

**Combining ability for crude protein  
in six selected inbred  
*x Triticosecale*  
genotypes.**

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**Combining ability for crude  
protein in six selected inbred  
*x Triticosecale* genotypes.**

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# Preface

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# List of abbreviations

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ANOVA	Analysis of Variance
$\alpha = 0.01$	Maximum probability to commit a Type 1 error; in this case 1/100
$\alpha = 0.05$	Maximum probability to commit a Type 1 error; in this case 5/100
b	number of blocks(replications) used in the trial
(bv)	block x genotype interaction
c	number of individual observations per block
CR <sub>y</sub>	Correlated Response of character y
CV	Coefficient of Variation given as a %
df	degrees of freedom given in the ANOVA
e	error term
gca	general combining ability
$h_b^2$	broad sense heritability
$h_n^2$	narrow sense heritability
LSD <sub>0.01</sub>	Least Significant Difference at confidence level $\alpha=0.01$
LSD <sub>0.05</sub>	Least Significant Difference at confidence level $\alpha=0.05$
MS	Mean Squares
MS <sub>e</sub>	Mean Squares error in the initial ANOVA
M' <sub>e</sub>	MS <sub>error</sub> in the combining ability ANOVA
MS <sub>gca</sub>	Mean Squares for general combining ability in the combining ability ANOVA
MS <sub>sca</sub>	Mean Squares for specific combining ability in the combining ability ANOVA
p	number of parents used in the diallel
sca	specific combining ability
SS	Sum of Squares
SS <sub>gca</sub>	Sum of Squares for general combining ability in the combining ability ANOVA
SS <sub>sca</sub>	Sum of Squares for specific combining ability in the combining ability ANOVA
v	number of genotypes to be analysed in the initial ANOVA
$\sigma^2$	variance
$\sigma^2_A$	additive genetic variance
$\sigma^2_D$	dominance variance
$\sigma^2_{D+I}$	total non-additive genetic variance
$\sigma_e^2$	expectation of the MS' <sub>error</sub> in the combining ability ANOVA ( $M'_e = \sigma_e^2$ );depicting the environmental variance when the variance components are listed.
$\sigma^2_G$	genotypic variance
$\sigma^2_{gca}$	variance of gca in the fixed parent population

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## Abbreviations

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$\sigma^2_P$	phenotypic variance
$\sigma^2_{sca}$	variance of sca in the fixed group of F <sub>1</sub> hybrids
*	Significantly different at level $\alpha = 0.05$
**	Significantly different at level $\alpha = 0.01$
***	Significantly different at level $\alpha = 0.001$

### Introduction

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Triticale received generous scientific attention in the past because of its interesting cytogenetic behaviour and its deemed potential as a feed grain for human consumption. Triticale, however, has now found a different application in the market place where it is mostly used as either a feed grain or forage crop or to a limited extent as both.

Genetic studies to determine the combining ability of selected triticale genotypes for dual purpose applications are practically non-existent.

The influence of utilisation as a forage crop on the subsequent grain yield is important in the selection for a dual purpose triticale. The resultant crude protein content and more importantly, the grain crude protein yield, is vital when the role of triticale as a source of crude protein is considered.

The forage crude protein content and more specifically, the crude protein yield of the forage, are important vegetative characteristics in the initial screening of genotypes for use in a dual purpose application.

The evaluation of combining ability of triticale genotypes for these characteristics will help in identification of genotypes which could be good parental components for developing both hybrids and standard varieties.

It is also important to know the genetic correlations between the characteristics of interest, in the selected genetic material a person is working with. This will enable the plant breeder to have a better view where he is heading, when selection is done based on one or more of the easier measured characteristics in the initial stages of selection.

The genetic correlation between vegetative crude protein yield when used as forage and the resultant grain yield is of particular interest. This correlation will give the answer if the triticale genotypes under consideration will be changed from generous grain producing plants to a pasture type with low seed production. This will have consequences on the viability of a potential cultivar for seed production and the production cost per kg of such seed.

# Literature review

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## 2.1 Triticale development, types and properties

Triticale is a man-made hybrid, derived from an initial cross between wheat and rye (Briggle, 1969; Sapra, Sharma, Hughes & Bradford, 1973). Triticale is the common name that has been given to amphidiploids between wheat and rye and combines the names of the two genera involved in its production, *Triticum* L. and *Secale* L. The correct generic name for such amphidiploids is *x Triticosecale* Wittmack. It is applied to crosses between hexaploid wheat and diploid rye and between tetraploid wheat and diploid rye. The name should in theory, also apply to crosses between diploid wheat and diploid rye and the crosses involving the wheats and tetraploid rye (Scoles & Kaltsikes, 1974). Development has concentrated on hexaploid varieties although both octoploid and more recently tetraploids types have been studied (Briggle, 1969; Krolow, 1973; Zillinski, 1974).

Wheat  $\times$  rye hybrids have been reported infrequently between 1875 and 1937 (Briggle, 1969). The first amphidiploid was produced by Rimpau in 1888, obtained from a naturally doubled sector of an F<sub>1</sub> plant from the cross of a hexaploid wheat with a diploid rye (Scoles & Kaltsikes, 1974). The development in 1937 of the colchicine technique for doubling the chromosomes of sterile F<sub>1</sub> hybrids to produce fertile plants created new interest among plant breeders. Since then triticale has been an object of extensive breeding and cytogenetic studies (Briggle, 1969; Larter, Tsuchiya & Evans, 1968). The objectives of plant breeders with the development of triticale included the combination of grain quality, productivity and disease resistance of *Triticum* with the vigor and hardiness of *Secale* (Briggle, 1969).

The first triticales to be produced were octoploid, resulting from the cross of hexaploid wheat (*Triticum aestivum* L. em Tell) with diploid rye (*Secale cereale* L.) (Gustafson & Qualset, 1974; Scoles & Kaltsikes, 1974). This may have been because this cross produces seed which can give rise to the F<sub>1</sub> plant without the need for embryo-culture, unlike that of a tetraploid wheat with rye. The other reason could be that hexaploid wheat was more commonly grown in northern Europe than

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tetraploid wheat, the area in which the first triticales were produced (Scoles & Kaltsikes, 1974). According to Scoles & Kaltsikes (1974) octoploid triticales as such has not proven to be of much practical value. These types were therefore largely discarded in favour of hexaploid triticales (Larter *et al.*, 1968; Gustafson & Qualset, 1974). The octoploid triticales still have a role to play however in the production of secondary hexaploid triticales (Scoles & Kaltsikes, 1974).

The first hexaploid triticales was reported by Derzhaven (1938) from the cross *T.durum* x *S.montanum*. The first hexaploid triticales resulting from the cross of tetraploid wheat with commercial diploid rye, is that of O'Mara (1948) obtained by crossing *Triticum durum* L. with *Secale cereale* L. According to Scoles & Kaltsikes (1974) there is a wide range of variation within the tetraploid wheats which might be utilised in hexaploid triticales. Müntzing (1956) suggested that the hexaploid triticales involving *T.durum* was superior in fertility to a triticales between *T.turgidum* and *S.cereale*. Kiss (1965) reported that of the triticales produced by him using *T.turgidum*, *T.carthlicum*, *T. durum* and *T.timopheevi*, those with *T.turgidum* seemed to be the most promising. Kiss (1965) also reports that using both cultivated and wild rye species the hybrids involving *S.cereale* were the best. Other wheat or rye varieties exhibited various disadvantageous characteristics such as very low fertility, fragile ears and very shrivelled grain. A large majority of the lines that are being used in triticales programmes involve either *T.turgidum* or *T.durum* and either *S.cereale* or *S.montanum* (Scoles & Kaltsikes, 1974).

The term primary triticales describes the triticales lines obtained by hybridising already existing triticales lines (Kaltsikes, 1974). These lines handled through conventional breeding programmes can incorporate characteristics originating from several wheat and rye parents. Most of the breeding work is concentrated at the hexaploid level and the term primary triticales usually refers to this ploidy level (Kaltsikes, 1974).

The most promising hexaploid triticales are the so-called secondary types (Gustafson & Qualset, 1974; Kaltsikes, 1974; Scoles & Kaltsikes, 1974). The secondary types are lines derived from intercrosses of hexaploid triticales with octoploid triticales (Kiss, 1966; Pissarev, 1966) or with hexaploid wheats (Sanchez-Monge, 1959; Nakajima & Zennyozzi, 1966; Larter *et al.*, 1968). Higher fertility is the major improvement of these types over the primary hexaploids (Pissarev, 1966; Sisodia & McGinnis, 1970a; Thomas & Kaltsikes, 1972; Gustafson & Qualset, 1974; Hsam &

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Larter, 1974). Sisodia & McGinnis (1970*b*) proposed two more methods for the production of new secondary triticale lines. In the first method a 6x wheat (AABBDD) line, or F<sub>1</sub> among different wheat cultivars is crossed to rye (RR) followed by hybridisation of the ABDR hybrid with a hexaploid triticale. The second method suggested by Sisodia & McGinnis (1970*b*) is to cross the pentaploid hybrid (AABBD) between 4x and 6x wheats to rye. The hybrid, thus obtained is then crossed to an existing hexaploid triticale line. In both these methods care must be taken to ensure that the cytoplasm of the resulting triticale is derived from hexaploid wheat.

Krolow (1973) reported the first successful production of tetraploid triticale by crossing hexaploid triticale with diploid rye and selfing the ABRR hybrid to obtain AARR, BBRR and (AB)(AB)RR (mixed genomes). After five to six generations the twenty-eight chromosome lines were stable with a very low level of aneuploid frequency.

Larter *et al.* (1968) state that the major weakness of triticale lies in its reproductive system. From the work of Sanchez-Monge (1959), Krolow (1966), Nakajima & Zennyozzi (1966) and Hsam & Larter (1974), it is known that varying degrees of cytological instability exists in hexaploid triticale. The level of such instability varies with genetic background and the number of generations removed from the original hybrid state. Larter *et al.* (1968) and Krolow (1966) found a rather high frequency of aneuploids when they examined plants of several triticales. Most aneuploid types were hypoploid. Gustafson & Qualset (1974) reported that sterility and malformed kernels are especially common in progeny from intercrosses among 42-chromosome triticales and remarked that the nature of sterility in intertriticale crosses is not understood. Larter *et al.* (1968) state that in the immediate progeny of known euploid plants ( $2n = 6x = 42$ ), aneuploids were again present, although some selected lines were more stable than others. It was according to Larter *et al.* (1968) apparent that considerable aneuploidy can exist in triticale strains and that a continuous cytological programme must be operated in conjunction with the breeding project. Larter *et al.* (1968) found an increase in meiotic instability with physiological stress due to water or heat stress in some of the advanced breeding lines. This resulted in considerable sterility. Scoles & Kaltsikes (1974) and Gupta & Priyadarshan (1982) did comprehensive literature studies on the detail of genetic abnormalities at the

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various stages of meiosis, as well as the theories regarding the genetic instability and role of the cytoplasm in triticales.

Gustafson & Qualset (1974) made the following conclusion after their study of various secondary hexaploid triticales: These results have important implications in triticales breeding because a particular triticales plant may have any of a large number of possible combinations of R and D chromosomes (assuming no variation in the A and B genomes). Intercrosses among triticales lines would then result in unbalanced chromosomal segregation. Most plants from such crosses would be expected to show varying degrees of sterility and only rare plants would have good fertility on the basis of chromosomal balance. This sterility has been observed in F<sub>1</sub>'s and segregating generations of intercrosses among triticales lines and the hypothesis is supported in this study by the rather large range in the number of univalent chromosomes found in the F<sub>2</sub> populations. Each triticales intercross should be considered as an interspecific hybrid with a low probability for obtaining progeny with good fertility and desirable combinations of agronomic characters unless the parents are closely related.

Triticales is a most useful cereal however. Even though it was developed as a food grain, it has more potential as a grain feed for ruminants according to McColey, Sherrod, Albin & Hansen (1971) and for nonruminants according to Briggles (1969), Knipfel (1969), Longnecker (1973) and Shimada, Martinez & Bravo (1971), than as food for humans (Brown & Almodares, 1976). The quality of protein in triticales grain is also superior to that of wheat in terms of higher lysine and threonine content, the amino acids found to be most limiting in cereals (Larter *et al.*, 1968). This is confirmed by the work of Heger & Eggum (1991) who found that triticales has a higher lysine content and protein of a better biological value for nonruminants than wheat grain. When evaluated as a source of grain protein, Villegas, Amaya & Bauer (1973) of CIMMIYT showed that a marked decrease in protein content of triticales grain has occurred with improvement in yield capacity and kernel plumpness. The increase in yield has, however, more than compensated for the loss in protein so that the production of grain protein per unit area has increased.

Apart from use as a feed grain, triticales is also a good supplemental forage according to Brown & Almodares (1976) and a very good silage crop (Bishnoi, Chitapong, Hughes & Nishimuta, 1978).



It has long been known that anther and pollen properties of triticale are far more favourable for cross pollination compared to wheat (D'Souza, 1970). Pollen dissemination, pollen supply, duration of flowering and outcrossing rates of triticale is higher in triticale than in wheat (Yeung & Larter, 1972). The conditions for the production of hybrids in triticale are therefore favourable (Oettler, Burger & Melchinger, 2003). Weißmann & Weißmann (2002) discussed triticale hybrid breeding from a plant breeder's point of view and compared the heterosis results from drilled small plot trials by Pfeiffer, Sayre & Mergaum (1998) and Oettler, Becker & Hoppe (2001) to the heterosis results obtained by Barker & Varughese (1992), Trethowan & Darvey (1994) and Góral, Węgrzyn & Spiss (1999). Weißmann & Weißmann (2002) argued that the heterosis estimated from single plants might be overestimated when compared to the results of the drilled small plots.

Oettler *et al.* (2003) and later, Oettler, Tams, Utz, Bauer & Melchinger (2005) completed heterosis studies using drilled big plot trials to verify the results of drilled small plot trials used by Pfeiffer *et al.* (1998) and Oettler *et al.* (2001). The results were in agreement and Oettler *et al.* (2003) came to the conclusion that mid-parent grain yield heterosis in winter triticale was more comparable to that of wheat than to rye. The range of heterosis was large, however, and it appeared feasible to reach a mid parent heterosis of 20 percent by selecting parents for combining ability and establishing heterotic groups. Although triticale is normally treated as a self pollinated crop in applied breeding, Fossati, Jaquierey & Fossati (1998) already reported that pilot production of commercial triticale hybrids has been successful and that several hybrids were being tested in official trials in Europe.

## **2.2 Effect of defoliation on crude protein characteristics of vegetative material**

Although triticale is grown mainly as feed grain for animals, its potential as a forage cereal has been highlighted by Bishnoi, Chitapong, Hughes & Nishimuta (1978) and Brignall, Ward & Whittington (1988).

The practice of grazing autumn sown winter cereals before the jointing stage and subsequently harvesting the grain is common in the southern U.S.A. (Hubbard &

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Harper, 1949; Brown & Almodares, 1976; Bishnoi & Hughes, 1979; Dunphy, McDaniel & Holt, 1982), the Ontario region of Canada (Poysa, 1985), the Mediterranean part of Europe (Skorda, 1978; García del Moral, 1992), southern and eastern Australia (Andrews, Wright, Simpson, Jessop, Reeves & Wheeler, 1991), Argentina (López, 1991) and is also practised in some parts of Syria (Nachit, 1983). Triticale has given similar forage yields to wheat (Brignall *et al.*, 1988), barley (Sapra, Sharma, Hughes & Bradford, 1973), oats (Brown & Almodares, 1976) and rye (Bishnoi & Hughes, 1979). Baron, Najda, Salmon & Dick (1993) even planted winter triticale in spring for grazing throughout the growing season in Canada and obtained higher total yields than with spring oats or barley.

Triticale has considerable potential as a source of protein (Skorda, 1978; Heger & Eggum, 1991). Forage crude protein contents from 19% to 30% have been reported for triticale harvested at the end of tillering (Skorda, 1978; Poysa, 1985; Royo, Montesinos, Molina-Cano & Serra, 1993; Royo, Insa, Boujenna, Ramos, Montesinos & Garcia del Moral, 1994; Royo & Pares, 1996). Brown & Almodares (1976) found that the percentage crude protein of triticale forage at comparable stages of growth was similar to rye, wheat and oat cultivars. Skorda (1978) found no significant differences between triticale, wheat and barley when the percentage crude protein of cut material at the jointing stage was considered.

Skorda (1978) found that cutting cereals for hay at the vegetative stages resulted in higher crude protein content than cutting at the flowering or seed stages. Crude protein content was found to be high at the jointing stage and to decrease rapidly until flowering stage. Poysa (1985) found an average difference of 1.5% in percentage crude protein of cereal forage between the early joint stage and the mid-joint stage. Skorda (1978) found that maximum forage yield of triticale was obtained by the delaying of harvest until the dough stage, but that the protein content had declined to 6.3% at this stage. A compromise is necessary between quantity and quality of forage in order to achieve the best combination of both (Droushiotis, 1984).

Skorda (1978) used forage crude protein yield as the compromise between forage yield and quality and obtained the highest yield of forage crude protein at the heading stage. Harvesting at this stage would give a better balance between dry matter yield and a crude protein content of 10.7%. Nachit (1983), Royo *et al.* (1994) and Royo & Pares (1996) determined the crude protein yield of triticale vegetative material cut at

the early joint stage just after the end of tillering and obtained values in the range of 351 kg/ha to 985 kg/ha. Royo & Pares (1996) tested for differences between triticale cultivars with regard to protein content at the early joint stage and found significant differences, although Royo *et al.* (1994) failed to show differences amongst the cultivars used in that study. Not one of these studies tested for significant differences between cultivars for crude protein yield of triticale vegetative material.

### **2.3 Effect of defoliation on crude protein characteristics of triticale grain**

The capacity of forage cereals for regrowth after defoliation in spring (Brignall *et al.*, 1988) enable them to be used for grazing first and then the regrowth may be left for grain production (Brown & Almodares, 1976; Poysa, 1985). The effect of forage removal on grain yield is an intricate process depending on many factors such as environmental conditions, moisture and fertility of the soil, animal grazing pressure, management practices, plant genotype and growth stage at cutting (Dunphy, McDaniel & Holt, 1982; Poysa, 1985). When grain yields have been measured following cutting or grazing in dual-purpose cereals, the results varied widely. Holliday (1956) found that a decrease in grain production occurred in most cases while only a few studies showed an increase in grain yield.

Increases in grain yield following grazing have been associated with reduced lodging in the grazed plots compared with the control plots (Day, Thompson & McCaughey, 1968). Skorda (1978) found in southern Europe also a reduction in lodging as well as a reduced rate of mildew and other disease infections when early sown cereals were used for forage production. The cutting of early sown triticale during the autumn and winter months in a season of adequate rainfall, will not adversely affect the grain yield but may actually increase it (Skorda, 1978).

