Genetic variability for forage yield and nutritive quality characteristics in selected inbred *x Triticosecale* genotypes.

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Genetic variability for forage yield and nutritive quality characteristics in selected inbred *x Triticosecale* genotypes.

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Preface

I wish to thank the following persons:

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Contents

List of abbreviations

ADF	Acid detergent fibre
ADL	Acid detergent lignin
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
CV	Coefficient of Variation given as a %
df	degrees of freedom given in the ANOVA
DM	100% Dry matter
DMI	Dry matter intake
e	error term
EE	ether extract
F_1	first generation progeny of a specific combination between two parents
gca	general combining ability
ha	hectare
h_b^2	broad sense heritability
h_n^2	narrow sense heritability
HPH%	Relative high-parent heterosis
IVDOM	*in vitro* digestible organic matter
$LSD_{0.01}$	Least Significant Difference at confidence level α=0.01
$LSD_{0.05}$	Least Significant Difference at confidence level α=0.05
LWG	Live weight gain
ME	Metabolic energy content
MPH%	Relative mid-parent heterosis
MS	Mean Squares
MS_e	Mean Squares error in the initial ANOVA
M'_e	MS_{error} in the combining ability ANOVA
MS_{gca}	Mean Squares for general combining ability in the combining ability ANOVA
MS_{sca}	Mean Squares for specific combining ability in the combining ability ANOVA
MRT	Predicted mean retention time of organic matter in the rumen
NDF	Neutral detergent fibre
NDF_{adj}	Adjusted neutral detergent fibre

Abbreviations

NSC	non structural carbohydrate
p	number of parents used in the diallel
sca	specific combining ability
S.E.	Standard error of the mean
SS	Sum of Squares
SS_{gca}	Sum of Squares for general combining ability in the combining ability ANOVA
SS_{sca}	Sum of Squares for specific combining ability in the combining ability ANOVA
v	number of genotypes to be analysed in the initial ANOVA
$\boldsymbol{X}$	mean phenotypic value of a specific F_1 combination across all replicates
σ^2	variance
σ^2_A	additive genetic variance
σ^2_D	dominance variance
σ^2_{D+I}	total non-additive genetic variance
σ_e^2	expectation of the MS'_{error} in the initial ANOVA done without parents, depicting the environmentall variance when the variance components are listed.
σ^2_G	genotypic variance
σ^2_{gca}	variance of gca in the fixed parent population
σ^2_P	phenotypic variance
σ^2_{sca}	variance of sca in the fixed group of F_1 hybrids
*	Significantly different at level $\alpha = 0.05$
**	Significantly different at level $\alpha = 0.01$
***	Significantly different at level $\alpha = 0.001$

Chapter 1

Introduction

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.

Triticale is mainly planted in Poland as well as Australia, Argentina, the U.S.A. and South Africa. Triticale is normally better adapted to poorer sandy or brackish soils than wheat and show generally better cold tolerance than oats. It can also grow better than rye in soils with a high clay content. In eastern Europe where a third of the world's triticale is grown, it is used as a grain crop to feed poultry, pigs and beef cattle. In Australia it is used both as a silage crop and for grain production. In the case of Argentina the crop is used as a pasture for winter feed, while it is used as a dual purpose crop in the U.S.A. In South Africa triticale is used mainly for winter grazing purposes in the summer rainfall areas while it is used for silage, grazing as well as grain production in the winter rainfall parts of the country. The size of the triticale seed market in South Africa is about 1633 metric ton and roughly 36300 ha is planted to this crop per year.

Genetic studies to determine the genetic variability for forage yield and nutritive quality characteristics in selected triticale genotypes are practically non existent.

The evaluation of combining ability of triticale genotypes for these plant quality-, plant production- as well as animal production characteristics will help in identification of genotypes which could be good parental components for developing both hybrids and standard varieties.

The calculations of the various heterosis parameters for these characteristics are necessary information to decide on the viability in the use of hybrids for further improvement thereof.

It is also important to know the heritability and 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 nutritive quality when used as forage and the resultant forage yield and predicted animal production per hectare is of particular interest. This correlation will give the answer if the triticale genotypes under consideration can be bred for both high forage yield and good nutritive quality. This will have consequences on the viability of a potential cultivar for improved animal production per hectare.

Chapter 2

Literature review

2.1 Triticale development and properties

Triticale is a man-made crop, 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 *x* 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_1 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_1 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_1 plant without the need for embrio-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 tetraploid wheat, the area in which the first triticales were produced (Scoles & Kaltsikes, 1974). According to Scoles & Kaltsikes (1974) octoploid triticale 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 triticale was reported by Derzhaven (1938) from the cross *T.durum x S.montanum.* The first hexaploid triticale 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 triticale involving *T.durum* was superior in fertility to a triticale 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 triticale programmes involve either *T.turgidum* or *T.durum* and either *S.cereale* or *S.montanum* (Scoles & Kaltsikes, 1974).

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 & Zennyozi (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 various stages of meiosis, as well as the theories regarding the genetic instability and role of the cytoplasm in triticale.

Triticale 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 McColoy, Sherrod, Albin & Hansen (1971) and for nonruminants according to Briggle (1969), Knipfel (1969), Longnecker (1973) and Shimada, Martinez & Bravo (1971), than as food for humans (Brown & Almodares, 1976). The quality of protein in triticale 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 triticale has a higher lysine content and protein of a better biological value for non ruminants than wheat grain.

Apart from use as a feed grain, triticale 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). Although triticale is normally treated as a self pollinated crop in applied breeding, Fossati, Jaquiery & 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 Forage yield and nutritive quality characteristics in triticale and other temperate grasses

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 & 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.

Skorda (1978) found that maximum forage yield of triticale was obtained by the delaying of harvest until the dough stage, but that the crude fibre content had risen to 28.2% at this stage. When the triticale was cut twice at the jointing stage, the average crude fibre content was only 16.0%, but the total dry matter production over the two cuts was 2234 kg/ha *versus* 15450 kg/ha when the triticale was cut at the dough stage. A compromise is necessary between quantity and quality of forage in order to achieve the best combination of both (Droushiotis, 1984). In a system of repeated harvests, Brignall et al., (1988) found a clear reduction in subsequent yield in triticale when apical meristems were removed by harvesting, thus requiring the regrowth from the slower and less productive tiller buds (Droushiotis,1984). Royo et al. (1994) found that forage yield in triticale was less influenced by sowing date and soil fertility than grain yield. Royo & Pares (1996) stated that no significant year *x* genotype interaction was detected for triticale forage production.

The importance of incorporating digestibility into herbage breeding programs was discussed already by Cooper, Tilley, Raymond & Terry (1962). Tan, Tan & Walton (1978) stated that the increased emphasis in breeding for quality forages is due partly to improved methods of evaluation. Selection for high forage yield has reached a plateau in many cases, whereas the demand for quality animal products continues to increase (Tan et al., 1978).

Dry matter digestibility can be increased either by improving the digestibility of the fibre or by increasing the ratio of cell contents to fibre. The cell contents of grasses consist mainly of crude protein and water-soluble carbohydrate, with smaller quantities of fatty acids, starch, nucleic acids and minerals, which are all highly digestible. Fibre content and *in vitro* dry matter digestibility are usually strongly correlated, but the correlation is weaker at higher levels of dry matter digestibility (Wilkens, 1997). Although there is genetic variation in fibre content within both cocksfoot and smooth bromegrass, a considerable proportion of the genetic variation in dry matter digestibility results from differences in fibre digestibility (Casler & Carpenter, 1989; Buxton, 1990). This finding was supported by the research of Wilkens (1997) who found that the differences for *in vitro* dry matter digestibility among varieties of temperate perennial grasses tend to be much greater in mid and late summer when the digestibility of the fibre is at its lowest compared to the values in spring and autumn. The results of Casler & Carpenter (1989) provided evidence that *in vitro* dry matter digestibility can be improved by genetic modification of the cell wall composition, without reducing the total cell wall content.

Suitable evaluation for herbage quality in a plant breeding program should be rapid and inexpensive, require small amounts of herbage and provide precise, meaningful etimates (Bughrara, Sleper & Krause, 1991). The two main approaches to determine the feeding value of plant material which seem to have stood the test of time are the Tilley & Terry (1963) *in vitro* analysis and the detergent methods of analysis (Pienaar, 1993). The two-stage *in vitro* digestibility procedure of Tilley & Terry (1963), or some modification thereof, has been one of the most popular techniques used to obtain herbage digestibility estimates (Bughrara et al., 1991). The *in vitro* digestibility procedure of Tilley & Terry (1963) is strictly speaking not a chemical analysis since it uses live micro-organisms to digest the feed (Pienaar 1993). Pienaar (1993) also noted that in the majority of studies reported, the *in vitro* method has performed consistently better than all the chemical analysis when predicting digestibility. In the few cases where the detergent methods of analysis gave a closer fit within a small group of samples, the *in vitro* method gave a better overall fit over all samples (Givens, Moss & Adamson, 1993). The work of Givens et al., (1993) showed the *in vitro* method to be the one analysis which gave a regression between actual and predicted digestibility in which the intercept did not differ significantly from zero and the slope did not differ significantly from one.

The primary disadvantages of the *in vitro* fermentation procedure for screening purposes in a plant improvement program are that it is rather laborious and maintenance of a fistulated donor animal is required (Bughrara et al., 1991).

The phenotypic and genetic correlation between digestibility according to the *in vitro* method and forage yield varies between studies. Mason & Shenk (1976) found a negative phenotypic correlation between *in vitro* dry matter digestibility and yield in orchardgrass. Stratton, Sleper & Matches (1979) found differing phenotypic correlations between *in vitro* dry matter digestibility and yield in orchardgrass between different populations and also at different times of the year. Nguyen, Sleper & Matches (1982) also found low and differing phenotypic correlations between *in vitro* dry matter digestibility and yield in tall fescue as well as a highly significant negative correlation in spring. Vogel, Gorz & Haskins (1981) found negative genetic correlations between *in vitro* dry matter digestibility and yield in indiangrass for one population, but a low, positive correlation for the other population.

Vogel, Reece & Lamb (1986) found significant genotype *x* location and genotype *x* year interaction effects for first-cut forage yield in intermediate wheatgrass, but not for *in vitro* dry matter digestibility. The authors concluded that *in vitro* dry matter digestibility is a character that appears to be relatively stable over environments. In a follow-up study, Vogel, Reece and Nichols (1993) found genotype *x* location and genotype *x* year interaction effects to be not significant for *in vitro* dry matter digestibility for intermediate wheatgrass planted in swards. The character, *in vitro* dry matter digestibility is therefore quite stable across environments Vogel et al., 1993).

The ability of various methods of feed analysis to predict the energy value of feeds, has been studied and reviewed by Weiss (1993). When the results of these analyses are used as single components in regression equations, they are population dependent. This means that an equation developed for one set of feeds will not be suitable for another set. Even when more than one component is used in empirical regressions, such as the components of the proximate analysis, the results remain population dependent and are not really more accurate than the single component analyses (Weiss, 1993). Pienaar (1993) concluded that all chemical methods of feed analysis are population dependent, but the Tilley & Terry (1963) *in vitro* analysis seems to be more closely related to rumen digestion than any chemical method and therefore the least population dependent in all studies conducted.

The estimates of the metabolic energy content of feeds were in most cases close to actual values when the *in vitro* digestibility analysis was used as the basis (Pienaar, 1993).

Weiss (1993) stated that other factors affecting energy values of feed, such as rate of digestion, rate of passage, as well as particle size should also be considered when the energy values of feed have to calculated.

2.3 Prediction of voluntary dry matter intake in herbivores

Voluntary feed intake is the most important criterion of roughage ‘quality’ for ruminants (Pienaar & Roux, 1989b). A reliable estimate of voluntary feed intake is therefore very important according to Pienaar & Roux (1989b). Voluntary feed intake is a complex process however, and is dependent on the animal’s characteristics as well as those of the forage (Jarrige, Demarquilly & Dulphy, 1973). According to Jarrige et al. (1973) voluntary feed intake must be measured in animals of similar ingestive capacity and under standardized conditions, if comparisons are to be made between forages.

Donefer, Crampton & Lloyd (1960) found good relationships between amount of animal intake and rate of dry matter and cellulose digestion for timothy and smooth bromegrass. Orr, Cook, Champion & Rook (2001) found that live weight gain in grazing animals was strongly correlated with voluntary intake of ryegrass dry matter but only weakly correlated with water-soluble carbohydrate content.

Numerous different dry matter intake models are found in the literature. In this literature study, only a selection with application to this study will be discussed.

The intake model of Pienaar & Roux (1989a) made use of not only of the digestibility of the feed, but also of the rate of digestion, rate of passage of the feed through the rumen as well as the rumen fill effect. According to Pienaar & Roux (1989b) a linear relationship exists only between rumen fill and the voluntary intake. A first-order mathematical model which describes the relationship between voluntary intake and flow as well as fermentation, was published by Pienaar, Roux, Morgan & Grattarola (1980). However, since first-order kinetics are mostly not adequate to describe the fermentation or outflow curves, Pienaar & Roux (1989a) modified their first-order mathematical model by using the gamma function to describe both the fermentation and outflow curves of organic matter disappearance from the rumen (Pienaar & Roux, 1989b). The advantage of these dynamic models like the one of Pienaar & Roux (1989a) is that they include more of the relevant variables and usually yield more realistic estimates of voluntary feed intake than static models. However, their big disadvantage for acceptance and application in practical animal nutrition is their complexity (Pienaar & Roux, 1989b). Pienaar (1993) acknowledged that the use of published values for both rate of passage and rumen fill could be a source of error, since these differ from feed to feed. There was according to Pienaar (1993) no viable indirect method for estimating rates of passage of feeds in the laboratory available for inclusion in their model.

The National Research Council of the U.S.A. uses the energy concentration of the feed to calculate the voluntary dry matter intake per steer per day (NRC, 1996). The dry matter intake predictions of this static model uses equations developed from experimental feeding period averages as reported in a wide variety of published feeding trials (NRC, 1996). The NRC (1996) model showed an increase in dry matter intake with higher total digestible nutrient concentrations up to about sixty to sixty five percent, which equates to metabolic energy levels of 9.08 MJ/kg to 9.83 MJ/kg. When the total digestible nutrient concentration increase to seventy percent, which equates to a metabolic energy level of 10.59 MJ/kg, a decline in voluntary dry matter intake occurred already in the case of growing and finishing cattle because of the physiological regulation effect in the animals (NRC, 1996).

Mertens (1987) developed a feed intake model based on the concepts presented by Conrad (1966). Mertens (1987) proposed that neutral detergent fibre (*NDF*) be used to represent the fill effect of the diet and that gut capacity be expressed in terms of *NDF* intake capacity This part of the feed intake model of Mertens (1987) is applicable to the part of the graph to the left of the *b* in Fig 1, as shown by Williams, Oltenaco & Sniffen (1989). In this part of the graph in Fig. 1, physical regulation limits voluntary feed intake. The intake model of Mertens (1987) had some limitations that restrict its accuracy as summarised by Williams et al. (1989). Most importantly, because it used strictly *NDF* to quantify the fill effect of the diet, it failed to reflect differences in dry matter (*DM*) intake between legume and grass-based diets formulated at equal *NDF* content.

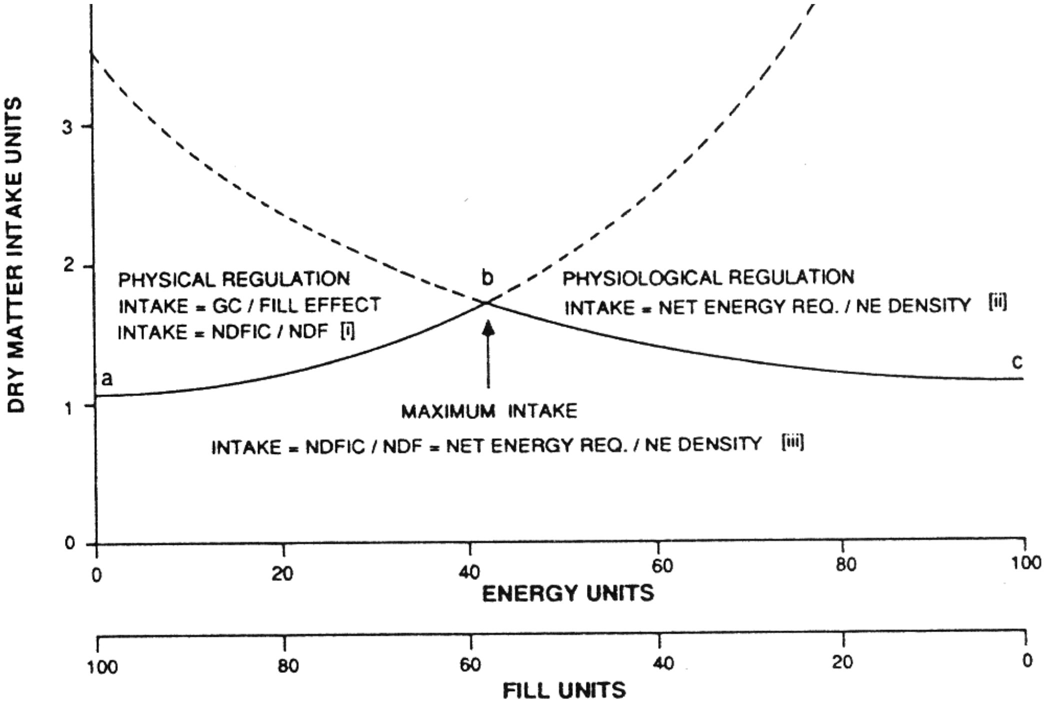

Figure 1. Mertens's (1987) dry matter intake model, adapted from those of Conrad (1966).

Mertens (1983) observed decreased intakes with three forage-based rations as the ratio of hemicellulose plus cellulose to lignin increased. Williams et al. (1989) came to the conclusion that any adjustment factor for *NDF* quality should take into account the fraction of forage in the total diet, the fraction of *NDF* in the forage and the ratio of structural carbohydrate to lignin. Williams et al. (1989) developed a formula for the adjustment of *NDF* quality and found a very good agreement between observed and predicted intakes of such diverse feeds as lucerne (alfalfa) hay, maize (corn) silage as well as Bermuda grass.

2.4 Relation between available food, animal gain and animal production per hectare

Jones & Sandland (1974) studied the relation between animal gain and stocking rate in previously completed pasture trials involving thirty three different pastures. The various stocking rates used on these pastures provided 114 values on which a regression equation was based upon. To combine the results of all pastures, the gains per animal were expressed as ratios of the calculated gain per animal at optimal stocking rate and similarly the stocking rates were expressed as ratios of the calculated optimum stocking rate. The result of this combination of trials is shown in Fig. 2. Jones & Sandland (1974) found that a linear model fit the data with a correlation coefficient of r = 0.992. This means that gain per animal will decline in a linear fashion with increased stocking rate. Although the gain per animal must level off at low stocking rates, the results suggested that this only occurred at stocking rates which experimenters rarely used in practice. It is also clear from Fig. 2 that zero animal gain is only reached when the stocking rate is double that required for maximum gain per hectare. This stocking rate where maximum gain per hectare can be achieved was considered by Jones & Sandland (1974) as the optimum stocking rate.

