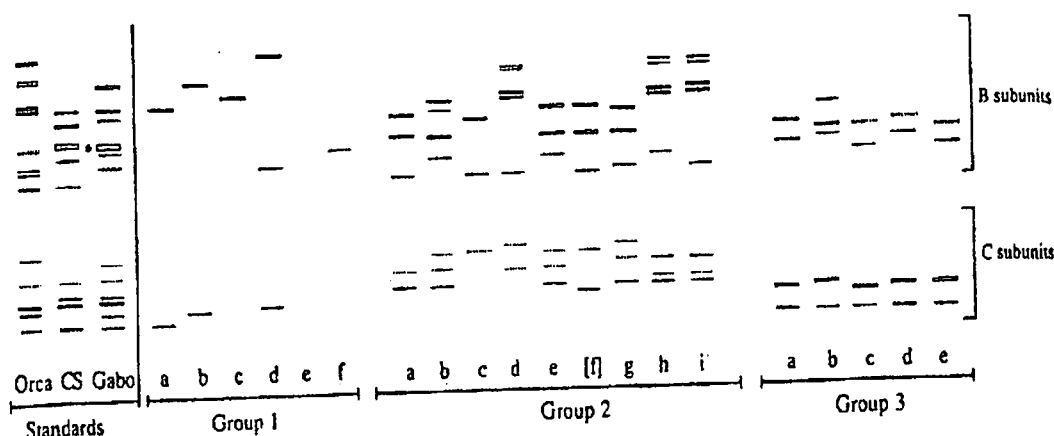


Fig. 2.3 Diagram showing the three groups of B and C subunit or subunit combinations identified by two-step SDS-PAGE analysis of 222 bread wheat cultivars. The grouping is based on the mutual exclusiveness of these bands or band combinations among the cultivars. This diagram also incorporates the information obtained on these subunits from analysis of substitution lines and the testcross progeny. Combinations 'a' and 'b' in each group are from Chinese Spring and Gabo, respectively. [f] = direct evidence for the chromosomal location of pattern 'f' has not been obtained. Faintly stained bands are shown by broken lines. * denotes that this thick band represents two bands of the same mobility, one controlled by 1BS and the other by 1DS in Chinese Spring and Gabo. These two bands have been included in group 2 and group 3 combinations of these as well as other cultivars having the denoted thick band (Gupta and Shepherd, 1990).

The number of band combinations found in the LMW glutenin subunits of hexaploid wheat is much lower than the expected number of such combinations on the basis of random association, indicating that genes coding for these bands are closely linked. Such close linkage has been demonstrated by Singh and Shepherd (1988) by detecting a low level of recombination between LMW glutenin subunits on chromosome 1B. The exact genetic and molecular nature of variation of LMW glutenin subunits is not known yet; however, rare recombination and point mutation can generate new LMW subunit combinations. Moreover, the analysis of nucleotide sequences of a LMW glutenin gene

has revealed the presence of repetitive sequences and if differences in their size and number exist between the genes, unequal crossing-over between these repeats might produce new subunits and will thus contribute towards the multiplicity and variation of LMW glutenin subunits.

The LMW subunits have shown the greatest polymorphism for chromosome 1B and this is in agreement with the hypothesis that the B chromosome in polyploid wheat is polyphyletic. The alternative hypothesis of a monophyletic origin of the B chromosome, however, cannot be rejected since the B chromosome may have undergone preferential changes during the evolution of the polyploid wheats. As a result, genes on chromosomes 1B coding for these storage proteins might have duplicated and diverged more extensively than the genes on chromosomes 1A and 1D.

The results also showed that chromosome 1A encoded for a minimum number of LMW subunits and many cultivars did not exhibit any band controlled by this chromosome. Interestingly, this chromosome 1A also controls a minimum number of HMW subunits of glutenin and gliadins in bread wheat, and it has been suggested that massive nonrandom diploidisation and silencing of genes have occurred on chromosome 1A (Gupta and Shepherd, 1990b).

LMW glutenin subunits are important in determining the dough viscoelastic properties of hexaploid and tetraploid wheat flours. However, the effects of different LMW subunit alleles on dough properties are still largely unknown. Gupta and MacRitchie (1994) have shown that the *Glu-A3e* allele produces no major B subunits. This allelic difference was found to be responsible for variation in both the size distribution of the glutenin polymers and dough strength. The results of Redaelli *et al* (1995) show that the *e* allele codes for two C subunits, whereas its counterpart allele *c* produces one major plus one minor B subunit as well as one C-type polypeptide. Therefore, the main difference between these two alleles is in their effects on the ratio of B and C subunit quantities, as suggested by Gupta and MacRitchie (1994).

3.2.3 Monosomic lines

Aneuploidy is used to describe organisms which chromosome number is not a whole-number multiple of the basis number of the group. Bread and durum wheats are allopolyploids (Baenziger *et al*, 1994). Common winter and spring wheats have a close cytogenetic relationship with durum wheat as they originated from a cross between the tetraploid emmer wheats (chromosome 1AABB) and *T. tauschii* (chromosome 1DD) (McFadden and Sears, 1946). As the A, B, and D chromosomes are derived from related diploid species, they have genes that encode related proteins. These proteins are however not identical. The interactions of proteins encoded by the different chromosomes are important when one wants to determine the precise physical and technological properties of doughs that are produced from bread and durum wheats (Tatham *et al*, 1990).

Monosomics can be used to determine the chromosome carrying a particular gene. If the 21 monosomics of a variety are crossed with another variety, homozygous for the gene to be located, and monosomic hybrids are selected from their resulting progeny, then the hemizygous chromosome in each of the crosses must be derived from the donor variety under investigation. If the gene is recessive to the allele carried by the recipient monosomic variety, then one of the monosomic hybrids will have the recessive phenotype and all of the other monosomic hybrids will have the dominant phenotype. The chromosome carrying the recessive gene can thus be determined.

Monosomics occur spontaneously. It is therefore possible to establish a complete set of monosomics in a variety by the observation of phenotypes and the counting of chromosomes. It was estimated that monosomics occur at a frequency of about one percent in varietal populations, but the phenotypes of most monosomics are not obviously different from the euploid. It is thus, not possible to obtain many of the monosomics by selecting adult plants in the field. Identification must therefore be made in the laboratory on the basis of chromosome counts at the seedling stage. This is however, a time consuming process and it can take many years before a complete set of monosomics can be isolated.

A more acceptable method is to use an existing set of monosomics, like Chinese Spring and through the use of backcrossing, to develop a further set in another variety. This

method has some disadvantages, but the ability to ensure that all 21 monosomics can be developed in a reasonable time is an important advantage over other methods.

It is possible to identify important chromosomal differences between varieties by comparing the monosomic series. Since many monosomic series exist in wheat, this comparative method can be useful in the rapid identification of the chromosomes responsible for major varietal differences (Law *et al*, 1987).

In South Africa, three sets of monosomic lines are available, namely Flamink, Inia and SST 3. The monosomic lines were developed through the use of the backcrossing technique and the existing set of monosomic Chinese Spring (Marais, 1999; personal communication).

3.3. Materials and Methods

3.3.1 Materials

Chinese Spring, Flamink, Inia and SST 3 were screened together with their monosomic lines for their LMW subunit composition. The cultivars of Chapter 1 were also used as a help to determine the chromosomes responsible for the expression of a given group of LMW glutenin bands. Please refer to Appendix C for all the replications and intensities of the four cultivars and their monosomic lines. The three standards (Gabo, Chinese Spring and Orca) used by Gupta and Shepherd (1990) was included in the studies of Maartens (1997). These results were used to compare the results of this thesis. Chinese Spring was again used as a standard in this thesis.

3.3.2 Methods

3.3.2.1 Extraction of glutenins

The same method (Singh *et al*, 1991) as in Chapter 1 was used to extract the glutenin proteins. Please refer to Chapter 1 for a detailed discussion. Six replications of each cultivar and monosomic line were evaluated.

3.3.2.2 Sodium dodecyl sulphate gel electrophoresis (SDS-PAGE)

The same gel concentrations as in Chapter 1 were used. The gels were also run at 66 mA at a temperature of 15°C. Please refer to Chapter 1 for a detailed discussion.

3.3.2.3 Staining of the gel

The staining method of Wrigley (1992) was used as in Chapter 1.

3.3.2.4 Gel analysis

The "Molecular Analyst Fingerprinting" software was also used. All the settings used were exactly the same as was done with the bread wheats in Chapter 1.

3.4 Results and discussion

In Table 3.2 a summary of all the LMW glutenin bands present in the cultivars and their monosomic lines, are given.

Table 3.2 The different LMW glutenin bands in the cultivars and their monosomic lines.

	CS	1A	1B	1D	Flam	1A	1B	1D	Inia	1A	1B	1D	SST3	1A	1B	1D
1																
2	—	—	—	—	—	—	—	—		—	—	—		—	—	—
3									—				—			—
4		—	—	—	—			—	—	—	—	—	—	—	—	
5	—		—													
6		—		—	—	—	—			—			—		—	—
7					—				—		—	—				
8	—					—	—			—	—	—		—		—
9		—		—				—			—	—			—	
10	—		—	—	—	—			—			—	—	—	—	—
11			—	—							—		—	—		
12		—							—	—						
13			—		—	—	—					—	—	—		—
14	—	—	—	—	—	—		—			—		—	—	—	—
15																
16	—							—		—	—	—	—	—	—	
17		—	—	—	—	—			—							
18							—	—		—				—		
19	—	—	—	—	—	—				—	—	—			—	—
20									—	—			—	—	—	—
21								—	—		—	—			—	—
22	—	—	—		—	—	—	—		—			—	—		—
23				—	—	—			—	—		—	—	—		—
24	—	—					—		—		—	—	—		—	—
25			—		—	—		—		—			—	—		—
26					—		—	—				—	—	—	—	—
27		—	—	—					—							—
28							—	—		—					—	
29	—	—	—	—	—	—					—	—	—	—		
30													—	—		—
31	—			—		—	—	—	—			—				
32					—					—	—					
33		—	—	—				—	—			—		—	—	—
34				—	—	—	—	—			—		—	—		
35										—	—	—	—	—		
36	—		—	—					—		—		—	—	—	—
37	—	—		—	—	—	—		—	—	—	—				
38	—	—	—	—	—	—	—	—		—	—	—	—	—	—	—
39													—			

* Please note that in the first four columns Chinese Spring and the monosomic lines of Chinese Spring are shown, followed by Flamink and its monosomic lines, followed by Inia and its monosomic lines, followed by SST 3 and its monosomic lines.

Group 1

This band was not present in any of the cultivars or monosomic lines.

Group 2

Group 2 was present in Chinese Spring and in all the monosomic lines of Chinese Spring. It was also present in Flamink and in the monosomic lines of Flamink. It was however, not present in Inia or SST 3, but it was present in both of their monosomic lines. It was possibly expressed from Chinese Spring.

Group 3

This group was only present in Inia and in SST 3 and in the monosomic line 1D of SST 3.

Group 4

Group 4 was present in the monosomic lines 1A and 1D of Chinese Spring. It was also present in Flamink and Flamink monosomic line 1D, in Inia and all of its monosomic lines and in SST 3 and monosomic SST 3 1B.

Group 5

Group 5 was present in Chinese Spring and monosomic Chinese Spring 1B and in monosomic SST 3 1A.

Group 6

This group was present in monosomic Chinese Spring 1A and 1D and in Flamink and monosomic Flamink 1A and 1B. It was also present in the monosomic 1A of Inia and in SST 3 and monosomic SST 3 1B and 1D.

Group 7

This band was present in Flamink, but in none of its monosomic lines. It was also present in Inia and monosomic 1B and 1D of Inia.

Group 8

Group 8 was present in Chinese Spring, but in none of the monosomic lines of Chinese Spring. It was present in the monosomic 1A and 1B of Flamink and monosomic 1A of Inia and in monosomic 1A and 1D of SST 3.

Group 9

This band was present in monosomic 1A and 1D of Chinese Spring, in monosomic 1D of Flamink, in monosomic 1B and 1D of Inia and in monosomic 1B of SST 3.

Group 10

This band was present in Chinese Spring and monosomic 1B and 1D of Chinese Spring. It was also present in Flamink and monosomic 1A of Flamink, in Inia and monosomic 1D of Inia and in monosomic 1B and 1D of SST 3.

Group 11

This band was present in monosomic 1B of Inia and in SST 3 and monosomic 1A of SST 3.

Group 12

This band was only present in monosomic 1A of Chinese Spring and in Inia and monosomic 1A of Inia.

Group 13

This band was present in monosomic 1B of Chinese Spring, in Flamink and in monosomic 1A and 1B of Flamink. It was also present in monosomic 1D of Inia, in SST 3 and in monosomic 1D of SST 3.

Group 14

This band was present in Chinese Spring and in all of its monosomic lines. It was present in monosomic 1A and 1D of Flamink and in monosomic 1B of Inia. It was also present in SST 3 and in monosomic 1A and 1D of SST 3.

Group 15

This band was not present in any of the cultivars or monosomic lines.

Group 16

This band was present in Chinese Spring, in monosomic 1D of Flamink, in monosomic 1A, 1B and 1D of Inia, in SST 3 and in monosomic 1A and 1B of SST 3.

Group 17

This band was present in all the monosomic lines of Chinese Spring. It was also present in Flamink, in monosomic 1A of Flamink and in Inia.

Group 18

This band was present in monosomic 1B and 1D of Flamink, in monosomic 1A of Inia and in monosomic 1A of SST 3.

Group 19

This band was present in Chinese Spring and all the monosomic lines of Chinese Spring. It was also present in Flamink and monosomic 1A of Flamink, in all the monosomic lines of Inia and in monosomic 1B and 1D of SST 3.

Group 20

This band was present in Inia, but in none of its monosomic lines. It was also present in SST 3 and monosomic 1A and 1D of SST 3.

Group 21

This band was present in monosomic 1D of Flamink, in Inia and monosomic 1B and 1D of Inia and in monosomic 1B and 1D of SST 3.

Group 22

This band was present in Chinese Spring, in monosomic 1A and 1B of Chinese Spring, In Flamink and all of the monosomic lines of Flamink, in monosomic 1A of Inia and in SST 3 and monosomic 1A of SST 3.

Group 23

This band was present in monosomic 1D of Chinese Spring, in Flamink and monosomic 1A of Flamink, in Inia and monosomic 1A and 1D of Inia in monosomic 1A and 1D of SST 3.

Group 24

This band was present in Chinese Spring and monosomic 1A of Chinese Spring, in monosomic 1B of Flamink and in Inia and monosomic 1B and 1D of Inia. It was also present in SST 3 and monosomic 1B and 1D of SST 3.

Group 25

This band was present in monosomic 1B of Chinese Spring, in monosomic 1A and 1D of Flamink, in monosomic 1A of Inia and in monosomic 1D of Inia.

Group 26

This band is absent in Chinese Spring and all of its monosomic lines. It is present in Flamink and in monosomic 1B and 1D of Flamink, in monosomic 1D of Inia and in SST 3 and in monosomic 1A and 1B of SST 3.

Group 27

This band is present in all the monosomic lines of Chinese Spring. It is also present in Inia and in monosomic 1D of SST 3.

Group 28

It is present in monosomic 1B and 1D of Flamink, in monosomic 1A of Inia and in monosomic 1B of SST 3.

Group 29

This band is present in Chinese Spring and all of its monosomic lines. It is also present in Flamink and monosomic 1A of Flamink, in monosomic 1B and 1D of Inia and in SST 3 and monosomic 1A of SST 3.

Group 30

This band was only present in SST 3 and in monosomic 1A and 1D of SST 3.

Group 31

This band was present in Chinese Spring and monosomic 1D of Chinese Spring. It was also present in monosomic 1A, 1B and 1D of Flamink and in monosomic 1D of Inia.

Group 32

This band was only present in Flamink and in monosomic 1A and 1B in Inia.

Group 33

It was present in all the monosomic lines of Chinese Spring, in monosomic 1D of Flamink, in Inia and monosomic 1D of Inia and also in all the monosomic lines of SST 3.

Group 34

This band was present in monosomic 1D of Chinese Spring, in Flamink and all the monosomic lines of Flamink, in monosomic 1B of Inia, in SST 3 and in monosomic 1A of SST 3.

Group 35

This band was only present in monosomic 1A and 1D of Inia.

Group 36

This band was present in Chinese Spring and monosomic 1B and 1D of Chinese Spring. It was also present in Inia and monosomic 1B of Inia and in SST 3 and all the monosomic lines of SST 3.

Group 37

This band was present in Chinese Spring, in monosomic 1A and 1D of Chinese Spring, in Flamink and monosomic 1A and 1B of Flamink, and in Inia and all the monosomic lines of Inia.

Group 38

This band was present in Chinese Spring and all the monosomic lines of Chinese Spring, it was present in Flamink and all the monosomic lines of Flamink, in all the monosomic lines of Inia and in SST 3 and in all the monosomic lines of SST 3.

Group 39

This band was only present in SST 3.

If all the results are taken into account, it is possible to determine which chromosomes are responsible for the expression of certain bands. This data are presented in Table 3.3. A Y indicates that the certain chromosome is responsible in the expression of bands in a given group, while a N indicates that the chromosome is not responsible. A question mark indicates that it is not known for sure if the chromosomes have an influence.

Group 1

This band was not present in any of the cultivars or monosomic lines. It was therefore impossible to determine which chromosome is responsible for the control of the expression of this band.

Group 2

This band is present in all the monosomic lines. It is however not present in Inia or SST 3. This raises the question if this band is perhaps a dominant band expressed from Chinese Spring. If it is true, then chromosome 1A is perhaps not responsible for its control. This band does occur in durum wheats and also in bread wheats and therefore will chromosome 1D be responsible for its control. Another chromosome is also responsible and it is more likely chromosome 1B than A.

Group 3

This band is present in Inia, but not in the monosomic lines of Inia. It is also present in SST 3 and in the monosomic 1D of SST 3. It is therefore likely that all the chromosome 1's are responsible for its control. However, it is also possible that the 0 band could be expressed from Chinese Spring in the monosomic lines of Inia. Please note that the 0 band is rather the absence of a band (the band is not expressed) than an actual band. It will however be called a 0 band for the sake of simplicity.

Table 3.3 The group of bands with the chromosomes that have an influence on the expression of the bands.

Group	Chromosome 1 A	Chromosome 1B	Chromosome 1D
1	?	?	?
2	N	Y	Y
3	Y	Y	Y
4	Y	Y	Y
5	Y	N	Y
6	Y	?	Y
7	Y	N	N
8	Y	Y	Y
9	Y	Y	N
10	Y	Y	Y
11	N	Y	Y
12	N	Y	Y
13	Y	Y	Y
14	N	Y	Y
15	?	?	?
16	Y	Y	Y
17	Y	Y	Y
18	Y	?	?
19	?	Y	Y
20	N	Y	N
21	Y	N	N
22	N	Y	Y
23	N	Y	Y
24	Y	Y	Y
25	?	?	?
26	Y	N	Y
27	Y	Y	Y
28	Y	Y	Y
29	Y	Y	Y
30	N	Y	N
31	Y	Y	N
32	?	Y	Y
33	Y	Y	N
34	N	Y	Y
35	N	Y	N
36	Y	N	Y
37	N	Y	Y
38	Y	Y	?
39	?	?	?

Group 4

It is likely that all the chromosome 1's are responsible for the control of this band. It is absent in the monosomic 1B of Chinese Spring, that makes chromosome 1B responsible for its control. It is also absent in monosomic 1A and 1B of Flamink, which makes chromosome 1A and 1B responsible for its control. It is also absent in monosomic 1A and 1D of SST 3, that makes chromosome 1A and 1D responsible for its expression.

Group 5

This band is absent in monosomic 1A and 1D of Chinese Spring. It is therefore likely that these two chromosomes are responsible for its control.

Group 6

It is not possible to say if chromosome 1B is responsible for the expression, because it could be that monosomic 1B of Chinese Spring inherit the 0 band (absent band) of Chinese Spring. The band was however absent in monosomic 1D of Flamink and monosomic 1A of SST 3. It is therefore likely that chromosome 1A and 1D are responsible for its expression.

Group 7

This band is absent in the monosomic 1A line of Inia and this makes chromosome 1A responsible for its control. It is also absent in all the monosomic lines of Flamink, but it is more likely that the monosomic lines had the 0 band (absent band) from Chinese Spring.

Group 8

It is likely that all the chromosome 1's are responsible for the control of this group, since it is not present in any of the monosomic lines of Chinese Spring.

Group 9

It looks as if chromosome 1A and 1B is responsible for the control of this band.

Group 10

This band is absent in monosomic 1A of Chinese Spring, monosomic 1B and 1D of Flamink, monosomic 1A and 1B of Inia and in monosomic 1A of SST 3. It is therefore possible that all three chromosomes are responsible for the expression of this band.

Group 11

This band is absent in monosomic 1B and 1D of SST 3, making these two chromosomes responsible for its expression.

Group 12

This band is absent in monosomic 1B and 1D of Inia, making these two chromosomes responsible for its expression.

Group 13

This band is absent in monosomic 1D of Flamink and also monosomic 1A and 1B of SST 3. It is therefore possible that all the chromosomes (1A, 1B and 1D) are responsible for the control of this band.

Group 14

This band is absent in monosomic 1B of Flamink and also in monosomic 1D of SST 3, making these two chromosomes responsible for its control.

Group 15

This band was not present in any of the cultivars or monosomic lines, making it impossible to determine its control.

Group 16

Chromosome 1D is definitely responsible for the control of this band, since it is absent in the monosomic 1D of SST 3. It is not present in any of the monosomic lines of Chinese Spring, making it also possible for chromosome 1A and 1B to have an influence on its expression.

Group 17

This band is not present in monosomic 1B and 1D of Flamink and in none of the monosomic lines of Inia. It is thus, likely that all the chromosome (1A, 1B and 1D) have an influence on the control of this band.

Group 18

It is possible that chromosome 1A is responsible for the control of this band, because it is not present in monosomic 1A of Flamink, but it is present in monosomic 1B and 1D. It could also be control by chromosome 1B and 1D, because it is not present in monosomic 1B and 1D of Inia or SST 3. It is not present in these two cultivars, either, making it impossible to say for sure if it is controlled by chromosome 1B and 1D.

Group 19

Chromosome 1B and 1D are responsible for the control of this band, because it is absent in monosomic 1B and 1D of Flamink. It is also absent in monosomic 1A of SST 3, but it is also absent in the cultivar SST 3, making it impossible to say for sure if this band is controlled by chromosome 1A. It could be that the no band (0 band) is controlled by monosomic 1A from SST 3.

Group 20

This band is definitely controlled by chromosome 1B, as it is only absent in monosomic 1B of SST 3. It is also possible that all the chromosomes are responsible, since it is absent in all the monosomic lines of Inia, but it is more likely that the monosomic lines had the 0 band from Chinese Spring.

Group 21

This band is definitely controlled by chromosome 1A, since it is not present in the 1A monosomic lines of Inia or SST 3.

Group 22

This band is controlled by chromosome 1B and 1D, since it is not present in monosomic 1D of Chinese Spring and also not in the 1B and 1D monosomic lines of Inia and SST 3.

Group 23

This band is also controlled by chromosome 1B and 1D, since it is not present in monosomic 1B or 1D of Flamink. It is also not present in the monosomic 1B lines of Inia and SST 3.

Group 24

This band is controlled by all the three chromosomes, since it is absent in monosomic 1B and 1D of Chinese Spring and also in monosomic 1A of SST 3.

Group 25

It is difficult to say which chromosome is responsible for the expression of this band, since it is not present in any of the cultivars, only in some of the monosomic lines. It is likely that no band (the 0 band) is expressed in some of the monosomic lines from the cultivars.

Group 26

This band is controlled by chromosome 1A and 1D, since it is absent in monosomic 1A of Flamink and also in monosomic 1D of SST 3.

Group 27

The expression of this band is probably controlled by all the chromosomes. It is present in all the monosomic lines of Chinese Spring, but it is not present in Chinese Spring. It is however present in Inia, but not in any of the monosomic lines of Inia, making it possible to be controlled by the different chromosomes. The possibility of the non-expression of the band (0 band) of Chinese Spring could however, not be excluded.

Group 28

It is not certain which of the chromosomes are responsible for the expression of this band, since it is absent in Chinese Spring and all the monosomic lines of Chinese Spring. It will be assumed for simplicity, that all the chromosomes are responsible, but this will be tested further.

Group 29

This band is definitely controlled by chromosome 1B and 1D, because it is absent in monosomic 1B and 1D of Flamink and SST 3. The possibility that it is controlled by chromosome 1A could however, not be excluded, since it is also absent monosomic 1A of Inia. It is also absent in Inia, making the non-expression of the band also possible.

Group 30

This band is controlled by chromosome 1B, since it is absent in monosomic 1B of SST 3.

Group 31

This band is controlled by chromosome 1A and 1B, since it is absent in monosomic 1A and 1B of Chinese Spring and Inia.

Group 32

It is possible that this band is controlled by all the chromosomes, because it is absent in all the monosomic lines of Flamink. It is however, also absent in Chinese Spring and all the monosomic lines of Chinese Spring, making the non-expression of the 0 band from Chinese Spring possible. It is likely that this band is controlled by chromosome 1D, since it is only absent in monosomic 1D of Inia. However, this band occurred in 31 percent of the durum cultivars. If the close genetic relationship between durum and bread wheat is taken into account, it must be that a chromosome other than D must be responsible for the expression. Taken also into account that LMW glutenins have shown the greatest polymorphism for the B chromosome (Gupta and Shepherd, 1990b), it is more likely that chromosome 1B is also responsible for the expression of this band.

Group 33

This band is likely controlled by chromosome 1A and 1B, since it is absent in the monosomic lines of 1A and 1B of Inia.

Group 34

This band is controlled by chromosome 1B and 1D, since it is absent in the monosomic lines 1B and 1D of SST 3.

Group 35

It is impossible to say which chromosome is responsible for the expression of this band, but it is probably chromosome 1B, since it is also absent in monosomic 1B Inia. It is however, also absent in Inia, making the non-expression of the band (0 band) also possible.

Group 36

This band is controlled by chromosome 1A and 1D, since it is absent in monosomic 1A of Chinese Spring and it is also absent in monosomic 1A and 1D of Inia.

Group 37

This band is controlled by chromosome 1B and 1D, since it is absent in monosomic 1B of Chinese Spring and monosomic 1D of Flamink.

Group 38

It is possible that all the chromosomes 1's have an influence on the expression of this band, because it is present in all the cultivars and monosomic lines, except Inia.

Group 39

This band was only present in SST 3 and it could therefore not be determined which chromosome is responsible for its expression. It could be that all the monosomic lines of SST 3 had the 0 band from Chinese Spring.

Please refer to Chapter 1 for all the correlations between the different groups. If the correlations are taken into account that were found between the different bands, it is possible to determine which chromosomes are responsible for the expression of the band, if some bands are absent or present in certain cultivars or monosomic lines.

Expression of the bands

If two bands are positively correlated, it means that if one is present, the other one will also be present. If two bands are negatively correlated, it means that if the one is present, the other one will be absent. This will be tested with the data obtained in Table 3.3. Only the correlations will be discussed that are definitely a result of a certain chromosome. In some correlations, no definite chromosome was indicated as being responsible for the expression of a certain chromosome and it will be discussed later on.

Group 1

This group will be excluded in the discussion for the time being.

Group 2

Group 2 is positively correlated with group 36. This means that if group 2 is present, that group 36 is probably also present. If one looks at Table 3.3., the only chromosomes where this is not true, are chromosomes 1A and 1B. It could thus be assumed that if group 2 is present together with group 36, it will be controlled by chromosome 1D. If group 36 is not present, but group 2 is present, then this combination will be controlled by chromosome 1B. The reverse is true for chromosome 1A.

Group 2 is also positively correlated with group 37. The only chromosome where these two bands are not present together, is chromosome 1A. Therefore, if bands in group 2 and group 37 are present in the same cultivar, it is probably controlled by chromosome 1B and 1D and if no band in this combination is present, then it will be controlled by chromosome 1A.

Group 3

This group is negatively correlated with group 33. This is true for chromosome 1D. If group 3 and group 33 are both present, it will be controlled by chromosome 1A or 1B. If it is absent, it will be controlled by chromosome 1D.

Group 3 is also positively correlated with group 35. According to Table 3.3 this is not true for chromosome 1A and 1D, but it is however, true for chromosome 1B. Group 3 is also positively correlated with group 36. This is however, not true for chromosome 1B and if only group 3 is present, this band will be controlled by chromosome 1B. Group 3 is also positively correlated with group 37. This is however not true for chromosome 1A.

Group 4

Group 4 is negatively correlated with group 5. This is true for chromosome 1B, but not for chromosome 1A and 1D. Group 4 is also positively correlated with group 26. This is true for chromosome 1A and 1D, but not for chromosome 1B. Group 4 is positively correlated with group 36, but this was not true for chromosome 1B. Group 4 was also positively correlated with group 37, but it was not true for chromosome 1A.

Group 5

Group 5 is negatively correlated with group 27. This was only true for chromosome 1B. It is also negatively correlated with group 32, and it was also only true for chromosome 1B. Group 5 was positively correlated with group 35. This was however, not true for any of the chromosomes. If group 5 is present and 35 absent, then it is probably controlled by chromosome 1A or 1D. If group 5 is absent and group 35 is present, then the band is probably controlled by chromosome 1B.

Group 6

This group was negatively correlated with group 7. This was true for chromosome 1D, uncertain for chromosome 1B and false for chromosome 1A. It was positively correlated with group 19, which was true for chromosome 1D, but uncertain for chromosome 1A and 1B.

Group 7

Group 7 is negatively correlated with group 8, which was true for chromosome 1B and 1D, but false for chromosome 1A. It was also negatively correlated with group 22. This was true for all the chromosomes, but if group 7 is present and group 22 absent, this band is controlled by chromosome 1A. If group 7 is absent and group 22 present, then this band is controlled by chromosome 1B or 1D.

Group 8

Group 8 is negatively correlated with group 9, which is only true for chromosome 1D.

Group 9

Group 9 is negatively correlated with group 10, which was only true for chromosome 1D.

Group 10

Group 10 was negatively correlated with group 11, which was true for chromosome 1A. It was positively correlated with group 28, which was true for all the chromosomes. It was negatively correlated with group 35, which was true for chromosome 1A and 1D, but not true for chromosome 1B. It was also negatively correlated with group 37, which was only true for chromosome 1A.

Group 11

Group 11 is positively correlated with group 17. This was however, not true for chromosome 1A. It was further negatively correlated with group 18, which was true for chromosome 1A, but uncertain for chromosome 1B and 1D. It was also negatively correlated with group 28, which was true for chromosome 1A. It was negatively correlated with group 33. If group 11 is absent and group 33 is present, it is probably controlled by chromosome 1A. If group 11 is present and group 33 absent, this band is controlled by chromosome 1D. If both bands are present, it is controlled by chromosome 1B.

Group 12

This group is negatively correlated with group 13, which is only true for chromosome 1A. It is positively correlated with group 18, which is not true for chromosome 1A and uncertain for chromosome 1B. It is also positively correlated with group 26. If group 12 is absent and group 26 present, it is expressed by chromosome 1A. If group 12 is present and group 26 absent, this band is controlled by chromosome 1B. If both groups are present, chromosome 1D is responsible for the expression of this band.

Group 13

This group is negatively correlated with group 14, which is only true for chromosome 1A. It is also negatively correlated with group 26, which is true for chromosome 1B. It is further also negatively correlated with group 36, which is also only true for chromosome 1B.

Group 16

This group was positively correlated with group 32, which was true for chromosome 1B and 1D.

Group 19

This group was negatively correlated with group 20, which was true for chromosome 1D.

Group 20

Group 20 was negatively correlated with group 21, which was true for chromosome 1A and 1B, and not true for chromosome 1D. If group 20 is absent, and group 21 is present, then chromosome 1A is responsible for the expression of this band. The reverse is true for chromosome 1B. If both bands are absent, chromosome 1D is responsible for the expression of group 20.