Decreases in grain yield after defoliation are normally associated with the removal of shoot apices, or growing points, by grazing (Hubbard & Harper, 1949; Morris & Gardner, 1958 and Droushiotis, 1984), or to decreased leaf area at anthesis or leaf area duration from jointing to anthesis (Dunphy, Holt & McDaniel, 1984; García del Moral, 1992).

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Hubbard & Harper (1949) found that removal of the developing ear at the height at which the plants were cut or grazed is likely to reduce the grain yield. The removed developing ears do not regenerate and can be replaced only by the production of a new tiller (Hubbard & Harper, 1949). Dunphy *et al.* (1982) and Brignall *et al.* (1988) found that the reduction in grain yield, after defoliation were mainly attributed to a reduced number of ears per m<sup>2</sup> at harvest. Royo *et al.* (1993) also found the reductions observed in the number of ears per plant, to be the yield component most influenced by defoliation. The stage when the growing points begin to elevate above ground level (jointing) is the critical stage of development for determining the date of livestock removal (Hubbard & Harper, 1949; Dunphy *et al.*, 1982; Poysa, 1985; Winter & Thompson, 1987). Forage harvested at a later stage decreased grain yield due to less tiller survival (Dunphy *et al.*, 1982). However, when triticale was grown under favourable environmental conditions, grain yield was not reduced by cutting, despite the removal of the growing points (Royo *et al.*, 1993). A feasible explanation may be that in spite of the advanced state of development when cut, cutting was performed very early in the season and the plants therefore had a long time to recover before the grain harvest (Royo *et al.*, 1993).

Moreover, substantial grain yield reductions have occurred even without the removal of the terminal meristem, or growing point (Kilcher, 1982; Dunphy *et al.*, 1982; Poysa, 1985; García del Moral, 1992; Royo *et al.*, 1994; Royo & Pares, 1996). Under poor weather and fertility conditions, grain yield losses can be expected even if cereals are grazed during the vegetative phase (Kilcher, 1982). Additional factors in the decrease of the grain yield may also be inhibition of tiller formation, increase of tiller death, leaf area decrease at anthesis and decrease in leaf area duration from jointing to anthesis, which reduce the availability of assimilate for grain set and grain growth (Dunphy *et al.*, 1982; 1984). The grain yield in cereals subjected to cutting is highly dependant upon the ability of the plant to rapidly produce new leaf area during the period from the last cut to anthesis (Dunphy *et al.*, 1984; Winter & Thompson, 1987; García del Moral, 1992). This implies that managing triticale for dual purposes requires consideration not simply for the stage of growth at cutting, but also for the regrowth capacity of the cultivar to be used (García del Moral, 1992).

The lack of consistency between the results of many studies may be partially attributed to the arbitrary dates for forage removal, which in many cases did not take

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into account the stage of development of the plant (Dunphy *et al.*, 1982). More consistent results may be obtained by timing the forage harvest in relation to the stage of plant development rather than by calendar date (Dunphy *et al.*, 1982). Previous studies have recorded grain yield decreases of 4% to 33% on a means per study basis for a one cut treatment of triticale at the early joint stage (Skorda, 1978; Nachit, 1983; Poysa, 1985; Royo *et al.*, 1994; Royo & Pares, 1996). When the results of individual triticale cultivars given by Nachit (1983), Poysa (1985) and Royo *et al.* (1994) are studied however, the range of grain yield response to a one cut treatment at the early joint stage of Dunphy *et al.* (1982), varies from an increase of 52% in production to a decrease of 56% in grain production. García del Moral (1992) took a first cut at the pseudostem erect stage and then a second cut when the regrowth reached the early joint stage. The mean decrease in grain yield was 49%. Unfortunately no results of the individual triticale cultivars used in this study, was given by García del Moral (1992).

Royo *et al.* (1993) studied the response of different triticale cultivars to a one cut treatment at the mid joint stage and found a mean decrease in grain yield of 19%. The range of response of the individual cultivars however, varied from an increase of 7% in production to a decrease of 53% in grain production. The differential response of the triticale genotypes to cutting seems to indicate that there is variability among genotypes, and selection for dual purpose use is possible (Royo *et al.*, 1993).

Petterson & Åman (1987) found that the crude protein content of twenty-seven triticale cultivars ranged from 9.4% to 16.5%. Grain crude protein percentages of 11.2 – 14.8% have also been recorded in a study by Heger & Eggum (1991). Grain protein content did not differ between grain and dual-purpose treatments when a one cut treatment at the early joint stage was applied (Skorda, 1978; Royo *et al.*, 1994; Royo & Pares, 1996). Triticale can produce up to 1000kg of grain crude protein per hectare under suitable conditions, when used only for grain production (Royo & Pares, 1996). When the total crude protein production of the vegetative harvest plus grain in a one cut treatment is considered, values of 684kg/ha to 1300kg/ha were found by Royo *et al.* (1993) and Royo & Pares (1996).

Nachit (1983) studied the phenotypic correlation between the vegetative harvest and the grain yield in a one cut treatment done at the early joint stage. The crude protein yield of the vegetative harvest had a better correlation to grain yield than the forage

dry matter yield. Nachit (1983) found therefore that genotypes with the highest dry matter and protein content during the early stages of development were the highest grain producers.

### 2.4 Diallel designs and analysis

Before the different possible diallel designs are discussed, the alternative mating designs which could also possibly be used, must first be considered. The parents-offspring covariance, the polycross as well as the topcross only enable the estimation of  $\sigma^2_A$  (Wricke & Weber, 1986). From the standpoint of efficiency the topcross test should be used primarily for the preliminary evaluation of lines on the basis of their general combining ability (Sprague & Tatum, 1942).

With the hierarchal design, the precision of  $\sigma^2_A$  is less than in the case of parent-offspring covariance and topcross or polycross. The precision of  $\sigma^2_D$  is very low. The factorial design is an improvement on the hierarchal design, but the estimation of  $\sigma^2_D$  is unsatisfactory if the parents are not inbred or if the number of sets is not large (Wricke & Weber, 1986). Becker (1985) indicated that both the hierarchal and the factorial mating designs have the precondition of a random, or Model 2 (Eisenhart, 1947), set of genotypes for parents. Most of the breeding material in which plant breeders are interested has been highly selected for traits of economic importance. With such selected material, the assumption that the varieties are a random sample from some equilibrium base population is completely invalid, and estimation of variance components does not provide useful information (Eberhart & Gardner, 1966).

The diallel mating design can accommodate a selected, fixed, set of parents for the determining of general combining ability (gca) and specific combining ability (sca) (Griffing, 1956*b*). Sprague & Tatum (1942) defined gca and sca for the first time. They defined the terms as follows: "The term 'general combining ability' is used to designate the average performance of a line in hybrid combinations", and "The term 'specific combining ability' is used to designate those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved." The gca provides therefore an estimate of the importance of genes which are largely additive in their effects, while sca provides an estimate which is largely dependant on genes with dominance or

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epistatic effects (Sprague & Tatum, 1942). Varieties displaying significant positive effects of gca will increase the value of a given trait in offspring, while those where the effects of gca are significant but negative, will decrease the value of the trait in their offspring (Węgrzyn & Grzesik, 1996).

Although failure to obtain estimates of these genetic effects can occur when the effects are in fact present, owing to cancelling of opposite effects at different loci or pairs of loci, the probability of such an occurrence is less in a diallel when each genotype is crossed with all other genotypes (Eberhart & Gardner, 1966).

In plant breeding, diallel analysis is used to investigate quantitative characters (Weber, 1976). For hybrid varieties sca is very important, so individual crosses must be made to find the desired sca effect (Wricke & Weber, 1986).

Diallel crossing techniques may vary depending upon whether or not the parental inbreds or the reciprocal F<sub>1</sub>'s are included or both (Griffing, 1956*b*). With this as a basis for classification there are four possible experimental methods: (1) parents, one set of F<sub>1</sub>'s and reciprocal F<sub>1</sub>'s are included; (2) parents and one set of F<sub>1</sub>'s are included, but reciprocal F<sub>1</sub>'s are not; (3) one set of F<sub>1</sub>'s and reciprocals are included but not the parents and (4) one set of F<sub>1</sub>'s, but neither parents nor reciprocal F<sub>1</sub>'s is included (Griffing, 1956*b*). Each of these methods necessitates a different form of analysis (Griffing, 1956*b*).

There are four sets of assumptions which can be considered with regard to the variety (genotypic) and block effects (Griffing, 1956*b*). These are: (1) the variety and block effects are constants. This is the situation in which the parental lines are deliberately chosen, or fixed, and cannot be regarded as a random sample from any population. This assumption can also be expressed somewhat differently by stating that the experimental material constitutes the entire population about which valid inferences can be made. This set of assumptions leads to a model in which all effects except the error are regarded as constants (Griffing, 1956*b*). This class of model have been designated as model 1 by Eisenhart (1947). In assumption (2) the variety effects are random variables and the block effects are constants. This second set of assumptions leads to a mixed model designated as mixed A (Griffing, 1956*b*). In assumption (3) the variety effects are constants, like in assumption 1, but the block effects are random. This third set of assumptions leads to another mixed model designated as mixed B (Griffing, 1956*b*). In assumption (4) the variety and block

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effects are both random variables. This is the situation in which the parental lines or the experimental material as a whole are assumed to be a random sample from some population about which inferences are to be made. This last set of assumptions leads to a model in which all effects except the population mean are random variables. This class of model has been designated as model 2 by Eisenhart (1947). The four methods can be combined with each of the four models to give a total of 16 different diallels. The objectives of the analyses and the analyses themselves are different for the two basic assumptions regarding the parental lines or experimental material (Griffing, 1956*b*).

The objectives of the diallel analyses where the parents are selected are to compare combining abilities of the parents when the parents themselves are used as testers, and to identify the higher yielding combinations. The estimation of combining ability effects are therefore of particular interest (Griffing, 1956*b*). When information on general and specific combining ability for a specific set of lines is desired in connection with a plant breeding problem, experimental methods 3 or 4 are most applicable. In plant material, if it can be assumed that there will be no genotypic reciprocal effects, method 4 is most suitable (Griffing, 1956*b*). Maternal effects, which are very important in animals, can mostly be neglected in plants (Wricke & Weber, 1986).

It should be pointed out that to obtain unbiased estimates of the variance components, diallel crossing methods 3 or 4 must be used. Therefore the parental lines must not be included in the combining ability analysis (Griffing, 1956*b*). It is advisable however, to include the parents in the experimental material grown in the experiment so that comparisons of hybrids with their parents can be made in other types of analyses (Griffing, 1956*b*). It cannot be stressed too heavily, that only the simple diallel analysis of methods 3 and 4 can be used to estimate variance components of the population (Wricke & Weber, 1986).

Kempthorne (1956) summarised the basic assumptions in the theory of the diallel cross design. The starting point of the assumptions is a random mating population at equilibrium. The second basic assumption is that the inbred lines are obtained from this population without selection. The further assumptions applicable to the diallel are normal diploid segregation; no difference between reciprocal crosses, that is no maternal effects; arbitrary epistacy; an arbitrary number of alleles at each locus; the



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parents are homozygous; the phenotypical expression is equal to the sum of a genotypic contribution and an environmental contribution, the latter being associated at random with the genotype (Kempthorne, 1956). The absence of reciprocal effects is a requirement for diallel experimental method 4 (Griffing, 1956b).

There are two more approaches to diallel analysis which differ from the Griffing (1956a;b) way of analysis. The diallel analysis of Hayman (1954a) combined with the  $V_r/W_r$ -technique of Hayman (1954b) and Jinks (1954) include a test of the  $F_1$ 's together with completely inbred parents. The crossing designs corresponds with methods 1 and 2 of Griffing (1956b). Hayman (1954b) stated that this model would allow a description of the genetic situation, if amongst others, the following assumptions are met: (1) no multiple allelism and (2) independent distribution of genes. Kempthorne (1956) stated that the first assumption would be true if the original population were an  $F_2$  of two homozygous lines, which in most cases it is not. Gilbert (1958) also criticized the assumptions on which the Jinks-Hayman analysis is based as well as the regression of  $W_r$ , on  $V_r$ , concluding that the method is not directly relevant to plant breeding. No multiple allelism and independent gene distribution are assumptions which surely are not fulfilled in a diallel analysis (Weber, 1976). According to Griffing (1956a) the including of selfs of the parents, as well as crosses causes bias. Weber (1976) compared Griffing's methods 2 and 4 and found that with method 2 the mean squares for gca and sca are enlarged compared with method 4, since the varieties as pure lines show great differences. The values for gca were relatively more enlarged than the sca. Wricke & Weber (1986) came to the conclusion that the Jinks-Hayman analyses do not provide estimates of variance components which can be used in selection theory.

Gardner & Eberhart (1966) and Eberhart & Gardner (1966) proposed an extended diallel analysis where parents,  $F_1$ 's and  $F_2$ 's are analysed in one step. When these various kinds of relatives are derived from the same base population and are evaluated in the same experiment, a large set of equations can be solved simultaneously for  $\sigma^2_A$ ,  $\sigma^2_D$  and various epistatic variance components (Wricke & Weber, 1986). However, Gardner & Eberhart (1966) stated that when parents are homozygous lines and only the diallel cross is considered, the model reduces to the Hayman's (1954a;b) model. The objections to this model had been dealt with in the previous paragraph. Weber (1976) evaluated all three the diallel analysis approaches

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on the same set of parents, F<sub>1</sub>'s and in the case of the extended diallel analysis of Gardner & Eberhart (1966), the F<sub>2</sub>'s as well. Weber (1976) came to the conclusion that the three statistical methods all gave similar results. The main difference between the extended diallel analysis of Gardner & Eberhart (1966) and Eberhart & Gardner (1966) and the method of Griffing (1956*b*) was that the number of genetic parameters is increased in the Gardner-Eberhart analysis.

The variance component for gca in the diallel design is the covariance between half sibs like  $\sigma^2_m$  and  $\sigma^2_f$  in the factorial design,  $\sigma^2_m$  in the hierarchal design or general combining ability in the topcross or polycross (Wricke & Weber, 1986). The variance component for sca in the diallel design corresponds to the interaction component between males and females in the factorial design (Wricke & Weber, 1986).

With homozygous lines as parents, the following relationship holds in the F<sub>1</sub> of a diallel cross (Weber, 1976):

$$\sigma^2_{gca} = 1/2 \sigma^2_A + 1/4 \sigma^2_{AA} + \dots$$

$$\sigma^2_{sca} = \sigma^2_D + 1/2 \sigma^2_{AA} + \sigma^2_{AD} + \dots$$

The estimates of the variance components in a diallel analysis are unbiased only in the absence of epistatic effects (Griffing, 1956*b*) The additive by additive epistasis effect is the interaction of two alleles at different loci, while the dominance effect is the interaction of two alleles at the same locus (Eberhart & Gardner, 1966). Since there is only one parental group, no epistasis can be estimated in a diallel design (Wricke & Weber, 1986). However, no efficient design exist to estimate the three genetic variances  $\sigma^2_A$ ,  $\sigma^2_D$  and  $\sigma^2_{AA}$  (epistasis) simultaneously with sufficient accuracy (Wricke & Weber, 1986).

Diallel experiments with triticale which could be studied as references are those done by Kaltsikes & Lee (1973), Reddy (1976), Gill, Sandha & Dhindsa (1978), Gill, Bhardwaj & Dhindsa (1979), Rao & Joshi (1979), Carrillo, Monteagudo & Sanchez-Monge (1983), Brar, Sandha & Virk (1985), Dhindsa, Sandha & Gill (1985), Barker & Varughese (1992), Mangat, Dhindsa & Sandha (1992), Mangat & Dhindsa (1995), Węgrzyn, Goral & Spiss (1995), Dhindsa, Maini, Nanda & Singh (1998), Oettler, Heinrich & Miedaner (2004) and Herrmann (2007). Ten of these diallel experiments studied grain yield as either production per plant or production per unit area, while none studied crude protein characteristics in either vegetative material or grain. Five

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of these diallel studies used method 4 of Griffing (1956*b*) and all of those who used the half diallel without parental lines in the combining ability analysis, also considered the parental lines used by them as a selected, fixed group.

When breeding strategies based on the results of a diallel study are considered, it must be remembered that in a crop like triticale, only the genetic variability resulting from additive gene action can be effectively utilised when treated as a self pollinated crop in a breeding programme. This is because of the retainment of this component in subsequent self- fertilisation (Reddy, 1976). The sca effects would not contribute appreciably to improvement unless heterosis is exploited in the form of hybrid triticale varieties (Reddy, 1976; Brar, Sandha & Virk, 1985).

The determination of genetic correlation coefficients between characteristics is useful because they give information about the effect of selection on other traits. The selection success can be estimated in the correlated feature if the heritabilities of both traits and the genetic correlation between them are known (Falconer, 1989).

## **Material and methods**

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### **3.1 Experimental material**

#### **3.1.1 Parents**

PAN 299, three hexaploid French cultivars as well as two inbred breeding lines were used as parents in a 6x6 half diallel cross. The names or codes and origin for the six parents as well as the corresponding numbers that will be used to identify the different parents and F<sub>1</sub> combinations are shown in Table 3.1.

**Table 3.1 List of six triticale parents used in the 6x6 half diallel cross.**

<b>No.</b>	<b>Name or code of parent</b>	<b>Origin</b>
1	PAN 299	Pannar Seed (Pty) Ltd , South Africa
2	Clercal	Causade , France
3	Central	Causade , France
4	Magistral	Causade , France
5	80 CI 562	Causade , France
6	83 TT 124	Causade , France

#### **3.1.2 Development of the F<sub>1</sub> hybrids**

In order to develop the F<sub>1</sub> hybrids, four replications of ten pots each were planted two weeks apart for each of the six parents. The seed of the parents were first germinated in Petri dishes and vernalized for six weeks at 5°C. Thereafter the seedlings were planted in the pots. This was done from 22<sup>nd</sup> May until the 3<sup>rd</sup> July. When the different plantings reached the flowering stage, the young ears were emasculated and pollinated six to ten days later.

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Up to 36 pollinations were done per combination. Seed from reciprocal crosses were pooled in order to have enough seed for the planting of the trial, because 378 plants per F<sub>1</sub> combination were needed to conduct the trial. The pollinations were done from 18<sup>th</sup> September until the 29<sup>th</sup> December and the seed was harvested when physiologically ripe.

Prior to planting representative soil samples were taken of the area that would be planted. Based upon the results of the soil analysis, 350kg 3:2:1(25) fertilizer was broadcast per hectare shortly before planting. The amount of N, P and K added to the soil was therefore 43.75kg/ha, 29.17kg/ha and 14.58kg/ha respectively.

The fertilizer was then incorporated into the soil to a depth of about 50mm -100mm to ensure even distribution under the system of irrigation used. The blocks of the randomised block design were measured out across the variance in soil fertility and water holding capacity.

### 3.1.3 Trial layout

The seed from the six parent lines and the 15 F<sub>1</sub> combinations was also germinated as mentioned previously and then vernalized for approximately four weeks. The seedlings were then planted in the trial site at the Modder river research station ± 40km south west of the city Kimberley in South Africa.