It is also clear from Fig. 2 that maximum gain per hectare is not achieved when gain per animal is also at its maximum. The linear model according to Jones & Sandland (1974), predicted that gain per animal at the optimal stocking rate is half that possible at an infinitely low stocking rate.

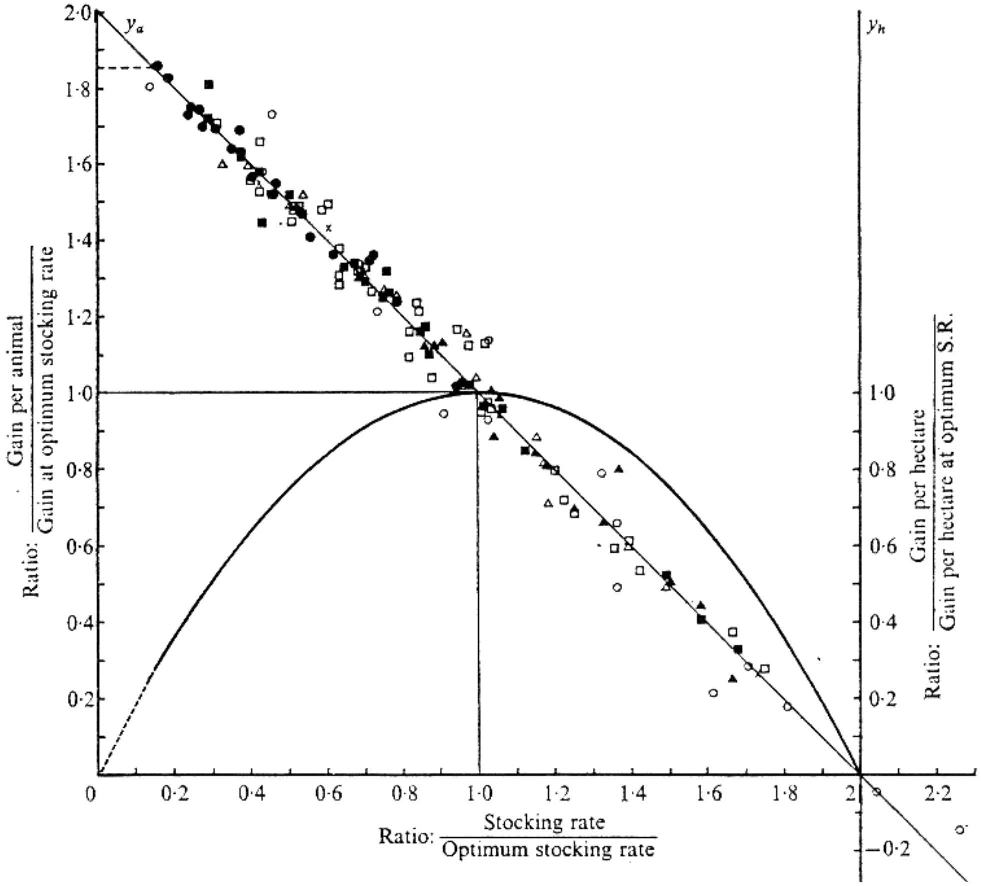

Figure 2. The relation between rate and both gain per animal and gain per hectare from grazing experiments conducted with a variety of pasture species in a wide range of environments.

Jones & Sandland (1974) conducted a grazing trial using four different fixed stocking reates to test the model which they developed. The results are shown in Fig. 3. The maximum gain per hectare occurred at half the intercept on the *X* – axis, while gain per animal at this stocking rate was at half the intercept on the *Y* – axis. These results were in agreement with the model. The implications of the existence of a plateau in gain per animal below a stocking rate of 1 animal per hectare in this case are also shown in Fig. 3. The effect of this plateau was found to be small on the graph of animal production per hectare and it does not influence the zero intercept on the *X* – axis nor the determination of the optimum stocking rate where maximum animal production per hectare occurred (Jones & Sandland, 1974).

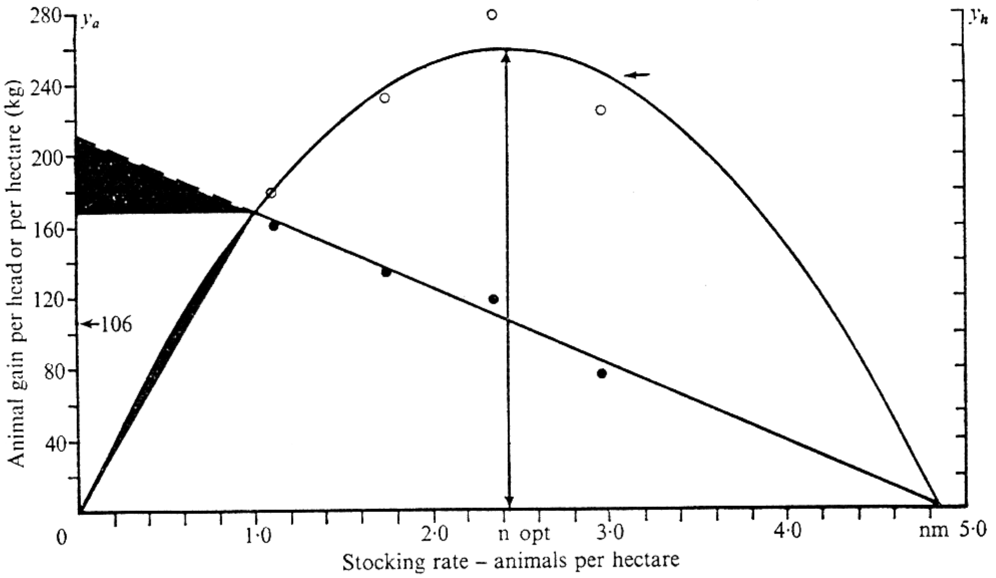

Figure 3. The relation between gain per animal and gain per hectare in response to increasing stocking rate for a *Setaria-Siratro* pasture.

Jones & Sandland (1974) came to the conclusion that it will be impossible to achieve an estimate of the maximum animal production per hectare under a ‘put and take’ system designed to give only one uniform grazing pressure. Since the relation between gain per animal and stocking rate remains linear over such a wide range of stocking rates, three different stocking rates would be able to provide an estimate of this linear relation without the need for replicates in the stocking rates. The animal gain per hectare is then calculated from the components of this relation, using a quadratic equation (Jones & Sandland, 1974).

2.5 Diallel designs and analysis

Before the different possible diallel designs are discussed, the possible alternative mating designs which could also be used, must first be considered. The parents-offspring covariance, the polycross as well as the topcross only enable the estimation of σ^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 σ^2_A is less than in the case of parent-offspring covariance and topcross or polycross. The precision of σ^2_D is very low. The factorial design is an improvement on the hierarchal design, but the estimation of σ^2_D is unsatisfactory if the parents are not inbred or if the number of sets is not large (Wricke & Weber, 1986). Becker (1984) 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 on this assumption 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 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_1'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_1's and reciprocal F_1's are included; (2) parents and one set of F_1's are included, but reciprocal F_1's are not; (3) one set of F_1's and reciprocals are included but not the parents and (4) one set of F_1's, but neither parents nor reciprocal F_1'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 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 general 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 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, 1956*b*).

There are two more approaches to diallel analysis which differ from the Griffing (1956*a*;*b*) way of analysis. The diallel analysis of Hayman (1954*a*) combined with the V_r/W_r-technique of Hayman (1954*b*) 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 (1956*b*). Hayman (1954*b*) 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 (1956*a*) 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 σ^2_A, σ^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 (1954*a*;*b*) model. The objections to this model had been dealt with in the previous paragraph. Weber (1976) evaluated all three the diallel analysis approaches on the same set of parents, F_1's and in the case of the extended diallel analysis of Gardner & Eberhart (1966), the F_2'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 σ^2_m and σ^2_f in the factorial design, σ^2_m in the hierarchal design or general combining ability in the topcross or polycross (Wricke & Weber, 1986). Hallauer & Miranda (1981) also stated that the variance component of gca in a diallel is equal to the covariance of half sibs because one parent is common. 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_1 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 σ^2_A, σ^2_D and σ^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, while none studied plant quality characteristics or plant production characteristics of the vegetative material. Five 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 variablility 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).

Chapter 3

Material and methods

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_1 combinations are shown in Table 3.1.

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

No.	Name or code of parent	Origin
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_1 hybrids

In order to develop the F_1 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℃. Thereafter the seedlings were planted in pots. This was done from 22nd May until the 3rd July. When the different plantings reached the flowering stage, the young ears were emasculated and pollinated six to ten days later.

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 126 plants per F_1 combination were needed to conduct the trial. The pollinations were done from 18th September until the 29th 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_1 combinations was also germinated in Petri dishes under controlled conditions in order to get the maximum number of seedlings possible. 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 split-plot in time 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^2 .

The planting date was the 30th 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.

3.1.4 Treatments

All the data used in this study came from two consecutive cuts of vegetative material in the split-plot in time experiment. Three 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 3rd July was the median cutting date for the first cut. This is normally the stage of growth when the triticale would be grazed for the first time.

The same three 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 & Wienhues, 1965), which corresponds to the mid–joint stage of Dunphy et al. (1982). The 1st 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.

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 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_1 hybrid combinations were included in this experiment.

All the cut material was dried in force draught ovens at temperatures of 60 - 65℃ 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.

Prior to the various analyses 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 except those specifically mentioned at the relevant character were performed in duplicate. The mean values were then taken for the calculation of percentages as were done by Petterson & Aman (1987) and Heger & Eggum (1991). At the same time as when the analyses were done, samples of the milled material were dried in an oven at 105℃ 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 the analyses were then calculated and the analysis results corrected to percentages on a 100% dry matter basis.

3.2 Characters measured

3.2.1 Plant quality characteristics

The plant quality characters which were determined by chemical analyses of the vegetative material were chosen carefully to make full use of the limited amount of material available for analysis. All the characters with the exception of the percentage ether extract and the non structural carbohydrate component were necessary inputs for the three different approaches to predict the voluntary dry matter intake per steer per day of the different genotypes. The percentage ether extract and the non structural carbohydrate component of the different genotypes were determined and calculated to look for possible useful additive genetic correlations between these characters and various animal production characteristics. The reason was that both of these easily digestible characters contribute to the metabolic energy content of the pasture. None of the three different approaches to predict the voluntary dry matter intake of a steer, nor the model used to predict live weight gain per steer per day used crude protein content as an input. The negative correlation between crude protein content and various fibre components is common knowledge by now. It was therefore decided to use crude protein in this study only in the background for the calculation of the non structural carbohydrate component. This study intended to focus rather on these quality characteristics with a direct quantifiable influence on voluntary dry matter intake per animal and live weight gain per steer per day.

3.2.1.1 NDF

Neutral detergent fibre percentage (%*NDF*) was determined according to Robertson & Van Soest (1981).

3.2.1.2 ADF

Acid detergent fibre percentage (%*ADF*) was determined in a sequential system from *NDF* as discussed by Van Soest, Robertson & Lewis (1991). The method of analysis described by Goering & Van Soest (1970) was used.

3.2.1.3 ADL

Acid detergent lignin percentage (%*ADL*) was determined according to the sequential analysis from *ADF* as described by Goering & Van Soest (1970). The sequential system of analysis for the fibre fractions was chosen because important interferences can be avoided according to Van Soest et al. (1991) and because the use of sample is more economical.

3.2.1.4 Hemicellulose

An estimate of hemicellulose content was calculated by the difference of %*NDF* and %*ADF* values as described by Goering & Van Soest (1970) and done by Nguyen et al. (1982) as well as Bughrara et al., (1991). The difference between *NDF* and *ADF* does include some protein attached to the cell walls (Goering & Van Soest, 1970). The principal advantage of the sequential analysis of *NDF* and *ADF* is that interferences can be minimised and that the estimate of hemicellulose is therefore more accurate (Van Soest et al., 1991).

3.2.1.5 Crude cellulose

According to Goering & Van Soest (1970) the *ADF* residue consists of cellulose, lignin, cutin and the acid-insoluble ash which consists mainly of silica. During the procedure to determine *ADL* the cellulose fraction is dissolved (Goering & Van Soest, 1970). After ashing of the residue of this process the crude lignin fraction (*ADL*) contains lignin and cutin (Goering & Van Soest, 1970). The difference between *ADF* and *ADL* will contain therefore except cellulose also the acid-insoluble ash fraction. Van Soest & Jones (1968) stated however that a considerable percentage of the biogenic silica is removed during the preparation of *NDF*, because of partial dissolvement in the neutral-detergent reagent. The term *crude cellulose* is therefore defined as *ADF – ADL*, to give an estimation of the cellulose content in the forage.

3.2.1.6 NDF_{adj}

The adjusted *NDF* content (NDF_{adj}) of the cut material was determined with the following formulas given by Williams et al. (1989):

The adjustment factor for *NDF* quality (*NDFADJ*) = A x *FNDF* x Ratio x 1.33^{-A}

A = the fraction of forage in the ration; taken as 1 in all the calculations

FNDF = the fraction of *NDF* in the forage

Ratio = $\frac{lignin}{hemicellulose + cellulose}$; the fraction of each component was used in the ratio

1.33^{-A} = 0.751880 in all the calculations because the forage fraction in the ration = 1

The following equation was then used to adjust for *NDF* quality:

Adjusted *NDF* fraction (*ANDF*) = *NDF* + (0.05 – *NDFADJ*)

The adjusted *NDF* content (NDF_{adj}) was then calculated as follows to get a value in percentage:

$NDF_{adj} = ANDF \times 100$

3.2.1.7 EE

The percentage ether extract (%*EE*) was determined according to AOAC (1984). The mean value of quadruple analyses was taken for the calculation of each of the percentages.

3.2.1.8 NSC

An estimate of the non structural carbohydrate (*NSC*) component was calculated according to a suggestion by Church (1986) as an alternative to Nitrogen-free extract (*NFE*) to give a reliable estimate of the readily available carbohydrates, namely the sugars and starch, in feeds high in hemicellulose.

$\%NSC = 100 - (\%\mathit{Crude\ Protein} + \%EE + \%NDF + \%\text{ash})$

3.2.1.9 IVDOM

In vitro digestible organic matter and rate of digestion were determined as described by Tilley & Terry (1963) and modified by Pienaar & Kühn (1991) to include measurement of gas production. The mean value of triplicate analyses was taken for the calculation of each of the percentages.

3.2.1.10 ME

The metabolic energy content (*ME*) was determined from the *IVDOM* values with the equation previously used in New Zealand by both Dexcel Laboratory and e-Lab Limited to predict *ME* of green pastures from *in vitro* digestible organic matter (Mann & Dugmore, 2004):

$ME = (\text{OMD} \times \text{OM}) \times 0.16$

ME in units of MJ/kg DM

OMD = organic matter digestibility percentage determined by the *in vitro* method, using rumen fluid.

OM = fraction of organic matter in the forage sample

3.2.1.11 MRT

The predicted mean retention time of organic matter in the rumen (*MRT*) was calculated according to the method as described by Pienaar & Roux (1989a).The unit of measurement for MRT is total amount of hours.

3.2.2 Plant production characteristics

The following plant production characters were calculated by multiplying the vegetative yield on an oven dry basis with the corresponding percentage of the relevant plant quality character. This was done for each genotype in both cuts. All the results are given in kg/ha. Only the plant production characters which could possibly have a positive correlation to the animal production potential of the pasture were calculated.

3.2.2.1 kg DM/ha

The dry matter (*DM*) yields given for every genotype in each cut are the vegetative yields based on oven dried mass as explained previously.

3.2.2.2 Crude cellulose yield/ha

3.2.2.3 EE yield/ha

3.2.2.4 NSC yield/ha

3.2.2.5 IVDOM yield/ha

3.2.2.6 ME yield/ha

3.2.3 Animal production characteristics

3.2.3.1 DM Intake/steer/day

A 300kg growing steer was taken as the basic animal unit in the calculation of all the following animal production characters.

3.2.3.1.1 DM Intake/steer/day (Pienaar)

The voluntary dry matter intake per steer per day, called (*Pienaar*) for this method, was calculated by dividing the predicted organic matter content at rumen fill by the predicted retention time of organic matter in the rumen as described by

Pienaar & Roux (1989a). This mechanistic dynamic mathematical model approach predicts intake from the rate and extent of digestion, using the gamma function to describe rates and *MRT* as discussed by Pienaar & Roux (1989a, 1989b). Published values for the organic matter contents at rumen fill as well as for the rates of passage of non-fermentable organic matter are used by this model (Pienaar & Roux, 1989b).

Pienaar & Roux (1989a) found that the above mentioned model fitted the data with at least the same accuracy as the generally accepted model of McDonald (1981) and also with an accuracy that is almost identical to that of the model of Mahlooji, Ellis, Matis & Pond (1984). In practice however, the *Pienaar* model is simpler to implement than the other two (Pienaar & Roux, 1989a).

3.2.3.1.2 DM Intake/steer/day (NRC)

The voluntary dry matter intake per steer per day (DMI), called (*NRC*) for this method, was calculated according to the following formulas of NRC (1996):

$\mathbf{NE_{ma}} = \{(1.37 \; x \; \text{MEC}) - (0.138 \; x \; \text{MEC}^2) + (0.0105 \; x \; \text{MEC}^3) - 1.12\}$

NE_{ma} = net energy value of diet for maintenance, *Mcal*/kg

MEC = metabolisable energy concentration of the diet, *Mcal*/kg

MEC was calculated for this study as follows:

$\mathbf{MEC} = \frac{ME}{4.184}$

ME = Metabolic energy content of the forage sample, MJ/kg DM, calculated from *IVDOM* as described in *3.2.1.10*

4.184 = conversion factor to convert MJ/kg to *Mcal*/kg (McDonald, Edwards & Greenhalgh, 1981)

$\text{DMI} = \{(\text{SBW}^{0.75} \; x \; (0.2435\text{NE}_{\text{ma}} - 0.0466\text{NE}_{\text{ma}}{}^2 - 0.0869))/\text{NE}_{\text{ma}}\} \; x \; \{(\text{BFAF})\,(\text{BI})\,(\text{ADTV})\,(\text{TEMP 1})\,(\text{MUD 1})\}$

DMI = kg DM/day

SBW = shrunk body weight, kg, (typically 0.96 *x* full weight)

BFAF = body fat adjustment factor, taken as 1.0 for weight up 350kg

BI = breed adjustment factor for DMI, taken as 1.04 for beef crossbreed

ADTV = feed additive adjustment factor for DMI, taken as 0.94 for no anabolic stimulant implantation.

TEMP 1 = temperature adjustment factor for DMI, taken as 5ºC - 15ºC ambient temperature

MUD 1 = is mud adjustment factor for DMI, taken as 1.0 for mudless conditions

This static model which uses the metabolic energy concentration in the forage as deciding factor in the DM intake calculations was used in order to evaluate the predicted intake of the forage samples from another perspective.

3.2.3.1.3 DM Intake/steer/day (Cornell)

The voluntary dry matter intake per steer per day, called (*Cornell*) for this method, was calculated according to the following formula of Williams et al. (1989):

$$\text{Intake} = \frac{NDFIC}{(A)FANDF + (1 - A)CNDF}$$

Intake = kg DM/day

NDFIC = NDF intake capacity at rumen fill, taken as 1.1% of live body weight (Mertens, 1987).