Group 21

This group is negatively correlated with group 22. This is true for all the chromosomes. If group 21 is present and group 22 is absent, chromosome 1A is responsible for the expression of this chromosome. The reverse is true for chromosome 1B and 1D. Group 21 is also negatively correlated with group 36, which is only true for chromosome 1D. It is further negatively correlated with group 38, which is true for chromosome 1B and uncertain for chromosome 1D.

Group 23

This group was negatively correlated with group 24. It was only true for chromosome 1A. It was also negatively correlated with group 26. If group 23 is absent and group 26 present, chromosome 1A is responsible for the expression of this band. The reverse is true for chromosome 1B. If both bands are present, then chromosome 1D is responsible for the expression. Group 23 is further positively correlated with group 27, which is true for chromosome 1B and 1D.

Group 24

This group is positively correlated with group 26, which is true for chromosome 1A and 1D. It is also positively correlated with group 31, which is true for chromosome 1A and 1B, but not true for chromosome 1D.

Group 26

Group 26 is negatively correlated with group 27, which is true for chromosome 1B. It is also negatively correlated with group 28, which is also only true for chromosome 1B.

Group 27

Group 27 is negatively correlated with group 37, which is only true for chromosome 1A.

Group 29

This group is negatively correlated with group 30, which is true for chromosome 1A and 1D.

Group 30

This group is negatively correlated with group 31, which is true for chromosome 1A.

Group 31

Group 31 is negatively correlated with group 32, which is true for chromosome 1D, but uncertain for chromosome 1A.

Group 32

This group is negatively correlated with group 33, which is true for chromosome 1D, but uncertain for chromosome 1A.

Group 33

Group 33 is negatively correlated with group 34, which is true for chromosome 1A and 1D. If group 33 is present and group 34 is absent, then chromosome 1A is responsible for the expression of this band. The reverse is true for chromosome 1D. Group 33 is also negatively correlated with group 36, which is true for chromosome 1B and 1D. If group 33 is present and group 36 is absent, then chromosome 1B is responsible for the expression of this band. The reverse is true for chromosome 1B.

Group 34

This group is negatively correlated with group 35, which is true for chromosome 1D.

Group 35

This group is positively correlated with group 37, which is true for chromosome 1A and 1B. If both groups are absent, then chromosome 1A is responsible for the expression and if both bands are present, then chromosome 1B is responsible for the expression.

Group 36

This group is positively correlated with group 38, which is true for chromosome 1A, but uncertain for chromosome 1D.

Groups not definitely assigned to specific chromosomes

As discussed previously, it was not always possible to say with certainty if a certain chromosome was responsible for the expression of a certain group. These groups had a question mark in Table 3.3. They will be discussed here. Please refer to Table 3.3 for the groups in question.

To determine the chromosomes responsible for the expression of certain groups, the following was taken into account:

1. Bread and durum wheats have a close cytogenetic relationship (McFadden and Sears, 1946). If a certain group does not occur frequently in the bread or durum wheats, it means that chromosome 1D could not have an influence, because chromosome 1D is absent in the durum wheats. The reverse is also true. If a certain group does not occur frequently in the durum wheats, but it does occur frequently in the bread wheats, then chromosome 1D must have an influence. It will be seen later on that a given band can be expressed by more than one chromosome.
2. Gupta and Shepherd (1990b) found that chromosome 1A encoded only a few LMW subunits and many cultivars did not exhibit any band controlled by this chromosome. However, LMW subunits have shown the greatest polymorphism for chromosome 1B. If this is taken into account, then a group where it is uncertain if the A or B chromosome have an influence, it could be assumed that the B would rather have the influence than the A chromosome.
3. The correlations of Chapter 1 were also taken into account. If a negative correlation was observed, then at least one of the chromosomes must not be responsible in one group for the expression of the band, but in the other group it must be responsible.

Group 1 (Chromosome 1A, 1B and 1D)

This group did not occur in many cultivars as seen in the bread or durum wheats. It does however occur more frequently in bread wheats and therefore it will be assumed that the D chromosome is responsible for its expression. To explain the occurrence in the durum

wheats, it will be assumed that the B rather than the A chromosome would be responsible.

The following will then be true:

1. There is a positive correlation between group 1 and group 2, 3 and 4. This makes the B and D chromosome responsible for the expression of these combinations.
2. Group 1 is negatively correlated with group 21. If the band in group 1 is absent, but present in group 21, then chromosome 1A will be responsible for the expression of this combination. The reverse is true for chromosome 1B and 1D.
3. Group 1 and group 33 is negatively correlated. If the band is absent in group 1, but present in group 33, then chromosome 1A will be responsible for the expression of this combination. The reverse is true for chromosome 1D. If both bands are present, then chromosome 1B will be responsible for the expression of this combination.
4. Group 1 and group 36 are positively correlated. If the band is absent in group 1, but present in group 36, then chromosome 1A will be responsible for the expression of this combination. The reverse is true for chromosome 1B. If both bands are present, then chromosome 1D will be responsible for the expression of this combination.

Group 6

Group 6 is negatively correlated with group 24. This will only be true if chromosome 1B, group 6 is not responsible for the expression of this group. It can thus be assumed that chromosome 1B is not responsible for the expression of group 6.

Group 15 (chromosome 1A, 1B and 1D)

This group does not occur frequently in durum or bread wheats. It can thus be assumed that chromosome 1D is not responsible for its expression.

If it is hypothesised that chromosome 1A and 1B are responsible for the expression of group 15, and chromosome 1D is not, then the following will be true:

1. Group 14 and 15 are negatively correlated and if band 15 is present and 14 is absent, then chromosome 1A will be responsible for the expression of group 15. However, if band 14 is present and band 15 absent then chromosome 1D will be responsible. If both bands are present, then chromosome 1B will be responsible.

2. Group 15 and 16 are negatively correlated and this hypothesis will make it true that chromosome 1D will be responsible for the expression of this combination.
3. Group 15 is also negatively correlated with group 27, and this will also make chromosome 1D responsible for the expression of this combination.
4. It is also positively correlated with group 28, and this makes chromosome 1A and 1B responsible for the expression of this combination.

Group 18 (Chromosome 1B and 1D)

1. Group 18 is not frequently found in durum wheats, but it does occur frequently in the bread wheats. It is thus safe to assume that chromosome 1D is responsible for the expression of this group. Group 17 and group 19 are negatively correlated to group 18. If this is true, then chromosome 1B cannot be responsible for the expression of group 18.

Group 19 (Chromosome 1A)

It will be taken into account that chromosome 1A encoded for a minimum number of LMW glutenin subunits and it is therefore not responsible for the expression of this group.

If it is assumed that chromosome 1A is not responsible for the expression of group 19, then the following will be true:

1. Group 6 is positively correlated with group 19, which makes chromosome 1D responsible for the expression of this combination.
2. Group 8 is positively correlated with group 19, which makes chromosome 1B and 1D responsible for the expression of this combination.
3. Group 18 is negatively correlated with group 19, which makes chromosome 1A and 1D responsible for the expression of this combination.
4. Group 19 and 20 is negatively correlated, which makes chromosome 1D responsible for the expression of this combination.

Group 25 (Chromosome 1A, 1B and 1D)

This group does not occur frequently in durum wheats, but it does occur frequently in bread wheats. It will thus be safe to assume that chromosome 1D is responsible for the expression of this group. To explain the occurrence of this group in durum wheats, it can

be assumed that the B chromosome is also responsible for the expression of this group, because only chromosome 1B is absent in the cultivar Flamink, Inia and SST 3. If it is assumed that the A chromosome is responsible, it would not be possible to explain the negative correlation between group 25 and 26. It is thus chromosome 1B and 1D that is responsible for the expression of this group and chromosome 1A is not responsible.

Group 32

If it is assumed that chromosome 1A is not responsible for the expression of group 32, more variation can be explained.

1. Group 4 is positively correlated with group 32. This makes chromosome 1B and 1D responsible for the expression of this combination. Chromosome 1A is not responsible.
2. Group 5 is negatively correlated with group 32. This makes chromosome 1A and 1B responsible for the expression of this combination. If the band is absent in group 5, but present in group 32, then chromosome 1B will be responsible for the expression. The reverse will be true for chromosome 1A.
3. Group 16 is positively correlated with group 32, which makes chromosome 1B and 1D responsible.
4. Group 22 is positively correlated with group 32, which makes chromosome 1B and 1D responsible.
5. Group 26 positively correlated with group 32, which makes chromosome 1D responsible for the expression of this combination.
6. Group 32 and 33 are negatively correlated. This makes chromosome 1A and 1D responsible for the expression of this combination. If the band is absent in group 32, but present in group 33, then chromosome 1A will be responsible for the expression. The reverse will be true for chromosome 1D.

Group 38 (Chromosome 1D)

Chromosome 1D is not responsible for the expression of this group. It looks more like this group is expressed by chromosome 1A and 1B, because it occurred frequently in both bread and durum wheats. If it is taken into account that chromosome 1D is absent in durum wheats, it looks as if this chromosome is not responsible for its expression.

Group 39 (Chromosome 1A, 1B and 1D)

This band did not occur frequently in bread or durum wheats. The 1B chromosome displays the most polymorphism and for that reason, it will be assumed that only chromosome 1B is responsible for the expression of this group and not chromosome 1A or D.

This new data are summarised in Table 3.4. The data of Table 3.3 are also given.

Table 3.4. The influence of the different chromosomes on the different groups.

Group	Genome A	Genome B	Genome D
1	N	Y	Y
2	N	Y	Y
3	Y	Y	Y
4	Y	Y	Y
5	Y	N	Y
6	Y	N	Y
7	Y	N	N
8	Y	Y	Y
9	Y	Y	N
10	Y	Y	Y
11	N	Y	Y
12	N	Y	Y
13	Y	Y	Y
14	N	Y	Y
15	Y	Y	N
16	Y	Y	Y
17	Y	Y	Y
18	Y	N	Y
19	N	Y	Y
20	N	Y	N
21	Y	N	N
22	N	Y	Y
23	N	Y	Y
24	Y	Y	Y
25	N	Y	Y
26	Y	N	Y
27	Y	Y	Y
28	Y	Y	Y
29	Y	Y	Y
30	N	Y	N
31	Y	Y	N
32	N	Y	Y
33	Y	Y	N
34	N	Y	Y
35	N	Y	N
36	Y	N	Y
37	N	Y	Y
38	Y	Y	N
39	N	Y	N

All these data are summarised in Table 3.5. The expression of the bands that are influenced by the different chromosomes are shown, with the correlations presented in Chapter 1 taken into account. For example, if the band in group 2 is alone in a given cultivar, then it is expressed by chromosome 1B. If it is present however, together with group 36, then chromosome 1A or D is responsible for its expression.

Table 3.5 The chromosomes responsible for the expression of certain combinations of LMW glutenin bands.

Combination	Chromosome 1A	Chromosome 1B	Chromosome 1D
1+2	2	1+2	1+2
1+3	3	1+3	1+3
1+4	4	1+4	1+4
1+21	21	1	1
1+33	33	1+33	1
1+34	-	1+34	1+34
1+36	36	1	1+36
1+37	-	1+37	1+37
1+38	38	1+38	1
1+39	-	1+39	1
2+4	4	2+4	2+4
2+13	13	2+13	2+13
2+27	27	2+27	2+27
2+36	36	2	2+36
2+37	-	2+37	2+37
2+38	38	2+38	2
2+39	-	2+39	2
3+33	3+33	3+33	3
3+35	3	3+35	3
3+36	3+36	3	3+36
3+37	3	3+37	3+37
3+38	3+38	3+38	3

Table 3.5 (Continued)

Combination	Chromosome 1A	Chromosome 1B	Chromosome 1D
4+5	4+5	4	4+5
4+26	4+26	4	4+26
4+32	4	4+32	4+32
4+36	4+36	4	4+36
4+37	4	4+37	4+37
4+38	4+38	4+38	4
5+27	5+27	27	5+27
5+32	5	32	5+32
5+35	5	35	5
6+7	6+7	-	6
6+19	6	19	6+19
6+24	6+24	24	6+24
7+8	7+8	8	8
7+22	7	22	22
8+9	8+9	8+9	8
8+19	8	8+19	8+19
8+38	8+38	8+38	8
9+10	9+10	9+10	10
10+11	10	10+11	10+11
10+28	10+28	10+28	10+28
10+35	10	10+35	10
10+37	10	10+37	10+37
11+12	-	11+12	11+12
11+17	17	11+17	11+17
11+18	18	11	11+18
11+28	28	11+28	11+28
11+33	33	11+33	11

Table 3.5 (Continued)

Combination	Chromosome 1A	Chromosome 1B	Chromosome 1D
12+13	13	12+13	12+13
12+18	18	12	12+18
12+26	26	12	12+26
13+14	13	13+14	13+14
13+26	13+26	13	13+26
13+36	13+36	13	13+36
14+15	15	14+15	14
14+22	-	14+22	14+22
15+16	15+16	15+16	16
15+27	15+27	15+27	27
15+28	15+28	15+28	28
16+17	16+17	16+17	16+17
16+33	16+33	16+33	16
16+39	16	16+39	16
17+18	17+18	17	17+18
17+39	17	17+39	17
18+19	18	19	18+19
18+29	18+29	29	18+29
18+36	18+36	-	18+36
19+20	-	19+20	19
20+21	21	20	-
20+37	-	20+37	37
21+22	21	22	22
21+36	21+36	-	36
21+38	21+38	38	-
22+23	-	22+23	22+23
22+32	-	22+32	22+32
22+37	-	22+37	22+37
23+24	24	23+24	23+24
23+26	26	23	23+26
23+27	27	23+27	23+27

Table 3.5 (Continued)

Combination	Chromosome 1A	Chromosome 1B	Chromosome 1D
24+25	24	24+25	24+25
24+26	24+26	24	24+26
25+26	26	25	25+26
25+28	28	25+28	25+28
26+27	26+27	27	26+27
26+28	26+28	28	26+28
26+32	26	32	26+32
27+37	27	27+37	27+37
28+29	28+29	28+29	28+29
29+30	29	29+30	29
30+31	31	30+31	-
31+32	31	31+32	32
32+33	33	32+33	32
32+39	-	32+39	32
33+34	33	33+34	34
33+36	33+36	33	36
33+38	33+38	33+38	-
34+35	-	34+35	34
34+39	-	34+39	34
35+37	-	35+37	37
36+38	36+38	38	36
36+39	36	39	36

If the data of Table 3.5 are taken into account, it is possible to class the different cultivars according to their LMW glutenins. For example, if the cultivar Adam Tas is classed according to its LMW bands, it will look as follow:

(In brackets are the chromosome/s responsible for the expression of the combination)

1+3 (B/D)
 3 (A)
 1+4 (B/D)
 4 (A)
 1+34 (B/D)
 1+36 (D)
 36 (A)
 1+38 (B)
 38 (A)
 3+36 (A/D)
 3+38 (A/B)
 18+36 (A/D)
 24+36 (A/D)
 24 (B)
 36+38 (A)

Another method of writing the above, will be

Chromosome 1A: 3,4,18,24,26,36,38

Chromosome 1B: 1,3,4,24,34,38

Chromosome 1C: 1,3,4,18,24,34,36

This method was used to class the cultivars used in the dendrogram of Chapter 1. It is summarised in Table 3.6.

Table 3.6 The different LMW bands expressed by chromosome 1 in South African cultivars

Cultivar	Chromosome 1A	Chromosome 1B	Chromosome 1D
Adam Tas	3,4,18,24,26,36,38	1,3,4,24,34,38	1,3,4,18,24,34,36
Belinda	3,8,15,28,36,38	3,8,15,19,28,38	3,8,19,36
Betta	10,18,21,24,27,29	10,11,20,23,24,27, 29,30	10,11,18,23,24,27, 29
Betta DN	9,10,18,26	9,10,12	10,12,18,26
Caledon	15,18,27,29	15,23,24,27,29	18,23,24,27,29
Eland	3,4,36,38	1,3,4,22,32,38	1,3,4,22,32,36
Flamink	3,4,18,29,38	3,4,11,14,22,32,35, 37,38	3,4,11,14,18,22,29, 32,37
Gamka	3,16,18,21,33,38	3,11,16,33,34,35, 37,38	3,11,18,34,37
Gamtoos	5,17,18	2,11,17,32,37	2,5,11,17,18,32,37
Gamtoos DN	5,16,17,21,31,36, 38	11,16,17,31,32,38	5,11,16,17,32,36
Gariep	24,27,29,33	23,24,27,29,30,33, 34	23,24,27,29,33,34
Gariep DN	15,21,27,28	15,19,20,23,25,27, 28	19,23,25,27,28
Harts	3,5,15,16,18,27,33, 38	3,12,15,16,20,23, 27,33,35,37,38	3,5,12,16,18,23,27, 37
Hugenoot	13,18,21,27	12,13,19,20,23,27	12,13,18,19,23,27
Inia	3,4,10,21,24,27,33, 36	3,4,10,20,23,24,27, 33,37	3,4,10,23,24,27,36, 37
Karee	2,6,15,21,33	1,2,14,15,19,33,37	1,2,6,14,19,37
Kanega	3,6,8,16,18,29,33, 38	3,8,11,16,19,20,29, 33,34,38	3,6,8,11,16,18,19, 20,29,34
Limpopo	6,17,18,27,33	11,17,19,22,23,27, 33	6,11,17,18,19,20, 22,23,27
Limpopo DN	18,21,26,27,33	12,14,19,22,23,27, 32,33	12,14,18,19,22,23, 27,32,36

* Please note that some bands can be expressed by more than one chromosome.

Table 3.6 (Continued)

Cultivar	Chromosome 1A	Chromosome 1B	Chromosome 1D
Marico	4,13,36	1,4,13,16,22,32,34,39	1,4,13,22,32,34,36
Molen	10,13,18,21,24,26,28,29,31	10,13,14,20,22,24,28,29,31,32	10,13,14,18,22,24,26,28,29,32
Molopo	24,28	14,22,24,25,28,32	14,22,24,25,28,32
Nantes	15,28,36,38	2,15,25,28,38	2,25,28,36
Oom Charl	3,5,7,8,13,24,26,38	1,3,8,13,20,24,35,37,38	1,3,5,8,13,24,26,37
Palmiet	13,18	11,12,13,22,32	11,12,13,18,22,32
Palmiet DN	10,18,24,27,28	10,12,23,24,25,27,28	10,12,18,23,24,25,27,28
Palmiet short	17,27,29,33	11,17,23,27,29,30,32,33	11,17,23,27,29,32
PAN 3211	10,13,28,31	10,13,14,25,28,30,31	10,13,14,25,28
PAN 3235	5,14,24,26,36	2,11,17,24,35	2,5,11,17,24,26,36
PAN 3349	7,8,18,21,29,36	8,12,29	8,12,18,29,36
PAN 3364	3,4,6,15,28,36,38	2,3,4,15,19,20,28,32,38	2,3,4,6,19,28,32,36
Sch 69	5,13,17,29,33	11,13,14,17,29,30,33,35	5,11,13,14,17,29
Snack	5,8,10,26	2,8,10,12,19,20,22,32,37	2,5,8,10,12,19,22,26,32,37
SST 66	4,6,15,16,18,24,26,27,29,36,38	2,4,15,16,22,24,27,29,32,37,38	2,4,6,16,18,22,24,26,27,29,32,36,37
SST 101	4,6,15,16,18,24,26,27,29,36,38,	2,4,15,16,22,24,27,29,32,37,38	2,4,6,16,18,22,24,26,27,29,32,36,37
SST 102	9,10,18,21,24,26,27,28,33,36	9,10,23,24,27,28,33	10,18,23,24,26,27,28,36
SST 363	5,18,24,27,29	19,23,24,27,29,32	5,18,19,23,24,27,29,32
SST 367	21	20,22,32	22,32

Table 3.6 (Continued)

Cultivar	Chromosome 1A	Chromosome 1B	Chromosome 1D
SST 822	4,6,8,17,24,26	2,4,8,11,17,19,24, 35,37	1,3,6,8,10,16,19, 22,25,28,32,34,37
SST 825	3,5,17,18,26,36	2,3,11,17,23,32	2,3,5,11,17,18,23, 26,32,36
T4	4,6,8,17,24,26	1,3,8,10,16,19,22, 25,28,32,34,37,39	1,3,6,8,10,16,19, 22,25,28,32,34,37
Tugela	10,15,18,21,28,29	10,12,15,20,25,28, 29	10,12,18,25,28,29
Tugela DN	7,9,10,18,24,28,29, 33	9,10,12,14,19,20, 22,26,25,28,29,33, 34	10,12,14,18,19,22, 24,25,28,29,34
Tugela f-g	5,13,15,18,27,29	13,14,15,23,27,29	5,13,14,18,23,27, 29
Tugela new	9,10,15,21,24,28	9,10,15,20,23,24, 28	10,23,24,28

Chromosome 1A

MacRitchie (1992) found that the least number of subunits was controlled by chromosome 1A. Forty percent of the cultivars he examined contained no band that was controlled by this chromosome. In this study it was also found that the least number of LMW bands are controlled by chromosome 1A. However, all of the cultivars contained a band that was controlled by this chromosome. SST 367 had only one band controlled by this chromosome. The maximum number of bands that were controlled by this chromosome was eleven and SST 101 and 102 had both 11 bands.

Chromosome 1B

SST 367 contained only three bands controlled by chromosome 1B. Tugela and Tugela DN contained 13 bands that were controlled by this chromosome.

Chromosome 1D

The least number of bands that were controlled by this chromosome were two in SST 367. SST 66, SST 101, SST 822 and T4 all had 13 bands that were controlled by this chromosome.

Variation between cultivars

All the cultivars could be distinguished using the above nomenclature. Cultivars like Tugela, Tugela DN, Tugela fast growing and Tugela new that are closely related could easily be distinguished as they had different band combinations on all three chromosomes. This makes this new nomenclature system very efficient for cultivar identification. The studies of Maartens (1997) showed that it was not possible to distinguish between Tugela and PAN 3235 using the nomenclature system of Gupta and Shepherd (1990). Many cultivars also had the same combination on the A, B or D chromosome 1. For example Gamtoos, Palmiet and PAN 3349 all had the combinations e and c on the B and D chromosome respectively, and they only differed in combinations on the A chromosome.

Another problem that was encountered using the nomenclature system of Gupta and Shepherd (1990), was that many bands that they reported as faint bands, were clear, dark bands in this study. For example, Tugela had combination e, group 2, but the faint bands reported in the nomenclature were clear dark bands in this study. It is possible that the computer software used in this study, is more sensitive, but there are definite differences in intensities of certain bands. This raises the question if there are perhaps differences between Australian and South African wheat cultivars in their band intensities and if the bands are perhaps expressed by different chromosomes.

In some South African cultivars the nomenclature of Gupta and Shepherd (1990) was unable to identify certain combinations. Belinda, Betta, Limpopo, Molopo and Nantes had no matching combinations in group 2 and Molen, Molopo and Nantes had no matching combinations in group 3. Polymorphism is common in wheat and new banding combinations are quite possible. Gupta and Shepherd (1990) have found that for LMW glutenins, chromosome 1B showed the greatest polymorphism. Rare recombination and point mutations can generate new LMW glutenin combinations. This can be the reason why new combinations were found, but it can also be possible that there are

combinations that are not yet included in the nomenclature of Gupta and Shepherd (1990).

In four of the 30 cultivars tested by Maartens (1997) banding combinations c and f (group 1) (nomenclature of Gupta and Shepherd, 1990) appeared together in the same South African cultivars. These combinations were therefore not alternatives to each other.

Jackson *et al* (1996) also encountered some problems when they used the nomenclature of Gupta and Shepherd (1990). Cultivars with the same name, but a different source gave different patterns. They have used the linkage demonstrated by Payne *et al* (1984) and Gupta and Shepherd (1988) between the genes for gliadins (*Gli-1*) and the genes for LMW subunits (*Glu-3*) on the short arms of chromosomes 1A, 1B and 1D. The cultivars they analysed had the same gliadin composition, and therefore, identical LMW glutenin patterns were expected. They suggested a nomenclature system based on gliadins as well as LMW glutenin subunits, where the format *Gli-A1*◊, *Glu-A3*□ is used, where ◊ is the *Gli-1* allele designated by Metakovsky (1991) and □ is the *Glu-3* allele designated by Gupta and Shepherd (1990). The gliadin composition were not determined in this thesis, but will be further investigated to comment on this nomenclature.

3.5 Conclusions

The monosomic lines proved to be effective to determine which chromosomes are responsible for the expression of certain bands. With the help of the correlations calculated in Chapter 1, combinations were determined that were expressed by certain chromosomes. This helped to develop a more effective nomenclature system for the identification of LMW glutenin subunits in bread wheat.

There are several advantages of this nomenclature system over the nomenclature of Gupta and Shepherd (1990):

1. All the cultivars tested could easily be distinguished.
2. It is very effective to determine differences between cultivars. Some cultivars had the same combinations in the nomenclature of Gupta and Shepherd (1990).
3. Researchers could determine correlations in wheat cultivars in their own countries and add new combinations to this nomenclature.
4. It is relatively easy to use once molecular distances are determined.

There are also disadvantages:

1. With the help of the nomenclature of Gupta and Shepherd (1990) molecular markers for bread wheat quality were identified. No genetic markers are yet identified with the new nomenclature system.
2. In some cases bands in the same group were expressed by all three chromosomes. These bands could have the same molecular weight, but different amino acid composition or quality effects. This could have an effect in identifying quality parameters.

Chapter 4

Conclusions

Electrophoresis has proved to be an effective and reliable method for cultivar identification. There was extensive heterogeneity between the different cultivars and the different patterns were also stable in response to environmental factors. This proves that, with the use of electrophoresis, differences between cultivars can be shown (Sapritstein and Bushuk, 1985).

Many practical applications have also stemmed from the use of electrophoresis. These applications are based on the understanding of the genetic control and heritability of the proteins and this enhances their reliability (Khan *et al*, 1990).

The one step one-dimensional method of Singh *et al* (1991) gave clear separation of the different bands. The HMW and LMW glutenins could also be read from the same gel in a gliadin-free background. Up to 20 samples could be analysed on a single gel.

It becomes more and more difficult to distinguish between newly released varieties. The accurate identification of plant breeding material is very important for the protection of plant breeders' rights and for effectiveness in breeding programmes. In South Africa, mainly the HMW glutenins are used to distinguish between wheat cultivars (Randall *et al*, 1992). This study has proved however, that the HMW glutenins are not reliable for cultivar identification since many cultivars in South Africa have the same banding combinations in both bread and durum wheats. It was, however, very effective to determine seed purity which is very useful before commercialising new varieties.

The LMW glutenins have proved to be more effective for cultivar identification in bread and durum wheats. All the cultivars had different banding patterns and it was also possible to distinguish between cultivars with a close genetic relationship, as well as between near isogenic lines.

The standard deviations of different cultivars showed some overlapping of bands. This was used to identify class intervals for the different banding patterns. Thirty-nine different LMW bands were identified. The correlations between the different banding patterns

were also determined. This proved that some banding combinations were negatively correlated while others were positively correlated.

With the help of four monosomic lines and these correlations, it was possible to identify a more effective nomenclature system for bread wheats. The nomenclature system currently used (Gupta and Shepherd, 1990) could not distinguish between all the South African cultivars and there were also banding combinations found in South African wheat cultivars that were not reported in this system. The combinations of c and f (group 1) were also not always alternatives to each other as reported by Gupta and Shepherd (1990). There were also differences in the band intensities reported by these researchers and the intensities found in this study.

The genetic distances between cultivars showed that there is genetic variation between South African durum wheats, but some bread wheat cultivars are very closely related. This study also showed that the LMW glutenins can be used to determine the genetic distances between cultivars that can help in the protection of plant breeders' rights.

A few questions were also raised in this study that will be looked at in the near future:

- 1) Is it possible to identify genetic markers for bread-making quality with the help of the new nomenclature system for LMW glutenins?
- 2) Are certain bands more prominent in determining bread-making quality or are certain LMW band combinations necessary to breed a better bread quality variety?
- 3) Can the differences in the intensities of different classes of bands have an influence on bread-making quality?

Chapter 5

Summary

1. The aim of this study was to identify:
 - a) The HMW glutenin subunit composition in South African bread and durum wheats.
 - b) The effectiveness of LMW glutenins for the identification of bread and durum wheat varieties.
 - c) Different classes of LMW glutenins.
 - d) The differences in the band intensities of the different classes.
 - e) The correlations between the certain combinations.
 - f) The genetic distances between cultivars in bread and durum varieties.
 - g) A new LMW glutenin nomenclature system that can help to distinguish between bread wheat cultivars.
2. The cultivars were screened in a gliadin-free background using a simplified one-dimensional procedure of Singh *et al* (1991). The HMW and LMW glutenins were run on a single gel.
3. The results were as follows:
 - a) Many cultivars had the same HMW banding combinations in bread and durum wheats. It was therefore not possible to use HMW glutenins to distinguish between cultivars.
 - b) The LMW glutenins were, however, very effective to distinguish between cultivars. It was also possible to distinguish between cultivars with a close genetic relationship and between near isogenic lines.
 - c) Thirty-nine different classes of LMW glutenins were determined with the help of the standard deviations of different cultivars.
 - d) It was possible to assign different band intensities to different classes. Some classes contained light bands, while other contained dark bands. There were also bands of medium intensity. In some classes light and dark bands occurred in the replications of the same cultivar.
 - e) Correlations were found between certain combinations.

- f) The genetic distances between cultivars showed that there are genetic variation between durum wheat varieties, but that some bread wheat varieties are very closely related.
 - g) A new nomenclature system was identified and this proved to be sufficient to distinguish between the different cultivars.
4. The conclusions of this study are:
- a) The HMW glutenins must not be used for cultivar identification in South Africa. It is only reliable to determine seed purity before commercialising new varieties.
 - b) The LMW glutenins are very effective to distinguish between cultivars.
 - c) The new nomenclature system is very effective for cultivar identification. It explains more of the variation between cultivars than the nomenclature system of Gupta and Shepherd (1990).
 - d) Using this system, genetic markers must be identified for bread-making quality. It must also be tested if certain bands alone are responsible for bread-making quality and if combinations of bands determine a good bread wheat cultivar.
 - e) The influence on quality of the intensities of bands in the different classes must also be tested.

Opsomming

1. Die doel van die studie was om:
- a) Die HMW gluteniene in Suid Afrikaanse brood en durum koring te bepaal.
 - b) Die effektiwiteit van LMW gluteniene te bepaal om tussen verskillende brood en durum kultivars te onderskei.
 - c) Verskillende klasse LMW gluteniene te bepaal.
 - d) The intensiteit verskille in bande tussen verskillende klasse te bepaal.
 - e) Korrelasies tussen die verskillende klasse te bepaal.
 - f) Die genetiese afstande tussen kultivars te bepaal.
 - g) 'n Nuwe LMW glutenien nomenklatuur sisteem te ontwikkel om tussen kultivars te onderskei.

2. Verskillende kultivars is ge-evalueer in 'n agtergrond wat vry is van gliadiene. 'n Vereenvoudigde een-dimensionele metode van Singh *et al* (1991) is gebruik. Die HMW en LMW gluteniene is op 'n enkele gel geëvalueer.

3. Die resultate was as volg:
 - a) Baie kultivars het dieselfde HMW glutenien bande gehad. Dit het bewys dat HMW gluteniene nie gebruik kan word om tussen kultivars te onderskei nie. Dit is egter ideaal om saad suiwerheid voor kultivar vrystelling te bepaal.
 - b) Die LMW gluteniene was baie effektief om tussen kultivars te onderskei. Dit was ook moontlik om tussen kultivars met naby genetiese agtergronde te onderskei.
 - c) Daar was 39 verskillende klasse LMW gluteniene. Dit is bepaal m.b.v. die standaard afwykings van sekere kultivars.
 - d) Sekere klasse het ook definitiewe intensiteit bande gehad. Bande in sommige klasse is uitgedruk as ligte bande terwyl ander donker bande was.
 - e) Sommige LMW kombinasies was hoogs gekorreleerd. Negatiewe en positiewe korrelasies is gevind.
 - f) Die genetiese afstande tussen kultivars is ook bepaal. Durum koring in Suid Afrika toon baie genetiese variasie tussen kultivars, maar daar is egter baie nabye genetiese verwantskappe tussen sekere brood korings.
 - g) 'n Nuwe nomenklatuur sisteem is ontwikkel en dit was baie effektief om tussen kultivars te onderskei.