The trial was a factorial experiment planted in a randomised block design. Three replications were planted, because this was an irrigated trial and variation was expected to be lower than in the case of a rain fed trial.

Forty two seedlings were planted per plot. The spacing was 150mm between plants in the row and 300mm between the rows. Three rows of fourteen plants each were planted per plot.

There was a spacing of 300mm between the long ends of the plots and 1.30m between the short ends of the rectangular plots. The effective plot size was 3.25m x 0.90m for a total area of 2.925m<sup>2</sup>.

The planting date was the 30<sup>th</sup> March.

The trial was watered when necessary by flood irrigation as the normal irrigation practice in this area. The purpose of the irrigation was to eliminate drought stress as a factor because this area receives practically no rain between end March and mid October.

### 3.2 Characters measured

#### 3.2.1 Vegetative characteristics

##### 3.2.1.1 Treatments

All the vegetative data used in this study came from two treatments in the factorial experiment. Six blocks of each genotype were cut the first time when the plants were approximately 15 – 25cm tall and all were still in the vegetative stage. The 3<sup>rd</sup> July was the median cutting date for the first cut. Cutting at this stage of development was selected to minimise the effect of cutting on grain yield while still having sufficient yield to warrant the harvest operation. This is normally the stage of growth when the triticale would be grazed for the first time.

Three of these six blocks were then cut for a second time when the tallest genotypes reached a height of approximately 45 – 50cm. These genotypes were at stage 7 – 9 (Bannerjee and Wienhues, 1965), which corresponds to the mid-joint stage of Dunphy *et al.* (1982). The 1<sup>st</sup> September was the median cutting date for the second cut. The mid-joint stage was chosen to maximise the forage yield, but without removing the developing ears, as was done by Poysa (1985). This is normally the stage when the last grazing would take place before the triticale would be left to produce grain in a dual purpose application.

These treatments resulted in three blocks of each genotype that were cut once and three blocks of each genotype that were cut twice. All the genotypes were cut as near as possible to the same time, so that growing conditions for all genotypes would be similar. All 42 plants per block were cut in each treatment because this was an irrigated trial and no edge effect was observed. All six parents as well as the 15 F<sub>1</sub> hybrid combinations were included in this experiment.

### **3.2.1.2 Measurement of characters**

For the purpose of this study the *percentage crude protein* as well as the *crude protein yield per hectare*, were determined from cuttings of vegetative material.

The plants in the different blocks were cut with a hand shear as was done by Brignall, *et al.* (1988). The cut height was 50mm above ground level as was the common cutting height by Morris & Gardner (1958), Droushiotis (1984) as well as Brignall *et al.* (1988). All the cut material was dried in force draught ovens at temperatures of 60 - 65°C as was recommended by Schmidt, Martin & Goodrich (1970) and done by Brown & Almodares (1976). The hot dried material was allowed to cool down in desiccators, before the weighing was done. All the vegetative yields were calculated on an oven dry basis.

Nitrogen (N) determinations were made on oven dried vegetative material with the standard Kjeldahl technique as discussed by Kirk (1950). Prior to the analysis all oven dried material of the different cuttings were milled with a Wiley electric mill to pass through a 0.8mm stainless steel sieve as recommended by Jones (1981). All analyses were performed in duplicate on the vegetative material from the two cut treatment and the mean values were taken for percentage crude protein calculations as were done by Petterson & Åman (1987) and Heger & Eggum (1991). The percentage crude protein of the vegetative material was calculated in each case by multiplying the percentage N by the conversion factor of 6.25 as were done for vegetative triticale material by Brown & Almodares (1976), Bishnoi & Hughes (1979), Nachit (1983) as well as Royo *et al.* (1993). At the same time as when the N analyses were done, samples of the milled material were dried in an oven at 105°C as was done by Petterson & Åman (1987) and allowed to cool down in desiccators before the samples were weighed. The moisture percentages at the time of N analyses were then calculated and the percentage crude protein corrected to percentage crude protein on a 100% dry basis.

The crude protein yield per hectare as calculated for the first time for triticale by Nachit (1983) was obtained by multiplying the percentage crude protein on a 100% dry matter basis with the corresponding vegetative yield also based on oven dried mass.

### 3.2.2 Grain characteristics

#### 3.2.2.1 Treatments

The grain related results came from three treatments in the factorial experiment. The control treatment was grain produced from three blocks of each genotype that were left uncut in the vegetative phase. The second and third treatments were grain produced from the three blocks of each cultivar that were cut once and twice respectively in the vegetative phase as explained under treatments of vegetative characters measured. Grain was harvested from all 42 plants per block in each of the treatments because this was an irrigated trial. The six parents as well as the 15 F<sub>1</sub> hybrid combinations were included in this experiment as well.

#### 3.2.2.2 Measurement of characters

The characters measured from the grain harvested were *grain yield per hectare*, *percentage crude protein* as well as the *crude protein yield per hectare*.

The grain was harvested from the second half of December to the first week of January when ripe and dry. The harvesting was done by cutting the ears from the plants with a hand shear. The threshing of the grain was done thereafter by using a Wintersteiger electric ear thresher. After drying milled samples of each grain lot at 105°C at the time of N analysis, as it was done in the case of the vegetative material, the percentages moisture were determined. The grain yield of each of the different genotypes, were then all corrected to yield at a moisture percentage of 12%.

The analyses to determine the N percentages were done in the same way as in the case of the vegetative material. The percentage crude protein in the grain was calculated by multiplying the percentage N by the conversion factor of 5.70 as recommended for small grain cereals by Tkachuk (1977) and used by Bishnoi & Hughes (1979), Royo *et al.* (1994) as well as Royo & Pares (1996) for calculation of percentage crude protein in triticale grain. The percentage crude protein of the grain was also corrected to percentage crude protein on a 100% dry basis in the same way as it was done in the case of the vegetative material.



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The crude protein yield per hectare was calculated by multiplying the percentage crude protein on a 100% dry matter basis with the corresponding grain yield on a 100% dry matter as was done in the case of the vegetative material.

### **3.2.3 Combination between vegetative and grain characters**

#### **3.2.3.1 Treatments**

The data used to calculate this character came from the two cut treatment in the factorial experiment.

#### **3.2.3.2 Character measured**

The character, *total herbivore utilisable crude protein yield per hectare* was calculated by summation of the total crude protein yield from the different vegetative cuttings and the total crude protein yield from grain in the corresponding treatment. The stubble of triticale that stays behind after harvesting is not considered to be palatable to herbivores and is best left standing in a no-till situation or else incorporated into the soil to help combat wind erosion in this area. The crude protein yield of this component was therefore not included in this crude protein production character.

## **3.3 Statistical analysis**

### **3.3.1 Factorial analysis**

The data from both the vegetative material as well as from the grain were separately subjected to factorial analyses. The factorial analyses were done with the AGROBASE (2000) program. Data from the six parents as well as from the 15 F<sub>1</sub> hybrid combinations were included in these analyses. The standard F-test was used to test if there were significant differences between genotypes across treatments as well as between the different treatments.

### 3.3.2 Randomised block analysis

After the factorial analyses were completed, the data from the different characters measured, were subjected to the standard analysis of variance of a randomised block experiment. This was done to test for differences between genotypes within each treatment. The program of AGROBASE (2000) was used to obtain the different ANOVA's. Data from the six parents as well as from the 15 F<sub>1</sub> hybrid combinations were included in these analyses as well. The standard F-test was used to test if there were significant differences between genotypes.

Instead of using the incorrect LSD values given by AGROBASE (2000), the LSD for means were determined with the following formulas given by Singh & Chaudhary (1979):

$$\text{S.E.} = \sqrt{\frac{2MS_e}{b}}$$

$$\text{LSD} = \text{S.E.} \times t_{0.05}$$

$t_{0.05}$  is the value of  $t$  in the  $t$  table at the level of significance of 0.05 (two tailed test) and  $df = df$  of  $MS_e$

If the mean difference between any two varieties was greater than the calculated LSD value then the difference was taken to be significant.

The same test was also performed using the  $t_{0.01}$  value to test for highly significant differences.

### 3.3.3 Diallel analysis

#### 3.3.3.1 Method used

Only the data from the 15 F<sub>1</sub> hybrid combinations were used for the diallel analysis as was recommended by Griffing (1956b). The data was analysed using the AGROBASE (2000) program. The *Method 4* with fixed effects was selected on the program for the diallel analysis. Since only one observation per block was available, AGROBASE (2000) used  $\{(v-1).(b-1)\}$  as the  $df$  for  $MS_e$  in the initial ANOVA (Personal communication from AGROBASE,2007). By using the  $df$ , of what is

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normally shown as the *df* for the  $MS_{(\text{block} \times \text{genotype})}$  interaction component in the initial ANOVA, as the *df* for  $MS_e$  in this analysis, implies that  $MS_{(bv)}$  was given as  $MS_e$  in the initial ANOVA and  $MS_{(bv)/bc}$  as  $M'_e$  in the combining ability ANOVA. This is effectively a *Method 4, mixed model B* analysis as described by Griffing (1956*b*), because  $M'_e$  in this particular case is  $MS_{(bv)/bc}$ . In the case of a *mixed model B* approach the genotype effects are regarded as constants, while the block effects are regarded as random variables (Griffing, 1956*b*). According to Griffing (1956*b*) is the combining ability analysis in the case of the *mixed model B* method essentially the same as for the *model 1* analysis except for the way in which  $M'_e$  is determined.

The model for the *Method 4, mixed model B* combining ability analysis given by Griffing (1956*b*) and adapted for the purpose of this study to cater for one observation per block is as follows:

$$X_{ij} = \mu + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + \frac{1}{b} \sum_k b_k + \frac{1}{b} \sum_k (bv)_{ijk} \quad \{\text{parent numbers: } i, j = 1, \dots, p\}$$

$$\quad \quad \quad \{\text{block numbers: } k = 1, \dots, b\}$$

$X_{ij}$  = the performance of the  $F_1$  cross between parents  $i$  and  $j$ ,

$\mu$  = population mean,

$\hat{g}_i$  and  $\hat{g}_j$  = the gca effect for the  $i$ th and the  $j$ th parent respectively,

$\hat{s}_{ij}$  = the sca effect for the cross between the  $i$ th and  $j$ th parents such that  $\hat{s}_{ij} = \hat{s}_{ji}$ .

All the other effects are random variables:

$b_k$  = the block effect,

$(bv)_{ijk}$  = the variety  $\times$  block interaction effect.

Restrictions:  $\sum_i \hat{g}_i = 0$

$$\sum_i \hat{s}_{ij} = 0 \text{ for each } j$$

$$\sum_k \sum_i (bv)_{ijk} = 0$$

Six diallel analyses were performed on the 15  $F_1$  hybrids for the six vegetative treatment combinations. Tests for significance of the  $MS_{gca}$  and the  $MS_{sca}$  were done with the standard F-test as for a *Method 4 model 1* analysis.

Nine diallel analyses were performed on the 15  $F_1$  hybrids for the nine grain related treatment combinations. Tests for significance of the  $MS_{gca}$  and the  $MS_{sca}$  were done in the same way as in the case of the vegetative treatment combinations.

### 3.3.3.2 General combining ability

The following three formulas given by Griffing (1956*b*) were used by AGROBASE (2000) to determine the  $SS_{gca}$ ,  $MS_{gca}$  as well as the individual gca effects, averaged for parents used as males and females:

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$$SS_{gca} = \frac{1}{(p-2)} \sum_i \mathbf{X}_i^2 - \frac{4}{p(p-2)} \mathbf{X}_{..}^2$$

$$MS_{gca} = \frac{SS_{gca}}{df_{gca}}$$

$$\text{gca effect of parent } i: \hat{g}_i = \frac{1}{p(p-2)} [p\mathbf{X}_{i.} - 2\mathbf{X}_{..}]$$

The following two formulas given by Griffing (1956*b*) were then used by AGROBASE (2000) to calculate the S.E. value for the variance between gca effects of the parents:

$$\text{var } (\hat{g}_i - \hat{g}_j) = \frac{2}{(p-2)} \times \sigma_e^2 \quad (i \neq j)$$

$$\text{S.E. } (\hat{g}_i - \hat{g}_j) = \sqrt{\text{var } (\hat{g}_i - \hat{g}_j)}$$

The formula given by Singh & Chaudhary (1979) was used in this study to calculate the LSD of gca effects within each treatment:

$$\text{LSD of } (\hat{g}_i - \hat{g}_j) = \text{S.E. } (\hat{g}_i - \hat{g}_j) \times t_{0.05}$$

$t_{0.05}$  is the value of  $t$  in the  $t$  table at the level of significance of 0.05 (two tailed test) and  $df = df$  of  $M'_e$

If the difference between the mean gca effects of two parents in the diallel was more than the LSD value, then it implied that the two gca effects were significantly different from each other. No test exists to test the differences of effects between treatments.

### 3.3.3.3 Specific combining ability

The following three formulas given by Griffing (1956*b*) were used by AGROBASE (2000) to determine the  $SS_{sca}$ ,  $MS_{sca}$  as well as the individual sca effects:

$$SS_{sca} = \sum_{i < j} \sum_j \mathbf{X}_{ij}^2 - \frac{1}{(p-2)} \sum_i \mathbf{X}_i^2 + \frac{2}{(p-1)(p-2)} \mathbf{X}_{..}^2$$

$$MS_{sca} = \frac{SS_{sca}}{df_{sca}}$$

$$\text{sca effect of cross } i \times j: \hat{s}_{ij} = \mathbf{X}_{ij} - \frac{1}{(p-2)} (\mathbf{X}_i + \mathbf{X}_j) + \frac{2}{(p-1)(p-2)} \mathbf{X}_{..}$$

The following two formulas given by Griffing (1956*b*) were then used by AGROBASE (2000) to calculate the S.E. value in this case:

$$\text{var } (\hat{s}_{ij} - \hat{s}_{ik}) = \frac{2(p-3)}{(p-2)} \times \sigma_e^2 \quad (i \neq j, k; j \neq k)$$

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$$\text{S.E. } (\hat{\sigma}_{ij} - \hat{\sigma}_{ik}) = \sqrt{\text{var}(\hat{\sigma}_{ij} - \hat{\sigma}_{ik})}$$

The formula given by Singh & Chaudhary (1979) was used in this study to calculate the LSD of sca effects within each treatment:

$$\text{LSD of } (\hat{\sigma}_{ij} - \hat{\sigma}_{ik}) = \text{S.E. } (\hat{\sigma}_{ij} - \hat{\sigma}_{ik}) \times t_{0.05}$$

$t_{0.05}$  is the value of  $t$  in the  $t$  table at the level of significance of 0.05 (two tailed test) and  $df = df$  of  $M'_e$

If the difference between the sca effects of two F1 hybrids in the diallel was more than the LSD value, then it implied that the two sca effects were significantly different from each other. No test exists to test the differences of effects between treatments.

### 3.3.3.4 Components of variance and heritabilities

Instead of changing the assumption about the randomness of the parents used in the diallel cross after the combining ability effects had been determined as was done previously by Weber (1976) and Carrillo *et al.* (1983) it was decided to keep to the original decision that the parents were a selected group and that the variety effects were therefore constants.

Griffing & Lindstrom (1954) as well as Griffing (1956*b*) determined the variance components from a *model 1* combining ability analysis where the variety effects were constants. As was already mentioned before, Griffing (1956*b*) stated when a *mixed model B* is used the combining ability analysis is essentially the same as the *model 1* analysis except for the way in which the error term  $M'_e$  is determined. It was therefore decided to determine the variance components for the *Method 4, mixed model B* diallel analysis also in the same way as Griffing & Lindstrom (1954) and Griffing (1956*b*) did in the case of a *Method 4 model 1* analysis, but with the appropriate error term.

The formulas as outlined by Griffing & Lindstrom (1954), Griffing (1956*b*) and elaborated on by Becker (1984) was used as follows:

$$\begin{aligned} \text{Variance of gca in the parent population: } \sigma^2_{gca} &= \frac{1}{df_{gca}} \times \frac{MS_{gca} - (MS_{e/bc})}{\frac{(p-2)}{(p-1)}} \\ &= \frac{1}{df_{gca}} \times \frac{MS_{gca} - M'_e}{\frac{(p-2)}{(p-1)}} \end{aligned}$$

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$$\begin{aligned} \text{Variance of sca in the group of F}_1 \text{ progeny: } \sigma^2_{\text{sca}} &= \frac{1}{df_{\text{sca}}} \times \frac{MS_{\text{sca}} - (MS_e/bc)}{\frac{2}{p(p-3)}} \\ &= \frac{1}{df_{\text{sca}}} \times \frac{MS_{\text{sca}} - M'_e}{\frac{2}{p(p-3)}} \end{aligned}$$

Griffing & Lindstrom (1954) stated clearly that inferences regarding these effects should be made only for the specific set of parents and their F1 progeny.

The  $\sigma^2_{\text{gca}}/\sigma^2_{\text{sca}}$  ratios were then determined for the different characters measured as was done for a fixed genotype situation by Carrillo et al. (1983). This was done to get an idea of the relative importance of  $\sigma^2_{\text{gca}}$  versus  $\sigma^2_{\text{sca}}$ .

The values of  $\sigma^2_{\text{gca}}$ ,  $\sigma^2_{\text{sca}}$  and  $\sigma^2_e$  were then used to determine the following variance components for variables as was done previously by Dehghani & Moghaddam (2004) for a *mixed model B* analysis. The formulas were originally given by Griffing (1956a) and Griffing (1956b).

$$\sigma^2_A = 2\sigma^2_{\text{gca}} \text{ (additive genetic variance)}$$

$$\sigma^2_{D+I} = \sigma^2_{\text{sca}} \text{ (originally given as } \sigma^2_{\text{na}} = \sigma^2_{\text{sca}} \text{ to indicate the non additive genetic variation.)}$$

$$\sigma^2_G = 2\sigma^2_{\text{gca}} + \sigma^2_{\text{sca}} \text{ (genotypic variance)}$$

$$\sigma^2_e = M'_e \text{ (error variance to indicate the variance due to the environment)}$$

$$\sigma^2_P = \sigma^2_G + \sigma^2_e \text{ (phenotypic variance)}$$

From these formulas the following formula for phenotypic variance were derived:

$$\sigma^2_P = 2\sigma^2_{\text{gca}} + \sigma^2_{\text{sca}} + \sigma^2_e$$

The variance components were used to determine the broad sense heritability as defined by Singh & Chaudhary (1979) as well as Falconer (1989):

$$h_b^2 = \sigma^2_G / \sigma^2_P$$

The narrow sense heritability as defined by Falconer (1989) was also determined for the various characters measured. The formula given by Falconer (1989) is as follows:

$$h_n^2 = \sigma^2_A / \sigma^2_P$$

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With the determination of S.E. for the various variance components as well as the two kinds of heritabilities it was decided to steer away from the usual way of estimating S.E. for these components, because the formulas given by Griffing (1956b) and Becker (1984) were always used in conjunction with a random *model 2* situation. In the context where these formulas were used, the S.E. values for the parameters in the larger population were estimated based upon the results from a random sample studied (Griffing, 1956b).