A = fraction of forage DM in the total ration, taken as 1 as in *3.2.1.6*

FANDF = the adjusted *NDF* fraction in the forage as determined under *3.2.1.6*

CNDF = the fraction of *NDF* in the concentrate

With only forage in the ration the formula reduced to the following:

$$\text{Intake} = \frac{0.011 x LiveBW}{FANDF}$$

This static intake model was favoured above later *NDF* based intake models because all the variable components in the formulas can be derived from chemical analyses; it is relatively simple without assumptions on rumen dynamics and the intakes predicted by this model fit a wide range of forage based rations very well as was shown by Williams et al. (1989).

3.2.3.2 ME Intake/steer/day

The *ME* intake per steer per day of the *Pienaar, NRC* and *Cornell* approaches were calculated by multiplying the *ME* content of the specific forage sample with the relevant predicted DM intake of the three different methods.

3.2.3.3 LWG/steer/day

The calculation of live weight gain per steer per day was calculated using the following formulas of NRC (1976, 1996). Protein and mineral content of the vegetative material was taken as adequate to sustain the predicted growth levels as energy content of young growing temperate pastures is normally the first limiting factor. When the name of an intermediate factor in front of the equal sign is printed in bold, it means that the factor will be used again in a later formula in the sequence of formulas. The meaning of the abbreviation will therefore not be explained in the later formula. The printing in bold of an abbreviation on the right hand side of the equal sign in a formula therefore corresponds with a previous result which was printed in bold.

$$\mathbf{TDN} = \frac{MEC}{0.036155}$$

This formula was deducted from ME (*Mcal*/kg) = TDN% *x* 0.036155 (NRC, 1976).

TDN = total digestible nutrient of the diet, %

MEC = metabolisable energy concentration of the diet, *Mcal*/kg, as calculated in *3.2.3.1.2*

All the following formulas were used according to NRC (1996):

pI = GRAZE *x* DMI

pI = kg predicted dry matter intake adjusted for grazing situations

GRAZE = 1, if FA > (DMI *x* 4)

FA = daily forage allowance, kg/day/head

DMI = voluntary dry matter intake per steer per day, kg DM/steer/day, using DMI values for *Pienaar, NRC* or *Cornell* as calculated in *3.2.3.1.1*, *3.2.3.1.2* or *3.2.3.1.3* respectively.

$\mathbf{NE_{mact}} = [\{0.006 \times \mathbf{pI} \times (0.9 - (\mathbf{TDN}/100))\} + (0.05 \times \text{TERRAIN})/(\text{p AVAIL} + 3)] \times \text{BW}/4.184$

NE_{mact} = activity effect on NE_m requirement

TERRAIN = Terrain factor taken as 1 for level land

p AVAIL = pasture mass available for grazing, 10^3kg/ha, taken as 0.333 x 10^3kg/ha, to allow for a theoretical stocking rate of up to 8 steers/ha and no limitation on the conditions of GRAZE

BW = Body weight, taken as 300kg as in the calculation of DMI

$\mathbf{NE_m} = [0.077\ \text{SBW}^{0.75}\ (\text{BE})\ (\text{L})\ (\text{SEX})\ \{0.8 + (\text{CS} - 1) \times 0.05)\}] + 0.0007 \times (20 - T_p)$

NE_m = net energy required for maintenance adjusted for acclimatization

SBW = shrunk body weight, kg, (typically 0.96 *x* full weight)

BE = breed effect on NE_m requirement, taken as 1 for beef type

L = lactation effect on NE_m requirement, taken as 1 for non lactating animal

SEX = 1, for steers

CS = condition score, taken as 5 on a scale of 1 to 9

T_p = previous average monthly temperature, taken as 20ºC

$\mathbf{I_m} = (\mathbf{NE_m} + \mathbf{NE_{mact}})/(NE_{ma} \times \text{ADTV})$

I_m = Intake for maintenance in the absence of heat stress, kg DM/day

NE_{ma} = net energy value of diet for maintenance, *Mcal*/kg, as calculated in *3.2.3.1.2*

ADTV = 1, for diets without ionophores

$\mathbf{NE_{ga}} = (1.42 \times \mathbf{MEC}) - (0.174 \times \mathbf{MEC}^2) + (0.0122 \times \mathbf{MEC}^3) - 1.65$

NE_{ga} = net energy value of diet for gain, *Mcal*/kg

$\mathbf{RE} = (\mathbf{DMI} - \mathbf{I_m}) \times \mathbf{NE_{ga}}$

RE = retained energy, *Mcal*/kg

$\mathbf{EQSBW} = \mathbf{SBW} \times (SRW/FSBW)$

EQSBW = equivalent shrunk body weight, kg

SRW = 435 kg for animals finishing at trace marbling

FSBW = actual final shrunk body weight at the body fat end point selected for steers, taken as (437kg x 0.96) = 420 kg. This was done to allow for a 2kg live weight loss on the way to the abattoir.

$\mathbf{SWG} = 13.91\ \mathbf{RE}^{0.9116} \times \mathbf{EQSBW}^{-0.6837}$

SWG = shrunk weight gain, kg

The live weight gain per steer per day (LWG/steer/day) was calculated from the SWG as follows:

$LWG = \mathbf{SWG} \times (100/96)$

LWG = kg/steer/day

The sequence of formulas were used with the same assumptions in the calculation of LWG for the *Pienaar, NRC* and *Cornell* approaches, only the relevant DMI values entered into the equation were different.

3.2.3.4 Live weight gain/ha

The relation between animal gain and stocking rate as described by Jones & Sandland (1974) and illustrated in Fig. 2, forms the basis of the reasoning behind the method used to calculate the live weight gain per hectare for a specific pasture genotype. It is clear from the literature review in 2.4 that it is impossible to determine the maximum potential animal gain per hectare with only one stocking rate. The proposed measure for animal production potential of a genotype is the calculated value of LWG per hectare at the highest stocking rate where maximum LWG per steer per day is still sustained, indicated by *A* on the graph in Fig. 2. It followed from the reasoning of Jones & Sandland (1974) that the LWG by a specified grazing animal on temperate species at this stocking rate is chiefly determined by the quality of the forage and that competition between animals for forage has no effect on DMI at this point yet. If the production of the pasture could be increased, point *A* will move to the right hand side of the *X* – axis, indicating that more animal units per hectare can be sustained at the same level of LWG. If the nutritional value of the pasture could be increased, point *A* will move vertically up the *Y* – axis, indicating that higher rates of LWG per animal can be achieved at the same stocking rate. Likewise the animal production per hectare at this stocking rate will only be influenced by the quantity and the quality of pasture available when all other factors like genetic potential of the steers, ambient temperature etc. are equal between the different pasture genotypes.

The Jones & Sandland (1974) model uses stocking rate in units of animals per hectare as input on the *X* – axis as shown in Fig. 2. The DMI of a steer is given as a specific rate however, namely *kg DM/steer/day*. In order to match the DMI of the grazing animal to the production of a specific pasture genotype, the production of the pasture also has to be given as a specific rate. The average DM growth rate of the pasture genotype gives a rate that can be used to this effect. Dividing of the average DM growth rate by the predicted DMI of a steer gives the average stocking rate which can be maintained for the period for which the average DM growth rate was determined. The stocking rate calculated in this way is now in the same units as used in Fig. 2 by Jones & Sandland (1974).

In order to comply with the conditions set in the first paragraph of this section, the condition for GRAZE in *3.2.3.3*, as well as the conditions for the predicted DMI and LWG in *3.2.3.1* and *3.2.3.3*, the calculations work on the assumption that a new set of 300kg steers adapted to this kind of pasture has to graze the pasture every day at the appropriate stocking rate.

The calculated average stocking rate is then multiplied by the predicted LWG per steer per day to give the predicted average LWG per hectare per day for the duration of the grazing period.

The animal production potential of a specific pasture genotype under the set of conditions stated above is then calculated by multiplying the predicted average LWG per hectare per day by the number of grazing days. This animal production potential was calculated for each genotype for both cuts and is given in units of kg *Live weight gain/ha*. This calculated animal production potential of a genotype is not the maximum possible animal production per hectare as explained in 2.4, but give an objective basis of comparison between different genotypes in a trial where plot sizes are too small to conduct grazing trials.

3.3 Statistical analysis

3.3.1 Split-plot in time analysis

The data from both cuts were subjected to split-plot in time analyses. The analyses were done with the AGROBASE (2000) program. Genotypes were taken as the whole plot treatment (*MP*), while cuts were taken as the subplot treatment. The interaction of genotype *x* cut was also calculated in order to test the significance thereof. Data from the six parents as well as from the 15 F_1 hybrid combinations were included in these analyses. The standard F-test was used to test if there were significant differences between genotypes across cuts as well as between the different cuts. The same F-test was also used to test for significance of the interaction that was considered.

3.3.2 Randomised block analysis

After the split-plot in time 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 cut. 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_1 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):

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

LSD = S.E. x $t_{0.05}$

$t_{0.05}$ 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_1 hybrid combinations were used for the diallel analysis as was recommended by Griffing (1956*b*). 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 normally shown as the *df* for the $MS_{(block\ x\ genotype)}$ 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:

$$\boldsymbol{X}_{ij} = \mu + \hat{g}_i + \hat{g}_j + \hat{s}_{ij} + \tfrac{1}{b} \sum_k b_k + \tfrac{1}{b} \sum_k (bv)_{ijk} \qquad \{\text{parent numbers: } i\text{ , } j = 1,\ldots.\text{p}\}$$

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

$\boldsymbol{X}_{ij}$ = the performance of the F_1 cross between parents *i* and *j,*

μ = 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 x block interaction effect.

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

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

$\sum_{i<}\sum_j (bv)_{ijk} = 0$

Sixty seven diallel analyses were performed on the 15 F_1 hybrids for the various forage yield and nutritive quality factors that were measured. 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.

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:

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

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

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

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:

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

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

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:

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

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

sca effect of cross *i* x *j* : $\hat{s}_{ij} = \boldsymbol{X}_{ij} - \frac{1}{(p-2)} (\boldsymbol{X}_i + \boldsymbol{X}_{j.}) + \frac{2}{(p-1)(p-2)} \boldsymbol{X}_{..}$

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

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

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

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

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

$t_{0.05}$ 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 F_1 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:

Variance of gca in the parent population: $\sigma^2_{\text{gca}} = \frac{1}{df_{gca}} \times \frac{MS_{gca} - (MS_e/bc)}{\frac{(p-2)}{(p-1)}}$

$$= \frac{1}{df_{gca}} \times \frac{MS_{gca} - M'_e}{\frac{(p-2)}{(p-1)}}$$

Variance of sca in the group of F1 progeny: $\sigma^2_{\mathrm{sca}} = \frac{1}{df_{sca}} \times \frac{MS_{sca} - \left(MS_e/bc\right)}{\frac{2}{p(p-3)}}$

$$= \frac{1}{df_{sca}} \times \frac{MS_{sca} - M'_e}{\frac{2}{p(p-3)}}$$

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 $\sigma^2_{\mathrm{gca}}/\sigma^2_{\mathrm{sca}}$ 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 σ^2_{gca} versus σ^2_{sca} .

The values of σ^2_{gca} , σ^2_{sca} and σ^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 (1956*a*) and Griffing (1956*b*).

$\sigma^2_{\mathrm{A}} = 2\sigma^2_{\mathrm{gca}}$ (additive genetic variance)

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

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

$\sigma^2_{\mathrm{e}} = MS_{\mathrm{e}}$ (error variance in the initial ANOVA done without parents to indicate the variance due to the environment, as used by Griffing (1956*b*)

$\sigma^2_{\mathrm{P}} = \sigma^2_{\mathrm{G}} + \sigma^2_{\mathrm{e}}$ (phenotypic variance)

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

$\sigma^2_{\mathrm{P}} = 2\sigma^2_{\mathrm{gca}} + \sigma^2_{\mathrm{sca}} + \sigma^2_{\mathrm{e}}$

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

$h_b^2 = \sigma^2_{\mathrm{G}}/\sigma^2_{\mathrm{P}}$

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:

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

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 (1956*b*) 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, 1956*b*).

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 (1956*b*):

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

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

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

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

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

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

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

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 σ_e^2 term was the same for all the parents.

This procedure was done for each of the characters measured.

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

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

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

S.E. = $\frac{S}{\sqrt{p}}$ (p was substituted for the *n* originally used to denote the number of individuals in the sample; in this case the population consisted of p 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 and phenotypic 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 θ in the following formula given by Griffing (1956*b*) with the additive effect A, the correlation between the additive genetic effects for two characters could be determined:

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

σ^2_{Aij} is the variance of the gca effects for the cross products,

σ^2_{Ai} is the variance of the gca effects for the independent character *i*,

σ^2_{Aj} is the variance of the gca effects for the dependent character y.

Correlations between characters were only calculated when the calculated σ^2_A values as described in 3.3.3.4 were positive for both characters. This was done to ensure reliable calculated additive genetic correlations.

In order to test the significance of the determined additive genetic correlations, the following formula of a *t* test given by Schefler (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.

In order to determine the phenotypic correlations between the selected characters, the phenotypic values of the F_1 hybrids for each of the two characters in all three replications were correlated with each other. This was done to be comparable with the values of the additive genetic correlations, because only the data from the 15 F_1 hybrid combinations were used for the diallel analysis to determine the gca effects which were used to calculate the additive genetic correlations. The calculation of the phenotypic correlations was done in the same way as explained for the additive genetic correlations, with the phenotypic value replacing the gca effect in the formula.

The tests for significance of the phenotypic correlations were done in the same way as explained for the additive genetic correlations.

3.3.4 Heterosis

The following parameters to express the degree of heterosis were calculated for each cross combination (P_1 *x* P_2).

Relative mid-parent heterosis (MPH%) with the following formula as used by Oettler et al. (2003) as well as Oettler, Tams, Utz, Bauer & Melchinger (2005):

$$MPH\% = (MPH/MP) \times 100$$

MPH indicated in the formula is the absolute mid-parent heterosis with the following formula as used by Oettler et al. (2003) and Oettler et al. (2005):

$$MPH = HYB - MP$$

HYB is the hybrid performance value of the F_1 hybrid from a specific cross combination.

MP is the mid-parent performance value in the same cross combination with the following formula as used by Burger, Oettler & Melchinger (2002), Oettler et al. (2003) and Oettler et al. (2005):

$$MP = (P_1 + P_2)/2$$

P_1 and P_2 are the performance values of parent 1 and parent 2 respectively.

Relative high-parent heterosis (HPH%) with the formula used by Oettler et al. (2005) for a parameter called relative better parent heterosis:

$$HPH\% = \{(HYB - P_{max})/ P_{max}\} \times 100$$

HYB has the same meaning as in the formula of mid-parent heterosis above.

P_{max} is the performance value of the best performing parent in the specific cross combination.

Both the *relative mid-parent heterosis* and the *relative high-parent heterosis* values from the 15 F_1 hybrid combinations for 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 F_1 hybrid combinations within each cut. The program of AGROBASE (2000) was used to obtain the different ANOVA's. The standard F-test was used to test if there were significant differences between the F_1 hybrid combinations.

The following formulas given by Singh & Chaudhary (1979) were used to calculate the LSD for the means of the heterosis values:

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

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

$t_{0.05}$ 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

Chapter 4

Phenotypic variability for forage yield and nutritive quality characteristics in triticale.

4.1 Plant quality characteristics

4.1.1 Split-plot in time analysis

4.1.1.1 Results

The mean squares for the different plant quality characteristics of the triticale vegetative material analysed in split-plot in time analyses of variance are presented in Tables 4.1 to 4.4.

4.1.1.2 Discussion

The analyses of variance in Tables 4.1, 4.2, 4.3 and 4.4 showed the following:

Highly significant differences between cuts existed for all the quality characteristics except %*EE.* The timing of the cuts was therefore chosen correctly in order to show differences between them.

The highly significant differences between blocks in the case of %*NDF*, % *ADF*, %*crude cellulose*, %NDF_{adj} and %*EE* as well as the significant difference in the case of %*ME* 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 the %*ADL*, %*hemicellulose*, %*NSC*, %*IVDOM* and *MRT* of the vegetative material.

A significant genotype *x* cut interaction occurred with %*ADF*, %*crude cellulose*, %NDF_{adj} and %*EE*, indicating that genotypes reacted differently to different cuts with regard to these characteristics.

The F-test showed in Table 4.1 that highly significant differences existed for %*NDF* between the genotypes used in this study. Significant differences were shown between genotypes for %*ADF*. No significant differences between genotypes were found for %*ADL*, indicating insignificant variability between genotypes.

Table 4.1 Mean squares for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters		
	df	%NDF	%ADF	%ADL
Genotypes	20	**39.521****	**18.693***	1.920
Blocks	2	**151.972****	**134.868****	0.211
Error (a)	40	12.885	9.419	1.512
Cuts	1	**5646.992****	**1641.763****	**13.354****
Gen. *x* **Cut**	20	15.780	**12.612***	1.572
Error (b)	42	10.597	6.677	0.881

The F-test showed in Table 4.2 that highly significant differences existed for %NDF_{adj} between the genotypes used in this study. No significant differences between genotypes were shown for %*hemicellulose* and %*crude cellulose.* This indicates limited variability between genotypes for these two characteristics.

Table 4.2 Mean squares for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters		
	df	%Hemicellulose	%Cr. cellulose	%NDF_{adj}
Genotypes	20	23.161	17.835	**34.404****
Blocks	2	30.368	**145.486****	**162.309****
Error (a)	40	20.483	10.215	12.958
Cuts	1	**1196.963****	**1359.057****	**5251.026****
Gen. *x* **Cut**	20	26.752	**9.531***	**23.041***
Error (b)	42	15.417	4.765	12.461

The F-test showed in Table 4.3 that highly significant differences existed for both %*EE* and %*NSC* between the genotypes used in this study. No significant differences between genotypes were shown for %*IVDOM*, indicating small differences between genotypes for this character.

Table 4.3 Mean squares for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters		
	df	%EE	%NSC	%IVDOM
Genotypes	20	**0.676****	**85.627****	21.785
Blocks	2	**1.936****	70.660	28.422
Error (a)	40	0.142	15.912	12.720
Cuts	1	0.101	**1380.813****	**3012.533****
Gen. *x* Cut	20	**0.268***	25.995	14.506
Error (b)	42	0.138	27.073	17.528

The F-test showed in Table 4.4 that highly significant differences existed for *ME* between the genotypes used in this study. Significant differences were shown between genotypes for *MRT*.

Table 4.4 Mean squares for the metabolic energy value and mean retention time of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters	
	df	ME (MJ/kg DM)	MRT (hour)
Genotypes	20	**0.787****	**4.202***
Blocks	2	**1.946***	0.452
Error (a)	40	0.256	2.073
Cuts	1	**38.288****	**879.543****
Gen. *x* Cut	20	0.384	3.220
Error (b)	42	0.564	5.411

The various significant differences for quality characteristics between the genotypes in the split-plot in time analyses justified more detailed statistical analyses to determine if the differences between the genotypes would continue in each of the two cuts.