4. Die volgende afleidings kan gemaak word:
 - a) Die HMW gluteniene is onvoldoende om te gebruik in Suid Afrika om tussen kultivars te onderskei. Dit kan egter met sukses gebruik word om saad suiwerheid te bepaal voor 'n kultivar vrygestel word.
 - b) Die LMW gluteniene is baie effektief om tussen kultivars te onderskei.
 - c) Die nuwe nomenklatuur sisteem is baie effektief om tussen kultivars te onderskei. Dit verklaar meer van die variasie tussen kultivars as die nomenklatuur van Gupta en Shepherd (1990).
 - d) Die volgende stap is om genetiese merkers te identifiseer vir broodbak kwaliteit deur van hierdie sisteem gebruik te maak. Daar moet ook bepaal word of sekere bande alleen verantwoordelik is om brood kwaliteit te bepaal en of sekere kombinasies eerder 'n invloed het.

- e) Daar moet ook gekyk word of die intensiteit van sekere bande 'n invloed het op die broodbak kwaliteit van 'n kultivar.

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Appendix A

This Appendix has all the tables of the bread wheat cultivars. Five to six replications of each cultivar are given (R1 to R5/R6) together with the band intensities (I1 to I5/I6). The last two columns of each cultivar have the average of the migration distances (Rav) and the class of intensity (I). As discussed in Chapter 1, a class of one means a very light band and a class of five is a very dark band.

Table 1. The migration distances and band intensities of the LMW glutenins of Adam Tas

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	2	8	1	6	1	9	1	11	1	8	1	9	1
-	-	17	3	19	1	18	1	15	1	12	1	16	1
21	3	28	1	-	-	23	1	20	1	25	3	23	1
44	3	46	2	48	2	40	2	49	1	44	1	45	2
50	1	53	3	57	3	50	1	55	1	55	1	53	1
70	4	77	4	72	5	72	2	75	5	75	5	74	5
98	1	95	1	92	1	95	5	92	5	92	5	94	6
101	1	101	1	98	1	104	5	100	1	-	-	101	1
120	4	124	4	-	-	-	-	120	1	119	3	121	6
135	3	133	4	130	5	134	2	131	2	-	-	133	6
-	-	154	2	155	3	157	3	151	3	146	3	153	3
174	1	173	1	174	1	173	2	176	1	175	1	174	1
179	1	185	1	182	1	182	1	187	1	186	1	184	1
192	1	194	2	194	3	192	1	189	1	189	1	192	1

Table 2. The migration distances and band intensities of the LMW glutenins of Australiese hard white

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
46	2	43	3	38	1	42	3	45	2	44	1	43	2
66	5	67	5	67	5	67	5	67	5	67	5	67	5
-	-	84	1	84	1	79	1	82	1	76	1	81	1
89	2	90	2	-	-	92	2	89	2	92	3	90	2
101	4	102	4	101	4	102	4	103	4	101	4	102	4
105	4	111	1	112	1	111	1	-	-	110	2	110	1
119	1	121	2	120	1	119	1	121	1	121	1	120	1
132	2	132	1	131	1	-	-	133	1	-	-	132	1
136	2	137	2	133	1	136	3	137	3	137	2	136	2
147	1	148	1/2	147	1	-	-	144	1	147	1	147	1
161	1	161	1	-	-	163	2	162	2	162	1	162	1
166	1	169	1	168	1	172	1	165	2	-	-	168	1

Table 3. The migration distance and band intensities of the LMW glutenins of Barta.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
18	1	19	1	17	1	12	1	10	1	12	1	15	1
27	1	22	1	21	1	20	1	24	1	22	1	23	1
37	3	39	4	-	-	40	4	36	4	37	4	38	4
51	2	50	3	53	3	-	-	56	3	59	2	54	3
80	5	87	5	91	5	87	5	81	5	83	5	85	5
95	2	100	2	98	4	96	2	91	3	-	-	96	2
107	4	108	2	110	2	111	2	104	2	107	2	108	2
119	4	124	4	125	4	128	4	120	3	126	2	124	4
139	1	138	4	140	4	145	5	138	4	140	4	140	4
155	2	156	2	157	1	155	2	157	2	157	1	156	2
173	1	171	3	173	3	-	-	173	3	171	2	172	3
182	1	181	1	-	-	180	2	-	-	179	1	181	1

Table 4. The migration distances and band intensities of the LMW glutenins of Belinda.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	3	10	1	14	1	21	1	18	1	10	1	15	1
40	3	43	4	46	4	42	3	38	3	48	3	43	3
62	3	64	3	68	3	66	4	59	3	63	5	64	3
75	5	77	5	82	5	78	5	72	5	75	4	77	5
99	1	92	4	95	4	91	4	97	1	100	4	96	4
111	2	114	2	118	2	116	2	109	3	112	1	113	2
148	2	141	5	145	5	147	5	140	5	138	4	143	5
158	3	169	5	163	4	162	3	160	3	154	3	159	3
180	1	185	1	185	1	187	1	182	1	185	1	184	1
187	1	190	1	190	1	193	1	191	1	194	1	191	1

Table 5. The migration distance and band intensities of the LMW glutenins of Bella.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
6	1	9	1	-	-	11	1	8	1	11	1	9	1
19	1	19	1	18	1	-	-	19	1	13	1	18	1
29	1	29	1	27	1	21	1	24	1	-	-	26	1
36	1	-	-	38	1	35	2	40	5	38	4	37	6
51	2	50	1	51	4	58	2	60	2	59	2	55	2
90	5	90	5	87	5	83	5	88	5	81	5	87	5
114	2	110	1	110	2	108	2	112	2	112	2	111	2
125	3	122	3	121	4	122	4	123	4	124	4	123	4
142	4	140	4	145	1	141	4	139	5	141	4	141	4
158	1	155	1	154	2	159	1	155	1	159	1	157	1
176	3	177	2	175	2	170	1	170	2	173	2	174	2
-	-	188	1	187	1	180	2	180	2	189	1	185	1

Table 6. The migration distance and band intensities of the LMW glutenins of Betana.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	18	1	12	1	10	1	11	1	9	1	13	1
21	1	20	1	20	1	19	1	27	1	20	1	21	1
31	1	32	1	34	1	40	3	39	3	34	1	35	1
65	2	61	2	64	2	60	2	59	1	59	2	61	2
85	5	84	5	82	5	80	5	80	5	79	5	82	5
106	2	106	2	102	2	103	2	101	2	100	2	103	2
110	2	109	2	113	3	111	2	110	2	108	2	110	2
118	3	113	3	119	3	120	2	117	2	117	3	117	3
135	3	135	4	132	4	136	4	133	3	132	4	134	4
151	1	151	1	150	1	154	1	153	1	150	1	152	1
165	2	164	2	165	3	-	-	169	2	167	3	166	2
180	1	178	1	177	1	171	2	180	1	177	1	177	1
186	1	182	1	189	1	185	1	186	1	186	1	186	1

Table 7. The migration distances and band intensities of the LMW glutenins of Betta

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
26	1	25	1	26	1	24	1	24	1	21	2	24	1
34	1	34	1	37	1	37	1	42	1	30	1	36	1
52	3	52	3	50	4	51	3	50	3	49	4	51	3
56	3	56	3	56	4	55	3	53	3	54	4	55	3
69	2	68	2	68	2	67	2	69	1	66	1	68	2
83	4	83	4	84	5	83	5	82	5	83	5	83	5
93	2	93	3	91	4	93	3	92	4	93	3	93	3
104	2	-	-	102	3	106	2	102	2	103	2	103	2
109	2	106	2	108	3	-	-	106	2	106	2	107	2
119	2	-	-	118	1	118	1	118	1	117	1	118	1
123	3	124	3	123	1	123	1	122	1	129	1	124	1
131	5	138	5	137	5	137	5	136	5	136	3	136	5
148	4	150	5	141	5	149	5	148	5	149	4	148	5
155	4	150	5	149	5	157	3	151	3	155	4	153	4
171	2	169	2	171	2	172	2	171	3	179	2	172	2

Table 8. The migration distances and band intensities of the LMW glutenins of Betta DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
22	1	25	1	24	1	28	1	28	1	28	2	26	1
49	4	48	4	49	4	48	5	51	3	46	5	49	4
52	2	52	4	47	4	52	5	55	4	50	5	52	4
	-	63	1	63	2	63	1	65	1	-	-	64	1
79	4	78	5	78	5	80	5	80	5	79	5	79	5
84	3	82	5	85	3	87	3	88	3	88	3	86	3
90	3	90	3	91	3	-	-	91	3	99	4	92	3
102	2	100	3	100	3	99	3	101	4	100	4	100	3
110	2	112	1	112	2	113	1	114	1	113	1	112	1
131	4	133	5	133	5	132	4	134	4	131	4	132	4
145	5	147	5	146	5	147	4	149	4	150	4	147	4
164	2	165	2	165	2	167	2	169	2	166	2	166	2

Table 9. The migration distance and band intensities of the LMW glutenins of Bona.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	1	16	1	10	1	11	1	11	1	15	1	13	1
27	1	20	1	20	1	28	3	20	1	-	-	23	1
48	3	47	3	40	1	42	3	47	2	44	3	45	3
63	2	62	2	65	5	62	5	62	5	60	2	62	6
82	5	81	5	82	5	87	2	84	2	80	5	83	5
103	2	104	3	106	3	107	3	107	3	110	4	106	3
119	4	115	5	118	3	119	4	-	-	120	4	118	4
132	4	132	4	135	4	137	1	138	1	137	1	135	6
147	1	148	1	150	1	153	2	153	1	152	2	151	1
165	2	165	5	167	1	168	1	165	1	169	1	167	1
184	1	184	1	186	1	186	1	183	1	180	1	184	1
188	1	191	1	191	1	193	1	190	1	194	2	191	1

Table 10. The migration distances and band intensities of the LMW glutenins of Caledon.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
35	1	-	-	40	-	40	1	36	1	40	1	38	1
66	5	66	5	69	5	67	5	68	5	69	5	68	5
74	2	75	2	77	2	77	2	78	2	77	2	76	2
92	2/3	93	3	95	3	93	3	94	3	94	2	94	3
106	3	106	3	106	4	103	3	103	3	105	3	105	3
114	2	114	2	116	2	112	2	115	2	117	2	115	2
122	1	123	1	124	1	123	1	123	1	124	1	123	1
138	2	139	2	140	2	139	2	137	2	139	2	139	2
148	1	151	1	150	1	150	1	150	1	147	1	149	1
168	2	169	2	170	2	164	2	165	2	165	2	167	2

Table 11. The migration distances and band intensities of the LMW glutenins of Carina.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	7	1	9	1	6	1	9	1	-	-	8	1
15	1	14	1	-	-	13	1	15	1	17	1	15	1
28	1	-	-	21	3	20	1	22	1	21	1	22	1
38	1	34	3	33	1	34	1	33	1	32	2	34	1
47	3	46	2	40	1	-	-	45	1	42	1	44	1
59	2	65	5	57	5	63	2	60	5	63	4	61	5
77	5	76	5	78	2	80	5	71	2	75	2	76	6
90	4	99	3	98	4	90	5	93	5	99	5	95	5
100	5	106	4	106	5	103	2	101	5	106	5	104	5
116	4	116	4	110	5	119	4	115	2	118	1	116	4
131	5	137	1	138	2	132	5	130	3	133	3	134	6
159	2	156	3	157	1	158	2	-	-	157	2	157	2
167	2	165	1	165	1	164	1	-	-	-	-	165	1
188	1	180	1	180	1	180	1	179	2	181	1	181	1
196	1	195	1	191	1	191	1	-	-	194	1	193	1

Table 12. The migration distances and band intensities of the LMW glutenins of Carolus.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	8	1	10	1	10	1	7	1	8	1	8	1
13	1	13	1	15	1	15	1	15	1	13	1	14	1
31	1	35	1	33	1	30	4	36	4	30	1	33	1
65	1	61	4	67	1	62	5	68	5	-	-	65	6
68	2	74	2	75	2	76	4	-	-	77	2	74	2
86	5	86	5	80	1	-	-	81	4	89	4	84	4
99	5	99	5	92	5	98	2	92	5	-	-	96	5
109	1	108	1	106	4	107	1	106	2	110	2	108	1
121	3	124	4	129	4	129	3	122	1	-	-	125	6
152	4	156	5	160	1	157	1	150	2	159	2	156	6
165	3	169	2	170	2	-	-	163	1	171	1	168	1
180	1	187	1	184	1	189	1	189	1	-	-	186	1

Table 13. The migration distance and band intensities of the LMW glutenins of Corella.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
6	1	10	2	10	1	9	1	13	1	14	2	10	1
25	2	30	5	28	1	23	1	22	1	23	1	25	1
-	-	30	5	39	2	36	2	31	2	30	1	33	2
41	5	47	1	-	-	48	1	41	1	45	2	44	1
60	1	53	2	58	1	54	1	54	1	-	-	56	1
68	2	72	5	73	1	71	1	72	1	72	1	71	1
-	-	92	1	98	5	97	5	91	5	99	2	95	5
111	1	106	1	107	2	105	2	111	1	110	2	108	1
115	1	117	1	120	2	118	2	120	2	123	3	119	2
120	1	122	1	129	2	126	2	127	2	127	2	125	2
138	1	138	2	135	2	132	2	139	2	133	1	136	2
143	1	142	2	147	3	143	2	-	-	143	1	144	2
163	1	167	1	162	1	160	1	160	1	162	3	162	1
177	1	170	1	180	2	176	2	170	3	174	2	175	2
185	1	184	2	-	-	186	1	184	1	181	1	184	1
190	1	190	3	197	1	193	1	192	1	194	1	193	1

Table 14. The migration distance and band intensities of the LMW glutenins of Dirkwin.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
4	1	6	1	7	1	9	1	8	1	8	1	7	1
12	2	13	1	12	1	11	1	-	-	12	1	12	1
18	1	15	1	-	-	18	1	16	1	19	1	17	1
-	-	26	1	21	1	30	1	29	1	28	1	27	1
51	4	47	2	50	2	45	1	40	1	45	1	46	1
71	5	70	5	71	5	70	5	75	5	80	5	73	5
87	1	82	4	89	5	83	5	88	5	89	5	86	5
98	3	97	3	99	3	103	2	-	-	92	3	98	3
-	-	119	3	-	-	114	3	118	3	117	2	117	3
120	4	-	-	121	3	126	3	127	2	124	3	124	3
150	3	143	1	147	2	145	1	147	1	140	3	145	1
171	1	-	-	178	1	177	1	176	2	176	2	176	1
180	1	182	1	-	-	180	1	186	1	182	1	182	1
185	1	-	-	189	2	184	1	188	1	186	1	186	1
191	2	193	1	-	-	190	1	194	1	191	1	192	1

Table 15. The migration distance and band intensities of the LMW glutenins of Eland.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
6	1	9	1	9	1	10	1	8	1	4	1	8	1
13	1	14	1	16	1	17	1	16	1	14	1	15	1
23	1	20	1	24	1	21	1	23	1	20	1	22	1
31	1	34	1	33	1	38	1	40	1	33	1	35	1
53	2	55	2	50	2	47	1	48	1	47	1	50	1
75	5	79	5	78	5	83	5	85	5	85	5	81	5
111	4	110	5	110	5	115	2	118	3	110	1	112	6
120	4	122	5	126	4	128	3	128	4	126	4	125	4
136	1	139	2	134	1	139	3	140	2	140	3	138	2
148	2	152	3	156	2	151	1	152	1	155	1	152	1
170	1	162	1	-	-	160	1	162	1	162	1	163	1
181	1	186	1	180	1	176	2	180	1	181	2	181	1
190	1	196	1	193	1	190	1	191	1	192	1	192	1

Table 16. The migration distance and band intensities of the LMW glutenins of Elize.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	1	6	1	9	5	6	1	12	1	6	1	8	1
23	5	20	2	21	2	20	1	18	2	20	2	20	2
32	1	30	2	-	-	30	4	33	5	30	5	31	6
47	1	42	1	48	2	49	1	50	1	52	1	48	1
62	4	60	4	61	3	66	3	68	3	68	3	64	3
80	5	78	3	76	2	70	3	70	3	71	3	74	3
-	-	88	4	87	1	84	4	86	4	88	4	87	4
91	4	-	-	94	1	91	5	97	5	95	5	94	5
105	3	103	2	106	2	107	1	-	-	110	1	108	2
114	2	111	2	118	2	-	-	120	3	118	1	116	2
-	-	129	3	126	2	125	3	128	3	126	3	127	3
133	4	134	3	-	-	139	5	140	3	135	2	136	4
-	-	141	2	-	-	148	2	145	3	141	2	144	2
159	2	158	2	150	1	152	4	155	3	156	3	155	2
169	1	-	-	168	1	169	1	163	2	164	1	167	1
179	1	175	2	172	1	-	-	173	1	172	1	174	1
188	1	184	1	186	1	187	1	188	3	187	3	187	1

Table 17. The migration distances and band intensities of the LMW glutenins of Elrina.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	2	11	2	11	2	14	3	-	-	10	1	12	2
27	1	26	1	22	1	24	1	28	4	22	3	25	1
38	1	35	1	34	1	32	1	34	4	33	2	34	1
55	4	53	4	52	4	51	5	50	4	49	3	52	4
68	2	69	2	60	1	-	-	60	4	63	5	64	6
90	5	86	5	88	5	87	2	90	4	85	5	88	5
94	5	92	5	92	5	97	4	96	4	96	5	95	5
106	1	106	1	104	1	104	5	109	5	104	3	106	6
125	3	122	3	120	3	124	1	-	-	125	2	123	3
136	3	139	4	137	3	-	-	132	2	134	2	136	3
153	5	151	5	150	5	156	1	151	5	153	5	152	5
169	1	167	1	166	1	161	1	165	1	-	-	166	1
177	1	177	1	178	2	173	1	-	-	171	1	175	1
186	2	183	2	182	2	185	2	189	1	184	1	185	2
-	-	194	1	192	1	190	2	194	1	190	1	192	1

Table 18. The migration distances and band intensities of the LMW glutenins of Flameks.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	1	11	1	5	1	4	2	4	1	5	1	6	1
20	1	20	1	15	1	12	1	16	1	16	1	17	1
33	1	32	3	-	-	35	3	38	3	37	3	35	3
48	3	53	3	48	3	53	5	-	-	52	3	51	3
67	3	-	-	68	5	61	5	62	5	60	5	64	5
84	2	79	5	79	1	79	1	83	1	83	1	81	1
97	1	94	1	91	1	94	1	91	1	94	2	94	1
101	1	104	1	107	2	103	2	101	2	-	-	103	2
115	3	116	2	-	-	110	2	117	3	112	3	114	3
130	3	136	3	136	1	132	1	134	1	133	1	134	1
159	1	154	1	160	2	156	2	157	2	157	2	157	2
-	-	167	2	164	2	169	1	169	1	-	-	167	1
176	1	174	2	177	1	-	-	171	1	170	1	174	1
185	1	189	1	187	1	181	1	187	1	186	1	186	1
192	1	196	1	195	1	196	2	196	2	193	1	195	1

Table 19. The migration distances and band intensities of the LMW glutenins of Flamink.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
-	-	19	3	15	1	15	1	13	1	13	1	15	1
22	3	-	-	20	1	21	1	21	1	23	1	21	1
48	5	48	5	43	5	43	1	51	5	38	1	45	5
57	5	56	5	53	5	66	5	57	5	-	-	58	5
73	1	69	1	74	1	75	5	74	1	73	1	73	1
83	1	82	1	78	1	82	1	-	-	-	-	81	1
93	2	90	2	88	2	90	1	91	2	94	1	91	2
109	2	108	3	109	4	-	-	110	3	105	1	108	3
112	2	112	3	-	-	112	2	-	-	109	1	111	2
129	2	129	3	128	3	132	5	127	3	128	3	129	3
149	1	148	1	142	1	151	4	-	-	145	2	147	1
-	-	-	-	159	1	163	2	163	3	157	1	161	2
171	1	169	1	171	1	171	1	175	1	-	-	171	1
175	1	174	1	177	2	-	-	183	1	181	4	178	1
181	1	178	2	188	1	188	3	188	4	187	4	185	6
-	-	196	1	192	1	193	1	193	1	193	3	193	1

Table 20. The migration distances and band intensities of the LMW glutenins of Gamka.

1	Int	2	Int	3	Int	4	Int	5	Int	6	Int	Av	Av
14	1	-	-	16	3	16	3	16	3	18	3	16	3
52	5	51	5	52	5	49	5	41	5	43	5	48	5
57	5	58	5	59	5	61	1	50	5	49	5	56	5
75	1	73	1	-	-	70	1	68	1	-	-	72	1
83	1	77	1	79	1	85	2	85	2	87	1	83	1
92	2	94	1	94	1	-	-	-	-	96	1	94	1
110	4	110	3	112	4	108	4	106	4	108	4	109	4
129	3	130	3	127	2	126	1	130	1	128	2	128	2
152	1	152	1	-	-	154	1	156	1	153	1	153	1
166	1	169	2	168	2	165	1	158	1	165	1	165	1
175	1	-	-	-	-	174	2	174	2	174	2	174	2
182	1	185	1	189	1	186	1	189	1	177	2	185	1
191	1	191	1	192	1	195	1	195	1	190	1	192	1

Table 21. The migration distances and band intensities of the LMW glutenins of Gamtoos.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	13	1	6	1	10	1	15	1	11	1	12	1
28	5	27	5	25	5	26	3	26	3	27	5	27	5
47	5	45	5	43	5	48	5	52	5	49	5	47	5
59	1	57	1	56	2	57	2	62	2	63	3	59	2
75	1	70	1	-	-	73	1	79	1	72	1	74	1
86	1	-	-	89	1	81	1	87	1	-	-	86	1
93	1	-	-	92	1	95	2	98	2	93	2	94	2
125	3	124	3	124	2	115	3	119	3	118	2	121	3
162	4	160	3	159	4	-	-	167	1	170	2	164	6
172	1	176	1	173	1	174	1	174	1	175	2	174	1
184	1	187	1	182	1	184	2	185	1	185	2	185	1

Table 22. The migration distances and band intensities of the LMW glutenins of Gamtoos DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
25	5	26	5	28	5	24	5	24	5	24	5	25	5
44	5	45	5	46	5	46	5	45	5	45	5	45	5
55	1	57	1	59	1	59	2	53	2	53	3	56	2
82	1	82	1	80	1	-	-	-	-	75	1	80	1
92	1	86	1	87	1	89	2	88	2	89	3	89	1
102	3	104	3	105	3	110	2	110	3	110	5	107	3
121	3	124	3	124	2	130	3	128	3	128	2	126	3
153	2	154	3	157	3	-	-	158	1	160	1	156	2
158	4	161	4	166	4	159	1	163	1	166	1	162	6
179	1	176	4	171	1	172	1	170	1	172	1	173	1
-	-	184	1	185	1	180	2	180	2	184	3	183	2
197	1	190	1	192	1	193	1	193	1	196	1	194	1

Table 23. The migration distances and band intensities of the LMW glutenins of Gandum I Fasai.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
25	2	25	4	25	2	28	2	25	3	28	2	26	2
38	1	37	1	39	1	35	1	33	1	35	1	36	1
49	4	47	3	48	3	46	4	44	2	45	3	47	3
59	5	59	3	59	5	62	5	67	5	64	5	62	5
67	5	66	4	68	5	70	5	72	5	70	5	70	5
78	2	79	3	80	3	77	2	78	3	77	3	78	3
91	3	93	4	91	3	90	3	90	2	89	3	91	3
95	3	97	3	94	3	94	3	96	3	96	3	95	3
104	5	104	5	103	5	102	5	101	4	101	5	103	5
-	-	108	5	109	4	-	-	108	3	107	4	108	4
123	1	123	1	122	1	123	1	121	1	123	1	123	1
127	2	126	1	126	1	127	1	127	1	129	1	127	1
-	-	132	1	133	1	132	1	134	2	137	1	134	1
145	1	145	1	142	1	146	1	142	1	142	1	144	1
150	1	151	2	155	2	150	1	-	-	152	1	152	1
164	1	167	1	169	1	168	1	169	1	163	1	167	1
173	1	172	1	172	1	173	1	174	1	173	3	173	1
178	1	174	1	174	1	177	1	177	1	176	2	176	1

Table 24. The migration distances and band intensities of the LMW glutenins of Gariép.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
61	3	62	3	-	-	-	-	66	4	64	5	63	4
73	5	74	5	73	5	73	5	73	5	71	5	73	5
96	3	97	3	97	4	96	3	97	3	97	5	97	2
105	5	107	5	107	5	107	5	108	4	109	5	107	3
114	1	115	2	118	1	117	1	119	1	115	2	116	5
121	1	123	1	124	1	125	1	127	1	125	1	124	1
134	1	136	1	133	1	135	1	139	1	137	2	136	1
147	1	148	1	141	1	145	2	145	1	144	3	145	1
155	1	-	-	153	1	154	1	154	1	150	1	153	1
164	2	166	1	167	1	165	1	167	1	167	2	166	1
175	1	176	1	177	1	170	2	171	1	-	-	174	1

Table 25. The migration distances and band intensities of the LMW glutenins of Gariep DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
47	1	48	2	47	1	43	1	42	1	43	1	45	1
70	5	70	5	71	5	69	5	69	5	66	5	69	5
77	2	78	2	79	2	79	2	79	2	76	2	78	2
94	3	94	3	97	3	96	3	95	2	93	2	95	3
103	4	104	3	102	4	-	-	104	4	-	-	103	4
107	4	106	3	105	4	106	4	107	4	107	4	106	4
117	1	117	1	119	1	116	1	117	1	114	1	117	1
125	1	126	1	127	1	125	1	124	1	122	1	125	1
137	1	139	1	139	1	138	1	138	1	135	2	138	1
144	2	144	2	146	2	141	2	142	2	146	1	144	2
152	1	-	-	153	1	149	1	150	1	151	1	151	1
169	1	168	2	170	2	167	2	167	2	168	2	168	2

Table 26. The migration distances and band intensities of the LMW glutenins of Gourits.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
18	1	16	1	11	1	18	1	10	1	16	1	15	1
31	1	29	1	32	5	32	1	29	1	28	1	30	1
50	4	47	5	45	5	49	5	52	5	43	5	48	5
-	-	65	5	64	5	58	4	58	5	59	5	61	5
71	4	78	3	75	4	71	1	73	1	70	4	73	6
94	1	97	1	92	1	93	4	94	4	-	-	94	6
-	-	101	4	102	3	98	4	100	4	100	4	100	4
114	4	114	3	110	3	111	5	114	5	110	4	112	4
135	5	133	5	130	5	133	1	135	1	132	2	133	6
147	1	144	1	144	1	142	1	150	2	144	2	145	1
160	2	157	1	157	2	157	5	160	4	165	5	159	6
183	4	182	4	183	5	183	1	183	1	183	1	183	6
193	1	195	1	193	1	190	1	194	1	194	1	193	1

Table 27. The migration distances and band intensities of the LMW glutenins of Harts.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	17	1	19	1	12	1	-	-	19	2	16	1
23	1	24	1	26	1	27	1	25	4	26	3	25	1
40	5	41	4	41	5	49	5	51	5	49	5	45	5
59	5	60	5	61	5	63	1	60	5	57	4	60	5
75	1	76	1	76	1	75	1	74	1	-	-	75	1
87	1	84	1	-	-	80	1	-	-	81	1	83	1
90	1	88	1	89	1	93	1	92	2	88	2	90	1
103	2	103	1	103	1	100	2	-	-	103	3	102	2
118	3	117	3	118	3	114	3	117	3	116	1	117	3
127	3	128	3	128	3	124	2	125	1	123	3	126	3
137	2	135	2	135	1	133	2	135	2	138	1	136	2
168	2	170	2	169	3	165	1	173	1	167	2	169	2
175	3	176	3	175	2	179	1	179	1	177	2	177	2
188	1	189	1	-	-	185	1	185	1	186	1	187	1
192	1	193	1	191	1	197	1	190	1	193	1	193	1

Table 28. The migration distances and band intensities of the LMW glutenins of Hugenoot.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
45	2	45	1	-	-	45	1	46	1	46	1	45	1
65	5	64	5	62	5	62	5	64	5	-	-	63	5
68	5	68	5	68	5	68	5	-	-	68	5	68	5
77	1	79	2	79	2	78	2	79	1	79	2	79	2
85	1	83	1	88	1	88	2	-	-	-	-	86	1
92	2	91	1	92	2	92	2	90	3	91	2	91	2
95	2	93	2	-	-	94	1	96	2	99	2	95	2
105	3	106	2	103	2	102	2	101	2	101	2	103	2
119	2	118	2	117	2	115	2	114	1	112	2	116	2
-	-	128	1	129	1	126	1	125	1	-	-	127	1
134	1	135	1	136	1	134	2	136	2	134	1	135	1
148	2	146	2	145	2	141	2	142	2	142	2	144	2
153	2	152	2	151	2	148	2	151	1	150	1	151	2
161	1	161	1	166	1	164	1	162	1	161	1	163	1
176	1	172	1	171	1	170	1	-	-	174	1	173	1

Table 29. The migration distances and band intensities of the LMW glutenins of Inia.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	3	17	3	11	2	14	3	15	3	17	3	16	3
28	5	26	4	24	3	21	3	22	3	23	3	24	3
40	5	40	5	39	5	31	5	33	5	33	5	36	5
53	4	53	4	53	5	50	5	51	5	53	5	52	5
59	4	59	4	-	-	64	4	64	4	66	4	62	4
86	2	85	2	87	2	83	1	86	2	86	1	86	2
101	3	100	4	99	3	101	4	103	4	97	4	100	4
104	3	104	4	106	3	-	-	108	3	105	4	105	3
114	3	115	4	117	4	119	5	119	5	113	3	116	4
120	3	120	3	123	4	126	3	126	3	122	3	123	3
134	1	134	1	-	-	140	1	142	1	143	1	139	1
156	2	156	3	157	2	158	5	161	4	162	4	158	6
163	5	164	4	164	3	166	5	169	5	170	5	166	5
180	1	183	1	176	1	181	1	181	1	185	1	181	1
189	1	192	1	180	1	189	1	189	1	191	1	188	1

Table 30. The migration distances and band intensities of the LMW glutenins of Jager.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	7	1	7	1	8	1	7	1	-	-	7	1
11	1	19	1	15	1	15	1	13	1	12	1	14	1
24	1	25	1	24	1	21	1	24	1	30	1	25	1
37	1	38	1	36	2	-	-	-	-	33	1	36	1
59	5	60	5	60	5	-	-	55	5	52	5	57	5
68	5	67	5	64	5	66	2	67	2	69	3	67	6
80	3	78	2	77	2	77	3	79	3	78	3	78	3
89	4	89	3	88	3	87	4	86	4	89	5	88	4
101	5	101	5	103	1	100	5	106	1	104	1	103	6
114	1	115	1	113	2	115	2	116	2	117	4	115	2
149	3	147	3	147	4	145	5	146	4	147	5	147	4
160	5	159	5	158	5	162	2	162	2	162	3	161	6
172	3	171	3	170	3	169	2	169	3	-	-	170	3
182	3	180	3	177	2	182	1	-	-	182	1	181	2
192	1	190	1	192	1	190	1	191	1	194	1	192	1