The S.E. values in this study were determined as follows:

The variance of the gca effect was firstly determined with the formula given by Griffing (1956b):

$$\text{Variance of the gca effect : } \text{var}(\hat{g}_i) = \frac{(\rho-1)}{\rho(\rho-2)} \times \sigma_e^2$$

The gca variance for each of the six parents used in the diallel was then determined using the following formula given by Griffing (1956b) and Becker (1984):

$$\text{gca variance of parent } i : \sigma_{g_i}^2 = (\hat{g}_i)^2 - \frac{(\rho-1)}{\rho(\rho-2)} \times \sigma_e^2$$

The variance of the sca effect was also determined using the formula used by Griffing (1956b):

$$\text{Variance of the sca effect : } \text{var}(\hat{s}_{ij}) = \frac{(\rho-3)}{(\rho-2)} \times \sigma_e^2$$

The sca variance for each of the six parents used in the diallel was then determined using the formula given by Griffing (1956b) and Becker (1984):

$$\text{sca variance of parent } i : \sigma_{s_i}^2 = \frac{1}{(\rho-2)} \sum_{j \neq i} \hat{s}_{ij}^2 - \frac{(\rho-3)}{(\rho-2)} \times \sigma_e^2$$

All the variance components that were previously determined for the fixed population used in the half diallel, were also determined for each of the six parents using the appropriate gca variance and sca variance determined for each parent. The  $\sigma_e^2$  term was the same for all the parents.

This procedure was done for each of the characters measured.

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Model 1 assumptions according to Eisenhart (1947) were used when a decision was made on possible formulas to use. Formulas as given by Scheffler (1979) to determine the variance, standard deviation and S.E. of a sample are as follows:

$$S^2 = \sum(x-\text{mean})^2/p \quad (\text{Variance})$$

$$S = \sqrt{S^2} \quad (\text{Standard deviation})$$

$$\text{S.E.} = \frac{S}{\sqrt{p}} \quad (\text{p was substituted for the } n \text{ originally used to denote the number of individuals in the sample; in this case the population consisted of } p \text{ parents.})$$

These formulas were used to determine the S.E. for each of the variance components and heritabilities in the closed population studied. This was done for each of the characters measured.

The S.E. values thus derived were then given as the S.E. attached to the value of the variance components and heritabilities determined for the fixed population used in this half diallel study.

### 3.3.3.5 Additive genetic correlations

In order to determine the additive genetic correlations between the selected characters, the gca effects of the parents for each of the two characters were correlated with each other.

Falconer (1989) gave the following general formula for the determination of a correlation:

$$r_A = \frac{\text{COV}_{xy}}{\sqrt{(\text{var}_x \cdot \text{var}_y)}}$$

By replacing  $\theta$  in the following formula given by Griffing (1956b) with the additive effect A, the correlation between the additive genetic variances of two characters could be determined:

$$r_{Aij} = \sigma^2_{Aij} / \sqrt{\{(\sigma^2_{Ai}) \cdot (\sigma^2_{Aj})\}}$$

$\sigma^2_{Aij}$  is the additive genetic variance for the cross products,

$\sigma^2_{Ai}$  is the additive genetic variance for the independent character  $i$ ,

$\sigma^2_{Aj}$  is the additive genetic variance for the dependent character  $y$ .



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In order to test the significance of the determined additive genetic correlations, the following formula of a  $t$  test given by Scheffler (1979) was used:

$t = r / \sqrt{\{(1-r^2)/(p-2)\}}$  (the original  $n$  in the formula was replaced by  $p$  for the sake of standardisation of symbols in this study.)

The  $t$  value determined in this way was then compared with  $t_{0.05}$ , the value of  $t$  in the  $t$  table at the level of significance of 0.05 (two tailed test) and  $df = p - 2$ .

If the calculated  $t$  value was greater than the table value of  $t$ , the correlation was deemed to be significant.

The test given by Rohlf & Sokal (1995) was used as an additional test to test the calculated additive genetic correlation coefficients for significance. In this test the value at  $df = n - 2$  was compared with the calculated additive genetic correlation coefficients. In the case of this study the value of  $n$  in the table was equal to  $p = 6$ .

If the value of the calculated correlation coefficient was greater than the table correlation coefficient, the correlation was deemed to be significant. The calculated correlation coefficients were only marked with asterisks to indicate significance if both of these tests were positive.

### **3.3.3.6 Correlated response**

The correlated response in the case of each additive genetic correlation was determined using the following formula given by Falconer (1989):

$$CR_y = i \times h_x \times h_y \times r_A \times \sigma_{py}$$

$CR_y$  is the correlated response of the dependent character  $y$ ,

$i$  is the intensity of selection read from the graph given by Falconer (1989),

$h_x$  is the square root of the narrow sense heritability for the independent character  $x$ ,

$h_y$  is the square root of the narrow sense heritability for the dependent character  $y$ ,

$r_A$  is the coefficient of the additive genetic correlation between the two characters,

$\sigma_{py}$  is the square root of the phenotypic variance for the dependent character  $y$ .

# Phenotypic variability for crude protein characteristics in triticale.

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## 4.1 Vegetative characteristics

### 4.1.1 Factorial analysis

#### 4.1.1.1 *Results*

The mean squares for percentage crude protein and crude protein yield of the triticale vegetative material in the factorial analysis of variance are presented in Table 4.1.

#### 4.1.1.2 *Discussion*

The analyses of variance in Table 4.1 showed that the treatment differences for both of the characters were highly significant. The treatments were therefore chosen correctly in order to show differences between them.

The highly significant differences between blocks in the case of percentage crude protein indicate that enough soil variation was present to justify the use of the randomised block design in order to minimise the MS error. No significant differences between blocks existed in the case of crude protein yield of the vegetative material.

No significant genotype x treatment interaction occurred for either of the two characters measured.

The F-test showed that highly significant differences existed between the genotypes used in this study. Highly significant differences were shown in this respect for both of the vegetative characters studied. This justified more detailed statistical analyses to establish if the differences between the genotypes would continue within the different treatments.

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**Table 4.1 Mean squares for percentage crude protein and crude protein yield of triticale vegetative material in the factorial ANOVA.**

		<b>Characters</b>	
	<b>df</b>	<b>% Crude protein</b>	<b>Crude protein yield</b>
<b>Genotypes</b>	20	16.877 **	52887.727 **
<b>Treatments</b>	1	282.089 **	2174821.690 **
<b>Genotype x Treatment</b>	20	3.108	4049.332
<b>Blocks</b>	2	175.115 **	8767.982
<b>Error</b>	82	3.390	7368.539

### 4.1.2 Randomised block design analyses

#### 4.1.2.1 Results

The mean squares for percentage crude protein of the triticale vegetative material in the normal randomised block design analysis of variance are presented in Table 4.2.

The mean squares for crude protein yield of the triticale vegetative material in the normal randomised block design analysis of variance are presented in Table 4.3.

#### 4.1.2.2 Discussion

The F-tests showed that the highly significant differences between blocks in the case of percentage crude protein also occurred within each of the treatments. This gave further justification for the use of blocks in the trial design. No significant differences between blocks were found in the case of crude protein yield in any one of the treatments.

The F-test showed highly significant differences between genotypes in each of the treatments, for percentage crude protein and also for the crude protein yield of the vegetative material. Royo & Pares (1996) also found significant differences between triticale genotypes for percentage crude protein. The results of this study indicated that both of the vegetative characters measured, can be genetically improved upon.

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**Table 4.2 Mean squares for percentage crude protein of the triticale vegetative material in the randomised block design ANOVA.**

		<b>% Crude protein</b>		
	<b>df</b>	<b>Cut 1</b>	<b>Cut 2</b>	<b>Combined[cut (1+2) treatment]</b>
<b>Genotypes</b>	20	15.609 **	2.827 **	4.376 **
<b>Blocks</b>	2	127.665 **	43.654 **	55.474 **
<b>Error</b>	40	5.134	1.039	1.414

**Table 4.3 Mean squares for crude protein yield of the triticale vegetative material in the randomised block design ANOVA.**

		<b>Crude protein yield</b>		
	<b>df</b>	<b>Cut 1</b>	<b>Cut 2</b>	<b>Total yield[cut (1+2) treatment]</b>
<b>Genotypes</b>	20	17272.875 **	8098.648 **	39664.173 **
<b>Blocks</b>	2	8629.795	7861.093	4068.726
<b>Error</b>	40	4079.003	3165.854	10829.976

### 4.1.3 Tables of means

#### 4.1.3.1 Results

The means for the different characters measured, were determined between the replications and are listed for both the parents as well as the 15 F<sub>1</sub> hybrids.

The highest value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The means of the treatment combinations for percentage crude protein of the triticale vegetative material are presented in Table 4.4.

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**Table 4.4 Means of treatment combinations for percentage crude protein of the triticale vegetative material.**

Genotypes	% Crude protein		
	Cut 1	Cut 2	Combined[cut (1+2) treatment]
<b>1</b>	<b>20.55</b>	<b>13.43</b>	<b>15.88</b>
<b>2</b>	16.30*	11.61 *	13.63 *
<b>3</b>	13.84 **	10.77 **	11.58 **
<b>4</b>	11.74 **	9.90 **	10.48 **
<b>5</b>	14.63 **	12.97	13.25 **
<b>6</b>	19.31	11.49 *	13.84 *
<b>1 x 2</b>	19.21	11.41 *	14.05
<b>1 x 3</b>	18.90	11.59 *	14.22
<b>1 x 4</b>	13.38 **	11.56 *	12.01 **
<b>1 x 5</b>	17.71	11.99	13.54 *
<b>1 x 6</b>	18.80	11.27 *	13.42 *
<b>2 x 3</b>	14.52 **	11.81	12.87 **
<b>2 x 4</b>	17.14	12.94	14.83
<b>2 x 5</b>	15.17 **	11.12 **	12.44 **
<b>2 x 6</b>	15.20 **	11.22 *	13.10 **
<b>3 x 4</b>	17.22	12.48	14.24
<b>3 x 5</b>	15.60 *	9.99 **	11.92 **
<b>3 x 6</b>	15.06 **	10.57 **	12.25 **
<b>4 x 5</b>	14.02 **	12.81	13.14 **
<b>4 x 6</b>	15.38 **	11.10 **	12.24 **
<b>5 x 6</b>	15.62 *	12.80	13.54 *
<b>Mean</b>	<b>16.16</b>	11.66	13.17** ← <b>LSD<sub>0.001</sub></b> <sup>Treatments</sup> = 1.12
<b>LSD<sub>0.05</sub></b>	3.74	1.68	1.96
<b>LSD<sub>0.01</sub></b>	5.00	2.25	2.63
<b>C.V.</b>	14.02	8.74	9.03

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The means of the treatment combinations for crude protein yield of the triticale vegetative material are presented in Table 4.5.

**Table 4.5 Means of treatment combinations for crude protein yield of the triticale vegetative material.**

Genotypes	Crude protein yield (kg/ha)		
	Cut 1	Cut 2	Total yield[cut (1+2) treatment]
1	254.51	316.25	570.76
2	228.49	199.00 **	427.49 *
3	123.28 **	232.05 *	355.34 **
4	79.10 **	114.03 **	193.13 **
5	85.60 **	204.43 **	290.04 **
6	232.78	301.12	533.89
1 x 2	263.98	300.59	564.57
1 x 3	297.17	324.35	<b>621.52</b>
1 x 4	94.60 **	231.29 *	325.88 **
1 x 5	144.80 **	274.38	419.18 *
1 x 6	226.04	<b>339.72</b>	565.76
2 x 3	201.41 *	204.95 **	406.36 *
2 x 4	<b>324.81</b>	292.84	617.65
2 x 5	211.33 *	298.83	510.16
2 x 6	321.42	275.86	597.28
3 x 4	204.34 *	251.20	455.54
3 x 5	234.66	282.29	516.95
3 x 6	227.68	271.31	498.99
4 x 5	116.36 **	284.37	400.73 *
4 x 6	135.31 **	264.98	400.29 *
5 x 6	129.99 **	254.07	384.07 **
<b>Mean</b>	197.03 ***	262.76	<b>459.79</b> ← $LSD_{0.001}^{Treatments} = 52.25$
<b>LSD<sub>0.05</sub></b>	105.39	92.85	171.73
<b>LSD<sub>0.01</sub></b>	141.01	124.22	229.76
<b>C.V.</b>	32.41	21.41	22.63

### 4.1.3.2 Discussion

The percentages crude protein of the vegetative material analysed in this study were generally lower than those found by Skorda (1978), Bishnoi & Hughes (1979), Royo *et al.* (1994) and Royo & Pares (1996), but more in agreement with the range of percentages found by Brown & Almodares (1976). There was a marked drop in percentage crude protein between the first cut and the second cut. In this study the two consecutive cuttings were done without a top dressing of N fertilizer between the cuttings. Brown & Almodares (1976) also took two more cuttings after the last fertilizer application in the second year of that trial and also found a marked drop in percentage crude protein in the last cut. Skorda (1978) found a rapidly rate of decline in percentage crude protein of triticale forage with phenological development beyond the vegetative stage. The lower value of percentage crude protein for the second cut may therefore be due to a combination of a lack of N to sustain a high percentage protein in the regrowth after the first cut as well as the effect of a more advanced phenological growth stage at the second cut.

The mean of the crude protein yields for the genotypes used in this study was lower than what was found by Nachit (1983), Royo *et al.* (1994) and Royo & Pares (1996) but the N fertilizer application in this study was lower and the cuttings were done at different phenological growth stages than in these studies.

The coefficients of variance (CV) for the different vegetative crude protein yields were higher than those obtained for the respective percentages crude protein. No value for the variation found for vegetative crude protein yield was given by Nachit (1983). The CV for the different vegetative crude protein yields were within the range given by Frame (1981) for herbage yield determination by means of cutting plots of comparable size to those used in this study.

When the means of percentage crude protein for each parent and F<sub>1</sub> hybrid are compared in Table 4.4 the following were found: Parent 1 had the highest value of all the parents in cut 1. The mean value of parent 1 showed highly significant differences with the means of parents 3, 4 and 5. A significant difference was shown with the means of parent 2. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in cut 1. The mean value of 1x2 showed a highly significant difference with the mean of 4x5 and significant differences were shown with the means of 2x3, 2x5, 2x6, 3x6 and 4x6.

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Parent 1 had the highest value of all the parents in cut 2 as well. The mean value of parent 1 showed highly significant differences with the means of parents 3 and 4 and significant differences were shown with the means of parents 2 and 6. Amongst the F<sub>1</sub> hybrids, 2x4 had the highest mean value in cut 2. The mean value of 2x4 showed highly significant differences with the means of 3x5 and 3x6 and significant differences with the means of 2x5, 2x6 and 4x6.

Parent 1 had the highest value of all the parents once again when the percentages crude protein of the total harvested vegetative material were considered. The mean value of parent 1 showed highly significant differences with the means of parents 3, 4 and 5 and significant differences were shown with the means of parents 2 and 6. Amongst the F<sub>1</sub> hybrids, 2x4 had the highest mean value as in the case of cut 2. The mean value of 2x4 showed highly significant differences with the means of 1x4 and 3x5 and significant differences were shown with the means of 2x3, 2x5, 3x6 and 4x6.

Parent 1 had the highest mean value of all the parents and F<sub>1</sub> hybrids across treatments when the percentage crude protein of the harvested vegetative material was considered. The mean values of parents 3 and 4 were in all cases highly significantly lower than the mean of parent 1. Amongst the F<sub>1</sub> hybrids, the means of 2x5, 2x6, 3x6 and 4x6 were in both treatments significantly lower than the mean value of the best respective hybrid.

When the means of the crude protein yield for each parent and F<sub>1</sub> hybrid are compared in Table 4.5 the following were found: Parent 1 had the highest value of all the parents in cut 1. The mean value of parent 1 showed highly significant differences with the means of parents 4 and 5 and a significant difference was shown with the mean of parent 3. Amongst the F<sub>1</sub> hybrids, 2x4 had the highest mean value in cut 1. The mean value of 2x4 showed highly significant differences with the means of 1x4, 1x5, 4x5, 4x6 and 5x6. Significant differences were shown with the means of 2x3, 2x5 and 3x4.

Parent 1 had the highest value of all the parents in cut 2 as well. The mean value of parent 1 showed a highly significant difference with the mean of parent 4 and significant differences were shown with the means of parents 2 and 5. Amongst the



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F<sub>1</sub> hybrids, 1x6 had the highest mean value in cut 2. The mean value of 1x6 showed a highly significant difference with the mean of 2x3 and a significant difference with the mean of 1x4.

Parent 1 had the highest value of all the parents once again when the total crude protein yield of the harvested vegetative material were considered. The mean value of parent 1 showed highly significant differences with the means of parents 4 and 5 and a significant difference was shown with the mean of parent 3. Amongst the F<sub>1</sub> hybrids, 1x3 had the highest mean value. The mean value of 1x3 showed highly significant differences with the means of 1x4 and 5x6 and significant differences were shown with the means of 1x5, 2x3, 4x5 and 4x6.

Three different hybrids had the highest mean values of all the parents and F<sub>1</sub> hybrids across treatments when the crude protein yield of the harvested vegetative material was considered. The mean values of parents 4 and 5 were in all cases at least significantly lower than the mean of parent 1. Amongst the F<sub>1</sub> hybrids, the means of 1x4 and 2x3 were in all cases significantly lower than the mean value of the best respective hybrid.

## 4.2 Grain characteristics

### 4.2.1 Factorial analysis

#### 4.2.1.1 *Results*

The mean squares for grain yield, percentage crude protein and crude protein yield of the triticale grain in the factorial analysis of variance are presented in Table 4.6.

#### 4.2.1.2 *Discussion*

The analyses of variance for the three characters showed that the treatment differences for all the characters were highly significant. The treatments were therefore chosen correctly in order to show differences between them.

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The highly significant differences between blocks for all the grain characters measured, indicate that enough soil variation was present to justify the use of blocks in the trial design in order to minimise the MS error.

No significant genotype  $\times$  treatment interaction occurred with any of the three characters measured.

The F-test showed that highly significant differences existed between the genotypes used in this study. Highly significant differences were shown in this respect for each of the grain characters studied. This justified more detailed statistical analyses to establish if the differences between the genotypes would continue within the different treatments.

**Table 4.6 Mean squares for grain yield, percentage crude protein and crude protein yield of triticale grain in the factorial ANOVA.**

	df	Characters		
		Grain yield	% Crude protein	Crude protein yield
<b>Genotypes</b>	20	1.632 **	3.435 **	12507.539 **
<b>Treatments</b>	2	117.276 **	51.299 **	984551.457 **
<b>Genotype <math>\times</math> Treatment</b>	40	0.584	1.005	4133.170
<b>Blocks</b>	2	12.213 **	15.618 **	101736.182 **
<b>Error</b>	124	0.531	1.387	5280.40

### 4.2.2 Randomised block design analysis

#### 4.2.2.1 Results

The mean squares for the triticale grain yield in the normal randomised block design analysis of variance are presented in Table 4.7.