4.1.2 Randomised block design analyses

4.1.2.1 Results

The mean squares for the different plant quality characteristics of the triticale vegetative material analysed in normal randomised block design analyses of variance are presented in Tables 4.5 to 4.8.

4.1.2.2 Discussion

The analyses of variance in Tables 4.5, 4.6, 4.7 and 4.8 showed the following:

The F-test showed that the highly significant differences between blocks in the case of %*ADF* and %*crude cellulose* also occurred within each of the cuts. In the case of %*NDF*, %NDF_{adj} and %*EE* highly significant differences were shown between blocks in cut 2, but only significant differences were shown in cut 1. The significant differences between blocks in cut 1 and cut 2 are in agreement with the results shown in the split-plot in time analysis for *MRT.* The split-plot in time analyses did not show any significant differences between blocks for the following characteristics, but highly significant differences between blocks were shown for %*NSC* in cut 1 and for *MRT* in cut 2. Likewise significant differences were shown between blocks for %*IVDOM* in cut 2 and for *MRT* in cut 1. No significant differences between blocks were found in the case of %*ADL* and %*hemicellulose* in any one of the two cuts. The results showed that the use of blocks in the trial design was justified for most of the plant quality characteristics evaluated in this study.

The F-test (Table 4.5) showed highly significant differences between genotypes in the case of %*NDF* and %*ADL* in cut 1, while significant differences were shown between genotypes for %*ADF* in cut 1. No significant differences between genotypes occurred for any of these plant quality characteristics in cut 2. This is in contrast to the agronomic study done in Spain by Royo, Montesinos, Molina-Cano &

Serra (1993) who cut only once, but at the same stage as cut 2 in this study. Royo et al., (1993) also found no significant differences between cultivars for %*NDF*, but significant differences were found for %*ADF.*

Table 4.5 Mean squares for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material in the randomised block design ANOVA's.

		Characters					
		%NDF		%ADF		%ADL	
	df	Cut1	Cut2	Cut1	Cut2	Cut1	Cut2
Genotypes	20	**26.312****	28.989	**15.843***	15.461	**2.566****	0.926
Blocks	2	**26.286***	**152.635****	**53.486****	**87.406****	1.266	1.802
Error	40	6.627	16.037	7.554	8.575	0.969	1.325

The F-test (Table 4.6) showed highly significant differences between genotypes only for %NDF_{adj} in cut 1. No significant differences between genotypes occurred for this character in cut 2. The lack of any significant differences between genotypes in the case of %*hemicellulose* and %*crude cellulose* is in agreement with the results from the split-plot in time analyses. The lack of any significant differences between genotypes for %NDF_{adj} in cut 2 is surprising because some of the genotypes were leafier while others had more reproductive tillers at this stage.

Table 4.6 Mean squares for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material in the randomised block design ANOVA's.

		Characters					
		%Hemi-cellulose		%Crude cellulose		%NDF_{adj}	
	df	Cut1	Cut2	Cut1	Cut2	Cut1	Cut2
Genotypes	20	14.756	35.157	13.457	13.910	**30.261****	27.184
Blocks	2	25.496	17.157	**53.891****	**94.529****	**34.118***	**155.500****
Error	40	12.556	23.501	7.457	7.614	7.642	17.035

The F-test (Table 4.7) showed highly significant differences between genotypes in the case of %*EE* and %*NSC* in cut 1, while significant differences were shown between genotypes for %*NSC* in cut 2. No significant differences between genotypes occurred for %EE in cut 2. The lack of any significant differences between genotypes in the case of %*IVDOM* is in agreement with the results from the split-plot in time analyses.

Table 4.7 Mean squares for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material in the randomised block design ANOVA's.

		Characters					
		%EE		**%NSC**		**%IVDOM**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Genotypes	20	**0.781****	0.163	**70.578****	**41.044***	9.861	26.430
Blocks	2	**0.853***	**1.482****	**164.141****	36.398	11.818	**54.224***
Error	40	0.168	0.099	15.530	22.315	13.996	15.247

The F-test (Table 4.8) showed highly significant differences between genotypes for *MRT* in cut 2, while significant differences were shown between genotypes for *ME* in cut 2. No significant differences between genotypes occurred for any of these plant quality characteristics in cut 1.

Table 4.8 Mean squares for metabolic energy value and mean retention time of the triticale vegetative material in the randomised block design ANOVA's.

		Characters			
		ME (MJ/kg DM)		**MRT (hour)**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Genotypes	20	0.553	**0.618***	2.527	**4.895****
Blocks	2	**1.684***	**1.533***	**18.816***	**26.065****
Error	40	0.453	0.331	3.644	1.890

The significant differences between genotypes indicated that %*NDF*, %*ADF*, %*ADL*, %NDF_{adj}, %*EE*, %*NSC*, *ME* as well as *MRT* can be genetically improved upon when evaluated in the appropriate treatment.

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_1 hybrids.

The best 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 combinations for the different plant quality characteristics of the triticale vegetative material are presented in Table 4.9 to 4.12.

4.1.3.2 Discussion

No triticale diallel study could be found where the %*NDF*, %*ADF* and %*ADL* from the different F_1 hybrids were investigated. Royo et al., (1993) found in an agronomic study done in Spain values in the range of 47.3% to 50.7% for %*NDF* and values of 23.9% to 26.9% for %*ADF.* Royo & Parés, (1996) found in a follow up agronomic study in Spain %*ADF* values in the range of 19.3% to 22.4% for triticale that was cut in the early joint stage. These values fall in a narrower range than the values of 42.15% to 55.84% for %*NDF* and 20.5% to 31.47% for %*ADF* found in this study.

The coefficients of variance (CV) for the different %*ADL* values were higher than those obtained for the %*ADF*. The CV for the different %*ADF* values were also higher than those obtained for the %*NDF*. No CV values were given by Royo et al., (1993) for either %*NDF* or %*ADF.*

When the means for %*NDF* of each parent and F_1 hybrid in Table 4.9 were compared, the following were found: Parent 5 had the lowest and therefore best value of the parents in cut 1. The mean value of parent 5 showed highly significant differences with the means of parents 1 and 2. A significant difference was shown with the mean of parent 6. Amongst the F_1 hybrids, 5*x*6 had the lowest mean value in cut 1. The mean value of 5*x*6 showed highly significant differences with the means of 1*x*3 and 2*x*4 and significant differences with the means of 1*x*2, 2*x*3, 2*x*6 and 3*x*4.

In cut 2 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 appeared to have the lowest value of the parents in cut 2 as well, although the differences with the other parents were not large enough to show significant differences. Amongst the F_1 hybrids, 2*x*5 had the lowest mean value in cut 2. The mean value of 2*x*5 showed highly significant differences with the means of 1*x*5 and 2*x*4.

The mean %*NDF* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.1 before.

Parent 5 had the lowest mean value of all the parents and F_1 hybrids across the two cuts when the %*NDF* of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 2*x*4 were in both cuts significantly higher than the mean value of the best respective hybrid.

The agronomic study of Royo et al., (1993) could not found any significant differences for %*NDF* between the cultivars used in their study.

When the means for %*ADF* of each parent and F_1 hybrid in Table 4.9 were compared, the following were found: Parent 5 had the lowest and therefore best value of the parents in cut 1. The mean value of parent 5 showed significant differences with the means of parents 1 and 2. Amongst the F_1 hybrids, 5*x*6 had the lowest mean value in cut 1. The mean value of 5*x*6 showed highly significant differences with the means of 1*x*2, 2*x*3 and 4*x*5 and significant differences with the means of 1*x*3, 2*x*4, 2*x*6 and 3*x*4.

In cut 2 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 lowest value of the parents in cut 2 as well. The mean value of parent 5 showed highly significant differences with the means of parents 1 and 2. A significant difference was shown with the mean of parent 4. Amongst the F_1 hybrids, 5*x*6 had the lowest mean value in cut 2. The mean value of 5*x*6 showed a highly significant difference with the mean of 1*x*6.

The mean %*ADF* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.1 before.

Parent 5 had the lowest mean value of all the parents and F_1 hybrids across the two cuts when the %*ADF* of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 5*x*6 were in both cuts significantly lower than the mean value of the highest respective hybrid.

The agronomic studies of Royo et al., (1993) and Royo & Parés, (1996) also found significant differences for %*ADF* between the cultivars used in their studies.

When the means for %*ADL* of each parent and F_1 hybrid in Table 4.9 were compared, the following were found: There were no significant differences between any of the six parents in cut 1. Amongst the F_1 hybrids, 3*x*5 had the lowest and therefore best mean value in cut 1. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*5 and 4*x*5 and significant differences with the means of 1*x*3, 2*x*4 and 3*x*4.

In cut 2 a significant difference between means was shown when using the LSD test although the F-test failed to indicate any significant differences between genotypes. There were no significant differences between any of the six parents in cut 2, as in the case of cut 1. Amongst the F_1 hybrids, 2*x*6 had the lowest mean value in cut 2. The mean value of 2*x*6 showed a significant difference with the mean of 2*x*4.

The mean %*ADL* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.1 before.

There was no common genotype with the lowest consistent mean value across the two cuts when the %*ADL* of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 2*x*4 were in both cuts significantly higher than the mean value of the best respective hybrid.

Table 4.9 Means of treatment combinations for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material.

	Characters					
	%NDF		**%ADF**		**%ADL**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	40.25**	47.97	18.31*	26.70**	2.10	4.32
2	38.05**	46.70	19.20*	26.71**	2.15	3.43
3	32.47	44.17	15.85	22.94	2.46	3.21
4	33.74	46.83	15.94	25.02*	2.04	3.17
5	***30.06***	***42.15***	***13.14***	***20.05***	2.77	3.39
6	34.62*	45.52	16.62	22.87	2.93	3.79
1 *x* **2**	35.74**	46.47	20.17**	25.18*	2.21	2.86
1 *x* **3**	37.07**	48.74	19.74**	25.94*	3.72*	3.39
1 *x* **4**	31.84	49.18*	17.49	23.78	3.23	2.90
1 *x* **5**	32.15	54.17**	17.90*	23.11	5.14**	3.36
1 *x* **6**	32.34	48.19	14.87	31.47**	2.59	4.54
2 *x* **3**	36.02**	46.20	20.20**	24.86	2.81	4.50
2 *x* **4**	41.23**	55.84**	19.70**	23.75	3.64*	4.77*
2 *x* **5**	32.08	44.98	16.28	24.15	2.14	3.90
2 *x* **6**	36.35**	47.65	19.57**	24.87	2.85	***2.85***
3 *x* **4**	35.44*	51.21**	19.06*	26.62**	3.60*	3.82
3 *x* **5**	32.55	48.68	15.28	24.00	***1.94***	3.40
3 *x* **6**	33.33	46.89	16.18	25.19*	2.44	3.40
4 *x* **5**	32.65	48.40	20.92**	22.75	5.31**	3.91
4 *x* **6**	32.95	48.06	14.80	24.73	3.11	3.38
5 *x* **6**	31.14	45.24	14.01	22.13	2.81	3.36
Mean	34.38	47.77	17.39	24.61	2.95	3.60
LSD$_{0.05}$	4.25	6.61	4.54	4.83	1.62	1.90
LSD$_{0.01}$	5.68	8.84	6.07	6.47	2.17	2.54
C.V.	7.49	8.38	15.80	11.90	33.36	31.97

No triticale diallel study could be found where the %*hemicellulose*, %*crude cellulose* and %NDF_{adj} from the different F_1 hybrids were investigated. No genetic study on any plant species could be found where the %*crude cellulose* and %NDF_{adj} from the different F_1 hybrids were investigated.

The coefficients of variance (CV) for the different %*hemicellulose* values were higher than those obtained for the %*crude cellulose*. The CV for the different %*crude cellulose* values were then higher than those obtained for the %NDF_{adj}. No value for the variation found in forage cereals for any of these three characters could be found in the literature.

When the means for %*hemicellulose* of each parent and F_1 hybrid in Table 4.10 were compared, the following were found: In cut 1 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. There were no significant differences between any of the six parents in cut 1. Amongst the F_1 hybrids, 4*x*5 had the lowest and therefore best mean value in cut 1. The mean value of 4*x*5 showed a highly significant difference with the mean of 2*x*4 and a significant difference was found with the mean of 4*x*6.

In cut 2 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. There were no significant differences between any of the six parents in cut 2. Amongst the F_1 hybrids, 1*x*6 had the lowest mean value in cut 2. The mean value of 1*x*6 showed highly significant differences with the means of 1*x*5 and 2*x*4 and significant differences were shown with the means of 1*x*4 and 4*x*5.

The mean %*hemicellulose* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.2 before.

There was no common genotype with the lowest consistent mean value across the two cuts when the %*hemicellulose* of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 2*x*4 were in both cuts significantly higher than the mean value of the best respective hybrid.

When the means for %*crude cellulose* of each parent and F_1 hybrid in Table 4.10 were compared, the following were found: In cut 1 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 2 had the highest value of the parents in cut 1. The mean value of parent 2 showed a highly significant difference with the mean of parent 5 and a significant difference was shown with the mean of parent 6. Amongst the F_1 hybrids, 1*x*2 had the highest mean value in cut 1. The mean value of 1*x*2 showed highly significant differences with the means of 4*x*6 and 5*x*6 and significant differences were shown with the means of 1*x*5, 1*x*6 and 3*x*5.

In cut 2 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 2 had the highest value of the parents in cut 2 as well. The mean value of parent 2 showed a highly significant difference with the mean of parent 5 as in the case of cut 1. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed highly significant differences with the means of 1*x*5, 2*x*3, 2*x*4, 2*x*5, 3*x*5, 4*x*5 and 5*x*6. Significant differences were shown between the mean of 1*x*6 and the means of 1*x*2, 1*x*4, 2*x*6, 3*x*6 and 4*x*6.

The mean %*crude cellulose* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.2 before.

There was no common genotype with the highest consistent mean value across the two cuts when the %*crude cellulose* of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 5*x*6 were in both cuts highly significantly lower than the mean value of the highest respective hybrid.

When the means for $\%NDF_{adj}$ of each parent and F_1 hybrid in Table 4.10 were compared, the following were found: Parent 5 had the lowest and therefore best value of the parents in cut 1. The mean value of parent 5 showed highly significant differences with the means of parents 1 and 2. Amongst the F_1 hybrids, 1*x*5 had the lowest mean value in cut 1. The mean value of 1*x*5 showed highly significant differences with the means of 1*x*2, 1*x*3, 2*x*3, 2*x*4 and 2*x*6 and a significant difference was shown with the mean of 3*x*4.

In cut 2 a significant difference between means was shown when using the LSD test although the F-test failed to indicate any significant differences between genotypes. There were no significant differences found between any of the six parents in cut 2.

Amongst the F_1 hybrids, 2*x*5 had the lowest mean value in cut 2. The mean value of 2*x*5 showed highly significant differences with the means of 1*x*5 and 2*x*4.

The mean $\%NDF_{adj}$ value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.2 before.

There was no common genotype with the lowest consistent mean value across the two cuts when the $\%NDF_{adj}$ of the harvested vegetative material was considered. Amongst the F_1 hybrids, the means of 2*x*4 were in both cuts highly significantly higher than the mean value of the best respective hybrid.

Table 4.10 Means of treatment combinations for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material.

	Characters					
	%Hemi-cellulose		**%Crude cellulose**		**%NDF$_{adj}$**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	21.95**	21.27	16.21	22.38	43.59**	49.37
2	18.85*	19.99	17.06	23.29	41.34**	48.91
3	16.62	21.23	13.39*	19.73**	35.47	46.57
4	17.80*	21.82	13.90	21.85*	37.11*	49.24
5	16.91	22.10	10.37**	16.66**	32.76	***44.36***
6	18.00*	22.65	13.69	19.08**	37.20*	47.40
1 *x* **2**	15.57	21.29	***17.96***	22.32*	38.97**	49.16
1 *x* **3**	17.34	22.79	16.02	22.56	38.89**	51.00
1 *x* **4**	14.36	25.40*	14.26	20.89*	34.13	51.87*
1 *x* **5**	14.25	31.06**	12.75*	19.75**	***32.43***	56.47**
1 *x* **6**	17.47	***16.72***	12.28*	***26.92***	35.21	49.28
2 *x* **3**	15.82	21.33	17.38	20.36**	38.67**	47.44
2 *x* **4**	21.53**	32.09**	16.07	18.98**	43.18**	56.88**
2 *x* **5**	15.80	20.84	14.15	20.24**	35.36	46.77
2 *x* **6**	16.78	22.78	16.72	22.02*	39.02**	50.37
3 *x* **4**	16.38	24.59	15.46	22.80	37.41*	53.08*
3 *x* **5**	17.27	24.68	13.34*	20.60**	36.00	50.92
3 *x* **6**	17.14	21.70	13.75	21.80*	36.35	49.14
4 *x* **5**	***11.85***	25.65*	15.61	18.84**	32.84	50.17
4 *x* **6**	18.16*	23.33	11.69**	21.35*	35.37	50.31
5 *x* **6**	17.13	23.11	11.20**	18.77**	33.80	47.50
Mean	17.00	23.16	14.44	21.01	36.91	49.82
LSD$_{0.05}$	5.85	8.00	4.51	4.55	4.56	6.81
LSD$_{0.01}$	7.82	10.70	6.03	6.09	6.10	9.11
C.V.	20.85	20.93	18.91	13.13	7.49	8.28

No triticale diallel study could be found where the %*EE*, %*NSC* and %*IVDOM* from the different F_1 hybrids were investigated. No genetic study on any plant species could be found where the %*EE* and %*NSC* from the different F_1 hybrids were investigated.

The coefficients of variance (CV) for the different %*NSC* values were higher than those obtained for the %*EE* The CV for the different %*EE* values were then higher than those obtained for the %*IVDOM.* No value for the variation found in forage cereals for any of these three characters could be found in the literature.

When the means for %*EE* of each parent and F_1 hybrid in Table 4.11 were compared, the following were found: Parent 6 had the highest and therefore best value of the parents in cut 1. The mean value of parent 6 showed highly significant differences with the means of parents 3, 4 and 5. Amongst the F_1 hybrids, 1*x*2 had the highest mean value in cut 1. The mean value of 1*x*2 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 2*x*4, 2*x*5, 3*x*4, 3*x*5, 3*x*6, 4*x*5, 4*x*6 and 5*x*6 and significant differences were shown with the means of 2*x*3 and 2*x*6.

In cut 2 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 1 had the highest value of the parents in cut 2. The mean value of both parents 1 and 6 showed significant differences with the mean of parent 4. Amongst the F_1 hybrids, 2*x*3 had the lowest mean value in cut 2. The mean value of 2*x*3 showed highly significant differences with the means of 3*x*6, 4*x*5 and 4*x*6.

As indicated in Table 4.3 before there were no significant differences between the mean %*EE* values of cuts 1 and 2. This was in contrast to all the other plant quality characters and indicated that the plant possibly needs a certain %*EE* for metabolism and tries to maintain this over cutting treatments.

Parent 4 had a significant lower mean value than the best respective parent when the %*EE* of the harvested vegetative material was considered across the two cuts. Amongst the F_1 hybrids, the means of 3*x*6, 4*x*5 and 4*x*6 were in both cuts highly significantly lower than the mean value of the best respective hybrids.