Table 31. The migration distance and band intensities of the LMW glutenins of K29-1.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
8	1	12	1	5	1	11	1	10	3	7	5	9	1
33	1	30	2	31	2	27	1	32	1	29	1	30	1
40	2	42	2	40	2	46	4	42	1	40	2	42	2
51	3	53	3	52	3	-	-	50	1	52	3	52	3
73	4	74	3	72	3	73	4	74	4	76	5	74	4
92	5	92	5	92	5	90	2	87	5	95	5	91	5
-	-	106	1	101	1	101	1	97	1	105	1	102	1
112	1	109	1	109	1	110	1	109	1	110	4	110	1
127	5	126	5	124	5	122	2	120	2	128	2	125	6
149	5	146	5	145	5	143	5	145	2	147	4	146	5
-	-	166	2	169	3	168	2	169	1	163	1	167	2
171	2	172	2	176	2	-	-	177	1	176	1	174	2
184	1	185	1	182	1	182	1	183	1	184	1	183	1

Table 32. The migration distances and band intensities of the LMW glutenins of K29-2.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	10	1	-	-	19	1	13	1	16	1	15	1
30	2	25	2	21	2	21	1	22	5	27	2	24	2
40	3	37	2	36	1	38	2	35	1	-	-	37	2
48	3	48	4	46	2	49	4	45	1	43	1	47	6
69	3	68	5	64	3	59	1	61	4	69	2	65	6
88	3	86	5	86	4	86	3	84	1	85	1	86	6
100	1	99	2	97	1	-	-	94	3	95	2	97	2
104	1	106	1	102	1	110	2	107	1	106	1	106	1
123	4	119	5	119	5	119	2	119	1	116	1	119	6
129	2	129	2	-	-	130	3	130	3	129	3	129	3
145	5	144	5	143	5	142	5	142	1	139	5	143	5
167	2	167	3	165	2	166	3	160	2	159	2	164	2
177	1	178	1	173	1	174	2	179	1	174	1	176	1
186	1	184	1	180	1	183	1	186	1	188	1	185	1

Table 33. The migration distances and band intensities of the LMW glutenins of K29-3.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
29	1	23	5	28	2	28	2	28	2	23	1	27	2
39	2	39	1	38	1	38	2	39	2	36	2	38	2
50	4	52	4	49	3	46	3	49	5	48	3	49	4
73	4	74	5	77	5	72	4	71	5	73	5	73	5
92	4	93	5	95	5	89	5	91	5	89	2	92	5
123	5	-	-	119	5	122	5	121	5	124	2	122	5
151	4	149	5	144	3	144	5	147	5	147	5	147	5
160	3	163	3	166	3	164	3	163	2	159	1	163	3
177	1	177	1	176	1	178	3	170	1	176	3	176	1
181	1	188	1	187	1	186	1	183	1	186	2	185	1
190	2	193	1	193	2	193	1	193	1	189	1	192	1

Table 34. The migration distances and band intensities of the LMW glutenins of K29-4.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
24	5	23	5	27	4	25	2	22	2	21	1	24	6
41	1	43	2	47	2	46	2	43	2	46	3	44	2
-	-	69	4	66	4	62	2	67	5	63	4	65	4
74	4	77	3	77	4	70	4	79	4	74	5	75	4
-	-	80	3	85	5	83	4	89	1	84	1	84	6
94	4	96	2	98	2	98	1	93	2	96	2	96	2
107	1	107	1	109	2	103	1	102	1	107	1	107	1
110	1	113	1	119	5	117	3	114	4	113	1	114	6
121	1	128	2	131	3	125	2	120	2	125	1	125	2
136	5	140	4	141	5	142	5	143	4	142	5	141	5
-	-	164	4	164	4	164	5	159	4	166	3	163	4
179	1	180	1	176	1	-	-	176	1	180	1	178	1
185	1	185	1	184	1	187	2	187	1	188	2	186	1
190	1	190	1	191	3	193	1	192	1	193	1	192	1

Table 35. The migration distances and band intensities of the LMW glutenins of K29-5.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
24	5	28	5	28	1	24	5	28	5	26	5
48	1	46	2	46	2	48	1	46	2	47	2
61	5	62	2	61	1	61	5	62	2	61	6
74	2	74	2	73	5	74	2	74	2	74	2
84	4	86	1	84	4	84	4	86	4	85	4
101	5	101	4	102	5	101	5	101	4	101	5
113	1	116	1	113	2	113	1	116	1	114	1
137	1	138	3	138	3	137	1	138	3	138	3
145	4	148	4	144	4	145	4	148	4	146	4
162	2	161	2	162	2	162	2	161	2	162	2
168	2	172	1	172	2	170	2	172	1	171	2
191	1	190	1	192	1	191	1	190	1	191	1

Table 36. The migration distances and band intensities of the LMW glutenins of K29-6.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
29	1	28	5	31	5	27	5	28	5	29	5
41	2	41	1	47	1	42	1	41	1	42	1
49	4	49	1	50	1	47	1	48	1	49	1
66	4	66	5	67	4	68	4	69	4	67	4
82	3	81	2	85	1	83	2	82	2	83	2
90	3	88	4	89	3	90	4	89	4	89	4
107	2	103	5	105	4	106	5	107	5	106	5
114	2	119	1	116	1	117	1	117	1	117	1
129	2	130	1	130	1	128	1	129	1	129	1
140	5	136	1	136	2	138	2	137	2	137	2
		148	5	147	4	146	4	147	4	147	4
170	2	171	5	171	4	170	4	171	4	171	4
185	1	185	1	186	1	187	1	188	1	186	1
191	2	193	1	193	1	192	1	193	1	192	1

Table 37. The migration distance of the LMW glutenins of K29-7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
24	3	22	1	22	1	21	1	22	1	22	1
36	5	33	5	35	5	36	5	37	4	35	5
59	1	55	1	59	1	57	1	58	1	58	1
66	2	67	3	64	1	65	2	66	2	66	2
80	3			79	2	77	3	76	3	78	3
88	3	89	4	88	2	90	3	88	3	89	3
110	3	107	4	108	4	109	4	110	4	109	4
122	1	121	1	124	1	123	1	120	2	122	1
129	1	126	1	127	1	128	1	129	1	128	1
145	3	148	3	144	3	146	3	147	3	146	3
156	1	158	3	152	3	155	3	157	3	156	3
169	2	166	3	172	2	170	2	167	2	169	2
182	1	180	1	185	1	184	1	183	1	183	1
192	1	190	1	190	1	193	1	194	1	192	2

Table 38. The migration distance of the LMW glutenins of K29-8.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
26	1	25	1	23	1	27	1	25	1	25	1
38	2	39	5	38	2	37	2	36	2	38	2
55	1	56	1	50	1	54	1	51	1	53	1
69	5	67	5	70	5	68	5	66	4	68	5
84	3	85	3	84	2	85	3	81	3	84	3
107	4	108	5	105	1	106	4	107	4	107	4
117	1	117	1	114	2	118	1	119	1	117	1
121	1	123	1	124	3	125	1	121	1	123	1
140	2	144	5	143	5	142	5	143	5	142	5
172	4	166	4	170	5	168	4	167	4	169	4
189	1	190	1	189	1	187	1	186	1	188	1

Table 39. The migration distance of the LMW glutenins of K29-9.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
17	1	15	1	13	2	16	1	17	1	16	1
38	2	37	2	39	1	36	2	35	2	37	2
51	4	48	1	49	2	47	2	46	2	48	2
61	1	61	4	65	4	62	4	63	4	62	4
82	2	81	4	84	2	83	2	84	2	83	2
87	4	85	4	87	2	88	4	89	4	87	4
103	1	106	4	100	1	104	1	102	1	103	1
113	2	117	1	114	1	112	1	110	1	113	1
116	2	119	1	117	1	118	1	119	1	118	1
126	2	122	1	128	5	127	5	128	5	126	6
	-	138	5	132	5	137	5	139	5	137	5
143	5	142	5	140	5	141	5	144	4	142	5
161	2	162	3	162	1	163	2	163	2	162	2
169	3	165	2	165	1	167	2	168	2	167	2
182	1	186	1	184	1	183	1	181	1	183	1

Table 40. The migration distances and band intensities of the LMW glutenins of K29-10.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
28	1	29	5	25	4	22	4	24	4	24	3	25	4
37	1	39	1	34	1	30	2	33	2	32	1	34	1
52	3	50	3	47	4	42	4	44	5	44	5	47	4
65	1	70	4	65	5	69	5	71	5	72	5	69	5
75	4	80	3	78	3	76	3	79	3	79	3	78	3
90	3	93	4	89	1	87	4	90	4	91	4	90	4
106	1	101	1	110	5	101	1	101	1	100	1	103	1
118	2	116	4	117	4	117	2	117	2	119	2	117	2
143	5	140	4	-	-	142	2	143	2	145	3	143	6
161	2	155	1	156	1	155	2	157	3	159	3	157	2
177	2	173	1	180	3	172	3	174	3	176	3	175	3
193	1	193	2	194	1	193	1	-	-	196	1	194	1

Table 41. The migration distances and band intensities of the LMW glutenins of K34-1.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
44	5	47	5	48	4	52	5	48	5	48	5	48	5
73	5	75	5	76	5	80	5	79	3	79	3	77	5
88	1	89	1	84	4	86	1	88	1	92	1	88	1
104	1	104	1	102	1	108	1	110	4	109	5	106	1
120	1	123	1	124	1	126	1	-	-	124	4	123	1
133	2	133	2	135	2	138	2	130	4	129	3	133	2
145	2	146	2	148	2	153	2	-	-	155	1	148	2
159	3	160	3	161	3	164	4	160	3	162	2	161	3
177	3	179	3	180	2	182	3	181	1	182	3	180	3

Table 42. The migration distances and band intensities of the LMW glutenins of K34-2.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
24	1	29	5	23	1	29	1	25	1	26	1
35	3	38	1	37	3	36	3	37	3	37	3
45	3	50	4	49	4	47	4	47	4	48	4
62	4	-	-	62	2	61	2	60	2	61	2
73	3	70	5	72	5	72	5	72	5	72	5
85	1	85	4	87	4	86	4	88	4	86	4
103	5	100	1	102	1	104	1	105	1	103	1
117	5	117	5	114	4	115	5	118	5	116	5
121	5	125	4	121	4	125	4	123	3	123	4
132	4	135	5	131	3	134	4	130	4	132	4
155	1	160	1	161	1	158	1	157	1	158	1
177	2	180	1	176	1	175	1	178	1	177	1
180	3	185	2	180	2	181	2	183	2	182	2
183	1	188	2	187	1	190	1	189	1	187	1

Table 43. The migration distance of1 the LMW glutenins of K34-3.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
14	1			15	1	13	1	12	1	14	1
18	1	18	1	18	1	17	1	15	1	17	1
35	1	36	4	39	4	37	4	38	4	37	4
46	5	46	1	46	4	47	4	48	4	47	4
56	1	58	3	60	1	55	1	57	1	57	1
74	4	77	4	72	5	73	4	70	4	73	4
89	5	91	3	90	2	87	3	86	3	89	3
98	1	100	1	101	1	97	1	96	1	98	1
102	1	103	1	104	1	101	1	103	1	103	1
104	1	108	1	108	1	105	1	107	1	106	1
112	2			117	3	115	3	120	3	116	3
124	5	129	5	122	3	123	5	122	5	124	5
138	3	139	5	140	5	137	5	136	5	138	5
144	4	149	4	145	5	147	4	147	4	146	4
157	1	160	1	158	1	155	1	160	1	158	1
164	1			161	1	162	1	165	1	163	1
170	1	170	1	172	2	173	1	173	1	172	1
181	1	180	1	179	1	178	1	177	1	179	1
188	1	190	1	190	1	189	1	188	1	189	1

Table 44. The migration distance of the LMW glutenins of K34-4.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
19	3	15	2	14	2	17	2	18	2	17	2
38	5	35	5	40	4	35	5	38	5	37	5
51	5			54	4	55	5	52	5	53	5
61	3	62	3	66	1	60	3	62	3	62	3
78	4	78	4	75	5	79	4	75	4	77	4
88	1	86	1	89	3	85	1	87	1	87	1
95	2	95	3	93	4	94	3	92	3	94	3
103	1	105	1	105	1	101	1	101	1	103	1
109	1	112	1	108	1	107	1	106	1	108	1
131	5	129	5	132	3	133	5	135	5	132	5
149	2	144	5	145	4	146	4	146	4	146	4
162	1	160	1	164	1	160	1	161	1	161	1
169	1			169	1	167	1	166	1	168	1
173	1	172	1	171	2	172	1	172	2	172	1
192	1	187	1	187	1	185	1	186	1	187	1

Table 45. The migration distance of the LMW glutenins of K34-6

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
14	1	17	1	14	1	19	1	15	1	16	1
24	2	25	2	26	2	30	2	27	2	26	2
43	4	40	5	38	1	39	2	38	1	40	6
68	4	68	4	68	3	69	5	67	4	68	4
85	5	86	5	84	3	84	4	83	4	84	4
99	1	99	3	98	1	102	1	98	1	99	1
113	1	110	1	116	5	115	5	114	5	114	6
133	5	132	5	132	5	132	5	135	5	133	5
153	5	156	4	154	4	155	3	154	4	154	4
		166	1	166	1	163	3	161	1	164	1
180	1	179	1	172	1	170	2	171	1	174	1
190	1			191	1	192	1	195	1	192	1

Table 46. The migration distances and band intensities of the LMW glutenins of K34-7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
33	3	32	2	33	2	36	2	36	2	34	2
45	3	49	3	46	3	47	3	49	3	47	3
66	5	67	5	68	4	69	5	62	3	66	5
81	5	85	5	84	4	79	5	82	5	82	5
97	1	99	1	99	1	98	1	101	1	99	1
113	4	119	5	119	5	114	3	117	3	116	4
132	4	137	4	135	5	135	4	137	4	135	4
155	2	157	3	160	3	160	1	162	1	159	2
190	1	189	1	187	1	185	2	188	2	188	1

Table 47. The migration distances and band intensities of the LMW glutenins of K34-8.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
37	1	38	3	42	1	34	2	38	2	38	2
51	4	50	4	50	1	54	3	50	2	51	6
73	5	72	5	69	3	73	4	72	3	72	4
84	5	85	5	86	2	81	2	89	4	85	6
129	4	131	4	121	4	122	5	121	5	125	4
140	5	142	5	135	5	139	5	136	5	138	5
169	1	164	1	160	2	169	1	161	3	165	1
189	3	189	1	189	1	193	1	196	1	191	1

Table 48. The migration distances and band intensities of the LMW glutenins of K34-9.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
28	1	25	4	27	3	-	-	27	1	27	6
42	2	41	2	40	1	45	2	45	2	43	2
52	4	50	4	52	4	51	3	-	-	51	4
78	4	72	5	74	5	75	3	80	4	76	4
94	4	98	2	100	1	92	5	95	4	96	6
127	4	119	4	120	4	121	5	125	4	122	4
143	5	141	5	140	5	140	5	143	5	141	5
164	2	163	2	169	2	163	3	164	2	165	2
190	1	187	3	188	2	192	1	188	1	185	1

Table 49. The migration distances and band intensities of the LMW glutenins of K34-10.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
42	2	41	2	38	3	40	2	42	2	41	2
55	4	55	4	59	4	61	3	60	3	58	4
75	5	78	5	81	4	80	3	83	3	79	4
87	5	90	5	94	5	96	5	98	5	93	5
122	5	123	4	124	4	128	5	129	5	125	5
144	5	144	5	147	5	151	5	151	5	147	5
-	-	169	1	164	2	167	3	168	2	167	2
172	1	176	1	170	1	175	1	175	2	173	1

Table 50. The migration distances and band intensities of the LMW glutenins of K35-2.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
14	1	12	1	11	1	11	1	16	1	13	1
-	-	25	1	22	1	20	1	25	1	23	1
62	3	63	3	-	-	60	4	60	3	61	3
82	4	84	3	82	3	80	5	82	4	82	4
87	3	94	2	90	2	89	4	89	3	90	3
127	4	127	4	123	4	124	4	126	4	125	4
152	5	150	5	147	5	146	5	147	5	148	5
167	3	166	2	163	2	169	1	161	2	165	2
174	2	173	2	170	2	176	1	171	1	173	2

Table 51. The migration distances and band intensities of the LMW glutenins of K35-3.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
26	1	29	1	30	1	26	3	23	2	27	1
40	2	42	2	43	3	48	3	44	3	43	3
52	2	54	2	51	2	-	-	-	-	52	2
62	3	66	3	-	-	66	3	63	3	64	3
85	5	87	4	86	4	82	4	80	5	84	4
-	-	110	1	115	3	114	5	111	5	113	6
136	5	132	4	-	-	136	5	135	5	135	5
149	5	151	5	151	5	152	3	151	4	151	5
164	1	166	1	160	2	161	2	167	1	164	1
192	1	191	1	195	2	191	1	190	1	192	1

Table 52. The migration distances and band intensities of the LMW glutenins of K35-4.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
22	2	24	3	23	2	27	1	23	1	24	2
44	3	46	3	44	3	40	4	49	2	45	3
65	3	66	3	65	3	65	4	60	4	64	3
79	4	80	5	79	5	78	4	79	4	79	4
110	5	111	5	109	5	113	1	108	1	110	6
135	5	134	5	134	5	132	5	130	5	133	5
151	4	150	5	150	4	145	5	147	5	149	5
160	3	159	2	158	2	153	2	160	1	158	2
168	1	169	1	167	1	166	2	170	1	168	1
190	1	190	1	188	1	181	1	-	-	187	1

Table 53. The migration distances and band intensities of the LMW glutenins of K35-5.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
10	1	18	2	19	2	18	2	10	2	15	2
28	2	26	1	29	1	27	2	20	1	26	1
41	2	38	3	41	3	39	2	35	3	39	3
52	3	58	5	60	3	59	3	53	3	56	3
74	5	70	5	78	5	74	5	71	5	73	5
100	5	106	3	109	5	107	5	-	-	106	5
124	4	128	2	130	5	130	5	121	5	127	5
151	1	148	1	150	3	150	2	148	2	149	2
189	2	189	1	191	1	190	1	188	1	189	1

Table 54. The migration distances and band intensities of the LMW glutenins of K35-6.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
19	1	13	1	-	-	19	2	19	1	18	1
31	2	30	3	31	3	32	4	31	4	31	3
41	4	45	4	49	4	52	5	50	5	47	4
69	5	66	4	68	4	65	5	61	5	66	5
96	4	-	-	91	5	94	4	92	4	93	4
118	5	110	4	112	5	116	5	111	5	113	5
136	2	130	5	134	5	136	1	138	1	135	6
-	-	146	2	150	3	141	2	153	2	148	2
180	1	179	1	178	1	180	1	179	1	179	1
194	1	191	1	193	1	198	4	196	1	194	1

Table 55. The migration distances and band intensities of the LMW glutenins of K35-7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
18	2	19	1	14	1	19	1	-	-	18	1
29	4	29	3	23	1	29	1	-	-	28	6
-	-	-	-	42	3	46	2	46	2	45	2
49	5	51	5	51	2	54	2	55	2	52	6
61	5	62	5	60	5	65	5	66	4	63	5
74	2	75	2	81	4	77	1	80	4	77	6
92	4	94	5	92	5	94	5	97	5	94	5
124	3	122	3	120	5	124	4	124	4	123	4
139	1	140	1	139	4	142	5	145	5	141	6
157	3	159	3	156	1	158	3	160	3	158	3
179	1	179	1	176	1	174	1	176	1	177	1
190	1	188	1	190	1	180	1	190	1	188	1

Table 56. The migration distances and band intensities of the LMW glutenins of K35-8.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
17	1	16	1	18	1	12	3	10	1	15	1
25	1	25	1	27	1	24	2	23	3	25	1
44	4	44	3	45	3	40	3	44	4	43	3
62	4	61	3	64	3	67	5	66	5	64	4
82	4	84	3	83	3	80	3	80	5	82	3
95	5	96	5	97	5	97	4	95	1	96	5
122	5	124	5	124	5	123	5	129	5	124	5
133	3	135	3	136	3	132	3	135	2	134	3
142	5	145	5	145	5	142	1	141	1	143	6
159	3	160	4	160	3	162	2	155	2	159	3
166	2	168	2	168	2	172	1	170	3	169	2
174	1	175	1	176	1	177	1	-	-	176	1
194	1	194	1	195	1	187	1	191	1	192	1

Table 57. The migration distances and band intensities of the LMW glutenins of K35-9.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
20	1	23	1	21	1	23	1	24	1	22	1
30	3	34	3	30	1	-	-	33	3	32	3
40	2	45	2	47	3	49	2	49	1	46	2
51	3	56	3	54	2	57	1	58	1	55	2
71	5	70	3	65	3	68	3	69	3	69	3
82	5	87	5	85	2	90	3	91	3	87	6
102	1	104	1	100	4	102	5	100	3	102	6
124	4	128	4	126	4	129	4	130	4	127	4
145	2	141	5	147	5	151	5	152	5	147	5
161	1	166	1	161	3	166	4	166	3	164	6
181	1	186	3	190	1	-	-	181	1	185	1

Table 58. The migration distances and band intensities of the LMW glutenins of K35-10.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
49	2	44	4	48	2	48	2	41	2	46	2
57	3	62	4	59	3	59	3	61	4	60	3
87	3	80	4	82	4	80	5	83	5	82	4
99	5	95	5	90	4	91	5	93	5	94	5
129	5	123	5	120	4	123	4	124	4	124	4
150	5	145	5	141	5	143	5	144	5	145	5
-	-	160	3	157	3	156	3	157	2	158	3
164	2	168	2	163	2	169	2	166	1	166	2
191	1	196	1	194	2	189	3	191	2	192	2

Table 59. The migration distances and band intensities of the LMW glutenins of K37-1.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
9	2	10	1	16	1	7	1	9	1	9	1
16	1	14	2	16	1	16	1	16	1	16	1
26	1	27	2	20	1	22	1	28	1	25	1
32	3	31	3	32	2	29	2	33	1	31	2
40	2	41	3	44	2	43	3	42	3	42	3
52	4	52	4	51	3	52	2	53	1	52	6
72	5	72	5	73	5	71	4	70	4	72	5
84	5	86	3	89	5	84	5	83	5	85	5
91	3	94	4	91	5	94	5	92	5	92	5
102	1	103	2	108	2	105	1	109	1	105	1
124	3	124	2	128	3	126	4	124	4	125	3
136	4	134	3	136	3	134	3	-	-	135	3
143	5	141	4	145	4	145	5	143	5	143	5
150	5	149	5	149	5	158	3	157	5	153	5
174	1	173	2	172	1	173	1	173	1	173	1
179	1	181	1	182	2	183	1	181	1	181	1
190	1	193	1	191	1	192	2	195	2	192	1

Table 60. The migration distances and band intensities of the LMW glutenins of K37-2.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
13	1	-	-	11	1	11	1	11	1	12	1
23	1	26	4	25	1	29	1	24	1	25	1
39	2	-	-	37	1	40	2	35	2	38	2
48	3	47	2	43	2	-	-	45	1	46	2
72	5	69	5	68	5	73	2	76	5	72	5
89	4	88	5	87	5	91	5	87	5	88	5
105	1	103	1	101	1	105	1	103	1	103	1
117	3	119	3	119	3	-	-	119	5	119	3
128	4	128	5	126	4	124	4	130	4	127	4
144	5	145	5	142	4	142	5	141	5	143	5
-	-	151	5	148	5	155	5	153	2	152	5
169	2	166	3	166	3	169	1	169	1	168	2
185	3	182	3	182	3	188	1	188	3	185	3
190	1	188	4	188	4	192	2	-	-	190	6

Table 61. The migration distances and band intensities of the LMW glutenins of K37-3.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
25	2	11	1	12	1	18	1	18	1	15	1
45	4	26	3	28	3	28	1	22	1	26	2
69	5	46	3	46	4	40	4	47	4	45	4
78	3	69	4	70	5	69	3	62	3	68	4
87	3	80	2	78	3	82	2	75	2	79	2
102	1	86	4	87	4	92	4	90	4	88	4
129	5	98	1	100	1	104	4	108	4	102	6
141	5	129	5	129	5	120	1	126	1	127	6
150	5	148	5	142	4	143	5	147	5	144	5
166	2	151	5	151	5	154	5	157	4	153	5
182	1	166	1	164	1	169	1	170	4	167	1
191	1	181	1	186	1	182	1	-	-	183	1
-	-	192	1	192	1	192	1	190	1	191	1

Table 62. The migration distances and band intensities of the LMW glutenins of K37-4.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
25	3	23	2	24	3	23	1	20	1	25	2
34	1	32	1	33	2	32	1	30	1	32	1
45	3	46	3	45	3	44	5	43	3	45	3
68	5	67	5	66	5	71	1	69	3	68	5
85	2	81	2	82	3	80	2	82	1	82	2
87	2	86	3	85	3	84	2	84	1	85	2
99	1	100	1	101	1	99	5	96	4	99	6
117	4	117	3	117	4	110	5	111	5	114	4
126	5	121	4	124	4	124	1	121	1	123	6
148	5	145	4	144	5	145	5	144	5	145	5
164	2	162	1	164	2	165	5	167	5	165	6
187	2	184	1	189	1	188	1	188	1	187	1
196	1	196	1	192	1	194	1	194	1	194	1

Table 63. The migration distances and band intensities of the LMW glutenins of K37-5.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
19	1	18	1	12	1	15	1	20	1	17	1
24	1	22	1	24	1	22	3	25	1	23	1
34	1	36	1	35	1	32	2	33	1	34	1
46	4	46	4	45	1	44	3	39	2	44	6
63	1	64	1	67	2	65	5	63	5	64	6
73	2	75	2	75	1	73	2	72	2	74	2
94	4	96	4	90	1	89	1	91	1	92	6
99	3	-	-	99	1	99	1	96	1	98	1
105	4	106	4	106	1	102	1	108	1	105	1
144	5	145	5	-	-	143	5	138	5	143	5
163	3	165	4	160	3	160	3	161	4	162	3
187	1	188	1	-	-	188	1	184	1	187	1
191	1	192	1	-	-	195	1	191	1	192	1

Table 64. The migration distances and band intensities of the LMW glutenins of K37-6.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
17	1	10	1	-	-	18	1	19	1	16	1
21	1	26	1	29	2	27	1	24	1	25	1
34	3	29	2	37	1	34	1	36	1	34	1
43	1	49	1	48	1	46	5	46	5	46	6
57	2	55	2	54	2	60	2	59	2	57	2
80	4	78	3	77	3	75	3	73	3	77	3
99	3	98	3	97	3	99	4	95	4	98	3
111	1	111	1	112	1	110	5	110	5	111	6
118	1	115	1	115	1	116	1	120	1	117	1
137	4	136	4	134	4	135	4	-	-	136	4
140	4	140	4	141	5	145	5	144	5	142	5
156	5	-	-	165	5	153	5	153	4	154	5
160	5	161	5	161	5	166	5	166	5	163	5
182	1	180	1	181	1	184	1	183	1	182	1

Table 65. The migration distances and band intensities of the LMW glutenins of K37-7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
18	1	12	1	17	1	21	1	17	1	17	1
27	1	-	-	29	2	30	2	28	2	28	2
42	4	39	4	41	1	38	1	40	2	40	6
59	1	54	1	54	2	50	1	53	1	54	1
70	2	66	3	63	1	62	1	62	1/2	65	2
91	3	89	3	89	3	86	2	84	4	88	3
95	3	99	5	94	3	93	3	90	2	94	3
103	5	-	-	107	1	104	1	103	1	104	1
112	1	114	1	112	1	110	1	112	1	112	1
116	1	116	1	121	1	117	1	119	1	118	1
142	5	138	5	140	5	147	5	142	4	142	5
150	4	151	4	150	5	158	5	153	5	152	5
164	4	165	4	172	1	172	1	168	1	168	6
-	-	177	1	177	1	176	1	173	2	176	1
186	1	-	-	188	1	188	1	185	1	187	1

Table 66. The migration distances and band intensities of the LMW glutenins of K37-8.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
21	2	15	2	11	1	20	1	16	1	17	1
24	2	25	3	25	3	26	1	30	2	26	2
39	4	33	2	38	1	35	4	42	1	37	6
48	2	49	2	48	3	50	1	46	1	48	2
58	1	62	2	61	2	62	3	55	3	60	2
71	5	71	4	72	4	75	2	80	4	74	4
85	4	83	3	90	5	85	4	84	4	85	4
89	4	90	4	90	1	88	4	91	5	91	4
104	1	103	2	103	1	108	1	107	1	105	1
133	5	133	4	132	5	134	5	129	5	132	5
143	4	143	5	143	5	144	5	140	5	143	5
153	4	151	5	152	5	156	5	152	5	153	5
169	2	173	3	172	2	179	1	173	1	173	2
192	2	191	1	189	1	193	1	192	1	191	1

Table 67. The migration distances and band intensities of the LMW glutenins of K37-9.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
10	1	10	1	12	1	16	2	15	1	13	1
24	5	24	5	25	4	26	4	28	3	25	4
38	1	34	1	39	2	35	2	38	2	37	2
49	3	45	3	47	3	44	5	51	3	47	3
73	5	77	5	72	4	71	5	72	4	73	5
83	5	90	1	81	4	80	2	81	3	83	6
99	1	99	1	89	4	90	4	90	2	93	6
103	1	-	-	102	1	104	2	105	1	104	1
123	5	129	4	125	4	122	4	123	4	124	4
133	5	135	5	131	5	131	5	131	4	132	5
147	5	-	-	148	5	145	5	151	5	148	5
166	1	160	1	168	1	163	1	165	1	164	1
174	1	176	1	172	1	170	1	174	1	173	1
184	1	183	1	185	1	181	1	184	1	183	1
191	1	188	1	191	2	186	2	191	1	189	1

Table 68. The migration distances and band intensities of the LMW glutenins of K37-10.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
24	1	25	3	22	3	25	2	28	1	25	2
30	1	33	2	34	1	35	1	33	1	33	1
47	1	49	3	44	3	-	-	46	3	47	3
61	1	60	2	-	-	63	5	61	5	61	6
72	1	71	4	66	4	-	-	75	4	71	4
76	1	79	1	81	3	82	1	-	-	80	1
82	1	83	2	84	3	85	1	86	2	84	2
100	1	100	1	99	1	101	5	98	1	100	1
108	1	109	1	105	1	107	5	101	1	106	1
127	4	125	4	126	4	123	5	126	4	125	4
144	1	147	5	147	5	146	5	142	5	145	5
179	5	176	1	178	1	177	1	176	1	177	1
-	-	188	1	185	1	187	1	188	1	187	1

Table 69. The migration distances and band intensities of the LMW glutenins of Karee.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
6	1	5	1	8	1	6	1	6	1	9	1	7	1
12	1	15	1	11	1	14	1	11	1	18	1	14	1
37	3	31	3	39	2	31	3	33	3	33	3	34	3
51	2	57	4	52	4	53	4	54	4	56	4	54	4
75	2	72	2	76	2	73	3	73	3	70	2	73	2
77	4	80	3	79	4	80	3	81	4	79	4	79	4
87	4	84	4	90	5	89	5	90	5	-	-	88	5
97	5	95	5	100	1	99	1	-	-	91	5	96	6
107	1	106	1	105	1	-	-	102	1	105	1	105	1
116	3	110	1	117	3	117	4	116	3	111	3	115	3
154	5	146	5	148	5	143	5	142	5	146	5	147	5
170	4	168	5	164	4	163	4	162	5	163	4	165	4
189	1	184	1	187	1	182	1	184	1	185	1	185	1

Table 70. The migration distances and band intensities of the LMW glutenins of Karioga.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
18	1	-	-	12	2	14	2	14	1	15	1	15	1
32	1	36	1	30	1	32	1	33	4	32	1	33	1
46	2	40	1	40	5	44	1	44	1	44	1	43	1
58	3	50	3	58	1	59	3	59	3	59	3	57	3
64	4	69	3	68	3	69	4	69	4	69	4	68	4
82	4	-	-	82	3	81	5	81	5	81	5	81	5
93	1	92	1	91	1	90	3	91	5	91	4	91	6
98	1	99	2	97	1	99	1	-	-	-	-	98	1
102	1	104	3	105	1	103	1	106	1	105	1	104	1
113	3	114	3	119	2	117	3	119	4	119	3	117	3
140	5	148	1	145	5	143	5	150	4	144	4	145	5
158	2	158	2	-	-	155	2	158	2	157	3	157	2
166	2	169	1	164	2	162	3	166	3	165	2	165	2
175	1	175	1	170	2	172	3	173	2	174	2	173	2
190	1	189	1	192	1	191	1	190	1	191	1	191	1