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**Table 4.7 Mean squares for triticale grain yield in the randomised block design ANOVA.**

		<b>Grain yield</b>		
	<b>df</b>	<b>Control</b>	<b>Cut 1</b>	<b>Cut (1+2)</b>
<b>Genotypes</b>	20	1.846 *	0.784	0.170 *
<b>Blocks</b>	2	5.818 **	6.835 **	3.400 **
<b>Error</b>	40	0.932	0.446	0.074

The mean squares for percentage crude protein of the triticale grain in the normal randomised block design analysis of variance are presented in Table 4.8.

**Table 4.8 Mean squares for percentage crude protein of the triticale grain in the randomised block design ANOVA.**

		<b>% Crude protein</b>		
	<b>df</b>	<b>Control</b>	<b>Cut 1</b>	<b>Cut (1+2)</b>
<b>Genotypes</b>	20	1.446 **	2.127 **	1.873
<b>Blocks</b>	2	0.037	0.824	40.725 **
<b>Error</b>	40	0.569	0.530	1.901

The mean squares for crude protein yield of the triticale grain in the normal randomised block design analysis of variance are presented in Table 4.9.

**Table 4.9 Mean squares for crude protein yield of triticale grain in the randomised block design ANOVA.**

		<b>Crude protein yield</b>		
	<b>df</b>	<b>Control</b>	<b>Cut 1</b>	<b>Cut (1+2)</b>
<b>Genotypes</b>	20	14034.676	5077.570	1661.632 **
<b>Blocks</b>	2	51761.665 *	55371.859 **	29846.803 **
<b>Error</b>	40	10053.998	3938.632	614.407

### 4.2.2.2 *Discussion*

The F-tests showed that the highly significant differences between blocks also occurred within six of the nine treatment combinations for grain characters. A significant difference between blocks was also shown for crude protein yield of the grain in the control treatment. This showed that the use of blocks in the trial design was justified in most cases for this study. No significant differences between blocks were found in the case of percentage crude protein for the control treatment and the cut 1 treatment.

The F-test showed significant differences between genotypes in the control treatment and the cut (1+2) treatment for grain yield. Highly significant differences between genotypes were shown in the control treatment and the cut 1 treatment for percentage crude protein and in the cut (1+2) treatment for crude protein yield of the grain. This indicated that all of the vegetative characters measured can be genetically improved upon when evaluated in the appropriate treatment combination.

### 4.2.3 Tables of means

#### 4.2.3.1 *Results*

The means for the different characters measured, were determined between the replications and are listed for both the parents as well as the 15 F<sub>1</sub> hybrids.

The highest value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The means of the treatment combinations for triticale grain yield are presented in Table 4.10.

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**Table 4.10 Means of treatment combinations for triticale grain yield.**

Genotypes	Grain yield (1000kg/ha)		
	Control	Cut 1	Cut (1+2)
1	3.91	1.73	1.03
2	3.53	2.28	0.70 *
3	3.29	2.36	0.55 **
4	2.05 **	0.57 **	0.16 **
5	1.67 **	1.30 **	0.34 **
6	3.50	1.59 *	0.59 **
1 x 2	4.23	<b>2.79</b>	<b>1.22</b>
1 x 3	<b>4.74</b>	2.03	0.59 **
1 x 4	4.07	2.22	0.86
1 x 5	2.74 *	1.90	0.75 *
1 x 6	4.42	1.49 *	0.69 *
2 x 3	2.70 *	2.28	0.87
2 x 4	3.17	2.48	0.54 **
2 x 5	3.61	2.57	0.87
2 x 6	4.21	2.36	0.87
3 x 4	3.55	1.98	0.64 *
3 x 5	4.23	2.43	0.48 **
3 x 6	3.25	2.04	0.95
4 x 5	3.03 *	2.29	0.66 *
4 x 6	2.58 **	1.88	0.56 **
5 x 6	3.49	1.49 *	0.76 *
<b>Mean</b>	<b>3.43</b>	2.00***	0.70*** ← <b>LSD</b> <sub>0.001</sub> Treatments = 0.44
<b>LSD</b> <sub>0.05</sub>	1.59	1.10	0.45
<b>LSD</b> <sub>0.01</sub>	2.13	1.47	0.60
<b>C.V.</b>	28.17	33.36	39.03

The means of the treatment combinations for percentage crude protein of the triticale grain are presented in Table 4.11.

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**Table 4.11 Means of treatment combinations for percentage crude protein of the triticale grain.**

Genotypes	%Crude protein		
	Control	Cut 1	Cut (1+2)
1	10.47 **	12.00	12.45
2	11.02 *	9.09 **	10.85 **
3	10.83 *	9.99 **	12.18
4	9.89 **	10.75 **	13.12
5	<b>12.28</b>	<b>12.41</b>	<b>13.90</b>
6	10.51 **	10.59 **	12.96
1 x 2	9.63 **	10.33 **	11.80
1 x 3	9.88 **	10.35 **	11.14 *
1 x 4	9.81 **	10.40 **	11.85
1 x 5	10.38 **	10.51 **	11.46 *
1 x 6	10.55 **	10.91 *	11.44 *
2 x 3	11.31	9.91 **	11.46 *
2 x 4	11.53	9.78 **	12.59
2 x 5	10.10 **	9.61 **	11.09 *
2 x 6	10.91 *	9.88 **	11.34 *
3 x 4	11.28	10.68 **	12.78
3 x 5	9.99 **	10.23 **	12.45
3 x 6	11.30	10.44 **	11.77
4 x 5	9.80 **	9.20 **	12.09
4 x 6	10.24 **	9.38 **	11.35 *
5 x 6	10.94 *	11.46	12.77
<b>Mean</b>	10.60 ***	10.38 ***	<b>12.04</b> ← <b>LSD<sub>0.001</sub></b> <sup>Treatments</sup> = 0.71
<b>LSD<sub>0.05</sub></b>	1.24	1.20	2.28
<b>LSD<sub>0.01</sub></b>	1.67	1.61	3.04
<b>C.V.</b>	7.12	7.01	11.45

The means of the treatment combinations for crude protein yield of the triticale grain are presented in Table 4.12.

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**Table 4.12 Means of treatment combinations for crude protein yield of the triticale grain.**

Genotypes	Crude protein yield (kg/ha)		
	Control	Cut 1	Cut (1+2)
1	362.90	184.20	113.68
2	340.56	182.17	65.58 **
3	314.45	207.67	54.77 **
4	182.10 **	54.55 **	16.57 **
5	179.23 **	143.38 *	35.36 **
6	323.87	144.96 *	64.35 **
1 x 2	356.08	<b>252.22</b>	<b>123.56</b>
1 x 3	413.37	183.99	57.92 **
1 x 4	351.36	202.09	82.34 *
1 x 5	245.34 *	176.14	70.00 *
1 x 6	<b>418.31</b>	134.29 *	69.47 *
2 x 3	262.94	201.27	79.20 *
2 x 4	322.67	218.10	56.31 **
2 x 5	324.37	217.01	79.91 *
2 x 6	401.76	206.47	84.49
3 x 4	355.06	184.19	71.60 *
3 x 5	379.98	218.44	51.25 **
3 x 6	325.77	183.00	88.74
4 x 5	262.09	185.72	59.76 **
4 x 6	232.31 *	155.93	53.66 **
5 x 6	338.51	150.98	74.48 *
<b>Mean</b>	<b>318.72</b>	180.32 ***	69.19 *** ← <b>LSD<sub>0.001</sub></b> <sup>Treatments</sup> = 43.65
<b>LSD<sub>0.05</sub></b>	165.46	103.56	40.90
<b>LSD<sub>0.01</sub></b>	221.38	138.56	54.73
<b>C.V.</b>	31.46	34.80	35.83

### 4.2.3.2 Discussion

The range of grain yields for the different genotypes of the control treatment in this study is lower than those found by Barker & Varughese (1992) in their triticale diallel study. The grain yields for the control treatment obtained in this study are in agreement with the yields obtained by Kaltsikes & Lee (1973) in their triticale diallel study. No triticale diallel study could be found where the changes in grain yields after different cutting treatments were investigated. Of the studies conducted with triticale cultivars, the results of the study of Andrews *et al.* (1991) showed the nearest similarities to the results of this study with regard to decline in grain yield after repeated cuttings. The decline in grain yields after 1 cut in this study, were even more severe than what was found by Nachit (1983), Poysa (1985), Andrews *et al.* (1991), García del Moral (1992) Royo *et al.* (1994) and Royo & Pares (1996). The fact that no N fertiliser topdressing was given after cut 1, could be responsible for this. The available N could probably not sustain a higher grain yield in this treatment. The decline in grain yields after cut 2 in this study, were also more severe than what was found by Andrews *et al.* (1991) and García del Moral (1992) after two cuts. The cuts of Andrews *et al.* (1991) were at fixed dates, while the second cut of García del Moral (1992) was done at a slightly earlier phenological stage compared to this study. The most probable reasons for the sharper decline in grain yield after the second cut in this study might be N availability as well as possible higher levels of meiotic instability due to physiological stress, because no N fertiliser topdressing was given after cut 2 as well. There is also the probability that the growing points of some tillers of the earliest maturing genotypes could have been above the cutting height and had been removed by the cutting process.

The cytoplasmic backgrounds of the six parents used in this study were unknown. As discussed earlier in the literature review, the origin of the cytoplasm plays an important role in the cytological stability of triticale. The inherent cytological and genetic instability of triticale was also shown in the literature review. With this in mind it would be worthwhile to look at the CV's for grain yield of triticale F<sub>1</sub> hybrids obtained by Barker & Varughese (1992). This was the only one of 10 triticale diallel studies found to work on grain yield, who reported the CV's for grain yield. A CV of 14.8% was found for one treatment which yielded a mean of 8300kg/ha and the CV increased to 22.6% at a mean yield of 5700kg/ha for the other treatment. Four



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replications were used in the study of Barker & Varughese (1992). In the case of this study three replications were used and the grain yields varied from a mean of only 700kg/ha for the cut (1+2) treatment to a mean of 3430kg/ha for the control treatment. The crossing of inbred triticale lines from diverse backgrounds, together with heat stress at flowering and induced N deficiency stress due to the cutting treatments, as well as highly significant differences between blocks in all treatments, may have had the effect to bring the inherent cytological instability to the surface and be largely responsible for the high CV's found.

No triticale diallel study could be found where the percentage crude protein of the grain and the resulted change in percentage crude protein in grain with different cutting treatments were investigated. Skorda (1978) worked with triticale cultivars and found a lowering of grain crude protein after two cuts compared with the control treatment. In this study the means of the grain crude protein percentage of the cut (1+2) treatment were highly significantly more than the means of the control treatment and the cut 1 treatment. This may be due to the common inverse correlation between grain yield and grain percentage crude protein, because a 79.6% decline in grain yield was observed in the cut (1+2) treatment compared to the mean grain yield of the control treatment, while Skorda (1978) only experienced a 10% decline in grain yield in his study. In this study no statistical difference could be found between the average percentage grain crude protein between the control, uncut treatment and the cut 1 treatment. This is consistent with the findings of Skorda (1978), Royo *et al.* (1994) and Royo & Pares (1996) who worked with triticale cultivars and also studied the response of percentage grain crude protein on a cutting treatment. The range of grain crude protein found in this study were lower than those found by Bishnoi & Hughes (1979), but more in agreement with the values found by Skorda (1978), Heger & Eggum (1991) and Royo & Pares (1996) for triticale grain. The CV for percentage crude protein in triticale grain found by Petterson & Åman (1987) is in agreement with the values obtained in this study.

No triticale diallel study could be found where the crude protein yields of the grain from the different F<sub>1</sub> hybrids were investigated. Royo & Pares (1996) worked with triticale cultivars and obtained higher values than those found in this study. The mean of the grain yields of the control treatment of Royo & Pares (1996) were also much higher than the grain yield of this study as well. Royo & Pares (1996) failed to supply

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a value for the CV of the triticale grain protein yields in their study, thus no comparison could be found for the CV's for triticale grain crude protein yields obtained in this study.

When the means for grain yield of each parent and F<sub>1</sub> hybrid in Table 4.10 are compared, the following were found: Parent 1 had the highest value of all the parents in the control uncut treatment. The mean value of parent 1 showed a highly significant difference with the mean of parent 5 and a significant difference was shown with the mean of parent 4. Amongst the F<sub>1</sub> hybrids, 1x3 had the highest mean value in control treatment. The mean value of 1x3 showed a highly significant difference with the mean of 4x6 and significant differences were shown with the means of 1x5, 2x3 and 4x5.

In the cut 1 treatment a few significant differences between means were shown when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 3 had the highest value of all the parents in this treatment. The mean value of parent 3 showed a highly significant difference with the mean of parent 4. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in the cut 1 treatment. The mean value of 1x2 showed a significant difference with the mean of 1x6 and 5x6.

Parent 1 had the highest value of all the parents in the cut (1+2) treatment as well. The mean value of parent 1 showed highly significant differences with the means of parents 4 and 5 and a significant difference was shown with the mean of parent 3. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in the cut (1+2) treatment. The mean value of 1x2 showed highly significant differences with the means of 1x3, 2x4, 3x5 and 4x6 and significant differences with the means of 1x5, 1x6, 3x4, 4x5 and 5x6.

When the means of the treatment combinations are used where both the F-test and LSD test are in agreement, parent 1 emerged as the parent with the highest mean grain yield. The means of parents 4 and 5 were always significantly lower than the mean of parent 1. Amongst the F<sub>1</sub> hybrids, there was no clear winner over treatment combinations. The hybrid 1x3 had the highest grain yield in the control treatment, as shown in Table 4.10 but the mean of the best hybrid combination in the cut (1+2) treatment, 1x2 was highly significantly better than the mean of 1x3 in that specific

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treatment. The means of 1x5 and 4x5 were however always significantly lower than the mean of the best hybrid in both treatment combinations.

When the means of the percentages crude protein of the grain for each parent and F<sub>1</sub> hybrid in Table 4.11 are compared, the following were found: Parent 5 had the highest value of all the parents in the control uncut treatment. The mean value of parent 5 showed highly significant differences with the means of parents 1, 4 and 6 and significant differences were shown with the means of parents 2 and 3. Amongst the F<sub>1</sub> hybrids, 2x4 had the highest mean value in the control treatment. The mean value of 2x4 showed highly significant differences with the means of 1x2, 1x4 and 4x5 and significant differences were shown with the means of 1x3, 2x5, 3x5 and 4x6.

Parent 5 had the highest value of all the parents in the cut 1 treatment as well. The mean value of parent 5 showed highly significant differences with the means of parents 2, 3, 4 and 6. Amongst the F<sub>1</sub> hybrids, 5x6 had the highest mean value in the cut 1 treatment. The mean value of 5x6 showed highly significant differences with the means of 2x4, 2x5, 4x5 and 4x6 and significant differences were shown with the means of 2x3, 2x6 and 3x5.

In the cut (1+2) treatment a few significant differences between means were shown when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 5 had the highest value of all the parents in the cut (1+2) treatment. The mean value of parent 5 showed a highly significant difference with the mean of parent 2. Amongst the F<sub>1</sub> hybrids, no significant differences were shown in this treatment.

When the means of the treatment combinations are used where both the F-test and LSD test are in agreement, parent 5 emerged as the parent with the highest mean percentage crude protein in the grain. The means of parents 2, 3, 4 and 6 were always significantly lower than the mean of parent 5. Amongst the F<sub>1</sub> hybrids, there was no clear winner over treatment combinations. The hybrid 2x4 had the highest mean percentage crude protein in the grain in the control treatment, but the mean of the best hybrid combination in the cut 1 treatment, 5x6 was highly significantly better than the mean of 2x4 in that specific treatment. The means of 2x5, 3x5, 4x5 and 4x6 were however always significantly lower than the mean of the best hybrid in both treatment combinations.

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When the means of the grain crude protein yield for each parent and F<sub>1</sub> hybrid in Table 4.12 are compared, the following were found: A few significant differences between means were shown in the control uncut treatment when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 1 had the highest value of all the parents in this treatment. The mean value of parent 1 showed significant differences with the means of parents 4 and 5. Amongst the F<sub>1</sub> hybrids, 1x6 had the highest mean value in the control treatment. The mean value of 1x6 showed significant differences with the means of 1x5, and 4x6.

In the cut 1 treatment a few significant differences between means were shown when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 3 had the highest value of all the parents in this treatment. The mean value of parent 3 showed a highly significant difference with the mean of parent 4. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in the cut 1 treatment. The mean value of 1x2 showed a significant difference with the mean of 1x6.

Parent 1 had the highest value of all the parents in the cut (1+2) treatment. The mean value of parent 1 showed highly significant differences with the means of parent 3, 4 and 5 and significant differences were shown with the means of parents 2 and 6. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in the cut (1+2) treatment. The mean value of 1x2 showed highly significant differences with the means of 1x3, 2x4, 3x5, 4x5 and 4x6. Significant differences were shown with the means of 1x4, 1x5, 1x6, 2x3, 2x5, 3x4 and 5x6.

When the means of the treatment combination are used where both the F-test and LSD test are in agreement, parent 1 emerged as the parent with the highest mean crude protein yield in the grain. The means of parents 4 and 5 were highly significantly lower than the mean of parent 1, as in the case of grain yield. Amongst the F<sub>1</sub> hybrids, the hybrid 1x2 had the highest mean crude protein yield in the grain in the cut (1+2) treatment, as in the case of grain yield in the cut (1+2) treatment. The means of 1x5 and 4x5 were however significantly lower than the mean of the best hybrid, as in the case of grain yield.

### 4.3 Combined characteristics

#### 4.3.1 Randomised block design analysis

##### 4.3.1.1 Results

The mean squares for total herbivore utilisable crude protein yield of triticale in the normal randomised block design analysis of variance are presented in Table 4.13.

**Table 4.13 Mean squares for total herbivore utilisable crude protein yield of triticale in the randomised block design ANOVA.**

		<b>Total herbivore utilisable crude protein yield</b>
	<b>df</b>	<b>Cut (1+2) + grain</b>
<b>Genotypes</b>	20	50018.413**
<b>Blocks</b>	2	45927.469*
<b>Error</b>	40	13389.155

##### 4.3.1.2 Discussion

The significant differences between blocks for this measured character, indicate that enough soil variation was present to justify the use of blocks in the trial design in order to minimise the MS error .

The F-test showed that highly significant differences existed between the genotypes used in this study. This indicated that this measured character can be genetically improved upon when evaluated in the way as done in this study.

#### 4.3.2 Tables of means

##### 4.3.2.1 Results

The means for the character measured, were determined between the replications and are listed for both the parents as well as the 15 F<sub>1</sub> hybrids.

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The highest value per treatment combination is presented in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The means of the treatment combination for total herbivore utilisable crude protein yield of triticale are presented in Table 4.14.