When the means for %*NSC* of each parent and F_1 hybrid in Table 4.11 were compared, the following were found: Parent 4 had the highest and therefore best value of the parents in cut 1. The mean value of parent 4 showed highly significant differences with the means of parents 1, 2 and 6. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 1. The mean value of 1*x*4 showed highly significant differences with the means of 1*x*2, 1*x*3 and 2*x*4 and significant differences were shown with the means of 1*x*5, 1*x*6, 2*x*6, 3*x*4 and 4*x*6.

Parent 3 had the highest value of the parents in cut 2. The mean value of parent 3 showed a significant difference with the mean of parent 1. Amongst the F_1 hybrids, 2*x*5 had the highest mean value in cut 2. The mean value of 2*x*5 showed highly significant differences with the means of 1*x*5 and 2*x*4.

The mean %*NSC* value of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.3 before.

Parents 3, 4 and 5 had high mean values across the two cuts when the %*NSC* of all the parents was considered. The mean values of %*NSC* of these three parents were never significantly lower than the mean of the best genotype in either of the two cuts. Amongst the F_1 hybrids, the means of 1*x*5 and 2*x*4 were in both cuts significantly lower than the mean value of the highest respective hybrid. The mean values for %*NSC* of 1*x*4, 2*x*5, 3*x*5 and 4*x*5 on the other hand, were never significantly lower than the mean of the best genotype in either of the two cuts.

When the means for %*IVDOM* of each parent and F_1 hybrid in Table 4.11 were compared, the following were found: In cut 1 a few significant differences between means were found when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 3 had the highest and therefore best value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1. Parent 3 also showed significant differences with hybrids 1*x*5, 2*x*4 and 2*x*5. There were no significant differences between the F_1 hybrids in cut 1 for %*IVDOM*.

In cut 2 a few significant differences between means were found when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 4 had the highest value of the parents in cut 2. The mean value of parent 4 showed significant differences with the means of parents 1 and 3. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 2*x*3, 2*x*6, 3*x*6 and 4*x*6, while significant differences were shown with the means of 1*x*3, 2*x*5, 3*x*4 and 5*x*6.

The mean %*IVDOM* value of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.3 before.

There was no common genotype with the highest consistent mean value across the two cuts when the %*IVDOM* of the harvested vegetative material was considered. Parents 4 and 5 had consistent high mean values across the two cuts when the %*IVDOM* of all the parents was considered. The mean values of %*IVDOM* of these two parents were never significantly lower than the mean of the best genotype in either of the two cuts. Amongst the F_1 hybrids, the means of 1*x*2, 1*x*4, 1*x*6, 3*x*5 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

The only other genetic research which could be found where differences in %*IVDOM* amongst F_1 hybrids were studied is the work of de Santis & Chiaravalle, (2001) who investigated %*IVDOM* in tall fescue. Their results agree with this study where no significant differences could be shown when the plants were in a predominantly vegetative stage with few reproductive tillers. Their study also show significant differences between F_1 hybrids for %*IVDOM* when samples were taken near heading stage of regrowth.

Table 4.11 Means of treatment combinations for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material.

	Characters					
	%EE		%NSC		%IVDOM	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	4.12	3.66	22.88**	23.64*	85.80*	77.77*
2	3.80*	3.58	32.05**	27.58	88.97	78.10*
3	3.31**	3.45	40.14	***32.70***	***93.00***	77.60*
4	2.98**	3.08**	***43.29***	31.80	87.87	84.27
5	2.70**	3.57	39.54	31.86	91.40	83.37
6	4.33	3.61	30.14**	29.54	89.90	78.73*
1 *x* **2**	***4.53***	3.62	29.66**	28.84	88.87	78.83
1 *x* **3**	4.07	3.73	29.87**	27.84	89.53	77.67*
1 *x* **4**	3.01**	3.51	40.00	25.77	88.67	***85.17***
1 *x* **5**	3.10**	3.38	32.24**	20.53**	86.80*	79.67
1 *x* **6**	3.52**	3.33	33.37**	27.50	88.50	79.20
2 *x* **3**	3.66*	***3.78***	35.35*	28.27	88.77	74.37**
2 *x* **4**	3.47**	3.50	28.47**	17.76**	86.30*	78.07*
2 *x* **5**	3.15**	3.45	37.91	31.09	86.73*	77.90*
2 *x* **6**	3.78*	3.41	31.45**	27.32	88.87	75.63**
3 *x* **4**	3.44**	3.35	33.11**	23.51*	87.60	77.77*
3 *x* **5**	3.30**	3.28	38.06	28.67	91.17	80.53
3 *x* **6**	3.62**	3.00**	35.76*	29.97	87.00	75.50**
4 *x* **5**	2.67**	3.00**	38.32	26.18	90.10	82.97
4 *x* **6**	2.90**	3.02**	31.70**	28.57	88.53	74.83**
5 *x* **6**	3.44**	3.39	33.61**	28.89	86.90	77.97*
Mean	3.47	3.41	34.14	27.52	88.63	78.85
$LSD_{0.05}$	0.68	0.52	6.50	7.80	6.17	6.44
$LSD_{0.01}$	0.91	0.69	8.70	10.43	8.26	8.62
C.V.	11.82	9.20	11.54	17.17	4.22	4.95

No genetic study on any plant species could be found where the *ME* and *MRT* from the different F_1 hybrids were investigated.

The coefficients of variance (CV) for the different *MRT* values were higher than those obtained for the *ME*. No value for the variation found in forage cereals for any of these two characters could be found in the literature.

When the means for *ME* of each parent and F_1 hybrid in Table 4.12 were compared, the following were found: In cut 1 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 and therefore best value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1. The mean value of 3*x*5 showed significant differences with the means of 1*x*5, 4*x*6 and 5*x*6.

Parent 4 had the highest mean value for *ME* amongst the parents in cut 2. The mean value of parent 4 showed a highly significant difference with the mean of parent 1 and significant differences were shown with the means of parents 2, 3 and 6. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 2*x*3, 2*x*6, 3*x*6 and 4*x*6 and significant differences were shown with the means of 2x4, 2x5, 3x4 and 5x6.

The mean *ME* value of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.4 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *ME* of the harvested vegetative material was considered. Parents 4 and 5 had consistent high mean values across the two cuts when the *ME* of all the parents was considered. The mean values of *ME* of these two parents were never significantly lower than the mean of the best genotype in either of the two cuts. Amongst the F_1 hybrids, the means of 4*x*6 and 5*x*6 were in both cuts significantly lower than the mean value of the best respective hybrid. The means of 1*x*3, 1*x*4, 1*x*6, 3*x*5 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for *MRT* of each parent and F_1 hybrid in Table 4.12 were compared, the following were found: In cut 1 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 shortest *MRT* and therefore best mean value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1. Amongst the F_1 hybrids, 3*x*5 had the shortest *MRT* mean value in cut 1. The mean value of 3*x*5 showed a significant difference with the mean of 2*x*4.

Parent 5 had the shortest mean value for *MRT* amongst the parents in cut 2. The mean value of parent 5 showed a highly significant difference with the mean of parent 1 and significant differences were shown with the means of parents 2 and 3. Amongst the F_1 hybrids, 1*x*4 had the shortest *MRT* mean value in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 1*x*2, 1*x*3, 2*x*3, 2*x*4, 2*x*5, 2*x*6, 3*x*4, 3*x*6, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*5 and 1*x*6.

Cut 1 had a highly significantly shorter mean *MRT* value than the mean value in cut 2, as was indicated in Table 4.4 before.

There was no common genotype with the shortest consistent mean value across the two cuts when the *MRT* of the harvested vegetative material was considered. Parents 4 and 5 had consistent short mean values across the two cuts when the *ME* of all the parents was considered. The mean values of *MRT* of these two parents were never significantly longer than the mean of the best genotype in either of the two cuts. Amongst the F_1 hybrids, the mean *MRT* values of 2*x*4 were in both cuts significantly longer than the mean value of the best respective hybrid. The means of 1*x*4, 3*x*5 and 4*x*5 were in both cuts never significantly longer than the mean value of the respective genotype with the shortest *MRT* value.

Table 4.12 Means of treatment combinations for metabolic energy value and mean retention time of the triticale vegetative material.

	Characters			
	ME (MJ/kg DM)		**MRT (hour)**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	12.06^{*}	11.04^{**}	16.57^{*}	21.40^{**}
2	12.84	11.18^{*}	15.13	21.17^{**}
3	***13.36***	11.31^{*}	***12.97***	20.93^{**}
4	12.90	***12.35***	15.33	18.43
5	12.72	12.08	14.80	18.33
6	12.71	11.36^{*}	14.53	20.13^{*}
1 *x* **2**	12.67	11.39^{*}	14.90	20.87^{**}
1 *x* **3**	12.88	11.42	14.90	20.87^{**}
1 *x* **4**	12.52	12.27	14.70	***17.10***
1 *x* **5**	11.83^{**}	11.47	14.10	20.07^{*}
1 *x* **6**	12.46	11.44	15.70	20.00^{*}
2 *x* **3**	12.71	10.72^{**}	14.63	21.97^{**}
2 *x* **4**	12.47	11.25^{*}	16.37^{*}	20.73^{**}
2 *x* **5**	12.25^{*}	11.30^{*}	15.17	20.17^{**}
2 *x* **6**	12.36	10.85^{**}	14.87	21.50^{**}
3 *x* **4**	12.50	11.27^{*}	15.00	20.93^{**}
3 *x* **5**	13.06	11.68	13.03	19.23
3 *x* **6**	12.22^{*}	10.92^{**}	16.07	20.87^{**}
4 *x* **5**	12.64	12.00	15.20	18.47
4 *x* **6**	11.75^{**}	10.86^{**}	14.60	21.73^{**}
5 *x* **6**	11.68^{**}	11.27^{*}	16.10	20.73^{**}
Mean	12.50	11.40	14.98	20.27
LSD$_{0.05}$	1.11	0.95	3.15	2.27
LSD$_{0.01}$	1.49	1.27	4.21	3.04
C.V.	5.39	5.05	12.74	6.78

4.2 Plant production characteristics

4.2.1 Split-plot in time analysis

4.2.1.1 Results

The mean squares for the different plant production characteristics of the triticale vegetative material analysed in split-plot in time analyses of variance are presented in Tables 4.13 and 4.14.

4.2.1.2 Discussion

The analyses of variance in Table 4.13 and Table 4.14 showed that the differences between cuts were highly significant for *kg DM/ha*, *crude cellulose* yield/ha, *EE* yield/ha, *NSC* yield/ha, *IVDOM* yield/ha as well as *ME* yield/ha. The timing of the cuts was therefore chosen correctly in order to show differences between these characteristics.

The highly significant differences between blocks in the case of *kg DM/ha*, *crude cellulose* yield/ha, *NSC* yield/ha, *IVDOM* yield/ha and *ME* yield/ha as well as the significant differences between blocks in the case of *EE* yield/ha indicate that enough soil variation was present to justify the use of the randomised block design in order to minimise the MS error.

The highly significant genotype *x* cut interactions in the case of *kg DM/ha*, *crude cellulose* yield/ha, *IVDOM* yield/ha and *ME* yield/ha as well as the significant genotype *x* cut interaction in the case of *NSC* yield/ha indicate that genotypes reacted differently to different cuts for these characteristics.

The F-test showed in Table 4.13 that highly significant differences existed for *kg DM/ha*, *crude cellulose* yield/ha as well as *EE* yield/ha between the genotypes used in this study.

Table 4.13 Mean squares for the dry matter yield, crude cellulose yield and ether extract yield of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters		
	df	kg DM/ha	Cr. cellulose yield/ha (kg/ha)	EE yield/ha (kg/ha)
Genotypes	20	**861796.713****	**45205.164****	**1448.574****
Blocks	2	**1677450.351****	**147720.959****	**705.189***
Error (a)	40	268505.244	18220.313	298.514
Cuts	1	**35309746.588****	**2916357.360****	**35564.054****
Gen. *x* **Cut**	20	**317679.981****	**24050.227****	375.156
Error (b)	42	125126.754	9382.039	223.902

The F-test showed in Table 4.14 that highly significant differences existed for *NSC* yield/ha, *IVDOM* yield/ha as well as *ME* yield/ha between the genotypes used in this study.

Table 4.14 Mean squares for the non structural carbohydrate yield, *in vitro* digestible organic matter yield and metabolic energy yield of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Characters		
	df	NSC yield/ha (kg/ha)	IVDOM yield/ha (kg/ha)	ME yield/ha (MJ/ha)
Genotypes	20	**83706.622****	**546205.638****	**113380491.000****
Blocks	2	**278907.276****	**1470603.255****	**338200087.400****
Error (a)	40	30323.374	183335.951	38521197.200
Cuts	1	**1414074.408****	**15994011.314****	**3542408665.300****
Gen. *x* **Cut**	20	**36854.667***	**238100.683****	**52022195.400****
Error (b)	42	16973.150	85532.688	18723812.146

The highly significant differences for plant production characteristics between the genotypes used in this study justified more detailed statistical analyses to establish if the differences between the genotypes would continue within each of the two cuts.

4.2.2 Randomised block design analysis

4.2.2.1 Results

The mean squares for the different plant production characteristics of the triticale vegetative material analysed in normal randomised block design analyses of variance are presented in Tables 4.15 to 4.20.

4.2.2.2 Discussion

The analyses of variance in Tables 4.15, 4.16, 4.17, 4.18, 4.19 and 4.20 showed the following:

The F-test showed that the highly significant differences between blocks shown with the split-plot in time analyses did not show in both cuts. In the case of *kg DM/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha* highly significant differences were shown between blocks in cut 1 and when the total production across both cuts were considered, but no significant differences were shown in cut 2. In the case of *crude cellulose yield/ha* highly significant differences were shown between blocks in cut 1 and when the total production across both cuts were considered. Significant differences were shown between blocks in cut 2. In the case of *EE yield/ha* highly significant differences were shown between blocks in cut 1, but no significant differences were shown in cut 2 or when the total production across both cuts were considered. The results showed that the use of blocks in the trial design was justified for all of the plant production characteristics evaluated in this study.

The F-test (Table 4.15) showed highly significant differences between genotypes in the case of *kg DM/ha* for cut 1, cut 2 and also when the total production across both cuts was considered.

Table 4.15 Mean squares for dry matter yield of the triticale vegetative material in the randomised block design ANOVA's.

		kg DM/ha		
	df	Cut1	Cut2	Total
Genotypes	20	**498099.685****	**681377.009****	**1723593.426****
Blocks	2	**1681767.475****	424358.898	**3354900.703****
Error	40	118522.983	259931.552	537010.488

The F-test (Table 4.16) showed highly significant differences between genotypes in the case of *crude cellulose yield/ha* for cut 1, and also when the total production across both cuts were considered. Significant differences between genotypes were found in cut 2.

Table 4.16 Mean squares for crude cellulose yield of the triticale vegetative material in the randomised block design ANOVA's.

		Crude cellulose yield/ha (kg/ha)		
	df	Cut1	Cut2	Total
Genotypes	20	**19520.205****	**49735.185***	**90410.286****
Blocks	2	**62489.289****	**108031.718***	**295442.404****
Error	40	4844.856	22086.596	36440.609

The F-test (Table 4.17) showed highly significant differences between genotypes in the case of *EE yield/ha* for cut 1, cut 2 and also when the total production across both cuts were considered.

Table 4.17 Mean squares for ether extract yield of the triticale vegetative material in the randomised block design ANOVA's.

		EE yield/ha (kg/ha)		
	df	Cut1	Cut2	Total
Genotypes	20	**1003.751****	**819.980****	**2897.171****
Blocks	2	**2302.035****	115.643	1410.386
Error	40	204.164	243.822	597.029

The F-test (Table 4.18) showed highly significant differences between genotypes in the case of *NSC yield/ha* for cut 1, cut 2 and also when the total production across both cuts were considered.

Table 4.18 Mean squares for non structural carbohydrate yield of the triticale vegetative material in the randomised block design ANOVA's.

		NSC yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Genotypes	20	**46649.592****	**73911.698****	**167413.226****
Blocks	2	**347825.648****	24905.362	**557813.442****
Error	40	15860.829	27593.165	60646.780

The F-test (Table 4.19) showed highly significant differences between genotypes in the case of *IVDOM yield/ha* for cut 1, cut 2 and also when the total production across both cuts were considered.

Table 4.19 Mean squares for *in vitro* digestible organic matter yield of the triticale vegetative material in the randomised block design ANOVA's.

		IVDOM yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Genotypes	20	**380834.564****	**403471.254****	**1092410.879****
Blocks	2	**1376331.014****	321719.927	**2941207.038****
Error	40	91642.374	170130.846	366671.965

The F-test (Table 4.20) showed highly significant differences between genotypes in the case of *ME yield/ha* in cut 1, cut 2 and also when the total production across both cuts were considered.

Table 4.20 Mean squares for metabolic energy yield of the triticale vegetative material in the randomised block design ANOVA's.

		ME yield/ha (MJ/ha)		
	df	**Cut1**	**Cut2**	**Total**
Genotypes	20	**80056377.300****	**85346309.100****	**226760979.500****
Blocks	2	**311692664.800****	74487834.500	**676400179.900****
Error	40	19975678.047	35806501.272	77042392.603

The significant differences between genotypes indicated that *kg DM/ha*, *crude cellulose yield/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* as well as *ME yield/ha* can be genetically improved upon when evaluated in the appropriate treatment.

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_1 hybrids.

The best 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 the different plant production characteristics of the triticale vegetative material are presented in Tables 4.21 to 4.24.

4.2.3.2 Discussion

The mean of the total *kg DM/ha* yield for the genotypes used in this study was slightly lower than what was found by Nachit (1983), but in this study the total *kg DM/ha* yield was the total of two cuts, while in the case of Nachit (1983) it was one cut taken at the end of the tillering stage. The mean of the total *kg DM/ha* yield for the genotypes used in this study was on the other hand higher than those found by

Royo et al. (1994) and Royo & Pares (1996).The cuttings in these studies were however one cut per life cycle of the plant and were done at a slightly earlier phenological growth stage than in the case of this study.

No triticale diallel study could be found where the vegetative *kg DM/ha* yield from the different F_1 hybrids were investigated.

The CV for the different vegetative *kg DM/ha* 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. No value for the variation found for vegetative *kg DM/ha* yield was given by Nachit (1983), Royo, Insa, Boujenna, Ramos, Montesinos & Garcia del Moral (1994) or Royo & Pares (1996).

When the means for *kg DM/ha* yield of each parent and F_1 hybrid in Table 4.21 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 showed a highly significant difference with the mean of parent 4 and a significant difference with the mean of parent 5. Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*2, 2*x*3, 2*x*5, 3*x*5 and 3*x*6.

Parent 6 had the highest value of the parents in cut 2. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and significant differences with the means of parents 2 and 5. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed a highly significant difference with the mean of 2*x*3 and significant differences with the means of 1*x*4, 3*x*4 and 5*x*6.

Parent 6 had the highest value of the parents when the total *kg DM/ha* yield across two cuts was considered. The mean value of parent 6 showed highly significant differences with the means of parents 4 and 5. Amongst the F_1 hybrids, 2*x*6 had the highest total mean value across the two cuts. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4 and 5*x*6 and significant differences with the means of 1*x*5, 2*x*3, 3*x*4, 4*x*5 and 4*x*6.