Table 71. The migration distances and band intensities of the LMW glutenins of Katyil.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
18	1	15	1	16	1	17	1	15	1	16	1
21	1	20	1	21	1	23	1	20	1	21	1
63	5	61	5	65	5	60	3	61	5	62	5
67	5	68	5	70	5	70	5	71	5	69	5
93	3	-	-	87	1	89	1	89	1	90	1
101	3	107	2	-	-	108	2	105	2	105	2
120	4	125	4	129	4	123	4	122	4	124	4
136	1	139	1	-	-	137	1	136	1	137	1
152	3	-	-	151	1	149	1	148	1	150	1
169	1	164	2	170	3	165	2	164	2	166	2
180	1	179	1	174	3	180	1	179	1	178	1
188	1	189	1	187	1	190	1	188	1	188	1

Table 72. The migration distances and band intensities of the LMW glutenins of Kavkaz.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	13	1	15	1	13	2	11	1	12	1	13	1
19	1	22	1	21	1	19	1	-	-	22	1	21	1
27	1	26	1	30	1	29	1	28	1	29	1	28	1
50	5	58	5	60	5	50	5	52	5	51	5	54	5
75	2	72	1	76	1	78	2	77	2	78	3	76	2
91	3	90	3	91	4	92	5	92	4	92	4	91	4
104	1	100	3	103	3	102	1	103	1	101	1	102	1
121	2	124	2	120	1	119	5	121	4	121	3	121	6
136	1	131	2	130	1	132	1	132	2	131	1	132	1
154	4	158	5	160	4	154	5	153	4	152	4	155	4
169	2	-	-	171	1	166	3	166	2	166	3	168	2
171	1	176	3	175	1	175	1	174	1	175	1	174	1
196	1	196	1	194	1	193	1	192	1	193	1	194	1

Table 73. The migration distances and band intensities of the LMW glutenins of Limpopo.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
-	-	-	-	36	1	31	2	31	2	30	2	32	2
46	2	46	2	48	2	43	1	-	-	45	1	46	2
60	4	59	4	60	4	56	3	56	4	54	3	58	4
68	5	68	5	69	5	66	5	68	5	67	5	68	5
88	2	88	2	90	3	88	2	88	1	87	2	88	2
-	-	95	2	95	3	99	4	97	4	97	4	97	4
101	5	102	5	103	5	-	-	108	1	108	2	104	6
111	2	113	2	114	1	110	1	110	1	110	1	111	1
119	1	119	1	119	1	116	1	116	1	115	1	117	1
130	1	129	2	-	-	128	2	129	2	127	3	129	2
136	2	135	2	137	2	139	1	137	1	-	-	137	2
145	2	147	1	147	1	147	1	149	1	-	-	147	1
157	1	151	1	-	-	158	1	158	2	156	2	156	1
169	1	162	1	166	1	164	1	164	1	164	1	165	1

Table 74. The migration distances and band intensities of the LMW glutenins of Limpopo DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
66	5	60	3	64	5	62	5	62	5	63	4	63	5
72	5	72	5	76	1	70	5	71	5	72	5	72	5
93	2	94	2	94	2	-	-	-	-	93	2	94	2
99	3	96	3	99	4	97	4	97	2	98	3	98	3
103	4	103	4	110	1	106	5	107	4	108	4	106	4
-	-	114	1	116	1	115	1	113	1	-	-	115	1
118	1	117	1	117	1	118	1	116	1	117	1	117	1
131	1	133	1	131	3	134	1	135	1	-	-	133	1
137	2	142	1	139	1	138	1	140	2	138	1	139	1
163	1	164	1	160	1	163	1	161	1	-	-	162	1
173	1	170	1	173	1	166	1	167	1	166	1	169	1

Table 75. The migration distances and band intensities of the LMW glutenins of M29519.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	16	1	12	1	15	1	10	1	17	1	15	1
45	5	45	5	46	5	44	5	40	5	40	5	43	5
65	4	63	4	64	4	62	5	64	3	64	4	64	4
70	5	70	5	70	5	70	4	71	1	-	-	70	5
90	1	90	1	91	1	90	1	-	-	90	1	90	1
96	1	98	1	96	1	97	2	94	2	96	1	96	1
103	1	100	1	101	1	100	2	108	1	103	3	103	1
116	4	113	3	115	4	114	4	116	5	117	5	115	4
137	5	135	5	134	5	133	2	140	1	130	1	135	6
158	1	-	-	156	1	150	1	158	2	159	2	156	1
174	2	175	2	174	2	176	1	173	1	175	2	175	1
184	1	188	1	187	1	185	1	-	-	182	1	185	1
194	1	192	1	194	1	192	1	196	1	-	-	194	1

Table 76. The migration distances and band intensities of the LMW glutenins of M29568.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	6	1	4	1	8	3	8	2	11	1	7	1
11	1	10	1	12	1	-	-	17	1	14	1	13	1
24	3	23	3	23	3	24	1	25	1	29	3	25	3
39	1	37	1	36	1	40	2	35	1	-	-	37	1
64	4	64	4	66	5	66	5	60	5	60	5	63	5
78	5	79	5	78	5	-	-	76	1	80	5	78	5
106	5	108	2	-	-	109	3	103	5	109	5	107	5
116	3	117	3	116	3	117	4	114	5	-	-	116	3
126	3	126	3	126	1	130	1	127	1	127	1	127	1
139	4	139	4	141	4	142	1	137	1	141	4	140	4
174	2	173	2	170	1	176	1	172	1	173	1	173	1
-	-	186	1	184	1	187	1	187	1	186	1	186	1
189	1	191	1	196	1	191	1	194	1	191	1	192	1

Table 77. The migration distances and band intensities of the LMW glutenins of Marico.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
5	1	11	1	8	1	3	3	6	3	9	1	8	1
21	3	24	2	28	2	27	2	20	2	23	1	24	2
47	4	40	3	41	1	45	3	47	3	40	3	43	3
69	5	71	4	71	5	60	5	61	5	65	4	66	5
80	5	82	5	85	5	85	3	90	5	-	-	84	5
101	1	102	1	102	1	101	5	106	5	100	3	102	6
112	3	115	4	117	5	110	5	110	5	111	5	113	5
139	5	130	2	134	1	130	1	135	1	139	1	135	1
-	-	140	4	140	2	143	2	146	2	150	1	144	2
151	1	153	1	153	1	154	3	156	3	155	1	154	1
160	1	164	1	160	1	165	1	168	1	163	2	163	1
-	-	174	2	175	2	173	1	175	1	172	1	174	1
181	3	184	3	185	1	182	1	181	1	183	1	183	1
194	1	194	1	195	1	193	1	196	1	196	1	195	1

Table 78. The migration distances and band intensities of the LMW glutenins of Molen.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
50	3	49	3	51	3	55	4	56	3	57	3	53	3
64	5	62	5	61	5	68	5	66	5	66	5	65	5
72	5	71	5	69	5	77	1	70	5	71	5	72	5
93	3	91	3	89	2	89	3	89	3	90	3	90	3
102	4	104	4	102	4	97	4	99	4	100	4	101	4
104	5	109	3	-	-	109	3	110	3	102	4	107	3
115	2	114	2	113	2	115	2	116	2	113	2	114	2
122	1	122	1	-	-	128	2	-	-	120	1	123	1
135	1	134	1	133	1	137	1	130	2	133	2	134	1
142	2	141	2	140	2	142	1	-	-	-	-	141	2
147	1	149	1	-	-	-	-	150	1	149	1	149	1
154	1	-	-	156	1	155	2	158	2	158	1	156	1
165	1	162	1	161	1	-	-	-	-	160	1	162	1
170	1	170	1	176	1	175	2	-	-	171	1	172	1

Table 79. The migration distances and band intensities of the LMW glutenins of Molopo.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
45	1	46	1	44	1	47	1	45	1	42	1	45	1
73	5	75	5	74	5	72	5	72	5	71	5	73	5
-	-	83	2	81	3	82	1	80	2	79	2	81	2
100	4	100	4	101	4	99	4	97	4	95	4	99	4
110	5	110	5	112	5	108	3	110	5	107	4	110	5
119	1	121	1	120	2	123	1	119	2	121	1	121	1
128	1	127	1	127	2	129	1	129	1	126	1	128	1
137	1	138	1	-	-	139	2	139	2	137	1	138	1
145	2	145	1	143	2	144	2	144	2	140	2	144	2
151	2	153	1	151	1	151	1	-	-	154	1	152	1
165	2	160	1	159	1	159	1	-	-	162	1	161	1
174	2	169	1	168	2	170	1	172	2	174	2	171	2

Table 80. The migration distances and band intensities of the LMW glutenins of Nantes.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	13	1	13	1	12	3	10	4	15	1	12	1
49	1	47	1	43	1	47	2	41	2	40	1	45	1
-	-	60	5	61	2	65	5	65	5	59	5	62	5
76	4	75	4	74	4	77	1	-	-	76	1	76	6
84	5	88	5	85	5	82	1	89	1	86	2	86	6
108	1	106	1	100	2	100	2	107	3	100	3	104	2
118	2	110	1	118	2	112	2	110	3	110	3	113	2
124	2	124	3	125	3	-	-	121	2	130	1	125	2
140	4	143	4	143	4	140	1	140	1	140	1	141	6
176	1	178	1	176	1	171	1	172	1	170	1	174	1
182	2	183	1	181	1	181	1	182	1	182	1	182	1
194	1	190	1	195	1	196	1	193	1	196	1	194	1

Table 81. The migration distances and band intensities of the LMW glutenins of Norstar

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
18	1	-	-	16	1	14	1	20	1	15	1	17	1
41	1	39	1	40	1	48	1	45	3	49	2	44	1
62	3	63	3	63	3	65	2	60	2	63	3	63	3
74	2	75	2	73	2	79	5	77	2	73	4	75	2
93	5	96	5	95	5	91	5	90	4	93	5	93	5
104	4	106	4	106	4	105	1	102	1	105	2	105	6
134	2	133	2	133	2	137	2	134	2	133	2	134	2
152	2	151	2	-	-	150	4	148	3	150	2	150	2
162	4	161	4	160	5	165	3	163	4	162	4	162	4
176	3	176	3	175	2	173	2	179	1	172	1	175	2
185	1	184	1	184	2	189	1	189	1	180	1	185	1
194	1	192	1	195	1	192	1	191	1	188	1	192	1

Table 82 The migration distances and band intensities of the LMW glutenins of Oom Charl.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
12	1	10	1	8	1	11	1	7	1	8	1	9	1
17	1	13	1	14	1	18	1	14	1	15	1	15	1
29	2	23	1	28	1	25	1	25	1	22	1	25	1
36	1	37	1	-	-	38	1	-	-	35	1	37	1
46	1	41	1	41	1	44	1	41	1	42	1	43	1
70	5	67	5	63	5	67	5	65	1	68	5	67	5
92	1	91	1	85	1	87	1	83	5	86	1	87	1
101	1	101	1	106	2	104	4	103	1	108	1	104	1
122	3	120	4	-	-	123	5	129	4	123	4	123	4
130	3	130	3	132	4	134	4	137	5	139	4	134	4
145	4	141	1	152	1	-	-	150	1	150	1	148	1
176	2	174	2	174	3	180	1	177	2	174	3	176	2
184	2	184	2	183	1	185	1	187	1	187	1	185	1
190	2	196	1	194	1	194	1	193	1	192	1	193	1

Table 83 The migration distances and band intensities of the LMW glutenins of Oranje.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	17	1	12	1	11	1	9	1	16	1	14	1
21	1	-	-	20	1	22	1	20	1	21	1	21	1
31	4	35	1	-	-	32	1	38	1	33	1	34	1
40	5	48	5	44	4	48	1	43	1	40	1	44	6
52	3	59	3	55	1	56	1	52	1	51	1	54	1
61	1	-	-	66	3	66	1	65	1	64	1	64	1
75	4	70	1	-	-	71	1	78	1	72	1	73	1
84	2	85	3	90	3	80	1	85	2	87	2	85	2
103	4	106	5	100	3	100	5	101	5	103	5	102	5
123	1	130	1	129	1	131	3	122	1	129	1	127	1
146	1	140	2	147	3	142	2	142	2	140	3	143	2
170	1	169	1	164	1	167	1	160	1	163	1	166	1
182	1	189	1	190	1	181	2	185	1	179	1	184	1
197	1	192	1	195	1	193	1	190	1	190	2	193	1

Table 84 The migration distances and band intensities of the LMW glutenins of Oubaard.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	2	9	3	12	4	10	2	9	2	12	1	11	2
21	1	-	-	20	1	22	1	20	1	21	1	21	1
28	2	27	2	29	2	26	1	23	1	26	2	27	2
43	5	48	3	48	3	46	5	44	5	40	5	45	5
60	5	62	5	64	5	60	1	64	1	65	2	63	6
69	3	70	4	71	4	79	3	75	2	-	-	73	3
90	3	96	3	90	3	-	-	98	4	97	3	94	3
102	4	104	4	105	4	102	5	106	4	108	1	105	4
120	5	121	5	124	5	121	2	120	1	121	3	121	6
132	1	132	1	135	1	132	4	131	4	133	4	133	6
153	2	150	2	150	1	153	5	151	5	150	5	151	6
165	1	162	1	163	1	170	1	171	1	163	1	166	1
178	1	176	2	177	1	180	2	182	2	177	2	178	2
189	1	184	1	189	1	189	2	185	2	186	1	187	1
195	1	193	1	191	1	-	-	196	1	193	1	194	1

Table 85 The migration distances and band intensities of the LMW glutenins of Owens.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
12	2	18	1	13	1	17	1	16	1	15	1	15	1
28	1	21	-	-	-	21	1	21	1	21	1	22	1
-	-	30	1	29	1	30	1	27	1	28	1	29	1
52	4	53	4	57	5	59	1	59	1	54	1	56	6
65	5	65	5	66	5	65	1	70	1	70	1	69	6
90	1	86	1	92	1	90	5	87	5	85	5	88	6
105	2	102	2	105	1	109	1	107	1	108	1	106	1
120	3	114	2	113	1	-	-	112	1	110	1	114	1
-	-	127	1	122	1	123	1	127	1	120	2	124	1
-	-	130	1	-	-	132	1	132	1	131	2	131	1
153	2	156	2	156	1	150	1	150	1	151	1	152	1
157	2	153	2	156	1	156	1	154	1	155	1	156	1
174	1	170	1	170	1	172	3	171	1	170	2	171	1
186	1	186	1	180	1	185	1	187	1	185	1	185	1

Table 86 The migration distance of the LMW glutenins of Palala.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	2	12	2	10	2	15	1	18	2	14	2	14	2
30	1	27	1	25	1	29	3	30	1	30	1	29	1
-	-	48	3	46	1	43	1	42	1	-	-	45	1
64	5	63	5	61	5	61	2	60	2	60	1	62	6
84	1	81	1	80	1	83	5	80	5	80	5	81	6
97	1	93	1	91	1	-	-	93	1	91	1	93	1
101	1	99	1	97	2	97	1	98	1	102	1	99	1
114	3	111	3	111	4	114	2	119	3	116	3	114	3
130	1	127	1	122	1	130	1	129	2	129	1	128	1
150	1	151	2	148	2	143	1	150	1	148	1	148	1
-	-	167	1	165	2	166	2	167	3	166	2	166	2
177	1	175	1	172	1	-	-	174	1	179	1	175	1
185	1	181	1	180	1	180	1	185	1	-	-	182	1
189	1	187	1	-	-	189	1	189	1	187	1	188	1
194	1	192	1	198	1	194	1	193	1	193	1	194	1

Table 87 The migration distances of the LMW glutenins of Palmiet.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
49	3	48	3	47	3	47	3	48	2	-	-	48	3
58	3	56	3	55	3	-	-	-	-	59	3	57	3
64	4	62	4	61	4	61	5	60	4	-	-	62	4
72	5	68	5	68	5	70	5	68	5	67	5	69	5
94	3	91	3	90	3	92	2	90	3	90	2	91	3
106	4	101	5	101	4	105	4	103	4	102	4	103	4
118	2	115	1	113	2	113	2	114	2	113	2	114	2
140	2	139	2	137	2	140	2	140	2	139	3	139	2
167	2	166	2	164	2	160	1	166	2	163	1	164	2

Table 88 The migration distances of the LMW glutenins of Palmiet DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
35	2	37	2	37	2	41	1	35	2	40	1	38	2
47	1	48	2	50	2	57	2	58	3	58	2	53	2
63	4	63	4	63	4	63	4	64	4	64	4	63	4
70	5	70	5	71	5	71	5	71	5	71	5	71	5
91	3	92	2	92	3	96	4	94	3	97	3	94	3
102	4	102	4	105	4	105	5	105	5	106	4	104	4
116	1	116	1	118	1	119	1	115	1	117	1	117	1
		121	1	122	1	119	1	120	1	124	1	121	1
125	1	125	1	126	1			124	1	126	1	125	1
135	1	135	2	136	1	136	1	135	1	133	1	135	1
139	2	141	3	141	2	141	2	139	2	142	1	141	2
151	1	152	1	156	1	155	2	151	1	159	1	154	1
167	1	168	1	167	1	168	1	160	1	166	1	166	1

Table 89 The migration distances of the LMW glutenins of Palmiet short.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
33	1	33	2	35	2	40	2	41	3	36	2	36	2
60	4	55	3	56	4	60	4	59	4	59	4	58	4
67	5	68	5	69	5	68	5	68	5	69	5	68	5
89	3	89	2	90	3	89	3	87	3	91	4	89	3
106	4	103	5	106	5	100	4	103	4	100	4	103	4
112	2	113	1	115	1	119	1	120	1	121	1	117	1
137	2	137	2	138	2	137	3	138	1	137	2	137	2
145	1	146	1			140	2	147	1			145	1
150	1	152	1	150	1	152	1	154	1	153	3	152	1
160	1			161	1	161	1	163	1	165	1	162	1
165	1	167	1	168	1	168	2	167	1	168	1	167	1
176	1	178	1			177	1	171	1	171	1	175	1

Table 90 The migration distances of the LMW glutenins of PAN 3211.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
37	1	38	1			35	1	38	1	38	1	37	1
54	5	55	5	56	5	51	4	52	5	52	3	53	5
64	5	65	5	66	5			65	5	64	2	65	5
71	4	72	4	73	5	70	4	73	4	70	3	72	4
95	3	97	3	97	3	95	3	94	4	95	2	96	3
108	5	110	5	110	5	108	5	110	5	107	5	109	5
127	2	129	2	128	2			126	1	125	1	127	2
142	3	144	2	144	2	143	2	142	2	142	1	143	2
152	1	157	1			155	1	154	1	153	1	154	1
159	1			160	1	161	1	160	1	157	1	159	1
171	2	172	2	171	2	173	2	172	2	174	1	172	2

Table 91 The migration distance of the LMW glutenins of PAN3232.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	1	20	1	19	1	14	1	19	1	14	1	18	1
27	1	25	1	23	1	30	1	25	1	22	1	25	1
40	1	40	1	36	1	39	1	32	1	31	1	36	1
50	1	54	1	59	1	50	1	60	2	56	2	55	1
79	5	77	5	76	2	75	5	78	5	72	5	76	5
95	5	94	4	93	4	90	3	92	4	90	4	92	4
108	4	108	3	107	4	103	4					107	4
119	1			118	1	115	1	118	2	114	1	117	1
129	2	128	1	127	2	122	1			120	1	125	1
134	2	134	2	134	2	135	2	140	4	131	2	135	2
142	3			149	4	144	3	145	4	142	3	144	3
156	3	150	4			159	3	160	3	161	2	157	3
177	3	174	3	175	1	179	1	177	1	180	1	177	1
183	2	183	1	184	2	189	1	183	1	190	1	185	1

Table 92 The migration distance of the LMW glutenins of PAN 3235.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
15	1	15	1	12	1	15	1	16	1	10	1	14	1
26	1	24	1	23	1	27	1	28	1	27	1	26	1
37	1	32	1	34	1	32	1	39	1	-	-	35	1
-	-	42	1	47	1	47	1	45	1	43	1	45	1
57	1	58	4	59	1	56	1	59	1	59	2	58	1
75	5	72	5	72	2	72	5	73	5	74	5	73	5
92	5	91	5	87	5	87	4	88	4	90	4	89	5
106	5	102	2	101	1	100	1	106	1	100	1	103	1
125	1	124	2	127	3	120	1	120	2	120	2	123	2
132	2	131	3	130	3	131	2	132	2	133	2	132	2
159	4	153	4	158	5	158	1	158	2	158	3	157	6
174	2	173	1	178	2	173	1	178	1	-	-	175	1
182	1	180	3	188	1	184	1	186	1	181	1	184	1

Table 93 The migration distances of the LMW glutenins of PAN 3349.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
38	2	38	2	38	2	33	2	34	1	34	2	36	2
-	-	43	2	42	2	44	3	44	2	43	2	43	2
50	5	51	4	50	4	52	4	53	4	52	4	51	4
61	3	59	2	60	2	61	2	62	2	63	2	61	2
73	3	69	3	70	3	72	4	72	3	72	4	71	3
92	2	91	2	91	3	95	3	95	2	94	2	93	2
105	5	104	5	104	5	107	5	109	5	109	5	106	5
123	1	121	1	124	1	125	1	125	1	127	1	124	1
139	3	139	3	140	3	137	3	137	2	134	2	138	3
149	1	150	1	149	1	146	2	-	-	146	1	148	1
157	1	157	2	158	4	158	1	156	1	154	1	157	1
170	2	170	2	168	3	169	2	171	1	173	2	170	2
178	1	181	1	-	-	185	1	-	-	182	1	182	1

Table 94 The migration distance of the LMW glutenins of PAN 3364.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
10	1	12	1	10	1	10	1	11	1	10	1	11	1
14	1	14	1	17	1	14	1	17	1	14	1	15	1
20	1	22	1	20	1	21	1	22	1	23	1	21	1
28	1	30	1	29	1	32	1	35	2	35	1	32	1
50	5	54	5	49	5	46	5	48	5	48	4	49	5
-	-	69	3	64	2	62	3	64	3	63	3	64	3
75	3	78	4	72	4	71	4	71	4	73	4	73	4
82	4	89	2	83	2	84	3	82	2	86	2	84	2
94	2	95	1	97	1	97	1	93	1	-	-	95	1
105	1	101	1	101	1	100	1	101	1	100	1	101	1
118	2	114	3	113	3	115	4	115	3	115	3	115	3
145	5	142	5	140	5	143	5	143	5	144	5	143	5
167	5	163	5	160	5	161	4	161	4	163	5	163	5
-	-	182	1	185	1	180	1	183	1	183	1	183	1
193	1	193	1	-	-	193	1	190	1	193	1	192	1

Table 95 The migration distance of the LMW glutenins of PAN 3377.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	7	1	6	1	12	1	12	4	6	1	9	1
30	5	31	5	33	5	31	5	37	5	27	4	32	5
50	5	48	4	50	4	42	4	49	3	50	2	48	4
68	1	66	1	68	1	61	5	69	3	60	1	65	1
93	3	94	3	97	3	99	2	98	1	93	3	96	3
108	3	106	3	108	3	107	4	105	3	101	3	106	3
118	5	119	4	120	4	120	3	113	2	119	2	118	6
138	1	139	1	132	1	134	2	136	1	135	1	136	1
151	1	152	2	155	1	153	1	155	2	150	1	153	1
161	1	169	1	-	-	166	1	163	2	169	1	166	1
172	1	-	-	173	1	170	1	170	1	175	1	172	1
176	1	176	1	176	1	176	1	175	1	178	1	176	1
181	1	180	1	-	-	181	1	181	1	182	1	181	1
187	1	-	-	190	1	187	1	190	1	186	1	188	1
192	1	197	1	193	1	195	1	195	1	195	1	195	1

Table 96 The migration distance of the LMW glutenins of PAN 9303.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
-	-	16	2	13	1	10	1	16	1	11	1	11	1
34	5	30	5	31	5	35	4	33	3	32	5	33	5
46	2	47	1	48	2	49	2	43	2	46	2	47	2
54	2	60	3	61	3	60	3	58	2	58	3	59	3
70	2	75	1	73	1	76	1	70	3	-	-	73	1
-	-	85	1	88	2	90	1	82	1	85	1	86	1
97	3	97	3	94	2	100	2	99	3	95	3	97	3
102	2	102	1	100	2	-	-	108	2	106	5	104	2
122	5	128	1	121	1	120	5	120	5	120	1	122	6
137	1	132	1	132	1	135	1	140	1	137	2	136	1
153	2	155	2	151	2	154	2	-	-	154	1	153	2
160	2	159	1	162	1	162	1	162	2	163	1	161	1
163	1	165	1	166	1	165	1	168	1	168	1	166	1
171	1	176	1	173	1	177	1	176	1	171	1	174	1
183	1	185	1	187	1	187	1	184	1	-	-	185	1
191	1	193	1	192	1	195	1	195	1	195	1	194	1

Table 97 The migration distance of the LMW glutenins of PAN 9316.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	1	14	1	14	1	10	-	10	1	13	1	12	1
16	1	16	1	16	1	-	-	-	-	17	1	16	1
29	1	27	1	26	1	26	5	30	1	23	1	27	1
41	5	39	4	42	5	45	5	-	-	40	5	41	5
50	3	50	3	51	4	52	2	51	3	56	3	52	3
65	5	65	4	67	5	64	1	68	1	70	1	67	6
78	1	75	2	76	2	80	1	80	1	77	1	78	1
84	1	82	1	84	1	85	4	88	3	80	1	84	1
90	1	89	1	88	1	92	4	92	1	-	-	90	1
94	4	-	-	-	-	98	4	95	4	96	5	96	4
101	4	104	5	106	5	101	5	109	4	104	5	104	5
118	4	119	5	121	5	118	4	-	-	112	4	118	4
125	2	126	4	-	-	122	1	125	2	120	4	124	6
137	1	-	-	130	3	131	1	135	1	131	2	133	1
144	1	144	2	144	1	140	1	141	1	145	1	143	1
156	2	157	1	158	2	160	1	153	1	154	1	156	1
172	1	171	1	171	1	168	1	172	2	168	1	170	1
174	1	175	1	174	1	172	1	178	3	175	1	175	1
183	1	181	1	180	1	180	1	180	1	182	1	181	1
186	1	188	1	186	1	-	-	187	1	185	1	186	1
190	2	193	1	193	1	191	1	194	1	196	1	193	1

Table 98 The migration distance of the LMW glutenins of PAN 9409.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
8	1	5	1	4	1	5	1	6	1	9	1	6	1
12	1	10	1	11	1	11	1	10	1	-	-	11	1
18	1	19	1	-	-	17	1	19	3	-	-	18	1
23	1	25	1	21	1	21	1	-	-	22	1	22	1
49	4	49	4	42	4	43	5	43	5	44	4	45	4
66	4	66	4	60	5	65	4	68	5	60	4	64	4
75	3	76	3	71	3	72	1	78	1	71	3	74	3
84	1	85	1	81	2	82	1	84	1	84	1	83	1
91	1	92	1	90	1	-	-	87	1	89	1	90	1
93	4	94	4	-	-	97	4	99	5	100	4	97	4
105	5	105	5	110	5	105	4	107	5	109	4	107	5
120	5	120	5	119	4	116	4	119	5	120	5	119	5
130	1	130	3	131	1	132	1	133	1	135	1	132	1
143	2	145	2	149	2	144	1	144	2	149	2	146	2
160	3	160	2	164	2	165	1	160	2	160	2	162	2
170	1	178	1	175	1	174	1	179	1	175	1	175	1
185	1	187	1	186	1	183	1	185	1	185	1	185	1
-	-	190	1	188	1	189	1	189	1	189	1	189	1
193	1	195	1	196	1	198	1	194	1	195	1	195	1

Table 99 The migration distance of the LMW glutenins of PAN 9413.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
12	1	-	-	-	-	16	1	13	1	13	1	14	1
23	3	24	4	21	3	24	3	25	3	23	1	23	3
34	1	-	-	34	1	35	2	37	2	33	1	35	1
47	1	49	1	42	1	46	3	47	2	50	1	47	1
60	1	63	2	-	-	63	2	64	3	66	2	63	2
-	-	-	-	79	5	72	5	73	5	74	5	75	5
84	5	85	5	81	5	84	1	81	1	83	1	93	6
100	1	99	1	99	1	90	1	91	1	92	2	95	1
102	1	-	-	109	3	101	3	102	3	100	3	103	3
111	3	111	3	117	2	112	3	113	4	113	3	113	3
121	2	123	2	120	2	121	2	121	2	125	3	122	2
132	1	132	4	130	1	132	1	133	1	132	1	132	1
149	1	-	-	148	1	-	-	142	1	146	1	146	1
152	1	150	1	152	1	151	1	150	1	154	1	152	1
161	2	161	2	168	2	163	1	167	2	166	1	164	2
170	2	178	1	174	1	-	-	178	1	178	1	176	1
181	1	183	1	180	1	-	-	180	1	182	1	181	1
185	1	188	1	186	1	188	1	187	1	189	1	187	1
-	-	191	1	192	1	190	1	190	1	191	1	191	1

Table 100 The migration distance of the LMW glutenins of PAN 9414.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	4	16	4	13	1	15	1	13	1	15	1	15	1
30	1	26	1	23	1	25	3	25	3	27	1	26	1
37	1	35	1	30	1	37	1	34	1	-	-	35	1
44	1	49	1	40	1	49	1	47	2	-	-	46	1
70	5	68	5	61	5	67	4	69	5	70	4	68	5
75	5	76	1	-	-	75	5	76	5	78	5	76	5
-	-	104	4	100	4	104	3	105	4	106	4	104	4
114	5	110	5	110	4	114	5	117	5	119	5	114	5
130	4	122	3	122	1	125	3	126	3	128	3	126	3
146	1	141	1	141	1	142	1	142	1	142	1	142	1
155	1	150	2	151	1	154	2	151	1	153	1	152	1
163	1	165	1	164	1	168	1	165	1	-	-	165	1
178	1	172	1	173	1	178	1	173	1	173	1	175	1
182	1	181	1	185	1	183	1	185	1	185	1	184	1
185	1	187	1	188	1	186	1	187	1	188	1	187	1
195	1	190	1	194	1	191	1	193	1	193	1	193	1

Table 101 The migration distance of the LMW glutenins of PAN 9416.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
		9	1	11	1	10	1	11	1	10	1	10	1
19	5	17	1	11	1	12	1	14	1	14	1	15	1
	-	37	5	31	1	33	1	34	1	34	1	34	1
41	5	45	5	45	5	43	3	46	5	48	5	45	5
59	1	59	1	54	5	53	1	57	1	59	1	57	1
79	3	78	3	76	3	78	5	78	3	79	2	78	3
90	1	90	5	89	1	89	1	89	1	81	1	88	1
115	5	-	-	113	3	115	5	115	5	116	5	115	5
120	1	119	1	116	3	119	5	119	5	-	-	119	6
138	1	130	1	136	1	131	4	132	5	130	5	133	6
144	1	149	1	147	1	144	2	146	1	144	1	146	1
154	1	154	1	150	1	155	2	154	1	155	1	154	1
159	2	160	1	160	1	163	1	165	1	163	1	162	1
174	1	175	1	170	2	-	-	175	1	170	1	173	1
182	1	182	1	186	2	180	1	182	1	181	1	182	1
192	1	191	1	192	1	192	1	192	1	193	1	192	1