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**Table 4.14 Means of the treatment combination for total herbivore utilisable crude protein yield of triticale.**

	<b>Total herbivore utilisable crude protein yield (kg/ha)</b>
<b>Genotypes</b>	<b>Cut (1+2) + grain</b>
<b>1</b>	684.44
<b>2</b>	493.07*
<b>3</b>	410.11**
<b>4</b>	209.70**
<b>5</b>	325.39**
<b>6</b>	598.24
<b>1 x 2</b>	<b>688.14</b>
<b>1 x 3</b>	679.45
<b>1 x 4</b>	408.22**
<b>1 x 5</b>	489.17*
<b>1 x 6</b>	635.23
<b>2 x 3</b>	485.55*
<b>2 x 4</b>	673.96
<b>2 x 5</b>	590.07
<b>2 x 6</b>	681.77
<b>3 x 4</b>	527.15
<b>3 x 5</b>	568.20
<b>3 x 6</b>	587.73
<b>4 x 5</b>	460.49*
<b>4 x 6</b>	453.95*
<b>5 x 6</b>	458.54*
<b>Mean</b>	528.98
<b>LSD<sub>0.05</sub></b>	190.94
<b>LSD<sub>0.01</sub></b>	255.47
<b>C.V.</b>	21.87

### 4.3.2.2 Discussion

Royo & Pares (1996) obtained higher values for total protein produced by means of both forage and grain, than what was found in this study. The study of Royo & Pares (1996) was, however, conducted in much more favourable conditions when the average grain yield of 7276kg/ha in the control treatment is compared with the 3430kg/ha obtained in this study. The best parent in this study equals the total crude protein produced by means of forage and grain of the triticale cultivar studied by Royo, et al. (1993).

When the means for total herbivore utilisable crude protein yield for each parent and F<sub>1</sub> hybrid in Table 4-14 are compared, the following were found: Parent 1 had the highest value of all the parents in the control uncut treatment. The mean value of parent 1 showed highly significant differences with the means of parents 3, 4 and 5 and a significant difference was shown with the mean of parent 2. Amongst the F<sub>1</sub> hybrids, 1x2 had the highest mean value in the control treatment. The mean value of 1x2 showed a highly significant difference with the mean of 1x4 and significant differences were shown with the means of 1x5, 2x3, 4x5, 4x6 and 5x6.

## 4.4 Conclusion

### 4.4.1 Vegetative characteristics

#### 4.4.1.1 % Crude protein

Parent 1 looked to be the best for this character because the means of all the other parents were significantly lower than the means of parent 1, when viewed across both cutting treatments. This parent should show good *gca* for this character in a combining ability analysis.

Amongst the F<sub>1</sub> hybrids, the means of 2x4, and 3x4 were never significantly different from the respective best performing genotype in the different treatments. These hybrid combinations should show above average *sca* for this character in a



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combining ability analysis, because none of their parents were good for this character.

### **4.4.1.2 Crude protein yield**

Parents 1 and 6 looked to be the best for this character because the means of all the other parents were significantly lower than the mean of the best performing parent, when viewed across both cutting treatments. These parents should show good *gca* for this character in a combining ability analysis.

Amongst the F<sub>1</sub> hybrids, the means of 1x2, 1x3, 1x6, 2x4, 2x6, 3x5 and 3x6 were never significantly different from the respective best performing genotype in the different treatments. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis, especially 2x4 and 3x5, because none of their parents were good for this character.

### **4.4.2 Grain characteristics**

#### **4.4.2.1 Grain yield**

Parent 1 looked to be the best for this character because the means of all the other parents were significantly lower than the means of parent 1, when viewed across the three treatments. This parent should show good *gca* for this character in a combining ability analysis.

Amongst the F<sub>1</sub> hybrids, the means of 1x2, 1x4, 2x5, 2x6 and 3x6 were never significantly different from the respective best performing genotype in the different treatments. The hybrid combinations 2x5, 2x6 and 3x6 should show above average *sca* for this character in a combining ability analysis, because none of their parents were good for this character across all treatments.

#### **4.4.2.2 % Crude protein**

Parent 5 looked to be the best for this character because the means of all the other parents were significantly lower than the means of parent 5, when viewed across the

three treatments. This parent should show good *gca* for this character in a combining ability analysis.

All of the F<sub>1</sub> hybrids were significantly different from the respective best performing genotype in the different treatments. It would be a surprise to find any combinations with consistent above average *sca* for this character in a combining ability analysis.

### **4.4.2.3 Crude protein yield**

Parent 1 looked to be the best for this character because the means of all the other parents were significantly lower than the means of parent 1, when viewed across the three treatments. This parent should show good *gca* for this character in a combining ability analysis.

Amongst the F<sub>1</sub> hybrids, the means of 1x2, 2x6, and 3x6 were never significantly different from the respective best performing genotype in the different treatments. The hybrid combinations 2x6 and 3x6 should show above average *sca* for this character in a combining ability analysis, because none of their parents were good for this character across all treatments.

### **4.4.3 Combined characteristics**

Parents 1 and 6 looked to be the best for total herbivore utilisable crude protein yield because the means of all the other parents were significantly lower than the mean of the best performing parent. These parents should show good *gca* for this character in a combining ability analysis.

Amongst the F<sub>1</sub> hybrids, the means of 1x2, 1x3, 1x6, 2x4, 2x5, 2x6, 3x4, 3x5 and 3x6 were not significantly different from the best performing genotype for this character. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis. The hybrid combinations 2x4, 2x5, 3x4 and 3x5 should show above average *sca* for this character in a combining ability analysis, because none of their parents were good for this character.

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These are all rough conclusions based upon the phenotypical performance of the parents and F<sub>1</sub> hybrid combinations across the different treatments. To know for certain the results of the different combining ability analyses must be studied.

## **Combining ability for crude protein characteristics in triticales.**

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### **5.1 Vegetative characteristics**

#### **5.1.1 Combining ability analysis**

##### **5.1.1.1 Results**

The mean squares for percentage crude protein of the triticales vegetative material in the combining ability analyses of variance are presented in Table 5.1.

**Table 5.1 Mean squares for percentage crude protein of the triticales vegetative material in the combining ability ANOVA's.**

		<b>% Crude protein</b>		
	<b>df</b>	<b>Cut 1</b>	<b>Cut 2</b>	<b>Combined[cut (1+2) treatment]</b>
<b>Blocks</b>	2	84.150**	32.113**	39.563**
<b>gca</b>	5	3.658	0.617	0.389
<b>sca</b>	9	3.252	0.775	1.046
<b>Error</b>	28	1.914	0.364	0.515

The mean squares for crude protein yield of the triticales vegetative material in the combining ability analyses of variance are presented in Table 5.2.

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**Table 5.2** Mean squares for crude protein yield of the triticale vegetative material in the combining ability ANOVA's.

		Crude protein yield		
	df	Cut 1	Cut 2	Total yield[cut (1+2) treatment]
<b>Blocks</b>	2	4698.587	7066.197	1395.089
<b>gca</b>	5	8202.176**	708.041	8636.305
<b>sca</b>	9	3853.857*	1406.435	9058.050*
<b>Error</b>	28	1304.833	1166.022	3473.305

### 5.1.1.2 Discussion

No reference of a genetic study on any forage cereal where the combining ability for percentage crude protein, or crude protein yield of vegetative material was investigated, could be found.

The combining ability analysis of variance for percentage crude protein of the triticale vegetative material showed no significant differences with regard to both the gca and sca effects across both the treatments. There were in all cases highly significant differences between blocks according to the F-test of the normal randomised block analysis. This meant that the environment had a bigger effect in differences amongst the F<sub>1</sub> genotypes than either the gca or sca effects. There might also be a case of scale effects in the percentage crude protein of the vegetative material, whereby the plant would produce rather less vegetative growth, than producing vegetative growth with a very low percentage crude protein. Based on the results of the F-test, it will not be worthwhile to try to increase the percentage crude protein of the vegetative material in the triticale genotypes used in this study, through selection.

In the combining ability analysis of variance for crude protein yield of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1, but no significant differences were shown in cut 2, or where the gca of the total crude protein yield was considered. The F-test showed significant differences with regard to sca effects in cut 1 and also in the case of the total crude

protein yield across the two cuts. No significant differences between blocks were detected with the F-test in the case of crude protein yield of the vegetative material. In this case selection for increased crude protein yield of the vegetative material would be effective if the selection is done at cut 1. Based on the results of the F-test, there would be no advantage to do a second cut and to do the selection on the second cut, or on the total crude protein yield over two cuts.

### 5.1.2 General combining ability

#### 5.1.2.1 Results

The highest gca value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The estimates of mean general combining ability effects of parents for percentage crude protein of the triticale vegetative material are presented in Table 5.3.

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**Table 5.3** Estimates of mean general combining ability effects of parents for percentage crude protein of the triticale vegetative material.

Genotypes	% Crude protein		
	Cut 1	Cut 2	Combined[cut (1+2) treatment]
<b>1</b>	<b>1.7546</b>	-0.1002	0.3252
<b>2</b>	0.0659	0.0665	0.3376
<b>3</b>	0.0820	-0.4449*	-0.1086
<b>4</b>	-0.9591**	<b>0.6681</b>	0.1334
<b>5</b>	-0.7149*	0.1235	-0.3409
<b>6</b>	-0.2286	-0.3129*	-0.3467
<b>LSD<sub>0.05</sub></b>	2.0033	0.8738	1.0393
<b>LSD<sub>0.01</sub></b>	2.7027	1.1788	1.4022

The estimates of mean general combining ability effects of parents for crude protein yield of the triticale vegetative material are presented in Table 5.4.

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**Tabel 5.4** Estimates of mean general combining ability effects of parents for crude protein yield of the triticale vegetative material.

Genotypes	Crude protein yield		
	Cut 1	Cut 2	Total yield[cut (1+2) treatment]
1	-4.5114**	21.6619	17.1505
2	<b>69.5793</b>	-2.6521	<b>66.9271</b>
3	30.1575	-12.3952	17.7623
4	-42.3023**	-14.7496	-57.0519**
5	-51.8753**	2.5682	-49.3069**
6	-1.0478**	5.5668	4.5190
<b>LSD<sub>0.05</sub></b>	52.3109	49.4502	85.3466
<b>LSD<sub>0.01</sub></b>	70.5738	66.7144	115.1429

### 5.1.2.2 Discussion

A few significant differences between gca effects for percentage crude protein were shown in cut 1 and cut 2 when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of cut 1, the estimated gca effect of parent 1 showed a highly significant difference with the gca effect of parents 4 and a significant difference was shown with the gca effect of parent 5. In the case of cut 2, the estimated gca effect of parent 4 showed a significant difference with the gca effects of parents 3 and 6. The strong gca effect of parent 4 in cut 2 was in contrast to expectations, because the mean phenotypic performance of parent 1 were highly significantly different from that of parent 4.

In the case of estimated gca effects for crude protein yield, the F-test and LSD test were in agreement for cut 1 and cut 2. In cut 1, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 1, 4, 5 and 6. In the case of the total crude protein yield, a few highly significant differences between



gca effects were shown when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. For total crude protein yield, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 4 and 5. The good gca effects of parent 2 in both cut 1 as well as in the case of total crude protein yield were in contrast to expectations from the phenotypical performances for this character. This shows that the breeding value of an inbred parent cannot be deducted from its phenotypic performance.

### **5.1.3 Specific combining ability**

#### **5.1.3.1 Results**

The highest sca value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The estimates of specific combining ability effects for percentage crude protein of the triticales vegetative material are presented in Table 5.5.

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**Table 5.5** Estimates of specific combining ability effects for percentage crude protein of the triticale vegetative material.

Genotypes	% Crude protein		
	Cut 1	Cut 2	Combined[cut (1+2) treatment]
<b>1 x 2</b>	1.192	-0.204*	0.199
<b>1 x 3</b>	0.866	0.486	0.816
<b>1 x 4</b>	-3.610**	-0.650*	-1.633**
<b>1 x 5</b>	0.472	0.325	0.365
<b>1 x 6</b>	1.080	0.044	0.253
<b>2 x 3</b>	-1.820*	0.548	-0.547
<b>2 x 4</b>	1.838	0.557	<b>1.175</b>
<b>2 x 5</b>	-0.375	-0.717**	-0.745*
<b>2 x 6</b>	-0.835	-0.183*	-0.081
<b>3 x 4</b>	<b>1.905</b>	0.612	1.030
<b>3 x 5</b>	0.039	-1.333**	-0.819*
<b>3 x 6</b>	-0.990	-0.313*	-0.480
<b>4 x 5</b>	-0.507	0.377	0.159
<b>4 x 6</b>	0.374	-0.896**	-0.731*
<b>5 x 6</b>	0.371	<b>1.349</b>	1.039
<b>LSD<sub>0.05</sub></b>	3.470	1.513	1.800
<b>LSD<sub>0.01</sub></b>	4.681	2.0418	2.429

The estimates of specific combining ability effects for crude protein yield of the triticale vegetative material are presented in Table 5.6.

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**Table 5.6** Estimates of specific combining ability effects for crude protein yield of the triticale vegetative material.

Genotypes	Crude protein yield		
	Cut 1	Cut 2	Total yield[cut (1+2) treatment]
1 x 2	-10.0*	4.9	-5.2
1 x 3	62.6	<b>38.3</b>	100.9
1 x 4	-67.5**	-52.4*	-119.9**
1 x 5	-7.7*	-26.6	-34.3*
1 x 6	22.7	35.8	58.4
2 x 3	-107.3**	-56.7*	-164.0**
2 x 4	<b>88.6</b>	33.5	<b>122.1</b>
2 x 5	-15.3*	22.2	6.9
2 x 6	44.0	-3.8	40.2
3 x 4	7.6	1.6	9.2
3 x 5	47.4	15.4	62.8
3 x 6	-10.4*	1.40	-9.0
4 x 5	1.6	19.8	21.4
4 x 6	-30.3*	-2.6	-32.8*
5 x 6	-26.0*	-30.8	-56.8*
<b>LSD<sub>0.05</sub></b>	90.6	85.7	147.8
<b>LSD<sub>0.01</sub></b>	122.2	115.5	199.4

### 5.1.3.2 Discussion

In cut 1 and cut 2, as well as in the combination of the two, a few significant differences between sca effects for percentage crude protein were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In cut 1, the estimated sca effect of 3x4 showed a highly significant difference with the sca effect of 1x4 and a significant difference was shown with the sca effect of 2x3. In cut 2, the estimated sca effect of 5x6 showed highly significant differences with the sca effects of 2x5; 3x5 and 4x6 and significant differences were shown with the sca effects of 1x2; 1x4; 2x6 and 3x6. In the case of the combined percentage crude protein of the total vegetative harvest, the estimated sca effect of 2x4 showed a highly significant difference with the sca effect of 1x4 and significant differences were shown with the sca effects of 2x5; 3x5 and 4x6. This confirmed the expectation made earlier about the possible strong sca effect of 2x4 and 3x4.

In the case of estimated sca effects for crude protein yield, the F-test and LSD test were in agreement for cut 1 and the total crude protein yield in so far as to indicate that significant differences existed. A few highly significant differences between sca effects for crude protein yield were shown when using the LSD test, although the F-test failed to indicate any highly significant differences between sca effects. In cut 1, the estimated sca effect 2x4 showed highly significant differences with the sca effects of 1x4 and 2x3 and significant differences were shown with the sca effects of 1x2; 1x5; 2x5; 3x6; 4x6 and 5x6. In the case of the total crude protein yield, the estimated sca effect of 2x4 showed highly significant differences with the sca effects of 1x4 and 2x3 and significant differences were shown with the sca effects of 1x5; 4x6 and 5x6.

A few significant differences between sca effects for crude protein yield were shown in cut 2 when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In cut 2, the estimated sca effect of 1x3 showed a significant difference with the sca effects of 1x4 and 2x3. This confirmed the expectation made earlier about the possible strong sca effect of at least 2x4.

### 5.1.4 GCA/SCA Ratios

#### 5.1.4.1 Results

The ratios of the gca variance to the sca variance for percentage crude protein and crude protein yield of the triticale vegetative material are presented in Table 5.7.

**Table 5.7** Ratios of the gca variance to the sca variance for percentage crude protein and crude protein yield of the triticale vegetative material.

	% Crude protein			Crude protein yield		
Ratio	Cut 1	Cut 2	Combined	Cut 1	Cut 2	Total yield
$\sigma^2_{\text{gca}}/\sigma^2_{\text{sca}}$	0.326	0.155	-	0.676	-	0.231

#### 5.1.4.2 Discussion

Both the estimated gca effects and the sca effects of the same genotype change between treatments when the same characteristic is considered, as was shown in Tables 5.3 to 5.6. When the ratio of  $\sigma^2_{\text{gca}}$  to  $\sigma^2_{\text{sca}}$  for each characteristic is viewed across treatments, the value obtained also changes between treatments. Each treatment was almost like a different environment for these genotypes, because the environmental conditions for growth between germination and cut 1 were different from those between cut 1 and cut 2. At the later cut, the role of morphology of the plant may have played a bigger role with specific gene action of vernalization genes and day length sensitivity genes coming into play. The ratios for cut 1 were the highest for both characters considered.

The variance of gca played a smaller role than the variance of sca in all cases with regard to the vegetative material. These give an indication that none of these vegetative characters will show high narrow sense heritabilities.

## 5.2 Grain characteristics

### 5.2.1 Combining ability analysis

#### 5.2.1.1 Results

The mean squares for triticale grain yield in the combining ability analyses of variance are presented in Table 5.8.

**Table 5.8** Mean squares for triticale grain yield in the combining ability ANOVA's.

		<b>Grain yield</b>		
	<b>df</b>	<b>Control</b>	<b>Cut 1</b>	<b>Cut (1+2)</b>
<b>Blocks</b>	2	4.910*	6.646**	2.945**
<b>gca</b>	5	0.423	0.265	0.043
<b>sca</b>	9	0.500	0.066	0.034
<b>Error</b>	28	0.364	0.170	0.028

The mean squares for percentage crude protein of the triticale grain in the combining ability analyses of variance are presented in Table 5.9.

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**Table 5.9** Mean squares for percentage crude protein of the triticale grain in the combining ability ANOVA's.

		% Crude protein		
	df	Control	Cut 1	Cut (1+2)
<b>Blocks</b>	2	0.414	0.447	26.424**
<b>gca</b>	5	0.570*	0.421	0.307
<b>sca</b>	9	0.344	0.315	0.355
<b>Error</b>	28	0.203	0.185	0.605

The mean squares for crude protein yield of the triticale grain in the combining ability analyses of variance are presented in Table 5.10.

**Table 5.10** Mean squares for crude protein yield of the triticale grain in the combining ability ANOVA's.

		Crude protein yield		
	df	Control	Cut 1	Cut (1+2)
<b>Blocks</b>	2	48802.021*	55555.536**	24995.155**
<b>gca</b>	5	2765.684	1774.032	386.482
<b>sca</b>	9	4024.862	440.437	303.032
<b>Error</b>	28	3884.005	1407.410	233.516

### 5.2.1.2 Discussion

The combining ability analysis of variance for grain yield of the triticale showed no significant differences with regard to both the gca and sca effects across all three the treatments. There were highly significant differences between blocks in the cut 1 treatment and the cut (1+2) treatment and a significant difference in the control uncut

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treatment according to the F-test of the normal randomised block analysis. This meant that the environment had a bigger effect in differences amongst the F<sub>1</sub> genotypes than either the gca or sca effects. Based on the results of the F-test, it will not be worthwhile to try to increase the grain yield in the triticale genotypes used in this study, through selection.