The mean *kg DM/ha* value of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.13 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *kg DM/ha* of the harvested vegetative material was considered. Parents 4 and 5 had in both cuts significant lower *kg DM/ha* values than the parent with the highest respective mean *kg DM/ha* value. Amongst the F_1 hybrids, the means of 1*x*3, 2*x*4 and 2*x*6 were in both cuts never significantly lower than the mean value of the highest respective genotypes.

The agronomic studies of Brown & Almodares, (1976), Royo et al., (1993) and Royo & Parés, (1996) also found significant differences for *kg DM/ha* yield between the cultivars used in their studies.

Table 4.21 Means of treatment combinations for dry matter yield of the triticale vegetative material.

	kg DM/ha		
Genotypes	**Cut1**	**Cut2**	**Total**
1	1247.45**	2351.37	3598.83
2	1417.85*	1715.07**	3132.91*
3	910.05**	2148.72*	3058.77*
4	649.96**	1159.72**	1809.68**
5	678.30**	1604.27**	2282.58**
6	1243.69**	2686.96	3930.66
1 *x* **2**	1411.29*	2691.80	4103.09
1 *x* **3**	1567.84	2860.67	4428.51
1 *x* **4**	701.91**	1964.00*	2665.92**
1 *x* **5**	788.98**	2316.21	3105.19*
1 *x* **6**	1179.38**	***3021.27***	4218.64
2 *x* **3**	1489.65*	1722.36**	3212.01*
2 *x* **4**	1890.29	2259.48	4149.77
2 *x* **5**	1453.49*	2721.52	4147.01
2 *x* **6**	***2128.71***	*2456.55*	***4585.25***
3 *x* **4**	1180.34**	2014.31*	3194.66*
3 *x* **5**	1555.41*	2857.77	4413.17
3 *x* **6**	1506.64*	2631.48	4138.12
4 *x* **5**	890.87**	2329.56	3220.43*
4 *x* **6**	871.33**	2384.34	3255.67*
5 *x* **6**	866.30**	1984.02*	2850.32**
Mean	1221.32	2280.07	3501.39
LSD$_{0.05}$	568.10	841.30	1209.24
LSD$_{0.01}$	760.09	1125.62	1617.90
C.V.	28.19	22.36	20.93

No genetic study on any plant species could be found where the vegetative *crude cellulose yield/ha* and *EE yield/ha* from the different F$_1$ hybrids were investigated.

The CV for the different vegetative *crude cellulose yield/ha* were higher than those found for *EE yield/ha.*

When the means for *crude cellulose yield/ha* of each parent and F_1 hybrid in Table 4.22 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 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_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 2*x*5, 3*x*5 and 3*x*6.

Parent 1 had the highest value of the parents in cut 2. The mean value of parent 1 showed significant differences with the means of parents 4 and 5. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 2*x*3, 2*x*4, 3*x*4, 4*x*5 and 5*x*6. Significant differences were shown with the means of 2*x*5, 2*x*6 and 4*x*6.

Parent 1 had the highest value of the parents when the total *crude cellulose yield/ha* across two cuts was considered. The mean value of parent 1 showed significant differences with the means of parents 4 and 5. Amongst the F_1 hybrids, 1*x*6 had the highest total mean value across the two cuts. The mean value of 1*x*6 showed highly significant differences with the means of 1*x*4 and 5*x*6 and significant differences with the means of 1*x*5, 2*x*3, 3*x*4, 4*x*5 and 4*x*6.

The mean *crude cellulose yield/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.13 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *crude cellulose yield/ha* of the harvested vegetative material was considered. Parents 4 and 5 had in both cuts significant lower values than the parent with the highest respective mean *crude cellulose yield/ha* value. Amongst the F_1 hybrids, the means of 1*x*2 and 1*x*3 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for *EE yield/ha* of each parent and F_1 hybrid in Table 4.22 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 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_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 2*x*5, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 2*x*3 and 3*x*5.

Parent 6 had the highest value of the parents in cut 2. The mean value of parent 6 showed highly significant differences with the means of parents 4 and 5 and a significant difference was shown with the mean of parent 2. Amongst the F_1 hybrids, 1*x*3 had the highest mean value in cut 2. The mean value of 1*x*3 showed highly significant differences with the means of 1*x*4, 2*x*3, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*5, 2*x*4 and 3*x*6.

Parent 6 had the highest value of the parents when the total *EE yield/ha* across two cuts was considered. The mean value of parent 6 showed highly significant differences with the means of parents 4 and 5 and a significant difference with the mean of parent 3. Amongst the F_1 hybrids, 1*x*3 had the highest total mean value across the two cuts. The mean value of 1*x*3 showed highly significant differences with the means of 1*x*4, 1*x*5, 3*x*4, 4*x*5, 4*x*6 and 5*x*6 and a significant difference with the mean of 2*x*3.

The mean *EE yield/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.13 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *EE yield/ha* of the harvested vegetative material was considered. Parents 4 and 5 had in both cuts significant lower values than the parent with the highest respective mean *EE yield/ha* value. Amongst the F_1 hybrids, the means of 1*x*2, 1*x*3 and 2*x*6 were in both cuts never significantly lower than the mean value of the best respective genotypes.

Table 4.22 Means of treatment combinations for crude cellulose yield and ether extract yield of the triticale vegetative material.

	Characters					
	Cr. cellulose yield/ha (kg/ha)			**EE yield/ha (kg/ha)**		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1	203.25**	525.45*	728.70	50.94*	86.02	136.96
2	247.61	399.38**	646.99	54.76*	61.42**	116.18**
3	122.95**	423.27**	546.22*	29.50**	73.59*	103.10**
4	90.59**	258.01**	348.60**	19.14**	36.67**	55.82**
5	72.39**	272.94**	345.33**	17.63**	56.91**	74.55**
6	181.53**	521.14*	702.67	54.31*	95.11	149.42
1 *x* **2**	259.72	604.40	864.12	63.60	95.62	159.22
1 *x* **3**	248.02	655.95	903.97	64.19	***105.94***	***170.14***
1 *x* **4**	95.23**	414.82**	510.05**	21.27**	70.11**	91.38**
1 *x* **5**	100.35**	477.33**	577.68*	25.11**	76.21*	101.32**
1 *x* **6**	147.48**	***810.52***	***958.00***	42.57**	99.96	142.52
2 *x* **3**	258.29	348.83**	607.12*	54.37*	65.21**	119.57*
2 *x* **4**	320.00	440.89**	760.88	65.41	78.89*	144.30
2 *x* **5**	209.84*	554.27*	764.11	44.57**	92.82	137.39
2 *x* **6**	***359.30***	549.03*	908.33	***81.38***	84.45	165.83
3 *x* **4**	181.28**	460.64**	641.92*	39.61**	67.37**	106.98**
3 *x* **5**	209.31*	596.32	805.63	50.63*	92.21	142.84
3 *x* **6**	220.74*	582.19	802.93	58.39	77.48*	135.88
4 *x* **5**	130.93**	455.52**	586.45*	23.03**	66.46**	89.48**
4 *x* **6**	101.16**	522.65*	623.81*	25.11**	71.33**	96.44**
5 *x* **6**	96.42**	372.59**	469.01**	29.72**	67.08**	96.80**
Mean	183.64	487.91	671.55	43.58	77.18	120.77
LSD$_{0.05}$	114.86	245.24	315.00	23.58	25.77	40.32
LSD$_{0.01}$	153.67	328.11	421.46	31.55	34.47	53.95
C.V.	37.90	30.46	28.43	32.78	20.23	20.23

No genetic study on any plant species could be found where the vegetative *NSC yield/ha* and *IVDOM yield/ha* from the different F_1 hybrids were investigated.

The CV for the different vegetative *NSC yield/ha* were higher than those found for *IVDOM yield/ha.*

When the means for *NSC yield/ha* of each parent and F_1 hybrid in Table 4.23 were compared, the following were found: There were no significant differences between any of the six parents in cut 1. Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*2, 1*x*3, 1*x*6 and 3*x*4.

Parent 6 had the highest value of the parents in cut 2. The mean value of parent 6 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 F_1 hybrids, 2*x*5 had the highest mean value in cut 2. The mean value of 2*x*5 showed highly significant differences with the means of 1*x*4, 1*x*5, 2*x*4 and 3*x*4. Significant differences were shown with the means of 2*x*3 and 5*x*6.

Parent 6 had the highest value of the parents when the total *NSC yield/ha* across two cuts was considered. The mean value of parent 6 showed a highly significant difference with the mean of parent 4. Amongst the F_1 hybrids, 3*x*5 had the highest total mean value across the two cuts. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*4, 1*x*5 and 5*x*6 and significant differences were shown with the means of 2*x*4, 3*x*4, 4*x*5 and 4*x*6.

The mean *NSC yield/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.14 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *NSC yield/ha* of the harvested vegetative material was considered. Parents 1, 3 and 6 had in both cuts never significant lower values than the parent with the highest respective mean *NSC yield/ha* value. Amongst the F_1 hybrids, the means of 2*x*5, 2*x*6, 3*x*5 and 3*x*6 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for *IVDOM yield/ha* of each parent and F_1 hybrid in Table 4.23 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 showed a highly significant difference with the mean of parents 4 and a significant difference with the mean of parent 5. Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*2, 1*x*3, 2*x*3, 2*x*5 and 3*x*6.

Parent 6 had the highest value of the parents in cut 2. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and significant differences with the means of parents 2 and 5. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed a highly significant difference with the mean of 2*x*3 and significant differences with the means of 1*x*4, 3*x*4 and 5*x*6.

Parent 6 had the highest value of the parents when the total *IVDOM yield/ha* across two cuts was considered. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and a significant difference with the mean of parent 5. Amongst the F_1 hybrids, 2*x*6 had the highest total mean value across the two cuts. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4 and 5*x*6 and significant differences with the means of 1*x*5, 2*x*3, 3*x*4 and 4*x*6.

The mean *IVDOM yield/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.14 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *IVDOM yield/ha* of the harvested vegetative material was considered. Parents 4 and 5 had in both cuts significant lower values than the parent with the highest respective mean *IVDOM yield/ha* value. Amongst the F_1 hybrids, the means of 2*x*4, 2*x*6 and 3*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

Table 4.23 Means of treatment combinations for non structural carbohydrate yield and *in vitro* digestible organic matter yield of the triticale vegetative material.

	Characters					
	NSC yield/ha (kg/ha)			**IVDOM yield/ha (kg/ha)**		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1	280.86**	556.43*	837.29**	1068.05**	1828.59	2896.64
2	447.63*	471.81**	919.43*	1253.57*	1338.77**	2592.34*
3	376.68**	702.13	1078.81	844.70**	1665.62*	2510.32*
4	273.45**	360.68**	634.14**	571.91**	965.92**	1537.83**
5	288.58**	515.45*	804.02**	625.30**	1342.50**	1967.80**
6	380.16**	800.04	1180.20	1113.72**	2111.45	3225.17
1 *x* **2**	423.13*	782.66	1205.79	1249.50*	2122.25	3371.76
1 *x* **3**	464.22*	796.61	1260.83	1393.52*	2212.51	3606.04
1 *x* **4**	281.02**	471.63**	752.65**	625.73**	1682.32*	2308.05**
1 *x* **5**	248.28**	470.18**	718.46**	686.29**	1842.91	2529.20*
1 *x* **6**	398.85*	823.48	1222.33	1060.98**	***2410.96***	3471.95
2 *x* **3**	541.36	490.35*	1031.70	1316.61*	1284.78**	2601.39*
2 *x* **4**	534.25	408.42**	942.67*	1626.49	1764.02	3390.52
2 *x* **5**	564.57	***848.45***	1413.02	1259.59*	2119.26	3378.86
2 *x* **6**	***673.28***	662.77	1336.05	***1898.63***	1845.54	***3744.17***
3 *x* **4**	409.00*	474.83**	883.83*	1030.30**	1567.19*	2597.49*
3 *x* **5**	603.40	816.09	***1419.49***	1411.78	2291.61	3703.39
3 *x* **6**	526.11	784.85	1310.96	1317.32*	1991.52	3308.83
4 *x* **5**	351.01**	618.71	969.72*	814.00**	1959.28	2773.28
4 *x* **6**	275.01**	658.60	933.61*	769.21**	1762.91	2532.12*
5 *x* **6**	295.83**	571.90*	867.73**	755.63**	1546.73*	2302.36**
Mean	411.27	623.15	1034.42	1080.61	1793.17	2873.79
LSD$_{0.05}$	207.82	274.11	406.37	499.54	680.63	999.22
LSD$_{0.01}$	278.05	366.74	543.71	668.36	910.65	1336.90
C.V.	30.62	26.66	23.81	28.01	23.00	21.07

No genetic study on any plant species could be found where the vegetative *ME yield/ha* from the different F_1 hybrids were investigated.

The CV for the different vegetative *ME yield/ha* were almost the same as those found for *IVDOM yield/ha.*

When the means for *ME yield/ha* of each parent and F_1 hybrid in Table 4.24 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 showed significant differences with the means of parents 4 and 5. Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*2, 2*x*3, 2*x*5 and 3*x*6.

Parent 6 had the highest value of the parents in cut 2. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and significant differences with the means of parents 2 and 5. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed a highly significant difference with the mean of 2*x*3 and significant differences with the means of 1*x*4, 3*x*4 and 5*x*6.

Parent 6 had the highest value of the parents when the total *ME yield/ha* across two cuts was considered. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and a significant difference with the mean of parent 5. Amongst the F_1 hybrids, 3*x*5 had the highest total mean value across the two cuts. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*4 and 5*x*6 and significant differences with the means of 1*x*5, 2*x*3, 3*x*4 and 4*x*6.

The mean *ME yield/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.14 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *ME yield/ha* of the harvested vegetative material was considered. Parents 4 and 5 had in both cuts significant lower values than the parent with the highest respective mean *ME yield/ha* value. Amongst the F_1 hybrids, the means of 1*x*3, 2*x*4, 2*x*6 and 3*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

Table 4.24 Means of treatment combinations for metabolic energy yield of the triticale vegetative material.

	ME yield/ha (MJ/ha)		
Genotypes	**Cut1**	**Cut2**	**Total**
1	15005.44**	25946.35	40951.79
2	18097.17*	19159.45**	37256.62*
3	12209.06**	24283.32*	36492.38*
4	8381.10**	14114.88**	22495.98**
5	8809.41**	19475.26**	28284.68**
6	15791.99**	30478.26	46270.25
1 *x* **2**	17830.92*	30706.82	48537.74
1 *x* **3**	20037.09	32522.00	52559.10
1 *x* **4**	8860.41**	24184.50*	33044.91**
1 *x* **5**	9357.41**	26553.37	35910.78*
1 *x* **6**	14953.24**	***34820.22***	49773.47
2 *x* **3**	19081.09*	18539.97**	37621.06*
2 *x* **4**	23510.70	25415.47	48926.17
2 *x* **5**	17859.19*	30747.09	48606.29
2 *x* **6**	***26598.53***	26447.55	53046.08
3 *x* **4**	14730.53**	22700.91*	37431.44*
3 *x* **5**	20266.57	33265.42	***53532.00***
3 *x* **6**	18682.66*	28806.35	47489.02
4 *x* **5**	11430.78**	28372.52	39803.30
4 *x* **6**	10187.81**	25608.39	35796.20*
5 *x* **6**	10122.22**	22351.69*	32473.91**
Mean	15323.97	25928.56	41252.53
$LSD_{0.05}$	7375.16	9874.19	14483.90
$LSD_{0.01}$	9867.61	13211.19	19378.76
C.V.	29.17	23.08	21.28

4.3 Animal production characteristics

4.3.1 Split-plot in time analysis

4.3.1.1 Results

The mean squares for the different animal production characteristics of the triticale vegetative material analysed in split-plot in time analyses of variance are presented in Tables 4.25 to 4.28.

4.3.1.2 Discussion

The analyses of variance in Table 4.25, 4.26, 4.27 and 4.28 showed that the differences between cuts were highly significant for predicted *DM intake/steer/day*, predicted *ME intake/steer/day*, predicted *LWG/steer/day* and predicted *Live weight gain/ha* according to the approaches of *Pienaar*, *NRC* as well as *Cornell*. The timing of the cuts was therefore chosen correctly in order to show differences between these characteristics.

There were highly significant differences between blocks in the case of the predicted *DM intake/steer/day* according to the *Cornell* approach and significant differences between blocks in the case of the *NRC* prediction. There were also significant differences between blocks in the case of predicted *ME intake/steer/day*, according to the approach of *Cornell.* Highly significant differences between blocks existed for predicted *Live weight gain/ha*, according to the approaches of *Pienaar*, *NRC* as well as *Cornell.* These significant differences indicate that enough soil variation was present to justify the use of the randomised block design in order to minimise the MS error.

Highly significant genotype *x* cut interactions occurred for the predicted *DM intake/steer/day* according to the *Cornell* approach. A highly significant genotype *x* cut interaction was shown for predicted *Live weight gain/ha*, according to the approach of *NRC.* A significant genotype *x* cut interaction was shown for predicted *Live weight gain/ha* according to the approaches of *Pienaar* and *Cornell.* This indicates that genotypes reacted differently to different cuts for these characteristics.

The F-test (Table 4.25) showed that highly significant differences existed between the genotypes used in this study for predicted *DM intake/steer/day*, according to both the *NRC* and *Cornell* approaches.

Table 4.25 Mean squares for the predicted dry matter intake per steer per day of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		DM Intake (kg/steer/day)		
	df	Pienaar	NRC	Cornell
Genotypes	20	1.194	**0.075****	**1.260****
Blocks	2	0.058	**0.236***	**4.707****
Error (a)	40	1.063	0.029	0.438
Cuts	1	**287.232****	**3.863****	**174.326****
Gen. *x* **Cut**	20	0.986	0.040	**0.837****
Error (b)	42	1.558	0.051	0.308

The F-test (Table 4.26) showed that highly significant differences existed between the genotypes used in this study for predicted *ME intake/steer/day*, according to both the *NRC* and *Cornell* approaches.

Table 4.26 Mean squares for the predicted metabolic energy intake per steer per day of the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		ME Intake (MJ/steer/day)		
	df	Pienaar	NRC	Cornell
Genotypes	20	359.795	**12.751****	**263.478****
Blocks	2	295.872	20.135	**315.429***
Error (a)	40	278.651	3.474	61.288
Cuts	1	**67214.949****	**555.979****	**42057.065****
Gen. *x* **Cut**	20	247.520	5.804	84.845
Error (b)	42	412.020	10.148	95.570

The F-test (Table 4.27) showed that highly significant differences existed between the genotypes used in this study for predicted *LWG/steer/day*, according to both the *NRC* and *Cornell* approaches.

Table 4.27 Mean squares for the predicted live weight gain per steer per day from the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		LWG/steer/day (kg/steer/day)		
	df	**Pienaar**	**NRC**	**Cornell**
Genotypes	20	0.310	**0.038****	**0.215****
Blocks	2	0.385	0.072	0.123
Error (a)	40	0.209	0.011	0.046
Cuts	1	**48.694****	**1.763****	**32.160****
Gen. *x* **Cut**	20	0.195	0.018	0.049
Error (b)	42	0.325	0.029	0.099

The F-test showed highly significant differences between the genotypes used in this study for predicted *Live weight gain/ha*, according to the approaches of *NRC* as well as *Cornell* and significant differences between the genotypes were shown for the approach of *Pienaar.*

Table 4.28 Mean squares for the predicted live weight gain of steers per ha from the triticale vegetative material in the ANOVA's of split-plot in time analyses.