Table 102 The migration distance of the LMW glutenins of PAN 9417.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
6	1	7	1	8	1	9	1	7	1	7	1
13	1	16	1	17	1	13	1	15	1	15	1
24	1	28	1	25	1	25	1	20	1	24	1
30	1	33	1	30	1	30	1	33	5	31	1
49	5	52	5	50	5	48	5	46	1	49	5
63	5	66	5	69	5	66	3	65	5	66	5
76	1	75	2	78	1	78	1	78	1	77	1
93	2	89	3	91	2	93	1	91	2	91	2
111	5	113	5	115	5	111	5	112	5	112	5
120	3	123	5	124	5	126	5	124	5	123	5
140	1	132	2	135	1	137	1	130	1	135	1
150	2	149	2	151	2	148	1	148	1	149	2
155	2	-	-	157	1	155	1	158	1	156	1
167	1	160	2	161	2	161	2	164	1	163	2
171	1	175	1	170	1	172	1	170	1	172	1
182	1	183	1	181	1	180	1	181	1	181	1
190	1	189	1	190	1	187	1	186	1	188	1
196	1	193	1	194	1	193	1	190	1	193	1

Table 103 The migration distance of the LMW glutenins of PAN 9418.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
4	1	6	1	6	1	6	1	7	1	7	1	6	1
11	1	13	1	10	1	10	1	12	1	12	1	11	1
16	1	18	1	14	1	15	1	17	1	15	1	16	1
36	5	40	1	-	-	41	5	40	5	40	5	39	5
51	5	51	4	51	4	53	2	53	2	53	2	52	6
66	3	66	3	67	4	62	2	61	3	61	3	64	3
78	3	75	1	-	-	75	1	75	1	76	1	76	1
82	1	84	2	85	2	80	1	83	1	82	1	83	1
89	2	89	2	90	1	95	3	95	2	94	2	92	2
101	1	99	1	101	1	103	4	102	2	101	1	101	1
113	5	115	5	116	5	112	5	116	4	115	4	115	5
122	5	124	5	125	5	125	1	129	1	126	1	125	6
141	1	143	1	144	1	148	1	147	2	147	2	145	1
151	2	152	2	153	2	152	3	158	1	159	2	154	2
175	1	176	1	172	1	172	1	174	1	172	1	174	1
181	1	182	1	183	1	182	1	182	1	183	1	182	1
192	1	192	1	190	1	191	1	191	1	191	1	191	1
196	1	197	1	195	1	195	1	193	1	193	1	195	1

Table 104 The migration distance of the LMW glutenins of PAN 9419.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
9	1	5	1	11	1	5	1	5	1	6	1	7	1
21	4	20	5	23	5	20	4	20	4	20	4	21	4
39	1	37	1	31	1	37	1	37	5	30	1	35	1
48	2	46	2	49	2	50	2	50	3	45	1	48	2
65	3	64	3	67	3	69	1	66	3	67	5	66	3
82	5	82	5	85	5	-	-	84	1	86	5	84	5
92	3	92	3	95	2	95	3	97	3	-	-	94	3
100	1	-	-	-	-	106	2	101	2	102	3	102	2
120	5	120	5	120	5	120	5	123	5	124	5	121	5
130	5	130	5	133	5	135	1	137	1	139	1	134	6
147	2	144	1	143	1	148	2	148	1	145	1	146	1
155	1	150	1	156	2	156	1	152	1	156	2	154	1
162	3	165	1	164	2	169	1	164	1	169	1	166	1
174	1	-	-	-	-	173	1	173	1	176	1	174	1
182	1	185	1	182	1	180	1	181	1	181	1	182	1
188	1	190	1	-	-	189	2	186	1	184	1	187	1
196	1	197	1	191	1	193	1	193	1	193	1	194	1

Table 106 The migration distances of the LMW glutenins of PAN 9711.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
49	5	48	5	49	5	52	5	51	5	50	5	50	5
60	5	58	4	60	5	62	5	62	5	60	5	60	5
78	1	79	1	79	1	79	1	78	1	81	1	79	1
90	3	90	3	89	4	93	3	92	3	91	3	91	3
100	5	100	5	101	5	102	3	103	5	104	5	102	5
117	2	114	2	114	2	112	2	110	2	115	2	114	2
121	1	123	1	128	1	125	1	124	1	122	1	124	1
134	2	131	2	131	2	139	3	137	2	137	2	135	2
145	1	146	1	144	1	146	1	-	-	144	1	145	1
154	2	161	3	160	2	159	2	158	2	156	1	158	2
167	3	166	3	166	3	169	3	168	2	165	1	167	3
179	1	178	1	177	1	178	1	178	1	177	1	178	1

Table 106 The migration distances of the LMW glutenins of Pan 9712

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
36	1	36	1	31	1	-	-	36	1	39	1	36	1
52	5	52	5	52	5	51	5	52	5	53	5	52	5
62	5	62	5	64	5	61	5	62	5	63	5	62	5
80	1	77	1	-	-	78	1	78	1	79	1	78	1
85	1	-	-	-	-	82	1	81	1	83	1	83	1
92	3	93	3	93	3	90	3	91	3	92	3	92	3
103	4	105	5	107	4	102	5	103	5	105	5	104	5
116	2	115	2	-	-	111	3	112	2	113	2	113	2
125	1	127	1	127	1	120	1	121	1	121	1	124	1
140	2	141	2	141	2	149	1	142	1	141	2	142	2
156	1	157	1	158	1	158	1	156	1	159	1	157	1
164	1	163	1	162	1	162	1	164	1	165	1	163	1
169	2	170	2	170	2	168	2	169	1	168	1	169	2
180	1	176	2	179	1	178	1	173	1	173	1	177	1

Table 107 The migration distances of the LMW glutenins of PAN 9713

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
33	1	35	1			32	1			33	1	33	1
49	5	50	5	49	5	50	5	50	5	50	5	50	5
60	5	61	5	65	5	60	5	60	5	61	5	61	5
79	1	77	1	79	1	70	1	71	1	72	3	75	1
90	4	90	3	90	2	90	3	91	3	90	3	90	3
101	5	102	5	100	4	103	5	103	5	104	5	102	5
109	3	110	2	110	2	114	2	113	2	115	2	112	2
115	2	118	1	115	1	120	1	117	1	115	2	117	1
131	2	131	2	131	2	135	3	137	2	138	3	134	2
147	1	144	1	149	1	146	1	148	1	147	1	147	1
150	1	151	1	154	1			151	1	152	1	152	1
159	1	159	1	157	1	157	1	155	1	158	1	158	1
165	1	164	1	162	1	162	1	165	2	162	1	163	1
168	1	166	1	165	1	167	1	165	2	168	1	167	1
172	1	171	1	170	1	172	1	171	1	173	1	172	1

Table 108 The migration distance of the LMW glutenins of PAN LE 4.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
6	2	8	1	10	1	9	1	8	1	8	1
24	3	23	4	23	5	24	4	22	4	23	4
31	2	32	1	36	1			33	1	33	1
35	2	37	1	38	1	38	1	37	1	37	1
45	5	43	1	42	1	43	1	44	1	43	1
59	2	54	1	59	1	55	1	56	1	57	1
63	1	65	1	64	1			62	1	64	1
78	4			75	5	76	5	77	5	77	5
83	5	87	5	89	5	90	1	88	5	87	5
100	1	97	1	102	1	97	1	96	1	98	1
108	3	106	2	106	2	105	2	103	2	106	2
123	3	122	5	123	5	124	5	121	5	123	5
134	1	132	5	133	4	136	1	131	2	133	6
146	1	143	2	146	1	146	1	147	1	146	1
157	2	158	2	158	2	155	1	156	2	157	2
169	2	167	2	166	2	165	2	168	2	167	2
183	1	183	1	183	1	184	1	185	1	184	1
190	1	191	1	189	1	190	1	188	1	190	1
193	1	194	1	192	1	194	1	193	1	193	1

Table 109 The migration distance of the LMW glutenins of PAN LE 7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
6	1	5	1	5	1	8	1	5	2	8	1	6	1
15	1	13	1			13	1	15	1	16	1	14	1
22	5	24	4	20	4	20	1	20	1	23	1	22	6
33	1			31	1	30	1	29	3	29	1	30	1
40	1	40	1	40	1	42	1	38	1	41	2	40	1
45	1	45	1	47	1	46	1	48	1			46	1
61	1	64	1			63	1	64	1	60	5	62	1
70	5			73	5	72	4	76	4	75	5	73	5
86	5	83	5	88	5	82	5	85	5	87	1	85	5
		98	1	96	1	97	1	97	1	98	1	97	1
107	2	104	2			104	1	101	1	105	1	104	1
122	5	120	5	120	4	120	3	122	4	124	4	121	4
132	5	130	4	130	3	133	4	135	4	136	4	133	4
156	2	150	3	153	2	153	2	152	1	156	2	153	2
164	3	160	2	165	1	164	2	164	2	167	2	164	2
176	1	174	2	175	1	175	2	173	2	172	2	174	2
184	1	183	1	185	1	185	1	183	1	181	1	184	1
191	1	195	1	192	1	195	1	193	1	193	1	193	1

Table 110 The migration distance of the LMW glutenins of PAN LE 9.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
9	1	8	1	-	-	9	1	9	1	9	1
14	1	14	2	14	1	16	1	14	1	14	1
22	1	25	1	20	1	25	1	24	1	23	1
30	1	36	1	35	5	32	1	34	1	33	1
-	-	50	3	47	1	45	3	47	3	47	3
58	5	59	5	63	4	60	1	60	1	60	6
75	4	75	5	76	1	70	4	75	4	74	4
82	3	81	2	85	1	84	2	-	-	83	2
94	1	91	1	95	2	93	1	93	1	93	1
99	1	98	1	98	2	96	1	99	1	98	1
115	3	117	4	116	4	119	5	115	4	116	4
126	2	126	3	124	3	-	-	128	3	126	3
135	4	135	3	131	4	137	5	137	4	135	4
158	1	162	1	158	1	162	1	163	1	161	1
174	2	172	2	174	1	171	1	171	1	172	1
182	1	180	1	183	1	180	1	179	1	181	1
188	1	184	1	189	1	186	1	186	1	186	1
193	1	190	1	193	1	190	1	190	1	191	1
197	1	196	1	-	-	195	1	196	1	196	1

Table 111 The migration distance of the LMW glutenins of PAN LE 10.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rev	I
13	1	11	1	11	1	13	1	16	1	13	1
21	1	21	1	24	1	20	1	25	1	22	1
45	5	47	5	50	5	51	5	50	5	49	5
65	2	60	1	60	1	66	1	-	-	63	1
80	4	80	1	79	4	80	4	78	4	79	4
92	1	92	1	95	1	-	-	92	1	93	1
96	1	97	1	99	1	-	-	97	1	97	1
117	1	-	-	119	2	118	1	116	1	117	1
137	5	130	5	134	5	137	5	132	5	134	5
146	4	143	5	142	4	144	4	142	5	143	4
153	1	155	1	151	4	153	4	150	5	152	6
170	1	170	2	167	1	168	1	163	1	168	1
173	1	179	2	173	1	-	-	178	1	176	1
185	1	186	1	188	1	190	1	190	1	188	1
192	1	190	1	191	1	192	1	-	-	191	1

Table 112 The migration distance of the LMW glutenins of PAN LE 12.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
8	1	8	1	-	-	6	1	9	1	6	1	9	1
-	-	12	1	12	2	18	1	16	1	15	1	15	1
23	4	21	2	25	4	-	-	25	5	24	4	24	4
-	-	35	1	35	1	31	1	30	1	31	1	32	1
42	1	46	1	43	2	42	1	41	1	40	1	42	1
57	1	57	1	58	1	58	1	53	1	55	1	56	1
78	5	79	5	79	4	77	5	75	1	75	5	77	5
84	5	-	-	85	2	82	5	81	5	85	5	83	5
102	1	103	1	103	1	102	1	103	1	102	1	103	1
-	-	107	1	109	1	108	1	110	1	109	1	109	1
132	5	130	5	130	5	130	5	130	4	130	2	130	5
150	1	147	2	146	2	145	2	148	2	145	3	147	2
164	2	164	2	163	1	162	1	161	1	165	1	163	1
174	2	175	1	172	1	174	1	175	1	175	1	174	1
186	1	187	1	185	1	189	1	188	1	185	1	187	1
190	1	193	1	192	1	194	1	193	1	195	1	193	1

Table 113 The migration distance of the LMW glutenins of Red Victory.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
5	1	6	1	6	1	9	1	8	1	8	1	7	1
10	1	13	1	14	1	14	1	13	1	14	1	13	1
18	1	20	1	22	1	17	1	19	1	17	1	19	1
21	1	26	1	25	1	24	1	24	1	25	1	24	1
27	1	29	1	29	1	29	1	30	3	30	1	29	1
43	5	40	5	41	5	43	5	44	5	45	1	43	5
60	1	65	1	60	1	63	2	63	1	61	2	62	1
75	4	73	4	75	4	79	5	78	4	78	5	76	4
93	1	94	1	93	1	93	1	90	4	-	-	93	1
100	1	98	1	97	1	97	1	99	1	97	1	98	1
-	-	102	1	105	1	105	1	104	1	103	1	104	1
109	1	110	1	109	1	111	1	114	1	110	1	111	1
116	1	118	2	117	1	119	2	117	1	117	1	117	1
124	3	122	2	127	2	-	-	121	1	125	2	124	2
-	-	136	5	137	5	133	5	134	2	-	-	135	5
158	1	158	1	157	1	157	1	157	1	154	1	157	1
162	1	165	1	-	-	161	1	162	1	161	1	162	1
173	1	170	1	-	-	175	1	172	1	171	1	172	1
177	2	179	3	175	2	178	2	-	-	178	1	177	2
181	2	185	1	185	1	186	1	184	1	184	1	184	1
192	1	190	1	191	1	-	-	190	1	192	1	191	1
195	1	196	1	196	1	195	1	193	1	-	-	195	1

Table 114 The migration distance of the LMW glutenins of Riemland.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
8	1	6	1	8	1	8	1	7	1	9	1	8	1
-	-	12	1	13	1	15	1	13	1	14	1	13	1
18	1	16	1	18	1	18	1	18	1	17	1	18	1
24	1	25	1	25	1	24	1	23	1	24	1	24	1
32	1	-	-	32	1	31	1	29	1	31	1	31	1
40	1	-	-	38	1	37	1	39	1	35	1	38	1
51	1	54	1	52	1	58	1	53	1	54	1	54	1
60	1	61	1	60	1	64	1	67	2	66	1	63	1
73	5	74	5	75	5	80	1	78	5	76	3	76	5
90	1	94	1	94	1	91	5	94	1	91	1	92	1
97	1	97	1	102	1	100	3	100	1	99	1	99	1
110	5	112	5	113	5	114	1	111	1	111	1	112	6
119	2	116	2	120	2	118	1	115	2	120	3	118	2
130	4	131	3	132	3	136	3	134	2	130	3	132	3
140	1	138	1	141	1	-	-	141	1	140	1	140	1
152	1	153	1	154	1	150	1	150	1	152	1	152	1
164	3	164	2	164	1	160	2	162	2	162	2	163	2
174	2	174	3	175	2	173	1	173	2	174	2	174	2
184	1	183	1	183	1	185	2	182	2	181	1	183	1
191	1	190	1	191	1	-	-	195	1	195	1	192	1

Table 115 The migration distances of the LMW glutenins of SA 1684.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
45	2	46	2	47	2	49	2	49	2	49	2	48	2
63	5	67	5	66	5	69	5	70	5	68	5	67	5
73	2	76	2	74	2	77	2	77	2	77	2	76	2
92	2	91	2	91	2	92	2	91	2	93	2	92	2
102	4	103	4	101	4	104	4	105	4	102	4	103	4
113	2	114	2	113	2	114	3	116	2	114	1	114	2
133	2	133	2	136	3	137	2	137	1	137	2	136	2
139	2	140	2	145	2	142	2	144	1	143	2	142	2
148	1	148	1	148	1	151	2	148	1	-	-	149	1
161	1	164	2	163	1	163	1	165	1	166	1	164	1
166	2	167	1	166	1	167	1	171	1	170	1	168	1

Table 116 The migration distances of the LMW glutenins of SA 463

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
43	1	41	1	42	1	-	-	43	1	-	-	42	1
67	5	68	5	67	5	70	5	68	5	67	5	68	5
74	3	75	3	74	3	-	-	-	-	73	3	74	3
89	1	90	2	90	2	91	2	90	2	88	2	90	2
104	4	105	4	105	4	106	4	104	4	103	4	105	4
112	1	112	1	112	2	115	1	113	1	112	1	113	1
121	1	119	1	119	1	122	1	121	1	120	1	120	1
141	2	140	2	138	2	-	-	139	1	140	2	140	2
146	1	146	1	146	1	143	2	142	1	148	1	145	1
166	1	165	2	164	1	169	1	169	2	168	1	167	1

Table 117 The migration distances of the LMW glutenins of Sch 69.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
31	1	27	1	-	-	30	1	30	1	29	1	29	1
36	1	32	1	-	-	38	1	37	1	36	1	36	1
52	4	51	4	59	3	55	5	55	4	55	4	55	4
64	4	63	3	64	4	66	5	66	4	65	4	65	4
70	4	71	3	74	4	71	4	72	4	73	4	72	4
-	-	87	1	-	-	83	1	89	1	87	1	87	1
94	3	96	2	96	3	93	3	97	3	95	3	95	3
110	5	111	5	110	5	107	5	108	5	107	5	109	5
117	3	117	3	-	-	118	3	119	3	115	3	117	3
124	1	128	1	-	-	125	2	124	2	122	1	125	1
141	3	141	2	140	2	139	3	139	3	138	3	140	3
150	1	154	1	-	-	153	1	154	1	153	1	153	1
166	2	169	2	168	2	166	2	166	2	168	2	167	2
180	1	180	1	-	-	176	1	176	1	178	1	178	1

Table 118 The migration distance of the LMW glutenins of Snack.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	2	13	1	17	2	10	1	15	1	9	1	13	1
27	1	30	1	-	-	24	2	25	1	22	2	26	1
42	1	44	1	45	4	42	1	44	1	41	1	43	1
53	2	56	2	-	-	52	1	53	2	53	2	53	2
65	5	68	3	-	-	63	3	62	2	60	3	64	3
73	4	77	5	71	5	76	5	74	5	74	5	74	5
90	4	89	3	82	4	86	4	84	2	84	4	86	4
99	1	94	1	95	1	98	1	96	1	94	1	96	1
102	1	100	1	100	1	105	1	102	1	100	1	102	1
114	1	110	2	115	3	116	2	116	2	115	2	114	2
130	3	136	3	-	-	134	2	134	2	134	2	134	2
150	3	-	-	144	-	144	4	142	3	143	3	145	3
-	-	161	3	167	3	164	3	163	2	162	2	163	3
171	1	171	1	-	-	-	-	174	1	177	1	173	1
189	1	184	1	187	1	185	1	185	1	181	1	185	1

Table 119 The migration distances of the LMW glutenins of Sonop.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	1	-	-	10	1	9	1	9	1	8	1	9	1
13	1	13	1	17	1	15	5	11	1	15	1	14	1
23	1	20	1	23	1	25	3	25	1	24	1	23	1
42	5	42	5	41	5	-	-	40	5	40	5	41	5
51	3	51	4	50	4	48	5	53	4	47	4	50	4
69	3	69	3	68	3	69	3	69	1	65	3	68	3
77	2	78	2	76	2	-	-	79	1	74	2	77	2
84	1	88	1	84	1	86	2	-	-	84	1	85	1
96	3	97	1	96	3	91	3	99	3	94	3	96	3
102	5	101	1	102	1	102	5	105	2	108	5	103	6
113	2	114	3	113	2	113	2	115	1	112	2	113	2
126	5	126	5	124	5	122	1	123	1	123	2	124	6
143	1	144	1	-	-	141	1	140	1	143	1	142	1
149	1	150	1	149	1	152	2	150	1	147	1	150	1
163	1	164	2	162	1	163	2	163	1	164	1	163	1
167	2	168	1	167	1	170	1	169	1	169	1	168	1
176	1	174	2	174	1	-	-	174	1	175	1	175	1
184	1	184	1	185	1	182	1	184	1	183	1	184	1
189	1	192	1	193	1	191	1	192	1	192	1	192	1

Table 120 The migration distance of the LMW glutenins of SST 3.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	2	16	2	17	1	14	1	17	1	-	-	16	1
22	1	27	1	25	1	20	1	23	1	26	1	24	1
30	1	33	1	34	1	30	1	30	1	35	1	32	1
60	2	58	2	58	2	55	1	56	2	-	-	57	5
65	2	62	2	65	2	69	2	68	2	66	3	66	2
71	2	76	3	-	-	-	-	74	2	74	2	74	1
85	5	86	5	82	5	81	4	80	5	85	4	83	5
105	1	104	1	102	1	100	1	102	2	105	2	103	1
115	2	110	1	114	2	109	1	110	2	115	2	112	2
122	3	126	3	126	3	119	1	121	3	125	3	123	3
130	3	133	2	131	2	132	2	133	2	135	2	132	2
146	3	143	3	143	3	-	-	147	3	-	-	145	3
155	1	156	2	155	2	152	2	153	2	151	2	154	2
173	1	174	1	171	1	175	1	175	1	-	-	174	1
183	1	-	-	185	1	180	1	181	1	182	1	182	1
192	1	191	1	195	1	193	1	190	1	191	1	192	1

Table 121 The migration distance of the LMW glutenins of SST 16.

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
8	1	8	1	8	1	11	1	9	1	8	1	9	1
17	4	16	1	16	1	15	1	14	1	15	1	16	1
26	1	29	3	27	1	25	1	24	1	28	1	27	1
34	1	40	1	37	1	38	1	37	1	38	1	37	1
47	1	45	2	-	-	47	2	47	2	46	3	46	2
59	2	56	1	56	4	57	1	56	1	-	-	57	1
68	5	66	1	69	1	68	1	64	1	-	-	67	1
-	-	75	1	77	1	79	1	73	1	79	1	77	1
82	1	81	5	-	1	84	1	84	1	85	1	83	1
91	1	95	1	92	5	-	-	90	1	89	1	91	1
109	5	106	5	103	5	106	5	108	5	109	5	107	5
127	1	125	1	-	-	120	1	124	1	124	1	124	1
133	1	-	-	134	5	130	1	131	1	134	1	132	1
154	2	152	3	154	3	152	3	153	4	153	3	153	3
164	2	165	2	162	1	163	1	-	-	166	1	164	1
175	1	176	2	177	2	175	1	177	1	177	1	176	1
183	1	-	-	181	1	182	1	183	1	182	1	182	1
190	1	187	1	185	1	184	1	187	1	-	-	187	1
195	1	194	1	192	1	194	1	195	1	196	1	194	1

Table 122 The migration distance of the LMW glutenins of SST 23.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
13	1	14	1	12	1	11	1	15	1	14	1	13	1
20	1	21	1	18	1	20	1	21	1	21	1	20	1
30	1	34	1	32	1	35	1	34	2	33	1	33	1
45	4	47	3	46	3	46	4	44	4	45	4	46	4
66	3	60	4	60	3	63	3	63	2	64	3	63	3
76	1	72	3	75	3	78	3	76	3	77	4	76	3
92	3	90	3	94	1	95	3	94	3	94	3	93	3
107	1	106	1	102	1	104	5	103	5	104	5	104	6
136	5	132	5	130	5	130	1	134	1	131	1	132	5
156	1	152	1	155	1	153	5	151	5	150	5	153	6
162	1	163	1	161	1	165	1	161	2	162	1	162	1
172	1	174	1	174	1	175	1	174	1	173	1	174	1
183	1	184	1	184	1	182	1	184	1	182	1	183	1
189	1	190	1	190	1	187	1	189	1	187	1	189	1
192	1	193	1	195	1	195	1	193	1	192	1	193	1

Table 123 The migration distance of the LMW glutenins of SST 33.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
13	1	14	1	17	1	18	1	14	1	17	1	13	1
32	4	30	3	30	3	29	3	29	1	30	3	30	3
49	1	50	1	47	1	42	3	48	1	48	1	47	1
-	-	59	1	55	1	57	1	56	1	58	1	57	1
65	1	-	-	65	1	63	1	62	1	64	2	64	1
86	5	86	5	83	5	84	5	80	1	84	5	84	5
97	1	100	1	100	1	102	1	99	5	98	1	99	1
131	5	130	4	129	5	131	5	135	5	130	5	131	5
153	1	153	1	156	1	156	1	151	1	153	1	154	1
167	1	167	1	170	1	166	1	167	1	168	1	168	1
174	1	173	1	174	1	172	1	-	-	172	1	173	1
180	1	183	1	183	1	182	1	182	1	183	1	182	1
186	1	187	1	186	1	188	1	185	1	187	1	187	1
190	1	190	1	195	1	195	1	192	1	192	1	192	1

Table 124 The migration distance of the LMW glutenins of SST 44.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
17	1	13	1	15	1	12	1	12	1	18	5	15	1
-	-	23	1	25	1	25	1	26	1	29	2	26	1
35	1	35	1	39	1	40	1	36	2	35	1	37	1
48	1	50	2	46	1	50	1	50	1	49	5	49	1
61	1	-	-	61	1	63	1	65	1	62	2	62	1
65	1	68	1	64	1	67	1	68	1	65	2	66	1
72	1	76	1	76	3	73	1	74	1	75	1	74	1
80	2	80	1	81	2	83	2	84	2	83	2	82	2
94	1	95	2	94	2	96	2	91	2	91	3	94	2
101	1	104	2	105	1	106	1	101	2	104	1	104	1
117	1	117	1	117	2	115	1	114	1	116	1	116	1
125	5	129	4	127	5	130	1	127	1	128	1	128	6
139	1	-	-	134	1	136	1	136	1	136	1	136	1
149	1	152	1	147	1	150	1	148	1	149	3	149	1
158	2	158	1	154	1	159	1	154	1	158	1	157	1
-	-	162	1	165	1	168	1	164	2	167	1	165	1
171	1	170	1	174	2	175	1	173	1	174	1	173	1
178	1	178	1	180	2	-	-	177	1	178	1	178	1
181	1	180	1	184	2	181	1	182	1	184	1	182	1
190	1	191	1	195	1	192	1	190	1	193	1	192	1

Table 125 The migration distances of the LMW glutenins of SST 55.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	1	14	1	13	1	11	1	11	1	13	1	13	1
30	4	29	4	28	4	23	1	23	1	24	1	26	6
41	1	41	1	42	1	42	5	39	5	39	4	41	6
49	1	46	1	50	1	47	5	46	5	46	5	47	6
63	1	-	-	62	1	65	1	60	1	61	1	62	1
76	2	74	2	72	2	77	1	75	2	70	1	74	2
83	5	82	5	81	5	-	-	82	1	82	5	82	5
94	1	92	1	92	1	96	5	94	5	92	5	93	6
110	1	111	1	110	1	113	1	115	1	114	1	112	1
-	-	137	1	137	1	132	1	136	1	130	1	134	1
145	1	148	1	146	1	141	1	147	1	145	1	145	1
154	1	153	1	151	1	152	2	-	-	153	1	153	1
179	1	179	1	174	1	174	1	175	1	177	1	176	1
185	1	185	1	185	1	183	1	180	1	185	1	184	1
190	1	189	1	188	1	190	1	192	1	192	1	190	1

Table 126 The migration distance of the LMW glutenins of SST 66.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	1	11	1	13	1	19	1	16	2	10	2	14	1
22	2	27	2	29	2	30	1	27	2	28	1	27	2
49	1	50	1	50	1	50	1	46	1	47	2	49	1
64	3	-	-	61	2	60	3	68	5	63	3	63	3
77	5	79	5	76	5	70	5	77	4	73	5	75	5
85	5	88	4	83	5	80	4	88	4	88	4	85	4
107	1	103	1	-	-	105	1	109	2	104	1	106	1
117	3	110	2	115	1	111	2	116	1	120	2	115	2
-	-	120	3	124	2	120	1	127	2	125	2	123	2
151	4	150	3	155	3	160	3	159	3	155	2	155	3
170	2	173	1	178	1	-	-	176	1	178	1	175	1
187	1	190	1	-	-	190	1	189	1	183	1	188	1

Table 127 The migration distance of the LMW glutenins of SST 101.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	12	1	11	1	12	1	12	1	14	1	12	1
20	1	21	1	25	1	21	1	20	1	25	1	22	1
32	1	34	1	36	1	34	1	34	1	31	1	34	1
45	5	49	5	50	5	49	1	46	1	45	1	47	6
74	1	79	1	77	1	79	1	72	5	74	1	76	1
82	1	83	1	85	2	84	1	81	1	83	1	83	1
92	2	93	1	95	2	90	1	95	1	95	1	93	1
110	1	110	3	111	4	110	3	110	3	109	3	110	3
122	1	125	1	122	1	126	1	120	3	123	1	123	1
133	1	134	1	134	1	135	1	130	1	132	1	133	1
140	1	138	1	141	1	-	-	140	1	138	1	139	1
149	1	147	1	150	1	150	5	150	1	147	1	149	1
161	3	162	2	163	1	-	-	164	2	164	2	163	2
177	1	173	1	173	1	175	1	170	1	175	1	174	1
180	1	182	1	182	1	184	1	184	1	182	1	182	1
189	1	187	1	190	1	189	1	190	1	-	-	189	1
192	1	190	1	184	1	193	1	-	-	191	1	192	1

Table 128 The migration distances of the LMW glutenins of SST 102.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
35	1	38	1	35	1	35	1	34	1	36	1	36	1
46	1	49	1	49	1	43	1	40	1	45	1	45	1
50	1	49	1	51	1	50	1	52	1	-	-	50	1
72	5	72	5	72	5	72	5	74	5	74	5	74	5
93	2	93	2	92	2	93	2	95	2	92	1	93	2
104	5	105	4	104	4	106	4	106	4	106	4	105	4
116	2	115	1	113	1	118	1	118	1	118	1	116	1
121	1	120	1	122	1	-	-	121	1	127	1	122	1
131	1	131	1	132	1	135	1	-	-	132	1	132	1
136	1	137	1	136	1	138	1	136	1	139	1	137	1
143	1	145	1	142	1	143	2	140	1	140	1	142	1
157	1	154	1	153	1	159	1	158	1	157	1	156	1
167	1	167	1	168	1	168	2	169	1	168	2	168	1
181	1	180	1	-	-	183	1	185	1	180	1	182	1

Table 129 The migration distance of the LMW glutenins of SST 107.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
8	1	9	1	8	1	7	1	6	1	8	1	8	1
14	1	15	1	-	-	11	1	13	1	15	1	14	1
26	5	28	4	30	4	28	1	30	1	30	1	29	6
42	1	46	2	46	2	46	2	48	2	47	2	46	2
76	1	-	-	76	1	77	1	77	5	75	1	76	1
91	1	89	1	89	1	94	1	91	1	91	1	91	1
101	1	101	1	101	1	105	1	103	1	106	2	103	1
117	3	116	4	118	4	113	4	117	4	116	2	116	4
130	1	127	1	130	1	125	1	125	3	123	1	127	1
140	1	140	1	143	1	140	1	141	1	141	1	141	1
155	1	150	1	151	1	151	1	150	1	152	2	152	1
158	1	158	1	-	-	158	1	160	1	160	1	159	1
170	2	172	2	171	2	171	2	170	1	173	1	171	2
186	1	186	1	184	1	-	-	188	1	189	1	187	1
189	1	191	1	193	1	193	1	193	1	193	1	192	1

Table 130 The migration distance of the LMW glutenins of SST 124.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
33	1	34	1	32	1	32	1	32	1	-	-	33	1
45	3	45	3	43	3	44	3	44	3	43	3	44	3
67	5	66	5	67	5	66	5	66	5	67	5	67	5
84	1	86	1	86	1	83	1	82	1	83	1	84	1
92	2	91	2	90	1	91	2	90	1	90	2	91	2
101	3	101	3	101	3	102	3	102	3	101	3	101	3
108	3	108	3	107	3	110	2	108	2	108	3	108	3
115	1	114	1	114	1	120	1	120	1	115	1	116	1
141	2	141	2	140	3	141	1	145	2	142	2	142	2
-	-	148	1	148	1	150	1	152	1	150	1	150	1
164	1	164	1	165	1	167	1	167	1	164	1	165	1
174	1	172	1	176	1	175	1	-	-	178	1	175	1