Of the four triticale genetic studies where the grain yield was expressed as yield per area unit instead of yield per plant, the following were found: Kaltsikes & Lee (1973) as well as Barker & Varughese (1992) found highly significant differences for both the gca and sca effects in the combining ability ANOVA's. Węgrzyn *et al.* (1995) as well as Oettler *et al.* (2003) however, found no significant difference between gca effects in either the studies although highly significant differences between sca effects were shown. The findings of the last two publications are in agreement with the present study in so far as the gca effects are concerned.

No reference of a genetic study could be found where the percentage crude protein of the grain and the resultant change in percentage crude protein of grain with different cutting treatments were investigated.

The combining ability analysis of variance for percentage crude protein of the triticale grain showed no significant differences with regard to both the gca and sca effects in the cut 1 treatment and the cut (1+2) treatment. A significant difference was shown in the control uncut treatment between gca effects, but no significant difference was shown for the sca effects in this treatment. There was a highly significant difference between blocks in the cut (1+2) treatment, according to the F-test of the normal randomised block analysis, but no significant difference was shown in the control treatment or the cut 1 treatment.

In the case of the control treatment there might have been more crude protein available for the grain, compared to the other two treatments. Differences between gca effects could therefore show in this treatment. In the case of the cut 1 treatment and cut (1+2) treatment, the available crude protein in the plant could have become the limiting factor and no significant combining ability effects were shown because the values of the different genotypes came closer to each other. There might also be a case of scale effects in the percentage crude protein of the grain, whereby the plant would rather produce less grain, than producing grain with a very low percentage crude protein. Based on the results of the F-test, it will only be worthwhile to try to



increase the percentage crude protein of the grain in the triticale genotypes used in this study, through selection in the control, uncut treatment.

No reference of a genetic study could be found where the crude protein yield of the grain and the resulting change in crude protein yield of grain with different cutting treatments were investigated.

The combining ability analysis of variance for crude protein yield of the triticale grain showed no significant differences with regard to both the gca and sca effects across all three the treatments. There were highly significant differences between blocks in the cut 1 treatment and the cut (1+2) treatment and a significant difference in the control uncut treatment according to the F-test of the normal randomised block analysis. This meant that the environment had a bigger effect in differences amongst the F<sub>1</sub> genotypes than either the gca or sca effects. Based on the results of the F-test, it will not be worthwhile to try to increase the crude protein yield of the grain in the triticale genotypes used in this study, through selection.

### 5.2.2 General combining ability

#### 5.2.2.1 Results

The highest gca value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The estimates of mean general combining ability effects of parents for triticale grain yield are presented in Table 5.11.

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**Table 5.11** Estimates of mean general combining ability effects of parents for triticale grain yield.

Genotypes	Grain yield		
	Control	Cut1	Cut (1+2)
<b>1</b>	<b>0.5489</b>	-0.0787	0.0838
<b>2</b>	-0.0225	<b>0.4325</b>	<b>0.1512</b>
<b>3</b>	0.1170	0.0049	-0.0623
<b>4</b>	-0.4023*	0.0260	-0.1263*
<b>5</b>	-0.2270	-0.0151	-0.0634
<b>6</b>	-0.0141	-0.3697*	0.0170
<b>LSD<sub>0.05</sub></b>	0.8742	0.5977	0.2432
<b>LSD<sub>0.01</sub></b>	1.1794	0.8064	0.3281

The estimates of mean general combining ability effects of parents for percentage crude protein of triticale grain are presented in Table 5.12.

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**Table 5.12** Estimates of mean general combining ability effects of parents for percentage crude protein of triticale grain.

Genotypes	% Crude protein		
	Control	Cut 1	Cut (1+2)
<b>1</b>	-0.5762**	<b>0.3683</b>	-0.3609
<b>2</b>	0.2315	-0.3789*	-0.2131
<b>3</b>	0.3049	0.1493	0.1194
<b>4</b>	0.0288	-0.3959*	0.3830
<b>5</b>	-0.3360*	-0.0032	0.1845
<b>6</b>	<b>0.3470</b>	0.2605	-0.1129
<b>LSD<sub>0.05</sub></b>	0.6517	0.6232	1.1264
<b>LSD<sub>0.01</sub></b>	0.8792	0.8407	1.5196

The estimates of mean general combining ability effects of parents for crude protein yield of triticale grain are presented in Table 5.13.

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**Table 5.13** Estimates of mean general combining ability effects of parents for crude protein yield of triticale grain.

Genotypes	Crude protein yield		
	Control	Cut 1	Cut (1+2)
1	30.2861	-1.9698	8.9315
2	1.1298	<b>34.6154</b>	<b>13.9775</b>
3	18.4539	3.5676	-4.7127
4	-34.9554	-2.6448	-10.9734*
5	-28.2531	-2.0824	-8.0414*
6	13.3387	-31.4861*	0.8184
<b>LSD<sub>0.05</sub></b>	90.2516	54.3282	21.6506
<b>LSD<sub>0.01</sub></b>	121.7603	73.2953	29.2093

### 5.2.2.2 Discussion

A few significant differences between gca effects for grain yield were shown in all three treatments when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of the control treatment, the estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 4. In the cut 1 treatment, the estimated gca effect of parent 2 showed a significant difference with the gca effect of parent 6. In the case of the cut (1+2) treatment, the estimated gca effect of parent 2 showed a significant difference with the gca effect of parent 4.

In the case of estimated gca effects for percentage crude protein of the grain, the F-test and LSD tests were in agreement for the control treatment in so far as to indicate that significant differences existed. A highly significant difference between gca effects for percentage crude protein were shown when using the LSD test, although the F-test failed to indicate any highly significant differences between gca effects. In the

control treatment, the estimated gca effect of parent 6 showed a highly significant difference with the gca effect of parent 1 and a significant difference was shown with the gca effect of parent 5. In the cut 1 treatment a few significant differences between gca effects for percentage crude protein were shown when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the cut 1 treatment, the estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2 and 4. The LSD test and F-test were in agreement in the case of the cut (1+2) treatment and no significant differences were shown between estimated gca effects.

In the case of estimated gca effects for crude protein yield, the F-test and LSD test were in agreement for the control treatment and no significant differences were shown between estimated gca effects. In the cut 1 treatment and the cut (1+2) treatment a few significant differences between gca effects for crude protein yield were shown when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the cut 1 treatment, the estimated gca effect of parent 2 showed a significant difference with the gca effect of parent 6. In the cut (1+2) treatment, the estimated gca effect of parent 2 showed significant differences with the gca effects of parents 4 and 5.

### 5.2.3 Specific combining ability

#### 5.2.3.1 Results

The highest sca value per treatment combination is presented in all cases in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The estimates of specific combining ability effects for triticale grain yield are presented in Table 5.14.

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**Table 5.14** Estimates of specific combining ability effects for triticale grain yield.

Genotypes	Grain yield		
	Control	Cut 1	Cut (1+2)
1 x 2	0.101	0.288	0.231
1 x 3	0.477	-0.043	-0.189*
1 x 4	0.324	0.120	0.150
1 x 5	-1.187*	-0.156	-0.029
1 x 6	0.285	-0.210	-0.162
2 x 3	-0.998*	-0.306	0.026
2 x 4	-0.006	-0.128	-0.236*
2 x 5	0.261	-0.002	0.031
2 x 6	0.642	0.147	-0.051
3 x 4	0.235	-0.204	0.073
3 x 5	<b>0.736</b>	0.294	-0.152
3 x 6	-0.451	0.258	<b>0.243</b>
4 x 5	0.055	0.134	0.097
4 x 6	-0.609	0.078	-0.084
5 x 6	0.133	-0.273	0.054
<b>LSD<sub>0.05</sub></b>	1.514	1.035	0.421
<b>LSD<sub>0.01</sub></b>	2.043	1.397	0.568

The estimates of specific combining ability effects for percentage crude protein of triticale grain are presented in Table 5.15.

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**Table 5.15** Estimates of specific combining ability effects for percentage crude protein of triticale grain.

Genotypes	% Crude protein		
	Control	Cut 1	Cut (1+2)
<b>1 x 2</b>	-0.536*	0.139	0.544
<b>1 x 3</b>	-0.357*	-0.370*	-0.442
<b>1 x 4</b>	-0.151	0.219	-0.001
<b>1 x 5</b>	<b>0.780</b>	-0.062	-0.192
<b>1 x 6</b>	0.264	0.075	0.090
<b>2 x 3</b>	0.268	-0.066	-0.274
<b>2 x 4</b>	0.759	0.350	0.591
<b>2 x 5</b>	-0.309	-0.216*	-0.704
<b>2 x 6</b>	-0.181	-0.208*	-0.156
<b>3 x 4</b>	0.440	0.725	0.454
<b>3 x 5</b>	-0.489*	-0.117*	0.324
<b>3 x 6</b>	0.137	-0.172*	-0.061
<b>4 x 5</b>	-0.405*	-0.601**	-0.299
<b>4 x 6</b>	-0.643*	-0.692**	-0.745
<b>5 x 6</b>	0.423	<b>0.996</b>	0.871
<b>LSD<sub>0.05</sub></b>	1.129	1.079	1.951
<b>LSD<sub>0.01</sub></b>	1.523	1.456	2.632

The estimates of specific combining ability effects for crude protein yield of triticale grain are presented in Table 5.16.

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**Table 5.16** Estimates of specific combining ability effects for crude protein yield of triticale grain.

Genotypes	Crude protein yield		
	Control	Cut 1	Cut (1+2)
<b>1 x 2</b>	-8.00	28.25	<b>27.14</b>
<b>1 x 3</b>	31.97	-8.93	-19.81*
<b>1 x 4</b>	23.36	15.38	10.87
<b>1 x 5</b>	-89.36	-11.13	-4.40
<b>1 x 6</b>	42.03	-23.58	-13.79*
<b>2 x 3</b>	-89.31	-28.24	-3.58
<b>2 x 4</b>	23.84	-5.19	-20.21*
<b>2 x 5</b>	18.84	-6.85	0.46
<b>2 x 6</b>	54.63	12.02	-3.82
<b>3 x 4</b>	38.90	-8.06	13.78
<b>3 x 5</b>	57.12	25.63	-9.51
<b>3 x 6</b>	-38.69	19.59	19.12
<b>4 x 5</b>	-7.36	-0.88	5.26
<b>4 x 6</b>	-78.74	-1.26	-9.70
<b>5 x 6</b>	20.77	-6.77	8.19
<b>LSD<sub>0.05</sub></b>	156.32	94.10	37.50
<b>LSD<sub>0.01</sub></b>	210.90	126.95	50.59



### 5.2.3.2 Discussion

In the control treatment as well as the cut (1+2) treatment, a few significant differences between sca effects for grain yield were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In the control treatment, the estimated sca effect of 3x5 showed significant differences with the sca effects of 1x5 and 2x3. In the cut (1+2) treatment, the estimated sca effect of 3x6 showed significant differences with the sca effects of 1x3 and 2x4. The LSD test and F-test were in agreement in the case of the cut 1 treatment and no significant differences were shown between estimated sca effects.

A few significant differences between sca effects for percentage crude protein were shown in the control treatment as well as in the cut 1 treatment when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In the control treatment, the estimated sca effect of 1x5 showed significant differences with the sca effects of 1x2; 1x3; 3x5; 4x5 and 4x6. In the cut 1 treatment, the estimated sca effect of 5x6 showed highly significant differences with the sca effects of 4x5 and 4x6 and significant differences were shown with the sca effects of 1x3; 2x5; 2x6; 3x5 and 3x6. The LSD test and F-test were in agreement in the case of the cut (1+2) treatment and no significant differences were shown between estimated sca effects.

In the case of estimated sca effects for crude protein yield, the F-test and LSD test were in agreement for the control treatment as well as the cut 1 treatment and no significant differences were shown between estimated sca effects. In the cut (1+2) treatment, a few significant differences between sca effects for crude protein yield were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In the cut (1+2) treatment, the estimated sca effect of 1x2 showed significant differences with the sca effects of 1x3; 1x6 and 2x4.

### 5.2.4 GCA/SCA Ratios

#### 5.2.4.1 Results

The ratios of the gca variance to the sca variance for grain yield, percentage crude protein and crude protein yield of triticale grain are presented in Table 5.17.

**Table 5.17 Ratios of the gca variance to the sca variance for grain yield, percentage crude protein and crude protein yield of triticale grain.**

Ratio	Grain yield			% Crude protein			Crude protein yield		
	Control	Cut 1	Cut (1+2)	Control	Cut 1	Cut (1+2)	Control	Cut 1	Cut (1+2)
$\sigma^2_{gca}/\sigma^2_{sca}$	0.110	-	0.667	0.652	0.454	-	-	-	0.512

#### 5.2.4.2 Discussion

Both the estimated gca effects and the sca effects of the same genotype change once again between treatments when the same characteristic is considered, as was shown in Tables 5.11 to 5.16. When the ratio of  $\sigma^2_{gca}$  to  $\sigma^2_{sca}$  for each characteristic is viewed across treatments, the value obtained also change between treatments. Each treatment was almost like a different environment for these genotypes, because the physiological stress conditions for flowering and seed set changed from the control, uncut treatment to the cut 1 treatment and the cut (1+2) treatment. At the second cut of the cut (1+2) treatment, the role of morphology of the plant may have played a bigger role with specific gene action of vernalization genes and day length sensitivity genes coming into play.

Mangat & Dhindsa (1995) found also in their half diallel study on triticale that both general combining ability and specific combining ability variances were influenced by environmental conditions, thereby suggesting that to have unbiased estimates of gca and sca, such studies be made over a range of environments.

The variance of sca played a much bigger role than the variance of gca in all cases with regard to the grain characters considered, probably because of the “compatibility” of the specific crossings with regard to meiotic stability. It must be

remembered that F<sub>2</sub> grain was harvested and meiotic instability in the F<sub>1</sub> hybrid plants would have an effect on grain yield. It is also a well known fact that grain yield and percentage crude protein in the grain is inversely related. All these facts give an indication that none of these grain characters will show high narrow sense heritabilities.

When the available triticale diallel publications where the genotypes were considered fixed effects were studied, the following information could be found in the articles or calculated from information given: Carrillo *et al.* (1983), Brar *et al.* (1985) and Mangat & Dhindsa (1995) using the proper formulas to calculate the fixed effect variances, found  $\sigma^2_{gca}/\sigma^2_{sca}$  variances of 0.331; 0.098 and 0.360 respectively for grain yield in a normal uncut grain production situation. These figures tend to support the low ratio for grain yield obtained for the control treatment in this study. In contrast with this, if the information given by Barker & Varughese (1992) are used, a ratio of 2.633 is obtained over environments. This information suggests that triticale is a variable species.

### 5.3 Combined characteristics

#### 5.3.1 Combining ability analysis

##### 5.3.1.1 Results

The mean squares for total herbivore utilisable crude protein yield of triticale in the combining ability analyses of variance are presented in Table 5.18.

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**Table 5.18 Mean squares for total herbivore utilisable crude protein yield of triticale in the combining ability ANOVA.**

<b>Total herbivore utilisable crude protein yield</b>		
	<b>df</b>	<b>Cut (1+2) + grain</b>
<b>Blocks</b>	2	37505.381
<b><i>gca</i></b>	5	12272.720*
<b>sca</b>	9	7849.233
<b>Error</b>	28	4339.286

### **5.3.1.2 Discussion**

The F-test showed that significant differences existed between estimated *gca* effects. This suggests that meaningful selections can be made to improve the additive value of genotypes for this characteristic.

### **5.3.2 General combining ability**

#### **5.3.2.1 Results**

The highest *gca* value is presented in bold, italic script and all significant differences of means from this highest value are indicated by a \* for a  $\alpha = 0.05$  level of confidence or by a \*\* for a  $\alpha = 0.01$  level of confidence.

The estimates of mean general combining ability effects of parents for total herbivore utilisable crude protein yield of triticale are presented in Table 5.19.

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**Table 5.19** Estimates of mean general combining ability effects of parents for total herbivore utilisable crude protein yield of triticale.

	<b>Total herbivore utilisable crude protein yield</b>
<b>Genotypes</b>	<b>Cut (1+2) + grain</b>
<b>1</b>	26.0820
<b>2</b>	<b>80.9048</b>
<b>3</b>	13.0497
<b>4</b>	-68.0253**
<b>5</b>	-57.3483**
<b>6</b>	5.3371
<b>LSD<sub>0.05</sub></b>	95.3947
<b>LSD<sub>0.01</sub></b>	128.6990

### **5.3.2.2 Discussion**

In the case of estimated gca effects for total herbivore utilisable crude protein yield, the F-test and LSD tests were in agreement in so far as to indicate that significant differences existed. Highly significant differences between gca effects were shown when using the LSD test, although the F-test failed to indicate any highly significant differences between gca effects. The estimated gca effect of parent 2 showed highly significant differences with the gca effects of parent 4 and 5, like in the case of crude protein yield of vegetative material in cut 1.

### **5.3.3 Specific combining ability**

#### **5.3.3.1 Results**

The estimates of specific combining ability effects for total herbivore utilisable crude protein yield of triticale are presented in Table 5.20.

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**Table 5.20** Estimates of specific combining ability effects for total herbivore utilisable crude protein yield of triticale grain.

	<b>Total herbivore utilisable crude protein yield</b>
<b>Genotypes</b>	<b>Cut (1+2) grain</b>
<b>1 x 2</b>	22.0
<b>1 x 3</b>	81.1
<b>1 x 4</b>	-109.0*
<b>1 x 5</b>	-38.7
<b>1 x 6</b>	44.6
<b>2 x 3</b>	-167.6**
<b>2 x 4</b>	<b>101.9</b>
<b>2 x 5</b>	7.3
<b>2 x 6</b>	36.4
<b>3 x 4</b>	22.9
<b>3 x 5</b>	53.3
<b>3 x 6</b>	10.2
<b>4 x 5</b>	26.7
<b>4 x 6</b>	-42.5
<b>5 x 6</b>	-48.6
<b>LSD<sub>0.05</sub></b>	165.2
<b>LSD<sub>0.01</sub></b>	222.9

### 5.3.3.2 Discussion

A few significant differences between sca effects for total herbivore utilisable crude protein yield were shown when using the LSD test, although the F-test failed to

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indicate any significant differences between sca effects. The estimated sca effect of 2x4 showed a highly significant difference with the sca effect 2x3 and a significant difference with the sca effect of 1x4 was shown.

### 5.3.4 GCA/SCA Ratio

#### 5.3.4.1 Results

The ratio of the gca variance to the sca variance for total herbivore utilisable crude protein yield of the triticale are presented in Table 5.21.