		Live weight gain/ha (kg/ha)		
	df	**Pienaar**	**NRC**	**Cornell**
Genotypes	20	**24352.880***	**22137.669****	**20135.237****
Blocks	2	**118657.728****	**106344.244****	**91871.364****
Error (a)	40	10300.820	8645.508	8059.450
Cuts	1	**109271.575****	**378555.351****	**47438.201****
Gen. *x* **Cut**	20	**20166.757***	**14391.731****	**14095.525***
Error (b)	42	9292.238	5811.212	6905.986

The highly significant differences for animal production characteristics between the genotypes in the split-plot in time analyses justified more detailed statistical analyses to determine if the differences between the genotypes would continue within each of the two cuts.

4.3.2 Randomised block analysis

4.3.2.1 Results

The mean squares for the different animal production characteristics of the triticale vegetative material analysed in normal randomised block design analyses of variance are presented in Tables 4.29 to 4.34.

4.3.2.2 Discussion

The analyses of variance in Tables 4.29, 4.30, 4.31, 4.32, 4.33 and 4.34 showed the following:

The F-test showed that the highly significant differences between blocks shown with the split-plot in time analyses did not show in both cuts. In the case of *DM intake/steer/day*, according to the *Cornell* approach, highly significant differences were shown between blocks in cut 2 but only significant differences were shown between blocks in cut 1. In the case of *Live weight gain/ha*, according to the *Pienaar*, *NRC* and *Cornell* approaches, highly significant differences were shown between blocks in cut 1 and when the total production across both cuts were considered, but no significant differences were shown in cut 2. The significant differences between blocks shown with the split-plot in time analyses did not show in both cuts when the cuts were separately tested with the F-test. In the case of *DM intake/steer/day*, according to the *NRC* approach, significant differences were shown between blocks in cut 1 but highly significant differences were shown between blocks in cut 2. In the case of *ME intake/steer/day*, according to the *Cornell* approach, highly significant differences were shown between blocks in cut 2 but no significant differences were shown in cut 1.

Even when no significant differences between blocks were shown with the split-plot in time analyses, some significant differences between blocks were shown when the cuts were separately tested with the F-test. In the case of *DM intake/steer/day*, according to the *Pienaar* approach, highly significant differences were shown between blocks in cut 1 but highly significant differences were shown between blocks in cut 2. In the case of *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches, highly significant differences and significant differences were shown respectively between blocks in cut 2 but no significant differences were shown in cut 1. In the case of *LWG/steer/day*, according to the *Pienaar* and *Cornell* approaches, highly significant differences were shown between blocks in cut 2 but no significant differences were shown in cut 1. In the case of *LWG/steer/day*, according to the *NRC* approach, significant differences were shown between blocks in both cut 1 and cut 2. The results showed that the use of blocks in the trial design was justified for all of the animal production characteristics evaluated in this study.

The F-test (Table 4.29) showed highly significant differences between the genotypes for predicted *DM intake/steer/day*, according to the *Pienaar* approach in cut 2 and the *Cornell* approach in cut 1. Significant differences were shown between genotypes for predicted *DM intake/steer/day*, according to the *NRC* approach in cut 2.

Table 4.29 Mean squares for the predicted dry matter intake per steer per day of the triticale vegetative material in the randomised block design ANOVA's.

		DM Intake (kg/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Genotypes	20	1.445	**0.735****	0.062	**0.053***	**1.652****	0.445
Blocks	2	3.850	**3.851****	**0.182***	**0.148****	**1.835***	**3.137****
Error	40	2.054	0.263	0.051	0.027	0.465	0.283

The F-test (Table 4.30) showed highly significant differences between the genotypes for predicted *ME intake/steer/day*, according to the *Pienaar* approach in cut 2 and the *Cornell* approach in cut 1. No significant differences were shown between genotypes for predicted *ME intake/steer/day*, in the case of the *NRC* approach in either cut 1 or cut 2.

Table 4.30 Mean squares for the predicted metabolic energy intake per steer per day of the triticale vegetative material in the randomised block design ANOVA's.

		ME Intake (MJ/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Genotypes	20	362.201	**254.114****	6.771	11.784	**259.983****	88.340
Blocks	2	1463.79	**637.393****	21.468	**26.980***	29.186	**512.281****
Error	40	528.903	92.103	5.656	7.057	85.210	65.124

The F-test (Table 4.31) showed highly significant differences between the genotypes for predicted *LWG/steer/day*, according to the *Pienaar* approach in cut 2. Significant differences were shown between genotypes for the *Cornell* approach in cut 1. No significant differences were shown between genotypes for predicted *LWG/steer/day*, in the case of the *NRC* approach in either cut 1 or cut 2.

Table 4.31 Mean squares for the predicted live weight gain per steer per day from the triticale vegetative material in the randomised block design ANOVA's.

		LWG/steer/day (kg/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Genotypes	20	0.287	**0.218****	0.022	0.034	**0.182***	0.081
Blocks	2	1.259	**0.476****	**0.070***	**0.079***	0.014	**0.378****
Error	40	0.396	0.087	0.019	0.019	0.079	0.058

The F-test (Table 4.32) showed highly significant differences between the genotypes for predicted *Live weight gain/ha* in cut 1, according to the *Pienaar*, *NRC* and *Cornell* approaches.

Table 4.32 **Mean squares for the predicted live weight gain of steers per ha for cut 1 of the triticale vegetative material in the randomised block design ANOVA's.**

		Live weight gain/ha (Cut1) (kg/ha)		
	df	Pienaar	NRC	Cornell
Genotypes	20	**25568.549****	**19850.237****	**20483.026****
Blocks	2	**127205.501****	**89712.690****	**95842.953****
Error	40	7589.541	5661.089	6201.952

The F-test (Table 4.33) showed significant differences between the genotypes for predicted *Live weight gain/ha*, according to the *NRC* approaches. No significant differences between the genotypes were shown in cut 2 for predicted *Live weight gain/ha*, according to either the *Pienaar* or *Cornell* approaches.

Table 4.33 **Mean squares for the predicted live weight gain of steers per ha for cut 2 of the triticale vegetative material in the randomised block design ANOVA's.**

		Live weight gain/ha (Cut2) (kg/ha)		
	df	Pienaar	NRC	Cornell
Genotypes	20	18951.088	**16679.163***	13747.736
Blocks	2	23894.521	26539.685	20670.878
Error	40	10846.014	8590.786	7876.659

The F-test (Table 4.34) showed highly significant differences between the genotypes for predicted *Live weight gain/ha*, according to the *NRC* and *Cornell* approaches. Significant differences between the genotypes were shown for predicted *Live weight gain/ha*, according to the *Pienaar* approach.

Table 4.34 Mean squares for the total predicted live weight gain of steers per ha from the triticale vegetative material in the randomised block design ANOVA's.

		Total live weight gain/ha (kg/ha)		
	df	Pienaar	NRC	Cornell
Genotypes	20	**48705.812***	**44275.357****	**39477.444****
Blocks	2	**237315.914****	**212687.804****	**195752.883****
Error	40	20601.633	17291.029	16341.106

The significant differences between genotypes indicated that predicted *DM intake/steer/day* as well as predicted *Live weight gain/ha* can be genetically improved upon when evaluated in the appropriate treatment according to any one of the *Pienaar*, *NRC* or *Cornell* approaches.

4.3.3 Tables of means

4.3.3.1 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_1 hybrids.

The best 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 α = 0.05 level of confidence or by a ****** for a α = 0.01 level of confidence.

The means of the treatment combinations for the different animal production characteristics of the triticale vegetative material are presented in Tables 4.35 to 4.39.

4.3.3.2 Discussion

No genetic study on any plant species could be found where the predicted *DM intake/steer/day* of vegetative material from the different F_1 hybrids were investigated.

The CV for the different predicted *DM intake/steer/day*, according to the *Pienaar* approach was higher in cut 1 than those of the *Cornell* approach. The CV for the different predicted *DM intake/steer/day*, according to the *NRC* approach was in both cuts lower than either the *Pienaar* approach or the *Cornell* approach.

When the means for predicted *DM intake/steer/day* of each parent and F_1 hybrid in Table 4.35 were compared, the following were found: The high *ME* values of the vegetative material in cut 1 were the first limiting factors which caused a limit in predicted *DM intake/steer/day*. The *NRC* approach therefore predicted the smallest *DM intake/steer/day* for all the genotypes in cut 1 except for parent 1. Parent 1 had the highest $\%NDF_{adj}$ (43.59), the lowest *%NSC* (22.88), the lowest *%IVDOM* (85.80), the lowest predicted *ME* (12.06) and the longest predicted *MRT* (16.57 hours) of all the genotypes in cut 1. Between the three different approaches, the *Cornell* approach predicted the lowest *DM intake/steer/day* for parent 1 in cut 1 and this predicted intake was only slightly lower than the prediction according to the *NRC* approach. As stated before the *Cornell* approach rely solely on the $\%\ NDF_{adj}$ for predicting *DM intake/steer/day.* The $\%\ NDF_{adj}$ value of 43.59% must be very near the cross-over value when $\%\ NDF_{adj}$ and therefore rumen fill become the limiting factor and the *Cornell* approach will give the most prudent prediction. The *Pienaar* approach gave the highest predicted intakes in cut 1 in relation to the other two approaches, indicating that *MRT* and *%IVDOM* were not the limiting factors in cut 1.

The *Cornell* approach gave the lowest predicted *DM intake/steer/day* for all the genotypes in cut 2. This indicates that the high $\%\ NDF_{adj}$ of the genotypes in cut 2 was the limiting factor for predicted intake. The *NRC* approach compensated for the lower *ME* values of the genotypes in cut 2 by predicting higher intakes for the genotypes than the case was in cut 1. The *Pienaar* approach gave higher predicted *DM intake/steer/day* than the *Cornell* approach for all the genotypes in cut 2, indicating that the rate and extend of digestion indicated by *MRT* and *%IVDOM* were not the most limiting factor in cut 2. In the case of F_1 hybrid 2*x*3, the predicted intake of the *Pienaar* approach came close to the predicted intake according to the *Cornell* approach. F_1 hybrid 2*x*3 had the longest *MRT* value (21.97 hours) and lowest *% IVDOM* (74.37) of all the genotypes in cut 2, although the $\%\ NDF_{adj}$ of 47.44 was significantly higher than the genotypes with highest $\%\ NDF_{adj}$ values. The *MRT* of 21.97 hours and the *%IVDOM* value of 74.37% must be very near the cross-over values when the rate and extend of digestion become the limiting factor and the *Pienaar* approach will give the most prudent prediction.

When the means for predicted *DM intake/steer/day*, according to the *Pienaar* approach of each parent and F_1 hybrid in Table 4.35 were compared, the following were found: In cut 1 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 mean and therefore best predicted value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1. This was in agreement with the results of %*IVDOM* and *MRT* as discussed in section 4.1.3.2. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1 as in the case of %*IVDOM* and *MRT*. The mean value of 3*x*5 showed a significant difference with the mean of only 2*x*4, as in the case of *MRT*. This agreement between the results of %*IVDOM* and *MRT* and the *DM intake/steer/day*, according to the *Pienaar* approach is logic, because *MRT* forms the basis of the calculation of this intake approach, as explained previously in section 3.2.3.1.1. It must be borne in mind that the genotypes with the highest %*IVDOM* values would have the quickest rate of digestion according to Pienaar & Roux (1989a) and therefore the shortest *MRT*, resulting in the highest predicted intake values for this intake approach as explained in section 3.2.1.11 and 3.2.3.1.1.

Parent 5 had the highest value of the parents in cut 2. The mean value of parent 5 showed significant differences with the means of parents 1, 2 and 3. These results were again in agreement with the results of *MRT* as discussed in section 4.1.3.2, although the level of significance with which parent 1 was identified differed. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2 as in the case of %*IVDOM* and *MRT*. The mean value of 1*x*4 showed highly significant differences with the means of 1*x*2, 1*x*3, 1*x*5, 1*x*6, 2*x*3, 2*x*4, 2*x*5, 2*x*6, 3*x*4, 3*x*6, 4*x*6 and 5*x*6. A significant difference was shown with the mean of 3*x*5. In the case of *MRT* there was agreement in the identification of all the F_1 hybrids which differed highly significant from the mean of 1*x*4, except for 1*x*5 and 1*x*6 which showed only significant differences with the mean of 1*x*4. The mean of 3*x*5 also failed to show a significant difference with the mean of 1*x*4 in the case of *MRT*.

The mean predicted *DM intake/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.25 before.

There was no common genotype with the highest consistent mean value across the two cuts when the predicted *DM intake/steer/day*, according to the *Pienaar* approach was considered. Parents 4 and 5 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest respective mean predicted *DM intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for predicted *DM intake/steer/day*, according to the *NRC* approach of each parent and F_1 hybrid in Table 4.35 were compared, the following were found: In cut 1 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 lowest and therefore best value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1 as in the case of *ME* as well as the predicted *DM intake/steer/day*, according to the *Pienaar* approach. Amongst the F_1 hybrids, 3*x*5 had the lowest mean value in cut 1. The mean value of 3*x*5 showed significant differences with the means of 1*x*5, 4*x*6 and 5*x*6. These results were in agreement with the results of *ME* as discussed in section 4.1.3.2. This agreement between the results of *ME* and the *DM intake/steer/day*, according to the *NRC* approach is logic, because *ME* forms the basis of the calculation of this intake approach, as explained previously in section 3.2.3.1.2. It must be borne in mind that the genotypes with the highest *ME* values would have the lowest predicted intake values because of the physiological regulation effect as explained in Chapter 2.

Parent 4 had the lowest value of the parents in cut 2. The mean value of parent 4 showed highly significant differences with the means of parents 1 and 2 and significant differences were shown with the means of parents 3 and 6. These results were in again in agreement with the results of *ME* as discussed in section 4.1.3.2, although the level of significance with which parent 2 was identified differed. Amongst the F_1 hybrids, 1*x*4 had the lowest mean value in cut 2. In the case of *ME*, 1*x*4 had the highest *ME* value of all the F_1 hybrids in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 2*x*3, 2*x*6, 3*x*6 and 4*x*6. Significant differences were shown with the means of 1*x*2, 1*x*3, 1*x*5, 2*x*4, 2*x*5, 3*x*4 and 5*x*6. In the case of *ME* there was agreement in the identification of all the F_1 hybrids which differed highly significant from the mean of 1*x*4, but no significant differences could be shown with the means of 1*x*2, 1*x*3 and 1*x*5.

The mean predicted *DM intake/steer/day* of cut 1 was highly significantly lower than the mean value in cut 2, as was indicated in Table 4.25 before.

There was no common genotype with the best consistent mean value across the two cuts when the predicted *DM intake/steer/day*, according to the *NRC* approach was considered. Parents 4 and 5 had in both cuts predicted intake values that were never significantly higher than those of the parent with the lowest respective mean predicted *DM intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4, 3*x*5 and 4*x*5 were in both cuts never significantly higher than the mean value of the genotype with the lowest respective predicted intake.

When the means for predicted *DM intake/steer/day*, according to the *Cornell* approach of each parent and F_1 hybrid in Table 4.35 were compared, the following were found: Parent 5 had the highest and therefore best value of the parents in cut 1. The mean value of parent 5 showed highly significant differences with the means of parents 1 and 2. This was in agreement with the results of $\%NDF_{adj}$ as discussed in section 4.1.3.2. Significant differences were shown with the means of parents 4 and 6. Amongst the F_1 hybrids, 1*x*5 had the highest mean value in cut 1. The mean value of 1*x*5 showed highly significant differences with the means of 1*x*2, 1*x*3, 2*x*3, 2*x*4 and 2*x*6. A significant difference was shown with the mean of 3*x*4. This was also in agreement with the findings in $\%NDF_{adj}$. This agreement between the results of $\%NDF_{adj}$ and the *DM intake/steer/day*, according to the *Cornell* approach is logic, because $\%NDF_{adj}$ forms the basis of the calculation of this intake approach, as explained previously in section 3.2.3.1.3. It must be borne in mind that the genotypes with the highest $\%NDF_{adj}$ values would have the lowest predicted intake values because of the rumen fill effect as explained in Chapter 2.

A few significant differences between means were shown in cut 2 when using the LSD test although the F-test failed to indicate any significant differences between genotypes. There were no significant differences between any of the six parents in cut 2. Amongst the F_1 hybrids, 5*x*6 had the highest mean value in cut 2. The mean value of 5*x*6 showed a highly significant difference with the mean of 2*x*4 and a significant difference was shown with the mean of 1*x*5. The means of the F_1 hybrids 1*x*5 and 2*x*4 were also identified in the results of $\%NDF_{adj}$ as having significant differences with the mean of the best F_1 hybrid, but the actual best F_1 hybrid differed and the level of significance in the case of 1*x*5 differed too.

The mean predicted *DM intake/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.25 before.

There was no common genotype with the highest consistent mean value across the two cuts when the *DM intake/steer/day*, according to the *Cornell* approach was considered. Parents 3 and 5 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest respective mean predicted *DM intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*6, 2*x*5, 3*x*6, 4*x*6 and 5*x*6 were in both cuts never significantly lower than the mean value of the genotype with the highest respective predicted intake.

When the means for predicted *DM intake/steer/day*, according to the three different approaches in Table 4.35 were compared, the following were found: Parents 3 and 5 had in cut 1 predicted intake values that were never significantly worse than those of the parent with the best respective mean predicted *DM intake/steer/day,* irrespective of the approach that were followed to calculate intake. Likewise in cut 2, parents 4 and 5 had predicted intake values that were never significantly worse than those of the parent with the best respective mean predicted *DM intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4, 1*x*6, 3*x*5 and 4*x*5 had in cut 1 predicted intake values that were never significantly worse than those of the genotype with the best respective mean predicted *DM intake/steer/day,* irrespective of the approach that were followed to calculate intake. There were no F_1 hybrids in cut 1 with predicted intake values that were always significantly worse than those of the genotype with the best respective mean predicted *DM intake/steer/day.* Amongst the F_1 hybrids in cut 2, the means of 1*x*3, 1*x*5, 2*x*4, 2*x*6 and 3*x*4 had predicted intake values that were always significantly worse than those of the genotype with the best respective mean predicted *DM intake/steer/day.* There were no F_1 hybrids in cut 2 with predicted intake values that were never significantly worse than those of the genotype with the best respective mean predicted *DM intake/steer/day.*

Table 4.35 Means of treatment combinations for the predicted dry matter intake per steer per day of the triticale vegetative material.