Table 131 The migration distances of the LMW glutenins of SST 333.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
43	3	43	3	44	3	43	3	43	3	43	3	43	3
62	5	62	5	62	5	61	5	63	5	61	5	62	5
67	5	66	5	67	5	66	5	67	5	67	5	67	5
		76	1	76	1	77	1	77	1	76	1	76	1
83	1	83	1	83	1	83	2	83	1	83	1	83	1
90	2	90	2	91	1	90	2	90	2	91	2	90	2
97	3	99	3	99	3	102	3	101	3	101	3	100	3
106	2	105	3	108	2	107	3	106	3	107	3	107	3
114	1	114	2	114	1	114	2	114	2	115	2	114	2
122	1	121	1	124	1	124	1	123	1	123	1	123	1
		128	1	129	1	126	1	130	1	128	1	128	1
141	2	142	2	141	1	140	2	140	2	141	2	141	2
		149	1	148	1	147	1	148	1	147	1	148	1
167	1	165	1	166	1	163	1	165	1	166	1	165	1

Table 132 The migration distances of the LMW glutenins of SST 363.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
28	1	27	1	29	1	26	1	26	1	28	1	27	1
46	3	46	3	46	3	43	4	44	3	45	3	45	3
74	5	73	5	74	5	70	5	71	5	71	5	72	5
84	1	82	1	82	1	82	1	-	-	-	-	83	1
90	3	-	-	93	2	92	2	92	2	92	2	92	2
95	3	-	-	-	-	95	2	96	2	97	2	96	2
103	5	102	4	106	4	106	4	105	4	106	4	105	4
-	-	118	1	-	-	113	2	114	1	119	1	116	1
-	-	122	1	-	-	121	1	122	1	122	1	122	1
133	1	134	1	135	1	135	1	137	1	139	2	136	1
-	-	148	1	140	1	144	1	-	-	146	1	145	1
162	1	160	2	162	1	163	1	164	1	165	1	163	1
171	1	-	-	170	1	173	1	174	1	171	1	172	1

Table 133 The migration distances of the LMW glutenins of SST 367.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
67	5	68	5	68	5	66	5	68	5	74	5	69	5
79	2	79	2	80	2	79	2	81	2	81	3	80	2
90	1	91	1	91	1	91	2	93	1	92	1	91	1
103	3	102	2	103	3	103	3	104	3	105	3	103	3
110	2	109	1	109	2	111	2	110	1	-	-	110	2
115	1	112	1	112	1	115	1	112	1	113	1	114	1
123	1	126	1	124	1	129	1	131	2	131	1	127	1
139	1	133	1	135	1	137	1	141	1	140	1	138	1
154	1	-	-	151	1	151	1	153	1	153	1	152	1
161	1	164	1	166	1	161	1	162	1	167	1	164	1
169	2	170	1	171	1	172	1	176	1	173	1	172	1

Table 134 The migration distance of the LMW glutenins of SST 822.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	17	1	11	1	-	-	12	1	13	1	14	1
23	1	28	1	20	1	20	1	21	1	23	2	23	1
30	1	33	1	30	1	32	1	35	1	33	1	32	1
48	2	41	2	40	1	40	2	46	3	45	2	43	2
54	4	54	3	56	4	50	4	56	5	58	4	55	4
86	5	86	5	88	5	90	2	86	1	87	1	87	6
97	2	-	-	-	-	94	2	98	2	97	1	97	2
-	-	103	1	108	1	104	1	104	1	105	2	105	1
121	3	-	-	-	-	122	3	120	3	124	2	122	3
131	2	131	3	132	3	-	-	135	2	133	3	132	3
150	2	142	2	140	2	150	1	151	1	147	2	147	2
177	1	178	1	171	2	172	1	174	1	177	1	175	1
190	1	-	-	183	2	183	2	187	1	186	1	186	1

Table 135 The migration distance of the LMW glutenins of SST 825.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
12	1	11	1	13	1	12	1	13	2	10	1	12	1
	-	17		19	1	16	1	17	1	15		17	1
23	1	21	1	22	1	22	1	29	1	20	1	27	1
33	1	34	1	30	1	30	1	32	1	35	1	32	1
57	4	57	5	56	5	50	5	55	5	56	5	55	5
68	3	68	5	68	3	65	3	67	3	67	3	67	3
84	2	83	2			82	3	86	2	88	2	85	2
90	4	92	4	93	5	96	1	95	1	99	1	94	6
104	2	104	2	103	3	102	2	107	2	105	1	104	2
112	2	114	1	112	2	113	2	117	3	113	2	114	2
134	3	133	3	134	4	131	2	134	3	134	3	133	3
161	4	163	5	162	5	160	4	161	4	160	4	161	4
180	1	182	1	183	3	182	1	182	1	183	1	182	1

Table 136 The migration distances of the LMW glutenins of SST 936.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
26	1	26	1	26	1	24	1	24	2	27	1	26	1
31	1	33	1	34	1	30	1	34	1	35	1	33	1
34	1	37	1	37	1	38	1	38	1	38	1	37	1
50	5	49	5	50	5	46	4	47	5	50	5	49	5
66	5	66	5	65	5	60	5	61	5	62	5	63	5
73	5	73	5	74	5	73	5	69	5	70	5	72	5
93	2	95	3	95	3	93	4	93	3	93	3	94	3
107	5	107	5	108	5	107	5	106	5	109	5	107	5
130	1	131	1			133	1	134	1	132	1	132	1
140	2	142	1	139	2	139	1	140	1			140	1
147	2	146	1	148	2	151	2	149	2	149	1	148	2
154	1	156	2			158	2	155	2	155	2	156	2
163	1	160	1	160	1	162	1	163	1	162	1	162	1
166	1	167	1	167	1	169	1	169	1	165	1	167	1

Table 137 The migration distances of the LMW glutenins of SST 966.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
27	1	26	2	26	1	27	1	25	1	28	1	26	1
	-	35	1	35	1	34	1	33	1	33	1	34	1
52	5	52	5	52	5	50	5	51	5	50	5	51	5
66	5	67	5	67	5	64	5	65	5	64	5	66	5
75	5	74	5	74	5	72	5	72	5	72	5	73	5
95	3	95	3	95	3	93	3	93	4	94	3	94	3
108	5	108	5	108	4	109	5	109	5	109	5	109	5
116	3	116	3	116	3	118	4	118	3	118	3	117	3
124	1	124	1	124	1			128	1	129	1	126	1
145	1	145	1	146	1	148	1	148	2	147	2	147	1
154	1	152	1	151	1	154	2	153	1	152	2	153	1
166	1	161	1	166	1	168	1	169	1	168	1	166	1

Table 138 The migration distance of the LMW glutenins of SST 972.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	10	1	15	1	14	1	13	1	12	1	13	1
25	5	20	5	25	5	27	1	23	5	21	5	24	5
38	1	37	1	37	1	40	4	39	1	40	1	39	1
56	4	58	3	57	3	55	3	60	4	58	3	57	3
79	1	75	1	76	1	79	1	79	1	75	1	77	1
84	1	81	1	82	1	82	1	83	1	80	1	82	1
100	2	105	2	104	2	102	1	102	2	100	3	102	2
114	5			117	5	115	4	116	5	115	5	115	5
140	1	141	1	144	1	140	1	141	1	142	1	141	1
150	1	150	1	149	1	152	1	149	1	150	1	150	1
161	1	164	1	160	1	163	2	161	1	163	2	162	1
172	1	172	1	175	1	170	2	170	1	174	1	172	1
181	1	180	1	182	1	181	1	180	1	182	1	181	1
192	1	192	1	190	1	191	1	194	1	195	1	192	1

Table 139 The migration distance of the LMW glutenins of Stirling.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
22	4	10	1	9	1	10	1	7	1	9	1	9	1
35	1	22	3	21	5	28	1	27	5	23	5	24	5
50	1	33	1	36	1	33	1	37	1	36	1	35	1
71	1	55	2	50	1	52	1	51	1	50	1	51	1
80	1	73	1	71	1	73	1	-	-	75	1	73	1
100	1	84	1	78	1	-	-	80	1	81	1	81	1
105	1	99	1	99	1	99	3	98	1	95	2	98	1
119	5	102	1	100	1	-	-	102	1	103	1	102	1
-	-	116	5	116	5	111	5	115	5	116	3	116	5
135	2	129	1	129	1	127	1	122	1	125	3	126	1
155	1	134	1	136	1	139	1	137	1	140	1	137	1
165	1	-	-	156	1	154	1	154	1	154	1	155	1
172	1	161	1	162	2	163	1	162	1	161	1	162	1
181	1	172	1	169	2	172	1	172	1	-	-	171	1
196	1	181	1	180	1	180	1	180	1	180	1	180	1
-	-	194	1	194	1	193	1	193	1	195	1	194	1

Table 140 The migration distance of the LMW glutenins of T4.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	11	1	9	1	7	1	9	1	9	1	9	1
14	1	16	1	15	1	16	1	17	1	18	1	16	1
30	4	34	5	35	5	35	4	30	4	30	4	32	4
40	1	-	-	45	1	43	1	42	1	40	1	42	1
50	1	51	1	55	1	55	5	50	1	-	-	52	1
62	4	64	4	68	5	66	5	63	5	66	5	65	5
85	1	82	1	84	1	81	1	82	1	81	1	83	1
98	2	99	1	94	2	95	1	96	2	99	2	97	2
107	2	104	1	107	2	101	1	107	2	107	2	106	2
112	2	110	3	115	3	116	3	115	3	111	2	113	3
122	5	125	5	127	5	127	1	130	5	-	-	126	5
146	1	144	1	140	1	144	1	144	1	144	1	144	1
163	2	163	1	162	1	161	1	163	1	164	1	163	1
171	1	172	2	174	2	170	1	173	1	175	1	173	1
187	1	188	1	183	2	185	1	189	1	-	-	186	1
196	1	194	1	197	1	194	1	196	1	-	-	195	1

Table 141 The migration distances of the LMW glutenins of Tugela.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
26	1	27	1	28	1	26	1	27	1	27	1	27	1
45	3	41	3	42	3	42	4	43	3	43	4	43	3
51	5	51	5	51	5	51	5	54	5	54	5	52	5
63	4	63	4	63	4	65	5	66	4	66	4	64	4
76	5	77	5	76	5	77	5	79	5	79	5	77	5
93	4	94	4	94	3	94	3	95	3	94	3	94	3
103	4	103	4	-	-	104	5	103	4	104	5	103	4
109	5	109	5	107	5	108	5	108	5	109	5	108	5
119	4	118	4	117	4	117	4	117	4	117	4	118	4
128	1	127	1	125	1	128	1	128	1	129	1	128	1
145	3	-	-	143	2	140	3	140	2	141	2	142	2
150	4	149	3	149	2	145	3	146	2	146	3	148	3
173	2	173	1	172	1	170	1	-	-	170	1	172	1

Table 142 The migration distances of the LMW glutenins of Tugela DN.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
25	1	25	1	24	3	28	1	29	1	29	1	27	1
36	2	36	2	35	2	39	2	39	2	39	2	37	2
46	4	48	4	47	4	44	4	44	4	44	3	46	4
54	4	56	3	56	4	51	5	52	4	51	4	53	4
59	3	-	-	-	-	60	4	61	4	61	4	60	4
71	4	72	5	70	5	70	5	75	4	74	5	72	5
93	3	92	3	90	4	90	3	92	3	92	3	92	3
96	3	-	-	96	4	95	3	96	3	97	3	96	3
100	5	103	5	105	5	102	5	104	5	106	5	103	5
112	1	-	-	114	3	111	1	114	1	114	1	113	1
122	2	122	3	124	2	121	2	-	-	124	-	123	2
124	2	127	-	127	2	127	1	126	2	-	-	126	2
140	1	-	-	139	1	143	1	143	1	144	1	142	1
146	1	146	1	149	1	148	1	150	1	150	1	148	1
154	1	154	1	153	1	-	-	154	1	158	1	155	1
166	1	167	1	163	1	163	1	164	1	166	1	165	1
173	1	174	1	175	1	170	1	170	1	170	1	172	1

Table 143 The migration distances of the LMW glutenins of Tugela fast-growing.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
27	1	29	1	29	1	27	1	27	1	29	1	28	1
35	1	-	-	36	1	35	1	-	-	36	1	36	1
50	5	52	5	52	5	55	5	54	5	55	5	53	5
64	3	64	4	66	3	66	4	66	4	66	4	65	4
71	3	72	4	-	-	75	4	74	4	76	4	74	4
74	3	75	3	74	3	79	3	79	3	79	3	77	3
92	2	92	3	93	3	94	3	93	3	94	2	93	3
107	5	108	5	109	5	109	5	103	3	109	5	108	5
115	3	116	3	116	3	117	3	117	3	117	3	116	3
140	1	140	1	136	1	140	1	140	2	139	1	139	1
147	1	147	2	144	2	146	2	147	2	146	2	146	2
157	1	158	1	159	1	156	1	159	1	156	1	158	1
167	1	168	1	162	1	165	1	168	1	160	1	165	1

Table 144 The migration distances of the LMW glutenins of Tugela nuut.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rev	I
28	1	29	1	28	1	29	1	27	1	28	1	28	1
43	3	-	-	47	3	48	3	48	3	43	2	45	3
52	5	52	5	54	4	54	5	52	5	52	5	53	5
66	4	66	4	65	4	66	5	65	4	65	4	66	4
79	5	78	4	76	5	79	5	77	5	78	5	78	5
94	3	93	3	93	4	94	3	94	3	93	2	94	3
-	-	105	5	104	5	103	4	102	5	102	5	103	5
108	5	-	-	-	-	108	5	108	5	107	5	108	5
117	3	114	3	114	4	116	3	116	3	115	3	115	3
124	1	123	1	120	3	124	1	124	1	123	1	123	1
146	2	143	2	144	3	146	2	140	2	146	3	144	2
156	1	155	3	155	1	154	1	163	2	152	1	154	1
169	1	168	1	166	1	166	1	-	-	166	1	167	1

Table 145 The migration distance of the LMW glutenins of Turpin 7.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	1	15	1	13	1	15	1	14	1	16	1	14	1
35	5	36	5	36	5	33	5	39	5	40	5	37	5
50	1	55	1	55	1	51	1	52	1	55	1	53	1
71	5	73	5	74	5	71	5	75	5	78	5	74	5
90	1	92	1	92	1	95	1	92	1	92	1	92	1
100	1	101	1	-	-	106	2	100	1	101	1	102	1
106	1	107	1	110	1	110	2	108	1	110	1	109	1
119	2	118	1	120	2	119	2	120	2	117	1	119	2
128	4	130	3	126	3	129	3	130	3	128	1	129	3
150	1	153	1	155	1	151	1	158	1	155	1	154	1
165	1	164	1	169	1	164	1	170	1	170	1	167	1
180	2	180	1	182	1	185	1	180	1	183	1	182	1
193	1	192	1	193	1	193	1	195	1	191	1	193	1

Table 146 The migration distances of the LMW glutenins of Turksikum.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
27	1	28	1	27	1	28	1	30	1	-	-	28	1
31	2	32	2	35	1	33	1	34	1	35	1	34	1
45	2	47	3	47	3	47	4	48	3	46	3	47	3
66	5	68	5	67	5	68	5	69	5	68	5	68	5
78	2	78	2	78	1	78	2	79	3	79	2	78	2
92	3	92	3	92	3	91	3	91	1	92	2	92	3
100	3	100	3	100	4	99	3	101	3	100	3	100	3
109	5	107	3	106	3	108	3	109	3	-	-	108	3
115	3	115	3	115	3	114	2	111	2	113	3	114	3
126	1	129	1	128	1	-	-	132	1	130	1	129	1
138	2	139	2	137	2	139	1	140	2	140	1	139	2
146	2	146	1	147	1	148	1	148	1	149	1	147	1
165	1	168	2	169	1	166	1	165	1	167	1	167	1

Table 147 The migration distance of the LMW glutenins of Verebterde Kenia.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	Rav	I
7	1	6	1	10	1	6	2	-	-	7	1
15	1	12	1	14	1	16	1	14	1	14	1
21	1	19	1	20	1	21	1	24	1	21	1
33	1	32	1	33	1	30	1	33	1	32	1
39	1	39	1	40	1	-	-	36	1	39	1
48	1	46	1	47	1	50	1	47	1	48	1
57	1	57	1	60	1	59	1	60	2	59	1
77	4	76	4	76	5	74	5	76	4	76	4
85	1	86	2	90	1	87	1	90	1	88	1
104	1	104	1	105	1	-	-	103	1	104	1
108	1	107	1	-	-	106	1	106	1	107	1
117	1	115	2	118	2	116	2	114	3	116	2
125	3	129	4	128	2	-	-	130	3	128	3
138	5	137	5	134	2	138	5	139	5	137	5
159	1	156	2	155	1	158	1	155	1	157	1
163	1	168	1	164	1	162	1	165	2	164	1
177	1	174	1	176	1	177	2	178	1	176	1
-	-	182	2	181	1	182	2	181	2	182	2
187	1	185	2	188	1	186	2	185	2	186	2
192	1	190	1	190	1	191	2	195	2	192	1

Appendix B

This Appendix has all the tables of the durum wheat cultivars. Six replications of each cultivar are given (R1 to R6) together with the band intensities (I1 to I6). The last two columns of each cultivar have the average of the migration distances (Rav) and the class of intensity (I).

Table 2.1. The migration distances and band intensities of Aconchi.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	17	1	17	1	10	1	15	1	21	1	16	1
27	1	22	1	26	1	24	4	30	4	36	4	28	6
44	4	42	3	45	4	48	4	41	5	48	5	45	4
58	4	56	4	58	5	62	4	54	4	61	4	58	4
72	5	72	4	73	4	70	1	69	5	77	5	72	5
91	5	91	5	93	5	90	1	95	1	94	2/3	92	6
100	1	99	1	101	1	98	2	104	3	101	1	101	2
113	3	112	3	114	4	110	3	117	3	111	3	113	3
129	4	131	3	130	4	121	3	128	2	124	3	127	3
148	4	146	3	148	4	145	1	140	1	147	1	146	6
159	4	158	3	158	4	156	2	162	3	-	-	159	3
171	2	172	1	172	1	171	1	-	-	169	2	171	1
193	1	196	3	190	2	191	1	190	1	191	1	192	1

Table 2.2. The migration distances and band intensities of Altar.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
27	1	29	1	-	-	26	1	25	1	17	1	25	1
43	4	46	4	46	3	44	4	40	4	46	5	44	4
54	5	58	5	59	5	58	5	53	5	60	5	57	5
67	4	70	4	71	4	73	5	66	4	70	5	70	4
82	5	86	5	87	5	87	5	84	5	-	-	85	5
91	1	93	1	93	1	99	1	97	1	90	1	94	1
100	2	103	2	104	2	-	-	108	3	102	2	103	2
106	2	109	2	109	1	114	3	110	3	-	-	110	2
118	3	120	3	120	3	-	-	124	4	120	4	120	3
129	3	132	3	133	2	131	5	-	-	132	3	131	3
140	2	143	2	143	2	147	2	140	3	145	3	143	2
152	1	155	1	156	1	159	4	159	1	153	1	156	1
176	2	178	2	179	2	172	2	177	1	173	1	176	2
192	1	193	1	195	1	192	1	193	1	194	1	193	1

Table 2.3. The migration distances and band intensities of Fargo.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
31	1	30	3	-	-	33	3	33	3	33	3	32	3
46	4	44	4	40	1	41	5	43	1	44	2	43	6
58	5	57	2	52	5	58	5	58	5	57	5	57	5
70	4	71	5	70	5	67	4	66	4	65	4	68	4
86	5	81	5	78	4	82	2	81	2	79	2	81	6
94	1	93	2	102	4	92	4	94	1	94	2	95	6
104	3	109	3	-	-	103	4	108	2	106	3	106	3
-	-	-	-	116	3	119	4	118	3	115	3	117	3
120	3	120	4	124	4	122	3	127	3	127	3	123	3
133	3	133	3	136	3	134	4	138	1	133	1	135	3
144	2/3	145	3	143	2	144	1	145	1	-	-	144	2
156	1	160	1	154	1	-	-	156	1	155	1	156	1
180	3	179	3	178	2	181	1	175	1	179	2	179	2
195	1	194	1	194	1	198	1	195	1	196	2	195	1

Table 2.4. The migration distances and band intensities of Goeie Hoop.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	17	3	16	1	20	1	21	1	20	1	19	1
33	3	32	3	31	4	38	4	36	4	34	4	34	4
57	5	56	5	53	5	51	5	48	5	59	5	54	5
65	5	69	5	66	5	65	4	62	5	-	-	65	5
79	2	80	1	-	-	79	4	76	5	73	5	77	6
94	3	89	4	86	5	87	4	94	4	92	4	90	4
108	4	103	3	101	3	103	2	-	-	-	-	104	3
115	4	117	3	114	5	116	4	111	4	111	4	114	4
128	4	126	3	125	4	128	1	125	4	122	4	126	4
-	-	135	2	131	3	141	3	137	4	135	3	136	3
143	3	141	3	140	2	145	2	140	1	145	1	142	2
163	2	163	4	162	1	167	1	167	1	163	1	164	1
187	1	179	2	189	3	188	1	186	1	185	1	186	1

Table 2.5. The migration distances and band intensities of Kronos.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
20	1	21	1	20	1	26	1	24	5	22	2	22	1
34	5	35	4	34	4	36	5	32	5	34	5	34	5
45	5	47	5	46	5	50	5	48	5	50	5	48	5
59	4	60	4	60	4	62	5	59	4	60	4	60	4
73	5	76	5	74	4	-	-	69	1	72	2	73	6
81	2	84	3	82	3	82	4	81	2	83	4	82	3
98	3	99	3	97	3	102	3	95	2	95	4	98	3
109	5	112	5	109	4	110	4	107	3	105	4	109	4
119	4	121	4	119	4	122	4	119	3	122	5	120	4
132	4	134	4	133	4	136	1	133	4	-	-	134	4
146	2	148	1	147	2	148	1	145	1	144	1	146	1
168	2	168	3	166	2	163	1	167	2	168	2	167	2
186	1	183	1	182	1	186	1	183	2	181	1	184	1
194	1	197	1	196	1	189	1	190	2	190	1	193	1

Table 2.6. The migration distances and band intensities of Mexicale 75.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	17	2	14	1	16	1	10	1	10	2	14	1
27	5	33	4	26	4	32	3	26	3	29	4	29	4
35	5	41	5	38	4	40	5	38	5	42	5	39	5
50	5	56	4	50	5	56	4	50	5	55	5	83	5
71	5	71	5	74	5	71	5	70	5	72	5	72	5
82	2	79	1	85	1	79	1	81	2	80	1	81	1
96	2	93	4	97	5	95	1	99	2	90	3	95	6
106	2	111	3	110	4	105	2	109	2	106	2	108	2
123	2	129	3	122	3	120	2	122	2	122	2	123	2
-	-	135	2	138	3	139	1	132	1	136	2	136	2
155	2	155	1	159	1	162	2	153	3	160	2	157	2
170	1	164	3	168	2/3	170	1	170	2	-	-	170	2
175	1	177	1	182	2	180	1	178	1	182	2	179	1
187	2	188	1	188	1	-	-	188	1	-	-	188	1

Table 2.7. The migration distances and band intensities of Moni.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	3	12	2	13	3	18	2	19	3	17	3	15	3
34	4	36	4	36	4	38	5	38	5	38	4	37	4
44	5	46	5	46	5	48	5	47	5	48	5	47	5
58	5	61	5	62	5	62	5	62	5	62	5	61	5
76	4	78	5	78	5	77	5	76	4	77	5	77	5
95	3	95	4	96	4	99	5	100	5	98	4	97	4
110	3	113	3	111	3	108	4	110	4	109	3	110	3
122	4	-	-	124	3	123	4	121	4	120	4	122	4
130	3	131	3	132	3	135	4	137	4	138	3	134	3
142	3	144	3	144	3	141	3	143	4	143	4	143	3
169	2	170	1	172	2	170	3	170	2	171	2	170	2
183	2	187	1	187	2	186	2	186	1	184	2	186	2

Table 2.8. The migration distances and band intensities of Nordum.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	3	14	1	18	1	12	1	13	1	15	1	15	1
37	4	36	3	31	4	34	4	32	4	34	5	34	4
47	5	48	1	45	2	47	2	45	2	46	2	46	2
61	5	61	5	63	5	66	5	66	5	64	5	64	5
77	5	69	4	78	5	75	5	75	5	73	5	75	5
87	2	85	4	90	5	85	4	85	4	86	4	86	4
98	5	98	4	107	4	102	3	102	4	103	4	102	4
120	5	113	4	120	3	115	4	115	4	116	5	117	4
127	5	130	3	129	4	129	4	130	4	129	4	129	4
142	5	141	3	149	4	143	4	143	4	142	4	143	4
170	2	172	2	173	1	174	2	174	3	175	2	173	2
185	2	186	2	189	2	189	2	191	1	194	1	189	2

Table 2.9. The migration distances and band intensities of Orania.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
38	3	40	3	41	4	33	4	33	4	31	4	36	4
51	5	50	5	50	5	45	5	46	5	45	5	48	5
65	4	69	4	-	-	64	5	61	4	63	5	64	4
74	1	76	1	71	5	77	4	76	4	75	3	75	6
89	3	93	4	87	5	90	4	89	3	88	4	89	4
105	1	109	3	109	5	107	3	107	3	105	3	107	3
118	4	123	5	123	5	121	3	121	4	125	3	122	4
131	3	137	4	139	3	138	3	134	3	137	4	136	3
144	3	149	4	150	5	151	3	148	3	149	3	149	3
-	-	160	1	155	3	157	2	157	1	155	3	157	2
-	-	166	1	166	1	166	1	166	1	166	1	166	1
181	1	179	1	183	2	181	1	179	1	178	1	180	1

Table 2.10. The migration distances and band intensities of USD 9302.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	18	1	-	-	19	1	19	1	17	1	18	1
33	4	32	4	31	5	42	5	42	5	39	5	37	5
44	5	45	5	42	5	50	5	49	5	51	5	47	5
61	4	61	5	63	5	70	5	70	5	67	5	65	5
75	5	76	5	77	5	77	2	-	-	73	5	76	5
87	2	88	4	87	5	87	5	87	5	86	5	87	5
100	3	100	4	101	4	95	3	95	4	93	4	97	4
121	4	118	4	117	3	111	3	111	4	110	4	115	4
		121	4	128	3	124	5	124	5	122	5	124	5
132	3	134	4	136	4	138	4	139	5	137	4	136	4
145	4	146	4	149	3	150	4	150	5	149	4	148	4
155	1	156	2	156	2	160	1	161	2	160	2	158	2
190	2	188	2	186	3	185	2	184	2	183	3	186	2

Table 2.11. The migration distances and band intensities of USD 9503.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	1	16	1	13	1	-	-	11	2	13	2	12	1
36	4	35	5	31	4	32	5	35	5	36	5	34	5
51	5	47	5	44	5	42	5	46	5	46	5	46	5
63	4	60	4	57	4	60	5	60	5	61	4	60	4
82	5	79	5	75	5	76	5	78	5	78	5	78	5
91	1	87	4	84	1	84	1	87	1	-	-	87	1
101	3	98	4	99	3	99	3	100	2	100	3	100	3
120	3	116	3	112	2	117	1	116	1	116	2	116	2
134	4	133	4	138	3	136	2	134	3	134	3	135	3
146	4	144	3	149	3	151	2	148	3	147	2	148	6
157	1	155	1	-	-	157	1	-	-	155	1	156	1
178	1	173	1	175	1	174	2	172	1	171	1	174	1

Table 2.12. The migration distances and band intensities of USD 9509.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
12	1	10	1	11	1	11	1	10	1	10	1	11	1
32	3	36	4	36	4	35	5	28	4	32	4	33	4
47	5	47	5	49	5	50	4	44	5	44	5	47	5
61	3	60	4	63	4	65	5	62	4	63	4	62	4
79	5	78	5	79	5	75	1	71	1	73	2	76	6
88	2	88	3	91	2	86	2	-	-	91	2	89	2
104	3	106	3	107	4	103	3	104	2	104	4	105	3
120	3	118	3	121	3	118	3	-	-	118	4	119	3
132	4	130	3	131	3	129	2	125	3	125	3	129	3
145	4	146	3	147	3	-	-	142	3	145	4	145	3
155	2	156	2	156	2	160	2	161	1	-	-	158	2
173	2	176	1	175	1	-	-	178	1	180	1	176	1
185	2	187	2	188	2	186	1	-	-	189	2	187	2
191	1	197	1	195	1	-	-	191	1	192	3	193	1

Table 2.13. The migration distances and band intensities of USD 9511.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
10	1	8	2	11	2	14	1	17	2	15	2	13	2
34	4	29	4	30	4	36	4	37	4	36	4	34	4
42	5	40	5	39	5	51	5	50	5	49	5	45	5
63	5	59	5	60	5	64	4	65	5	67	5	63	5
79	5	74	5	73	5	80	5	81	5	79	5	78	5
98	2	97	4	96	4	92	3	91	1	-	-	95	6
105	2	108	2	106	2	108	3	106	2	106	3	107	2
122	2	120	2	129	4	120	3	123	2	123	2	123	2
134	4	135	5	132	4	138	4	131	4	134	2	134	4
154	4	154	5	150	4	150	3	153	4	155	4	153	4
177	1	177	1	175	1	178	2	180	1	178	1	178	1
190	2	188	1	194	1	197	1	192	2	192	1	192	1

Table 2.14. The migration distances and band intensities of USD 9607.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	2	10	1	10	1	5	2	9	1	10	2	9	1
27	3	30	2	32	3	27	4	30	3	31	3	30	3
47	5	50	5	49	4	40	5	43	5	43	5	45	5
63	5	60	5	60	5	55	5	59	3	60	4	60	5
81	5	74	4	73	4	70	5	73	5	75	5	74	5
-	-	89	5	91	5	94	4	94	4	97	3	93	4
103	1	-	-	102	1	103	2	104	1	104	1	103	1
115	2	111	3	111	3	111	2	120	3	120	3	115	3
131	2	130	3	130	4	132	3	134	3	134	3	132	3
139	2	144	3	143	3	146	3	145	3	149	4	144	3
-	-	172	1	170	1	161	1	167	1	169	2	168	1
179	2	180	1	183	1	182	2	187	1	183	1	182	1
191	1	189	1	191	1	195	1	197	1	190	3	192	1

Table 2.15. The migration distances and band intensities of USD 9608.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
27	1	31	4	30	2	30	2	28	2	30	2	29	2
44	5	49	5	50	5	50	5	49	5	48	5	48	5
63	5	65	5	62	3	60	5	58	5	59	5	61	5
76	4	-	-	70	3	74	5	73	4	72	4	73	4
89	1	81	5	81	5	89	5	88	5	89	5	86	5
104	4	103	4	102	3	102	4	97	4	-	-	102	4
116	3	119	3	110	2	111	4	110	3	111	3	113	3
128	4	126	4	126	3	131	3	131	3	129	3	129	3
142	4	136	2	135	3	142	3	139	3	140	3	139	3
150	4	150	5	149	3	154	4	154	4	151	4	151	4
164	1	160	1	159	1	-	-	169	1	159	1	162	1
181	1	184	1	180	1	180	1	180	2	181	1	181	1
188	4	193	1	195	1	191	1	192	1	188	1	191	1

Table 2.16. The migration distances and band intensities of USD 9609.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
20	2	21	1	20	2	15	2	15	2	12	2	17	2
49	5	48	4	47	4	50	5	50	5	51	5	49	5
72	4	71	4	72	4	67	4	66	3	71	3	70	4
89	5	88	5	89	5	82	5	85	5	85	5	86	5
99	1	98	1	98	1	100	1	101	4	96	1	99	1
112	3	110	3	110	3	113	2	115	2	113	3	112	3
125	2	120	2	119	2	120	2	120	2	123	2	121	2
134	3	134	4	132	4	138	2	139	4	139	4	136	4
159	1	156	1	156	2	153	1	155	2	158	1	156	1
167	1	159	1	168	1	161	1	165	1	163	1	164	1
178	1	177	1	174	1	177	2	181	1	181	1	178	1
188	2	186	2	185	3	190	1	191	2	188	2	188	2