**Table 5.21** Ratio of the gca variance to the sca variance for total herbivore utilisable crude protein yield of the triticale.

	<b>Total herbivore utilisable crude protein yield</b>
<b>Ratio</b>	<b>Cut (1+2) + grain</b>
$\sigma^2_{gca}/\sigma^2_{sca}$	0.565

#### 5.3.4.2 Discussion

The variance of gca played a smaller role than the variance of sca for this characteristic. This gives an indication that specific combinations are more important than additive gene action and a relatively low narrow sense heritability is expected.

## 5.4 Conclusion

With the aim of evaluating the combining ability effects to select parents for a better dual purpose triticale cultivar and to identify possible good hybrid combinations in mind, the following conclusions can be made.

When the gca and sca results for vegetative crude protein yield of the two treatments are compared, it becomes clear that the second cut in order to get the cut (1+2)

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treatment, was not necessary in the evaluation for parents with good breeding value or the identification of possible good hybrid combinations. The results of the cut (1+2) treatment, namely total crude production yield showed no additional information to that of the cut 1 treatment. In fact, better selection for parents with good gca effects will be conducted if the results of cut 1 is used. The gca effects of parents 2 and 3 emerged as the best for this character in the cut 1 treatment. If a triticale hybrid is the aim, then the combinations to be considered for this character are 1x3; 1x6; 2x4; 2x6; 3x4; 3x5 and 4x5.

For grain yield, the two treatments where the gca and sca effects were considered in response of one or two cuttings, were taken for selection purposes. The gca effects of parents 1, 2, 3 and 5 were the best for this character. Hybrid combinations to be considered for this character are 1x2; 1x4; 1x5; 1x6; 2x3; 2x5; 2x6; 3x4; 3x5; 3x6; 4x5; 4x6 and 5x6.

For crude protein yield of the grain, the same two treatments were taken as in the case of grain yield. The gca effects of parents 1, 2 and 3 were the best for this character. Hybrid combinations to be considered for this character are 1x2; 1x4; 1x5; 2x3; 2x5; 2x6; 3x4; 3x5; 3x6; 4x5; 4x6 and 5x6.

When the gca and sca results for total herbivore utilisable crude protein yield are compared, the gca effects of parents 1, 2, 3 and 6 were the best for this combined character. Hybrid combinations to be considered here are 1x2; 1x3; 1x5; 1x6; 2x4; 2x5; 2x6; 3x4; 3x5; 3x6; 4x5; 4x6 and 5x6.

The parents who excelled in every one of the four characters are parents 2 and 3. They should form the parents in a breeding program if a good dual purpose cultivar wants to be bred.

If a dual purpose triticale hybrid is the aim, then the combinations to be considered are 2x6; 3x4; 3x5 and 4x5. These four hybrid combinations were the only ones who excelled in each of the four characters. These four hybrid combinations can be evaluated more intensively over several environments in order to identify the best hybrid.

The percentage crude protein of either the vegetative material or the grain, were not used directly in this selection, because they were already incorporated in the different characters where crude protein yield were used.



# Variance components, heritabilities, additive genetic correlations and correlated response for crude protein characteristics in triticale.

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## 6.1 Vegetative characteristics

### 6.1.1 Variance components and heritabilities

#### 6.1.1.1 Results

The variance components and heritabilities for percentage crude protein and crude protein yield of the triticale vegetative material are presented in Table 6.1. Calculated variance components which resulted in negative values were indicated with minus (-) signs.

#### 6.1.1.2 Discussion

No reference of a genetic study to investigate percentage crude protein, or crude protein yield of vegetative material on any forage cereal, could be found in literature.

The additive genetic variances are relatively small compared to the non-additive genetic variances and the environmental variance ( $\sigma^2_e$ ) for percentage crude protein in cut 1 and cut 2. This resulted in low narrow sense heritabilities for percentage crude protein in the vegetative material in both cuts. The narrow sense heritability for percentage crude protein showed a slightly higher value in cut 1 than in cut 2, although it cannot be of significance due to the high S.E. values in both cases.

The additive genetic variance for crude protein yield in cut 1 was relatively more than the non-additive genetic variance and  $\sigma^2_e$  and resulted in a relatively higher narrow sense heritability for this character in cut 1 compared to the cut (1+2) treatment. This corresponded with the higher  $\sigma^2_{gca}/\sigma^2_{sca}$  value obtained for cut 1 relative to the cut (1+2) treatment in Chapter 5. The higher availability of N in cut 1 compared to

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cut 2 could maybe promote better additive gene activity. The first cut removed available N from the plants and in the absence of a N topdressing, an environmental limit could be created which limited the additive variance in the second vegetative cut. This could then have the effect of lowering the additive genetic variance in the cut (1+2) treatment and hence the lower narrow sense heritability compared to cut 1.

**Table 6.1 Variance components and heritabilities for percentage crude protein and crude protein yield of triticale vegetative material.**

Components	% Crude protein			Crude protein yield		
	Cut 1	Cut 2	Combined [cut (1+2)]	Cut 1	Cut 2	Total yield [cut (1+2)]
$\sigma^2_A$	0.872 ± 0.843	0.127 ± 0.129	-	3448.672 ± 1382.018	-	2581.500 ± 1387.120
$\sigma^2_{D+I}$	1.338 ± 0.722	0.411 ± 0.125	0.531 ± 0.127	2549.024 ± 690.388	240.413 ± 137.541	5584.745 ± 1401.8069
$\sigma^2_G$	2.210 ± 1.394	0.538 ± 0.183	-	5997.696 ± 1834.248	-	8166.245 ± 2269.812
$\sigma^2_e$	1.914	0.364	0.515	1304.833	1166.022	3473 305
$\sigma^2_P$	4.124 ± 1.394	0.902 ± 0.183	-	7302.529 ± 1834.248	-	11639.550 ± 2269.812
$h_b^2$	0.536 ± 0.497	0.596 ± 0.484	-	0.821 ± 0.212	-	0.702 ± 0.242
$h_n^2$	0.211 ± 0.230	0.141 ± 0.244	-	0.472 ± 0.207	-	0.222 ± 0.180

### 6.2 Grain characteristics

#### 6.2.1 Variance components and heritabilities

##### 6.2.1.1 Results

The variance components and heritabilities for grain yield, percentage crude protein and crude protein yield of the triticale grain are presented in Table 6.2. Calculated variance components which resulted in negative values were indicated with minus (-) signs.

##### 6.2.1.2 Discussion

Of the various triticale diallel studies sourced, the study of Carrillo *et al.* (1983) were the only one where the variance components of grain yield were extended to heritabilities. Like Weber (1976) in his study of peas, Carrillo *et al.* (1983) changed from Model 1 to Model 2 assumptions to calculate the variance components and heritabilities and obtained a narrow sense heritability of 0.08 for grain yield. This low heritability compared well with the value of 0.06 for narrow sense heritability of the grain yield in the control uncut treatment in this study. The narrow sense heritability for grain yield showed a slightly higher value in the cut (1+2) treatment than in the control treatment, although it cannot be of significance due to the high S.E. values in both cases.

No reference of a genetic study could be found where the percentage crude protein of the grain and the resultant change in percentage crude protein of grain due to different cutting treatments were investigated.

The narrow sense heritability for the percentage crude protein of the grain showed a slightly higher value in the control uncut treatment than in the cut 1 treatment or in the case of grain yield, although it cannot be of significance due to the high S.E. values in all the cases.

The narrow sense heritability for crude protein yield of the grain for the cut (1+2) treatment gave almost the same low value as in the case of grain yield of the same treatment.

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**Table 6.2** Variance components and heritabilities for grain yield, percentage crude protein and crude protein yield of triticale grain.

Components	Grain yield			% Crude protein			Crude protein yield		
	Control	Cut 1	Cut (1+2)	Control	Cut 1	Cut (1+2)	Control	Cut 1	Cut (1+2)
$\sigma^2_A$	0.030 ± 0.090	0.048 ± 0.063	0.008 ± 0.006	0.184 ± 0.085	0.118 ± 0.050	-	-	183.311 ± 421.536	81.483 ± 52.504
$\sigma^2_{D+I}$	0.136 ± 0.056	-	0.006 ± 0.003	0.141 ± 0.027	0.130 ± 0.059	-	140.857 ± 194.109	-	79.516 ± 40.012
$\sigma^2_G$	0.166 ± 0.103	-	0.014 ± 0.008	0.325 ± 0.086	0.248 ± 0.064	-	-	-	160.999 ± 74.717
$\sigma^2_e$	0.364	0.170	0.028	0.203	0.185	0.605	3884.005	1407.410	233.516
$\sigma^2_P$	0.530 ± 0.103	-	0.042 ± 0.008	0.528 ± 0.086	0.433 ± 0.064	-	-	-	394.515 ± 74.717
$h_b^2$	0.313 ± 0.175	-	0.333 ± 0.259	0.615 ± 0.063	0.573 ± 0.089	-	-	-	0.408 ± 0.201
$h_n^2$	0.057 ± 0.178	-	0.190 ± 0.150	0.348 ± 0.116	0.273 ± 0.148	-	-	-	0.207 ± 0.151

### 6.3 Combined characteristics

#### 6.3.1 Variance components and heritabilities

##### 6.3.1.1 Results

The variance components and heritabilities for total herbivore utilisable crude protein yield of the triticale are presented in Table 6.3.

### 6.3.1.2 Discussion

The broad sense heritability of  $0.633 \pm 0.474$  showed that combined additive genetic variance plus non-additive genetic variance were generally more important than  $\sigma^2_e$  for this combined character.

The moderate narrow sense heritability for this combined character appeared to be higher than the heritabilities for grain yield and crude protein yield of the grain, but the S.E. value was high and differences would not be significant.

**Table 6.3 Variance components and heritabilities for total herbivore utilisable crude protein yield of triticale.**

Components	Total herbivore utilisable crude protein yield
$\sigma^2_A$	3966.717 $\pm$ 2009.505
$\sigma^2_{D+I}$	3510.298 $\pm$ 1325.743
$\sigma^2_G$	7477.015 $\pm$ 2764.462
$\sigma^2_e$	4339.286
$\sigma^2_P$	11816.301 $\pm$ 2764.462
$h_b^2$	0.633 $\pm$ 0.474
$h_n^2$	0.336 $\pm$ 0.286

## 6.4 Additive genetic correlations and correlated response

### 6.4.1 Results

The additive genetic correlations and correlated response for crude protein characteristics of the triticale are presented in Table 6.4.

### 6.4.2 Discussion

Highly significant additive genetic correlations were shown between the vegetative crude protein yield of cut 1 and the total vegetative crude protein yield as well as the total herbivore utilisable crude protein yield.

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A highly significant additive genetic correlation was shown between the total vegetative crude protein yield of the cut (1+2) treatment and the total herbivore utilisable crude protein yield. Significant additive genetic correlations were shown between the total vegetative crude protein yield of the cut (1+2) treatment and the grain yield of the cut (1+2) treatment as well as the grain crude protein yield of the cut (1+2) treatment.

Correlated response values were only determined for the significant and highly significant additive genetic correlations.

**Table 6.4 Additive genetic correlations and correlated response for crude protein characteristics of the triticale.**

Independent variables	Dependant variables				
	Grain yield (Control)	Grain yield [cut(1+2)]	Grain crude protein yield [cut(1+2)]	Total vegetative crude protein yield [cut (1+2)]	Total herbivore utilisable crude protein yield
Crude protein yield (Vegetative, Cut 1)	0.3842	0.7171	0.7507	0.9583**	0.9371**
Total crude protein yield [Vegetative, cut (1+2)]	0.5831	0.8637*	0.8894*		0.9967**
<b>Correlated response (kg/ha) at 20% selection pressure</b>					
Crude protein yield (Vegetative, Cut 1)				46.854	56.793
Total crude protein yield [Vegetative, cut(1+2)]		50.895	5.302		41.427

If the top 20% of individuals for vegetative crude protein yield in the cut 1 treatment were selected for instance, then the correlated response in the total vegetative crude

protein yield would be 46.854kg/ha and in the total herbivore utilisable crude protein yield, 56.793kg/ha.

If the top 20% of individuals for total vegetative crude protein in the cut (1+2) treatment were selected, then the correlated responses in grain yield of the cut (1+2) treatment, the grain crude protein yield of the cut (1+2) treatment and the total herbivore utilisable crude protein yield would be 50.895kg/ha, 5.302kg/ha and 41.427kg/ha respectively.

### 6.5 Conclusion

With the aim of selecting parents for a better dual purpose triticale cultivar and to identify possible good hybrid combinations in mind, the following conclusions can be made.

The narrow sense heritabilities for percentage crude protein of vegetative material, the grain yield as well as crude protein yield of grain were low to very low. It will therefore not be worthwhile to select for these characters directly in the fixed genotypes used for this study.

The combining ability analyses in Chapter 5 showed that significant differences existed amongst both the gca and sca effects for the vegetative crude protein in cut 1. The LSD values also showed that accurate identification of possible parents for a breeding program or hybrid combinations can be made for this character in cut 1. The narrow sense heritability for this character in cut 1 was also at an acceptable level for selection purposes. When the correlated responses are considered, this character when evaluated in cut 1 would also give highly significant correlated responses for both total vegetative crude protein yield and total herbivore utilisable crude protein yield. The crude protein yield of the grain was included in this last character, so an overall beneficial response for improved crude protein yield of both vegetative material and grain in a dual purpose application would be obtained when selection for this character was done in cut 1.

### Summary / Opsomming

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The objective of this study was to study the combining ability, heritability and additive genetic correlation of various crude protein characteristics in a selected fixed population.

Three treatments were used to obtain grain production. The control treatment was left uncut; the cut 1 treatment had one cut of vegetative material before left for grain production while the cut (1+2) treatment had two consecutive cuts before the plants were allowed to produce grain.

Characters measured for grain in all treatments were grain yield, percentage crude protein and crude protein yield. Characters measured for the vegetative material were percentage crude protein and crude protein yield. The total herbivore utilisable crude protein yield where the total crude protein yield of the vegetative material was combined with the grain crude protein yield of the cut (1+2) was also determined.

Highly significant differences were shown between both genotypes and treatments for vegetative and grain characters when the phenotypic means of parents and offspring were evaluated in factorial analyses.

The F<sub>1</sub> progeny of a 6 x 6 half diallel cross were evaluated in the combining ability analyses using the *Method 4, mixed model B* analysis of Griffing (1956b), because only one reading per plot was obtainable for each of the characteristics measured.

In the combining ability analyses of the F<sub>1</sub> progeny, highly significant and significant differences were shown for gca effects and sca effects respectively when vegetative crude protein yield was evaluated in the cut 1 treatment. The  $\sigma^2_{gca}/\sigma^2_{sca}$  ratio differed between treatments and was higher for vegetative crude protein yield in the cut 1 treatment than in the cut (1+2) treatment.

No significant differences between gca effects or sca effects could be found for grain yield or grain crude protein yield in the analyses of variance for any of the treatments.

A significant difference between gca effects was shown for the combination character, total herbivore utilisable crude protein yield.



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## Chapter 7

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With the aim of evaluating the combining ability effects to select parents for a better dual purpose triticale cultivar and to identify possible good hybrid combinations in mind, selections could be made with the available data of the cut 1 treatment as basis.

When the variance components, heritabilities and correlated responses were calculated, the decision to base selection on the vegetative crude protein yield of the cut 1 treatment was confirmed. This character showed highly significant additive genetic correlations with both the total vegetative crude protein yield and the total herbivore utilisable crude protein yield.

**Key words:** triticale, diallel, fixed, vegetative, protein, grain, yield, combining, heritability, correlation.

Die doel van hierdie studie was om die kombineervermoë, oorerflikhede en additiewe genetiese korrelasie van verskeie ruproteïen eienskappe in 'n geselekteerde populasie te bepaal.

Drie behandelings is gebruik om graanproduksie te bepaal. Die kontrole behandeling is nooit gesny nie; die een snysel behandeling is een keer gesny voordat dit gelos is om graan te produseer, terwyl die twee snysel behandeling twee agtereenvolgende snysels ontvang het voordat dit toegelaat is om graan te produseer.

Graaneienskappe wat in al die behandelings bepaal is, is graanopbrengs, persentasie ruproteïen asook ruproteïenopbrengs. Eienskappe wat in die vegetatiewe materiaal bepaal is, is ruproteïen, en ruproteïenopbrengs. Die totale herkouer toeganklike ruproteïenopbrengs, wat 'n kombinasie is van die totale ruproteïenopbrengs van die vegetatiewe materiaal en die graan ruproteïenopbrengs van die ooreenstemmende behandeling, is ook bepaal.

Daar was hoogs betekenisvolle verskille tussen genotipes asook behandelings met die ontleding van die fenotipiese gemiddeldes van beide ouers en nageslag d.m.v. faktoriaal analise.

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## Chapter 7

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Die F<sub>1</sub> nageslag van 'n 6 x 6 halfdialleel kruising is d.m.v. *Metode 4, gemengde model B* van Griffing (1956b) vir kombineervermoë ontleed, omdat daar slegs een waarde per perseel vir elke eienskap beskikbaar was.

By die ontleding van kombineervermoë vir vegetatiewe ruproteïenproduksie in die F<sub>1</sub> nageslag, is hoogs betekenisvolle en betekenisvolle verskille t.o.v. algemene kombineervermoë effekte en spesifieke kombineervermoë effekte onderskeidelik, in die een snysel behandeling verkry. Die verhouding tussen die variansie van die algemene kombineervermoë tot die variansie van die spesifieke kombineervermoë, het tussen behandelings verskil en was hoër vir vegetatiewe ruproteïen opbrengs in die een snysel behandeling as in die twee snysel behandeling.

Geen betekenisvolle verskille kon t.o.v. algemene kombineervermoë effekte en spesifieke kombineervermoë effekte in enige van die behandelings vir graanopbrengs of graan ruproteïenopbrengs gevind word nie.

Betekenisvolle verskille tussen algemene kombineervermoë effekte is t.o.v. die kombinasie eienskap, totale herkouer toeganklike ruproteïenopbrengs, verkry.

Waar die doel was om die kombineervermoë effekte so te evalueer ten einde ouers vir 'n beter dubbeldoel tritcale kultivar te selekteer en ook goeie baster kombinasies te identifiseer, kon seleksies met die beskikbare data vanaf die een snysel behandeling gedoen word.

Die geldigheid van die besluit om seleksie op die vegetatiewe ruproteïenopbrengs van die een snysel behandeling te grond, is bevestig toe die variansiekomponente, oorerflikhede en gekorreleerde respons bepaal is. Hierdie eienskap het hoogs betekenisvolle additiewe genetiese korrelasies getoon met die totale vegetatiewe ruproteïenopbrengs asook die totale herkouer toeganklike ruproteïenopbrengs.

**Sleutelwoorde:** tritcale, dialleel, vaste, vegetatiewe, proteïen, graan, opbrengs, kombineervermoë, oorerflikheid, korrelasie.

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