Table 2.17. The migration distances and band intensities of USD 9610.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	2	16	1	20	2	20	2	20	2	-	-	18	2
42	4	38	3	41	4	38	4	39	5	35	4	39	4
52	5	52	5	53	5	50	5	51	5	60	4	53	5
71	4	69	3	71	4	67	4	63	5	70	4	69	4
86	5	85	5	85	5	78	3	89	1	84	1	85	6
105	4	105	3	108	3	105	4	101	4	107	4	105	4
113	4	114	1	114	4	118	4	116	4	-	-	115	4
123	3	122	1	122	1	126	5	121	4	122	5	123	6
-	-	135	2	132	3	135	3	129	3	130	3	132	3
140	4	141	4	141	4	143	4	140	3	142	4	141	4
164	1	164	1	162	4	-	-	165	1	162	1	163	1
-	-	170	1	171	1	179	2	176	1	172	2	174	1
182	1	181	2	185	1	188	1	189	1	188	2	186	1
191	2	191	1	195	2	193	1	192	1	193	1	193	1

Table 2.18. The migration distances and band intensities of USD 9612.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
20	3	28	3	29	2	30	3	28	3	28	4	27	3
44	4	47	4	47	4	46	4	43	3	43	3	45	4
67	5	62	5	63	5	62	5	61	5	64	5	63	5
82	4	87	5	88	4	82	4	82	4	84	3	84	4
102	3	-	-	100	1	92	1	99	2	102	2	99	2
-	-	108	4	110	5	107	4	109	4	110	3	109	4
115	1	-	-	-	-	115	1	116	1	118	2	116	1
132	1	130	5	129	5	131	4	134	5	135	5	132	5
-	-	138	1	139	1	141	1	143	1	145	2	141	1
146	5	148	4	150	5	149	1	150	2	150	2	149	6
-	-	164	1	166	1	160	1	160	1	160	1	162	1
179	1	179	1	176	1	174	2	173	2	172	1	176	1
195	1	194	1	195	1	191	1	194	1	192	1	194	1

Table 2.19. The migration distances and band intensities of USD 9614.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
18	3	-	-	20	1	17	1	15	1	15	1	17	1
33	4	31	4	34	5	30	4	31	4	30	2	32	4
43	2	46	3	45	4	49	4	50	4	51	4	47	4
64	5	66	5	69	5	60	5	63	5	62	5	64	5
-	-	-	-	76	4	75	4	77	4	76	3	76	4
85	3	86	5	90	4	90	5	90	5	92	5	89	4
119	4	118	3	115	1	111	4	116	4	114	4	116	4
134	4	134	3	137	3	130	4	136	3	137	3	135	3
150	3	155	2	151	1	152	5	155	5	154	4	153	6
161	1	-	-	163	1	162	1	165	2	164	2	163	1
172	1	177	1	170	1	176	1	-	-	169	1	173	1
189	1	184	1	184	1	187	1	180	1	180	1	184	1
195	1	194	1	194	1	194	1	191	1	196	1	194	1

Table 2.20. The migration distances and band intensities of USD 9701.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
23	3	24	1	20	1	23	3	25	3	26	3	24	3
-	-	30	1	30	2	32	5	34	5	39	5	33	6
50	5	48	4	50	4	50	4	-	-	50	3	50	4
53	5	56	5	58	5	-	-	53	4	55	5	55	5
67	4	70	4	72	5	67	5	69	5	71	5	69	5
82	5	84	5	87	5	90	3	92	5	90	3	88	5
-	-	97	1	95	1	99	1	102	1	100	1	99	1
102	3	106	3	108	3	107	1	109	3	-	-	106	3
118	3	118	3	-	-	121	3	-	-	114	1	118	3
123	3	123	3	123	2	127	2	124	3	122	3	124	3
143	3	144	2	148	3	145	3	147	3	146	2	146	3
167	1	167	1	161	1	169	1	-	-	162	1	165	1
187	1	183	1	189	1	180	1	181	2	188	2	185	1
197	2	191	1	194	1	194	1	194	1	194	1	194	1

Table 2.21. The migration distances and band intensities of USD 9702.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
7	1	9	1	11	1	9	1	7	1	8	1	9	1
27	3	28	3	32	3	28	3	30	2	29	2	29	3
52	3	53	5	42	5	49	5	50	5	50	4	49	5
57	5	58	3	60	4	57	5	59	5	62	5	59	5
74	5	74	5	78	5	72	5	74	5	73	5	74	5
82	1	83	1	80	1	87	5	88	5	88	5	85	6
96	2	97	3	99	2	97	1	-	-	100	2	98	2
103	2	104	1	108	1	109	1	109	1	108	2	107	1
125	3	122	3	127	3	122	2	129	5	125	3	125	3
129	3	132	3	135	3	131	3	137	1	135	1	133	3
145	4	147	4	150	4	149	3	149	5	147	4	148	4
156	1	157	1	159	1	-	-	164	1	155	1	158	1
176	1	176	1	175	1	172	1	172	1	171	1	174	1
189	2	190	1	189	2	190	1	192	1	185	1	189	1

Table 2.22. The migration distances and band intensities of USD 9703.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	8	4	10	1	8	1	8	1	12	1	10	1
33	1	26	2	27	1	29	2	30	3	29	2	29	2
49	5	52	5	45	4	45	5	45	5	42	5	46	5
59	5	60	5	58	5	58	3	58	5	59	3	59	5
72	5	-	-	71	4	79	5	79	5	75	5	75	5
99	1	93	2	90	2	-	-	99	2	97	3	96	2
107	2	107	4	105	4	100	3	107	1	105	1	105	6
127	3	121	3	123	3	126	3	125	3	123	4	124	3
135	1	128	3	134	2	134	1	132	1	133	1	133	1
147	1	143	2	143	2	150	4	150	4	148	5	147	6
164	1	-	-	164	1	166	1	166	1	167	1	165	1
177	1	177	1	181	1	178	1	179	1	181	1	179	1
-	-	193	1	195	1	190	2	190	2	193	2	192	2

Table 2.23. The migration distances and band intensities of USD 9704.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
-	-	14	1	10	1	16	1	15	1	11	1	13	1
25	2	26	2	23	2	32	3	30	2	26	4	27	2
43	4	44	4	44	5	42	5	44	5	38	5	43	5
55	5	56	5	55	5	56	3	58	5	53	4	56	5
69	4	70	4	68	4	61	3	70	5	71	4	68	4
84	5	85	5	83	5	80	5	84	1	-	-	83	5
-	-	-	-	100	3	98	3	96	2	93	3	97	3
104	3	105	4	102	3	100	3	104	3	108	3	104	3
-	-	116	2	114	1	109	1	114	1	-	-	113	1
126	2	123	3	122	3	125	3	121	2	126	3	124	3
135	2	134	3	132	3	132	2	129	2	135	2	133	2
145	2	145	2	142	3	148	2	145	2	148	1	146	2
168	1	169	1	167	1	164	1	166	1	-	-	167	1
177	2	179	2	177	1	176	2	177	1	175	2	177	2
192	2	189	1	191	1	183	1	186	1	187	1	188	1
197	2	194	1	-	-	191	2	191	1	197	2	194	2

Table 2.24. The migration distances and band intensities of USD 9705.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
11	1	11	1	-	-	10	1	11	1	8	1	10	1
20	1	20	1	22	1	26	1	25	2	22	1	23	1
43	5	40	4	38	4	43	4	44	5	45	4	42	4
58	5	50	5	52	5	54	5	56	5	55	5	54	5
-	-	63	4	66	4	66	4	69	4	70	4	67	1
76	5	82	5	84	5	81	5	84	5	84	5	82	5
89	2	93	1	93	2	95	1	-	-	94	2	93	2
99	3	103	3	107	2	104	3	104	4	107	3	104	3
115	3	118	3	121	4	119	3	120	3	123	4	119	3
132	4	134	3	136	3	129	2	133	3	133	3	133	3
141	4	146	3	148	3	139	3	143	2	145	3	144	3
155	2	159	1	160	2	151	1	152	1	154	1	155	1
168	1	168	1	170	1	166	1	170	1	169	1	169	1
-	-	-	-	175	1	178	1	177	1	172	1	176	1
180	2	183	1	186	2	185	1	181	1	181	1	183	1
191	1	186	1	196	1	193	1	196	1	-	-	192	1

Table 2.25. The migration distances and band intensities of USD 9706.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	10	1	16	1	12	1	12	1	13	1	13	1
25	1	18	1	-	-	25	1	24	1	20	1	22	1
51	5	49	5	49	5	57	5	57	5	59	5	54	5
74	4	67	5	72	5	73	4	71	4	75	4	72	4
83	5	85	5	83	5	87	5	85	5	87	5	85	5
93	3	92	2	91	2	96	2	96	2	-	-	94	2
109	3	105	3	105	3	111	4	111	3	105	3	108	3
122	5	122	3	120	5	123	5	125	4	120	5	122	5
137	3	138	3	136	4	134	3	136	3	139	2	137	3
148	3	148	3	146	3	146	3	146	3	150	1	147	3
160	1	161	1	158	1	165	1	-	-	169	3	162	1
185	2	182	2	182	3	183	2	184	2	186	1	184	2
195	1	188	1	192	1	195	1	190	1	194	1	192	1

Table 2.26. The migration distances and band intensities of USD 9707.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	1	15	1	20	1	18	1	14	1	17	1	16	1
31	4	31	3	36	4	37	1	34	1	37	1	34	6
44	4	44	5	49	5	51	4	43	4	45	4	46	4
59	4	59	4	63	5	62	4	64	4	61	3	61	4
78	5	79	5	82	5	75	4	75	5	76	5	78	5
88	1	89	1	90	1	83	3	81	1	83	2	86	1
100	5	101	4	103	4	98	5	105	5	107	5	102	5
116	4	115	4	118	4	115	4	113	1	116	4	116	4
131	3	133	3	134	3	126	4	131	3	134	4	132	3
143	3	144	3	145	2	143	4	147	3	151	3	146	3
155	1	157	2	157	2	160	2	159	2	160	2	158	2
171	1	168	2	171	1	170	2	165	2	165	2	168	2
178	3	180	2	181	2	-	-	183	2	185	2	181	2
196	1	197	1	191	1	192	1	-	-	191	1	193	1

Table 2.27. The migration distances and band intensities of USD 9708.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	16	1	15	1	11	1	13	1	-	-	14	1
35	2	32	3	33	2	36	1	32	2	-	-	34	2
48	5	49	4	47	4	45	2	47	1	46	1	47	6
63	5	63	4	62	4	61	4	61	4	60	4	62	4
83	5	84	5	82	5	79	5	80	5	79	5	81	5
91	2	90	2	89	2	94	5	95	4	94	4	92	6
104	4	104	5	103	4	109	5	111	5	109	5	107	5
119	3	118	3	119	3	116	4	117	3	116	1	118	3
135	3	135	2	134	3	137	4	135	3	133	3	135	3
146	2	145	2	146	2	-	-	150	2	152	3	148	2
159	3	158	3	157	2	157	3	158	3	156	4	158	3
185	2	180	3	185	2	187	3	187	3	187	3	185	3
192	1	190	1	193	1	194	1	-	-	-	-	192	1

Table 2.28. The migration distances and band intensities of USD 9709

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
-	-	16	1	14	1	10	1	11	1	14	1	13	1
23	1	24	1	28	1	27	4	27	4	29	4	26	6
44	1	46	1	42	1	45	5	41	5	45	5	44	6
58	5	58	4	57	4	61	5	58	5	60	5	59	5
78	5	77	5	76	5	80	5	76	5	79	5	78	5
94	4	93	3	92	3	97	3	95	2	87	3	93	3
109	5	108	5	107	5	102	4	104	1	100	5	105	5
116	2	116	2	114	2	116	4	113	2	113	4	115	2
126	4	126	4	123	5	125	4	124	2	120	4	124	4
134	3	134	4	134	3	134	3	132	3	132	4	133	3
150	4	152	3	150	4	146	3	146	3	144	3	148	3
162	3	162	3	-	-	161	1	-	-	164	3	162	3
168	3	173	1	-	-	170	1	170	1	169	1	170	1
186	3	186	2	183	2	180	2	188	2	189	1	185	2
192	1	190	1	192	1	190	1	-	-	191	1	191	1
199	1	196	1	-	-	196	2	-	-	195	1	197	1

Table 2.29. The migration distances and band intensities of USD 9710.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	1	7	1	11	1	10	1	7	1	5	1	8	1
25	5	20	5	28	5	26	1	23	1	23	1	24	6
37	5	31	5	40	5	39	1	36	2	36	1	37	6
54	5	51	5	55	5	53	5	50	5	49	3	52	5
		60	5			61	4	58	4	57	4	59	4
71	5	73	1	72	5	73	5	71	5	69	5	72	5
93	4	85	3	90	4	89	4	86	4	84	4	88	4
105	4	101	4			105	5	101	4	99	5	102	4
109	3	117	3	112	3	111	1	116	4	115	3	113	3
127	3	128	4	129	3	120	4	130	4	125	4	127	4
143	2	139	4	140	3	148	4	147	4	143	4	143	4
169	3	162	3			163	2	160	3	158	3	162	3
178	1	179	2	177	2	172	1	178	2	175	2	177	2
187	2	188	2			181	2	191	1	188	1	187	2
191	2	194	2	192	1	191	1	194	1	192	1	192	1

Appendix C

This Appendix has all the tables of the monosomic wheat cultivars. Six replications of each cultivar are given (R1 to R6) together with the band intensities (I1 to I6). The last two columns of each cultivar have the average of the migration distances (Rav) and the class of intensity (I). As discussed earlier, a class of one means a very light band and a class of five is a very dark band.

Table 1 The migration distances and band intensities of the LMW glutenins of Chinese Spring.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	1	10	1	13	2	8	1	8	1	9	1	10	1
25	1	26	1	26	1	25	1	26	1	28	1	26	1
40	5	45	5	47	4	45	4	44	4	43	4	44	4
56	4	55	4	-	-	52	5	52	5	51	5	53	5
71	5	72	2	70	5	71	5	70	5	71	5	71	5
80	2	85	1	84	2	81	2	80	3	79	2	82	2
92	1	96	1	91	1	97	1	98	1	96	1	95	1
110	2	113	2	110	4	110	2	109	2	109	2	110	2
125	3	121	2	126	3	125	3	121	3	126	3	124	3
146	1	140	2	146	2	148	5	147	4	146	4	146	6
159	1	159	1	160	3	161	1	158	1	159	1	159	1
181	1	185	1	181	1	182	1	-	-	180	1	182	1
186	1	189	1	188	2	188	2	186	2	186	2	187	2
195	1	194	1	190	1	191	1	192	1	192	1	192	1

Table 2. The migration distances and band intensities of the LMW glutenins of Chinese Spring monosomic 1A.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	2	15	2	15	1	11	1	10	1	10	1	13	1
21	1	25	1	20	1	21	1	21	1	24	1	22	1
30	1	32	1	31	1	30	1	28	1	30	1	30	1
48	3	48	3	45	1	47	4	47	3	45	3	47	3
63	3	63	3	63	2	61	2	60	2	60	2	62	2
73	5	73	5	75	5	71	5	72	5	70	5	72	5
87	3	88	3	88	3	83	3	83	2	86	2	86	3
95	2	95	2	97	1	95	1	96	1	95	1	96	1
114	3	114	3	113	3	110	3	113	2	113	3	113	3
125	4	125	3	127	3	122	4	121	3	122	3	124	3
138	5	139	5	138	5	133	5	134	5	133	5	136	5
149	3	150	3	150	4	146	4	146	3	146	3	148	3
166	2	167	3	166	2	162	2	163	2	164	1	165	2
185	2	185	2	186	2	184	1	185	2	183	2	185	2
195	1	193	2	190	1	190	1	-	-	195	1	193	1

Table 3. The migration distances and band intensities of the LMW glutenins of Chinese Spring monosomic 1B

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
10	1	16	1	14	1	16	1	14	1	12	1	14	1
30	1	29	1	23	1	25	1	25	1	22	1	26	1
53	5	54	5	53	5	57	5	52	3	55	5	54	5
64	5	-	-	66	3	68	5	66	5	60	5	65	5
76	5	75	5	77	5	70	4	70	5	71	5	73	5
88	3	85	2	92	2	89	1	90	2	85	2	88	2
99	1	100	2	98	3	100	3	95	3	101	3	99	3
114	3	114	2	118	4	115	3	110	3	113	3	114	3
127	4	126	5	130	5	130	5	128	5	123	5	127	5
139	5	138	4	138	5	132	5	-	-	136	4	136	5
151	5	150	5	150	5	145	5	145	4	147	5	148	5
166	2	167	2	170	3	161	4	160	1	169	2	166	2
182	1	185	2	182	1	181	2	180	1	185	1	183	1
192	2	196	1	190	2	193	1	194	1	191	1	193	1

Table 4. The migration distances and band intensities of the LMW glutenins of Chinese Spring monosomic 1D

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	14	2	15	1	10	1	15	1	17	2	14	1
23	1	21	1	23	1	24	5	20	1	20	1	22	1
30	2	32	2	30	1	35	3	35	2	30	2	32	2
-	-	-	-	45	3	48	3	42	3	48	3	46	3
54	5	52	3	51	1	55	3	56	3	54	3	54	3
74	5	76	5	74	5	-	-	72	5	72	5	74	5
91	3	89	3	89	3	89	3	88	2	83	4	88	3
100	2	100	2	98	1	98	2	97	2	99	1	99	2
119	4	118	4	118	2	118	4	116	5	118	5	118	4
135	5	135	4	135	2	137	2	138	2	137	2	136	2
145	2	145	2	149	2	-	-	147	1	148	2	147	2
153	5	153	5	-	-	158	1	158	1	159	1	156	6
-	-	168	3	162	1	166	1	163	1	166	1	165	1
170	2	-	-	175	1	172	1	172	1	171	2	172	1
184	2	-	-	185	1	185	1	183	1	182	1	184	1
189	2	188	2	-	-	188	1	186	1	189	1	188	1
-	-	-	-	192	2	194	1	191	1	193	1	193	1

Table 5 The migration distances and band intensities of the LMW glutenins of Flamink

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	10	1	15	1	14	1	13	1	16	1	14	1
25	1	-	-	25	1	25	1	21	1	-	-	24	1
35	1	32	1	36	1	33	1	33	1	33	1	34	1
40	1	38	1	-	-	40	1	41	1	38	1	39	1
53	1	53	1	50	2	-	-	53	1	50	1	52	1
70	5	70	5	67	5	64	5	66	3	71	5	68	5
87	1	-	-	88	1	85	5	88	5	90	5	88	6
96	1	96	1	97	1	98	1	99	1	-	-	97	1
112	3	111	2	111	3	115	3	112	3	111	2	112	3
116	3	116	3	115	3	115	3	115	1	115	2	115	3
133	3	134	4	131	3	135	3	132	2	131	3	133	3
148	3	147	2	143	2	150	3	142	3	144	3	146	3
165	1	164	1	161	1	166	2	165	1	160	1	164	1
-	-	174	1	172	1	177	1	171	1	174	2	174	1
186	2	185	2	186	1	186	1	186	1	185	1	186	1
193	1	-	-	192	1	190	1	194	1	192	1	192	1

Table 6. The migration distances and band intensities of the LMW glutenins of Flamink monosomic 1A

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	1	14	1	10	1	14	1	17	1	15	1	14	1
-	-	33	2	39	-	35	1	35	1	33	1	34	1
44	1	-	-	-	-	45	1	43	1	40	1	43	1
50	1	56	5	-	-	54	1	51	1	54	1	53	1
66	5	-	-	62	5	97	2	97	2	66	3	67	3
68	5	79	1	-	-	73	1	70	2	71	2	72	1
89	1	88	1	80	1	88	5	86	4	90	5	88	6
-	-	100	3	100	2	99	2	100	3	98	3	99	3
110	3	114	3	114	2	111	1	114	1	114	2	113	2
118	2	118	3	-	-	113	1	-	-	117	1	117	1
128	3	131	2	123	3	127	3	126	2	129	4	128	3
142	2	149	1	140	1	146	3	147	3	147	3	146	3
158	1	-	-	152	1	159	2	159	1	160	1	158	1
-	-	174	2	177	5	173	2	173	2	178	2	174	2
182	3	186	1	-	-	187	1	187	1	187	1	186	1
-	-	-	-	191	1	194	1	194	1	192	1	193	1

Table 7. The migration distances and band intensities of the LMW glutenins of Flamink monosomic 1B

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
13	1	19	1	18	3	13	1	11	1	10	1	13	1
-	-	35	1	32	1	37	1	33	2	31	1	34	1
46	1	-	-	40	2	43	1	40	2	42	1	42	1
69	5	70	5	67	5	65	3	67	3	65	3	67	5
91	1	92	1	90	2	95	2	95	3	96	2	93	2
113	3	114	3	114	2	110	2	113	1	112	1	113	2
120	3	122	3	124	3	125	3	125	3	124	3	123	3
131	3	132	3	133	3	131	2	136	3	136	3	133	3
144	2	144	2	145	3	142	3	144	3	143	3	144	3
159	1	-	-	161	1	155	2	158	1	159	2	158	1
180	2	180	1	179	2	173	1	173	1	174	1	174	1
184	2	183	1	187	2	189	1	188	1	185	1	186	1
192	1	188	1	-	-	194	1	194	1	190	1	192	1

Table 8. The migration distances and band intensities of the LMW glutenins of Flamink monosomic 1D

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
16	1	10	1	15	1	16	1	15	1	16	1	14	1
20	1	-	-	23	1	25	1	22	1	23	2	23	1
45	3	45	5	49	4	41	2	50	4	45	2	47	4
72	5	72	5	74	5	80	5	78	5	71	1	74	5
-	-	80	4	81	4	83	5	82	5	82	5	82	5
91	2	93	3	90	1	91	3	91	3	92	2	91	3
109	3	113	5	-	-	107	1	107	1	107	1	108	1
113	3	116	5	117	4	112	2	111	2	110	1	113	2
126	4	125	5	125	4	125	5	125	3	125	5	125	5
131	4	131	5	132	4	132	4	138	5	130	5	132	5
145	4	147	5	148	5	141	5	140	4	141	5	143	5
154	1	155	1	157	1	157	2	155	1	157	3	156	1
163	2	165	2	167	2	168	2	170	2	-	-	167	2
173	1	176	1	174	1	173	2	173	1	171	2	173	1
188	4	190	4	192	3	192	1	193	1	189	2	191	3

Table 9. The migration distances and band intensities of the LMW glutenins of Inia.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
19	3	17	3	11	2	14	3	15	3	17	3	16	3
28	5	26	4	24	3	21	3	22	3	23	3	24	3
40	5	40	5	39	5	31	5	33	5	33	5	36	5
53	4	53	4	53	5	50	5	51	5	53	5	52	5
59	4	59	4	-	-	64	4	64	4	66	4	62	4
86	2	85	2	87	2	83	1	86	2	86	1	86	2
101	3	100	4	99	3	101	4	103	4	97	4	100	4
104	3	104	4	106	3	-	-	108	3	105	4	105	3
114	3	115	4	117	4	119	5	119	5	113	3	116	4
120	3	120	3	123	4	126	3	126	3	122	3	123	3
134	1	134	1	-	-	140	1	142	1	143	1	139	1
156	2	156	3	157	2	158	5	161	4	162	4	158	6
163	5	164	4	164	3	166	5	169	5	170	5	166	5
180	1	183	1	176	1	181	1	181	1	185	1	181	1
189	1	192	1	180	1	189	1	189	1	191	1	188	1

Table 10. The migration distances and band intensities of the LMW glutenins of Inia monosomic 1A

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	13	1	10	4	17	5	12	5	10	14	12	4
25	3	24	2	20	1	-	-	22	2	23	4	23	2
32	1	32	1	31	1	36	1	37	1	-	-	34	1
41	1	40	1	44	5	-	-	-	-	43	1	42	1
66	5	61	5	65	2	68	4	61	1	63	3	64	6
81	4	82	2	82	1	86	3	81	1	83	5	83	3
94	3	92	2	91	2	-	-	95	2	92	2	93	2
101	1	99	1	98	4	101	2	99	3	96	2	99	2
110	1	112	4	110	5	117	4	112	2	112	1	112	6
116	2	117	5	112	3	119	5	118	1	-	-	117	3
127	3	130	5	125	4	127	3	122	1	123	4	126	4
141	5	-	-	145	4	138	3	146	1	141	3	143	3
166	2	161	2	163	2	163	2	160	1	166	2	163	2
178	1	171	1	175	5	175	1	178	1	176	1	176	1
185	1	183	1	189	1	187	1	187	1	185	1	186	1
190	1	190	1	195	1	191	1	191	1	190	1	191	1

Table 11. The migration distances and band intensities of the LMW glutenins of Inia monosomic 1B

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	4	14	5	12	5	8	1	7	1	8	1	10	6
25	1	28	1	25	1	21	5	22	5	22	5	24	6
37	1	37	1	38	1	33	1	-	-	33	1	36	1
41	2	48	4	48	4	45	1	47	1	49	2	47	2
59	3	58	2	59	1	58	3	60	3	60	5	59	3
71	2	74	4	72	4	74	3	77	3	-	-	74	3
82	1	86	1	83	1	83	3	86	3	82	4	84	2
98	3	95	2	99	2	95	2	95	2	95	2	96	2
106	4	110	5	106	4	109	2	108	2	108	1	108	6
122	5	126	5	124	5	120	4	124	4	124	4	123	5
147	1	151	2	144	3	144	2	145	1	146	3	146	2
168	2	164	1	157	1	164	1	-	-	165	1	164	1
172	2	175	1	174	1	175	1	174	1	173	1	174	1
183	3	-	-	181	1	-	-	183	1	184	1	183	1
-	-	187	1	187	1	188	1	188	1	189	1	188	1
-	-	194	2	195	2	193	1	191	1	193	1	193	1

Table 10. The migration distances and band intensities of the LMW glutenins of Inia monosomic 1D

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
17	5	14	1	14	1	13	1	13	1	14	1	14	1
		24	3	24	3	26	1	23	5	26	5	24	4
38	1	32	1	35	1	33	1	34	1	36	1	35	1
41	1	47	1	49	2	40	1	-	-	46	1	46	1
56	5	-	-	-	-	50	3	52	1	53	1	53	1
70	4	63	5	66	5	68	5	65	4	66	2	66	5
82	4	83	3	83	3	84	4	85	4	90	5	84	4
95	1	97	2	99	2	94	2	100	2	95	5	97	2
105	1	107	1	110	1	103	1	108	1	103	1	106	1
120	3	115	2	115	2	116	2	-	-	116	1	116	2
123	3	122	3	124	4	125	4	124	4	127	4	124	4
128	2	132	4	131	3	-	-	132	3	127	4	130	3
137	4	141	5	144	5	145	3	147	2	150	3	145	4
153	3	158	1	152	3	157	2	158	1	155	2	156	2
167	1	167	1	156	2	157	2	167	1	164	1	166	1
177	1	175	1	170	1	173	1	178	1	179	1	176	1
185	1	188	1	187	1	188	1	188	1	-	-	187	1
188	1	194	1	192	1	195	1	194	1	190	1	192	1

Table 13 The migration distance of the LMW glutenins of SST 3.

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
15	2	16	2	17	1	14	1	17	1	-	-	16	1
22	1	27	1	25	1	20	1	23	1	26	1	24	1
30	1	33	1	34	1	30	1	30	1	35	1	32	1
60	2	58	2	58	2	55	1	56	2	-	-	57	5
65	2	62	2	65	2	69	2	68	2	66	3	66	2
71	2	76	3	-	-	-	-	74	2	74	2	74	1
85	5	86	5	82	5	81	4	80	5	85	4	83	5
105	1	104	1	102	1	100	1	102	2	105	2	103	1
115	2	110	1	114	2	109	1	110	2	115	2	112	2
122	3	126	3	126	3	119	1	121	3	125	3	123	3
130	3	133	2	131	2	132	2	133	2	135	2	132	2
146	3	143	3	143	3	-	-	147	3	-	-	145	3
155	1	156	2	155	2	152	2	153	2	151	2	154	2
173	1	174	1	171	1	175	1	175	1	-	-	174	1
183	1	-	-	185	1	180	1	181	1	182	1	182	1
192	1	191	1	195	1	193	1	190	1	191	1	192	1

Table 14. The migration distance of the LMW glutenins of SST 3 monosomic 1A

R1	I1	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	1	16	1	16	1	-	-	11	1	13	1	14	1
21	1	27	1	26	2	26	2	24	3	25	1	25	2
43	1	44	1	42	1	44	1	41	1	42	1	43	1
55	2	54	1	52	1	-	-	57	1	57	2	55	1
71	2	63	2	70	2	71	1	70	1	-	-	70	2
79	5	79	5	80	5	82	4	88	5	82	5	80	5
89	2	92	1	95	1	92	5	-	-	-	-	92	1
104	2	100	2	102	2	-	-	102	1	104	1	102	2
113	2	112	2	114	2	113	1	109	1	-	-	112	2
120	2	118	2	118	2	115	1	115	1	120	2	118	2
130	1	132	2	130	2	127	2	123	1	134	2	131	2
147	2	148	1	142	1	145	2	149	1	-	-	146	1
151	2	158	1	153	1	152	1	157	1	160	1	154	1
169	2	165	1	165	2	166	1	164	1	165	1	166	1
175	1	173	1	171	1	173	1	170	1	170	1	172	1
182	1	184	1	185	1	185	1	183	1	180	1	183	1
191	1	191	1	191	1	192	1	190	1	195	1	192	1

Table 15. The migration distance of the LMW glutenins of SST 3 monosomic 1B

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
14	2	16	2	15	1	13	4	12	2	15	2	14	2
25	1	25	1	22	1	20	1	23	1	24	2	23	1
34	1	34	1	34	1	35	1	36	1	33	1	34	1
46	1	48	1	46	1	45	1	47	2	46	1	46	1
53	1	52	1	54	2	54	1	56	2	52	2	54	2
79	5	71	5	69	5	70	5	75	5	-	-	72	5
84	4	85	1	83	2	82	1	84	2	85	2	84	2
101	1	98	1	97	1	-	-	96	2	99	2	98	1
110	1	108	2	111	4	110	4	107	3	-	-	109	3
119	3	114	4	121	2	125	3	123	3	120	2	121	3
135	3	131	3	134	1	139	1	134	1	138	2	134	2
146	1	140	2	145	1	-	-	146	1	145	2	144	1
168	1	166	2	167	1	171	1	165	1	164	2	167	1
185	1	184	1	181	1	184	1	183	1	180	1	183	1
191	1	196	1	194	1	191	1	193	1	192	2	193	1

Table 16. The migration distance of the LMW glutenins of SST 3 monosomic 1D

R1	M	R2	I2	R3	I3	R4	I4	R5	I5	R6	I6	Rav	I
9	2	10	1	12	2	11	1	12	2	11	2	11	2
12	2	17	2	18	1	16	1	-	-	18	1	16	1
38	1	36	1	33	5	-	-	35	2	33	1	33	1
-	-	41	5	40	3	41	1	40	2	45	1	41	2
57	5	50	5	56	5	53	1	52	1	52	1	53	6
61	5	-	-	-	-	68	3	63	2	67	2	66	2
92	1	96	3	97	3	91	5	94	5	98	5	95	4
100	3	105	2	105	2	100	3	104	3	106	5	103	3
110	4	109	3	109	2	110	1	109	1	-	-	109	2
114	3	115	3	115	3	116	1	114	1	116	1	115	2
121	1	120	3	122	1	125	3	-	-	123	3	122	3
128	3	-	-	123	3	129	2	129	2	129	2	128	2
135	3	137	2	-	-	137	3	136	3	137	3	136	3
150	2	151	1	149	1	152	3	152	3	153	2	151	2
165	1	169	3	169	1	167	2	168	1	162	1	167	1
180	1	185	1	184	1	184	1	178	2	186	1	183	1
191	2	193	1	190	1	193	1	193	2	193	1	192	1