	DM Intake (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	9.52*	7.24**	7.63*	7.93**	7.61**	6.71
2	10.05	7.25**	7.36	7.89**	8.00**	6.79
3	12.00	7.22**	***7.16***	7.86*	9.33	7.09
4	9.90	8.11	7.34	***7.52***	8.92*	6.71
5	10.93	8.27	7.39	7.63	10.08	***7.52***
6	10.71	7.58**	7.41	7.85*	8.88*	6.97
1 *x* **2**	10.34	7.28**	7.42	7.84*	8.50**	6.72
1 *x* **3**	10.47	7.18**	7.34	7.83*	8.57**	6.47*
1 *x* **4**	10.66	***8.93***	7.48	7.54	9.69	6.40*
1 *x* **5**	11.41	7.60**	7.70**	7.81*	***10.23***	6.00**
1 *x* **6**	10.26	7.66**	7.50	7.80*	9.38	6.77
2 *x* **3**	10.61	6.99**	7.40	7.99**	8.60**	6.97
2 *x* **4**	9.30*	7.34**	7.49	7.87*	7.67**	5.81**
2 *x* **5**	10.26	7.50**	7.57*	7.87*	9.35	7.07
2 *x* **6**	10.65	7.18**	7.50	7.96**	8.54**	6.56*
3 *x* **4**	10.51	7.24**	7.48	7.87*	8.92*	6.24**
3 *x* **5**	***12.01***	7.92*	7.27	7.74	9.17	6.51*
3 *x* **6**	9.98	7.29**	7.56*	7.96**	9.16	6.76
4 *x* **5**	10.56	8.29	7.43	7.64	10.07	6.60*
4 *x* **6**	11.33	7.05**	7.71**	7.95**	9.39	6.67
5 *x* **6**	10.50	7.39**	7.70**	7.86*	9.79	7.08
Mean	10.57	7.55	7.47	7.82	9.04	6.69
LSD$_{0.05}$	2.37	0.85	0.37	0.27	1.13	0.88
LSD$_{0.01}$	3.16	1.13	0.50	0.36	1.51	1.18
C.V.	13.56	6.79	3.02	2.09	7.54	7.96

No genetic study on any plant species could be found where the predicted *ME intake/steer/day* of vegetative material from the different F_1 hybrids were investigated.

The CV for the different predicted *ME intake/steer/day*, according to the *Pienaar* approach was higher than those of the *Cornell* approach. The CV for the different predicted *ME intake/steer/day*, according to the *NRC* approach was in both cuts lower than either the *Pienaar* approach or the *Cornell* approach.

When the means for predicted *ME intake/steer/day*, according to the *Pienaar* approach of each parent and F_1 hybrid in Table 4.36 were compared, the following were found: In cut 1 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 mean and therefore best predicted value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1. The mean value of 3*x*5 showed a significant difference with the mean of 2*x*4.

Parent 4 had the highest value of the parents in cut 2. The mean value of parent 4 showed significant differences with the means of parents 1, 2 and 3. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 1*x*2, 1*x*3, 1*x*5, 1*x*6, 2*x*3, 2*x*4, 2*x*5, 2*x*6, 3*x*4, 3*x*6, 4*x*6 and 5*x*6. A significant difference was shown with the mean of 3*x*5.

The mean predicted *ME intake/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.26 before.

There was no common genotype with the highest consistent mean value across the two cuts when the predicted *ME intake/steer/day*, according to the *Pienaar* approach was considered. Parents 4 and 5 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest respective mean predicted *ME intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for predicted *ME intake/steer/day*, according to the *NRC* approach of each parent and F_1 hybrid in Table 4.36 were compared, the following were found: In cut 1 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. There were no significant differences between any of the six parents in cut 1. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1. The mean value of 3*x*5 showed significant differences with the means of 4*x*6 and 5*x*6.

A few significant differences between means were shown in cut 2 when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 4 had the highest value of the parents in cut 2. The mean value of parent 4 showed significant differences with the means of parents 1 and 2. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2. The mean value of 1*x*4 showed highly significant differences with the means of 2*x*3, 2*x*6 and 4*x*6. A significant difference was shown with the mean of 3*x*6.

The mean predicted *ME intake/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.26 before.

There was no common genotype with the best consistent mean value across the two cuts when the predicted *ME intake/steer/day*, according to the *NRC* approach was considered. Parents 3, 4, 5 and 6 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest respective mean predicted *ME intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*2, 1*x*3, 1*x*4, 1*x*6, 2*x*4, 2*x*5, 3*x*4, 3*x*5 and 4*x*5 were in both cuts never significantly lower than the mean value of the genotype with the highest respective predicted intake.

When the means for predicted *ME intake/steer/day*, according to the *Cornell* approach of each parent and F_1 hybrid in Table 4.36 were compared, the following were found: Parent 5 had the highest and therefore best value of the parents in cut 1. The mean value of parent 5 showed highly significant differences with the means of parents 1 and 2. Amongst the F_1 hybrids, 4*x*5 had the highest mean value in cut 1. The mean value of 4*x*5 showed highly significant differences with the means of 2*x*4 and 2*x*6. Significant differences were shown with the means of 1*x*2, 1*x*3, 2*x*3, 3*x*4, 3x6 and 4*x*6.

In cut 2 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 the parents in cut 2. The mean value of parent 5 showed significant differences with the means of parents 1 and 2. Amongst the F_1 hybrids, 5*x*6 had the highest mean value in cut 2. The mean value of 5*x*6 showed a significant difference with the mean of 2*x*4.

The mean predicted *ME intake/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.26 before.

Parent 5 showed the highest consistent mean value across the two cuts when the *ME intake/steer/day*, according to the *Cornell* approach was considered. Parents 3, 4, 5 and 6 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest mean predicted *ME intake/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4, 1*x*6, 2*x*5, 4*x*5 and 5*x*6 were in both cuts never significantly lower than the mean value of the genotype with the highest predicted intake.

Table 4.36 Means of treatment combinations for the predicted metabolic energy intake per steer per day of the triticale vegetative material.

	ME Intake (MJ/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	114.65*	79.83**	91.93	87.55*	91.79**	74.10*
2	129.16	80.97**	94.49	88.24*	102.77**	75.89*
3	***160.94***	81.75**	***95.60***	88.89	124.46	80.24
4	127.94	100.35	94.62	***92.75***	115.04	82.91
5	140.33	99.85	93.77	92.07	***127.94***	***90.74***
6	136.22	86.22**	94.16	89.11	112.90	79.23
1 *x* **2**	131.06	82.89**	94.03	89.31	107.66*	76.50*
1 *x* **3**	136.01	82.11**	94.29	89.40	110.93*	73.97*
1 *x* **4**	133.67	***109.90***	93.55	92.35	121.21	78.31
1 *x* **5**	135.13	87.42**	91.13*	89.50	120.94	68.41**
1 *x* **6**	128.54	88.01**	93.30	89.11	116.81	77.50
2 *x* **3**	135.41	75.38**	94.02	85.53**	109.23*	74.95*
2 *x* **4**	115.98*	82.67**	93.44	88.40	95.71**	65.38**
2 *x* **5**	125.62	84.74**	92.73	88.86	114.50	79.90
2 *x* **6**	131.44	78.21**	92.40	86.24**	104.63**	71.35**
3 *x* **4**	131.99	81.61**	93.45	88.68	111.31*	70.41**
3 *x* **5**	157.67	92.64*	94.75	90.27	119.67	76.15*
3 *x* **6**	122.63*	79.82**	92.20	86.88**	111.52*	73.91*
4 *x* **5**	134.12	99.62	93.77	91.55	127.01	79.18
4 *x* **6**	132.80	77.13**	90.44*	86.26**	109.75*	73.10*
5 *x* **6**	123.64	83.78**	89.52**	88.40	114.04	80.39
Mean	132.62	86.424	93.22	89.02	112.85	76.31
LSD$_{0.05}$	37.95	15.84	3.92	4.38	15.23	13.32
LSD$_{0.01}$	50.78	21.19	5.25	5.87	20.38	17.82
C.V.	17.34	11.10	2.55	2.98	8.18	10.58

No genetic study on any plant species could be found where the predicted *LWG/steer/day*, from intake of vegetative material from the different F_1 hybrids were investigated.

The CV for the different predicted *LWG/steer/day*, according to the *Pienaar* approach was higher in cut 1 than those of the *Cornell* approach. The CV for the different predicted *LWG/steer/day,* according to the *NRC* approach was in both cuts lower than either the *Pienaar* approach or the *Cornell* approach.

When the means for predicted *LWG/steer/day*, according to the *Pienaar* approach of each parent and F_1 hybrid in Table 4.37 were compared, the following were found: In cut 1 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 mean and therefore best predicted value of the parents in cut 1, as in the case of %*IVDOM* and *MRT* as well as the results of the predicted *DM intake/steer/day* according to the *Pienaar* approach. This result was also in agreement with the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. The mean value of parent 3 showed a significant difference with the mean of parent 1. This was in agreement with the results of %*IVDOM* and *MRT* as well as the results of the predicted *DM intake/steer/day* and *ME intake/steer/day*, according to the *Pienaar* and NRC approaches. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1, as in the case of %*IVDOM* and *MRT* as well as the results of the predicted *DM intake/steer/day* according to the *Pienaar* approach. This result was also in agreement with the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. The mean value of 3*x*5 showed a significant difference with the mean of only 2*x*4, as in the case of *MRT* and the results of the predicted *DM intake/steer/day* and *ME intake/steer/day*, according to the *Pienaar* approach.

Parent 4 had the highest value of the parents in cut 2, as in the case of %*IVDOM* and the results of the predicted *ME intake/steer/day*, according to the *Pienaar* approach. The mean value of parent 4 showed a highly significant difference with the mean of parent 1 and significant differences with the means of parents 2 and 3. These results were in agreement with the results of the predicted *ME intake/steer/day*, according to the *Pienaar* approach, although the level of significance with which parent 1 was identified differed. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2, as in the case of *%IVDOM* and *MRT* as well as the results of the predicted *DM intake/steer/day* according to the *Pienaar* approach. This result was also in agreement with the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. The mean value of 1*x*4 showed highly significant differences with the means of 1*x*2, 1*x*3, 2*x*3, 2*x*4, 2*x*5, 2*x*6, 3*x*4, 3*x*6, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*5, 1*x*6 and 3*x*5. In the case of *MRT* there was agreement in the identification of all the F_1 hybrids which differed highly significant from the mean of 1*x*4. The mean of 3*x*5 failed to show a significant difference with the mean of 1*x*4 in the case of *MRT*. In the case of the predicted *DM intake/steer/day* and *ME intake/steer/day*, according to the *Pienaar* approach there was agreement in the identification of all the F_1 hybrids except for 1*x*5 and 1*x*6 which showed highly significant differences with the mean of 1*x*4, instead of significant differences.

The mean predicted *LWG/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.27 before.

There was no common genotype with the highest consistent mean value across the two cuts when the predicted *LWG/steer/day*, according to the *Pienaar* approach was considered. Parents 4, 5 and 6 had in both cuts predicted animal growth values that were never significantly lower than those of the parent with the highest respective mean predicted *LWG/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for predicted *LWG/steer/day*, according to the *NRC* approach of each parent and F_1 hybrid in Table 4.37 were compared, the following were found: In cut 1 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 mean and therefore best predicted value of the parents in cut 1. The mean value of parent 3 showed a significant difference with the mean of parent 1 as in the case of the *Pienaar* approach These results were in agreement with the *ME* results as well as the predicted *DM intake/steer/day*, according to the *Pienaar* and *NRC* approaches. This result was also in agreement with the predicted *ME intake/steer/day* and *LWG/steer/day*, according to the *Pienaar* approach. Amongst the F_1 hybrids, 3*x*5 had the highest mean value in cut 1, as in the case of %*IVDOM* and *ME* as well as the results of the predicted *DM intake/steer/day* and *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. This result was also in agreement with the predicted *LWG/steer/day*, according to the *Pienaar* approach. The mean value of 3*x*5 showed significant differences with the means of 4*x*6 and 5*x*6. These results were in agreement with the results of the predicted *ME intake/steer/day*, according to the *NRC* approach.

A few significant differences between means were shown in cut 2 when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 4 had the highest value of the parents in cut 2, as in the case of %*IVDOM* and *ME* as well as the results of the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. The mean value of parent 4 showed significant differences with the means of only parents 1 and 2, as in the case of the predicted *ME intake/steer/day*, according to the *NRC* approach. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2, as in the case of %*IVDOM* and *ME* as well as the results of the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches. This result was also in agreement with the predicted *DM intake/steer/day* and *LWG/steer/day*, according to the *Pienaar* approach. The mean value of 1*x*4 showed highly significant differences with the means of 2*x*3, 2*x*6 and 4*x*6. A significant difference was shown with the mean of 3*x*6. These results were in agreement with the results of the predicted *ME intake/steer/day*, according to the *NRC* approach.

The mean predicted *LWG/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.27 before.

There was no common genotype with the best consistent mean value across the two cuts when the predicted *LWG/steer/day*, according to the *NRC* approach was considered. Parents 3, 4, 5 and 6 had in both cuts predicted intake values that were never significantly lower than those of the parent with the highest respective mean predicted *LWG/steer/day.* Amongst the F_1 hybrids, the means of 1*x*2, 1*x*3, 1*x*4, 1*x*6, 3*x*5 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

When the means for predicted *LWG/steer/day*, according to the *Cornell* approach of each parent and F_1 hybrid in Table 4.37 were compared, the following were found:

Parent 3 had, as in the case of the *Pienaar* and *NRC* approaches, the highest value of the parents in cut 1. This result was also in agreement with the result of the highest %*IVDOM*, *ME* and *MRT* values. The mean value of parent 3 showed a highly significant difference with the mean of parent 1 and a significant difference was shown with the mean of parent 2. The results of both the %NDF_{adj} as well as the predicted *ME intake/steer/day*, according to the *Cornell* approach were in agreement with the identification of the parents with significantly lower values, although the level of significance with which parent 1 was identified differed. Amongst the F_1 hybrids, 4*x*5 had the highest mean value in cut 1, as in the case of the predicted *ME intake/steer/day*, according to the *Cornell* approach. The mean value of 4*x*5 showed a highly significant difference with the mean of 2*x*4 and significant differences were shown with the means of 1*x*2, 2*x*6, 4x6 and 5*x*6. The results of the predicted *ME intake/steer/day*, according to the *Pienaar* approach also identified 2*x*4, although the level of significance differed with the approach of *Cornell*. The results of the predicted *ME intake/steer/day*, according to the *NRC* approach identified 4x6 and 5*x*6, but the level of significance differed as well.

In cut 2 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 the parents in cut 2, as in the case of the parent with the lowest %NDF_{adj} value and the shortest *MRT.* The results of the predicted *DM intake/steer/day*, according to the *Pienaar* and *Cornell* approaches, as well as the predicted *ME intake/steer/day*, according to the *Cornell* approach also agree with this. The mean value of parent 5 showed significant differences with the means of only parents 1 and 2, as in the case of the predicted *ME intake/steer/day*, according to the *Cornell* approach. The results of the predicted *DM intake/steer/day and ME intake/steer/day*, according to the *NRC* approach also identified the means of parents 1 and 2 as significantly lower than the mean of parent 5. Amongst the F_1 hybrids, 1*x*4 had the highest mean value in cut 2, as in the case of the *Pienaar* and *NRC* approaches. The results of the predicted *DM intake/steer/day*, according to the *Pienaar* approach, as well as the predicted *ME intake/steer/day*, according to the *Pienaar* and *NRC* approaches also agree with this. The mean value of 1*x*4 showed a significant difference with the mean of only 2*x*4, as in the case of the predicted *ME intake/steer/day*, according to the *Cornell* approach.

The mean predicted *LWG/steer/day* of cut 1 was highly significantly higher than the mean value in cut 2, as was indicated in Table 4.27 before.

There was no common genotype with the highest consistent mean value across the two cuts when the predicted *LWG/steer/day*, according to the *Cornell* approach was considered. Parents 3, 4, 5 and 6 had in both cuts predicted animal growth values that were never significantly lower than those of the parent with the highest respective mean predicted *LWG/steer/day.* Amongst the F_1 hybrids, the means of 1*x*4, 2*x*5 and 4*x*5 were in both cuts never significantly lower than the mean value of the highest respective genotype.

Table 4.37 Means of treatment combinations for the predicted live weight gain per steer per day from the triticale vegetative material.

	LWG/steer/day (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	1.88^{*}	0.93^{**}	1.34^{*}	1.11^{*}	1.34^{**}	0.80^{*}
2	2.35	0.97^{**}	1.50	1.14^{*}	1.70^{*}	0.85^{*}
3	***3.19***	1.01^{**}	***1.57***	1.18	***2.30***	0.97
4	2.33	1.58	1.51	***1.40***	2.01	1.15
5	2.60	1.54	1.46	1.35	2.29	***1.32***
6	2.50	1.12^{**}	1.48	1.19	1.94	0.96
1 *x* **2**	2.37	1.05^{**}	1.47	1.20	1.80^{*}	0.90^{*}
1 *x* **3**	2.52	1.03^{**}	1.49	1.20	1.91	0.84^{*}
1 *x* **4**	2.41	***1.80***	1.44	1.37	2.11	1.03
1 *x* **5**	2.32	1.17^{*}	1.30^{*}	1.21	1.99	0.70^{**}
1 *x* **6**	2.28	1.18^{*}	1.42	1.19	1.99	0.92^{*}
2 *x* **3**	2.48	0.79^{**}	1.47	1.01^{**}	1.84^{*}	0.78^{**}
2 *x* **4**	1.98^{*}	1.02^{**}	1.43	1.15^{*}	1.49^{**}	0.61^{**}
2 *x* **5**	2.17	1.08^{**}	1.39	1.17^{*}	1.91	0.96
2 *x* **6**	2.32	0.87^{**}	1.38	1.05^{**}	1.67^{**}	0.71^{**}
3 *x* **4**	2.36	1.00^{**}	1.43	1.16^{*}	1.86	0.74^{**}
3 *x* **5**	3.06	1.31^{*}	1.52	1.25	2.14	0.92^{*}
3 *x* **6**	2.10^{*}	0.92^{**}	1.37	1.07^{**}	1.83^{*}	0.78^{**}
4 *x* **5**	2.43	1.52	1.45	1.33	2.26	1.02
4 *x* **6**	2.24	0.85^{**}	1.27^{**}	1.05^{**}	1.71^{*}	0.76^{**}
5 *x* **6**	2.03^{*}	1.06^{**}	1.23^{**}	1.16^{*}	1.80^{*}	0.98
Mean	2.38	1.13	1.42	1.19	1.90	0.89
$LSD_{0.05}$	1.04	0.49	0.23	0.23	0.46	0.40
$LSD_{0.01}$	1.39	0.65	0.30	0.31	0.62	0.53
C.V.	26.47	25.97	9.56	11.70	14.79	27.11

No genetic study on any plant species could be found where the predicted *Live weight gain/ha*, from intake of vegetative material from the different F_1 hybrids were investigated.

The CV for the different predicted *Live weight gain/ha*, according to the *Pienaar* approach was higher in both cuts than those of the *Cornell* approach. The CV for the different predicted *Live weight gain/ha,* according to the *NRC* approach was in cut 1 higher than the CV of the *Cornell* approach, but lower than either the *Pienaar* approach or the *Cornell* approach in cut 2. The CV for the different predicted *Live weight gain/ha* 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 for the predicted *Live weight gain/ha*, according to the *Pienaar* approach of each parent and F_1 hybrid in Table 4.38 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1, as in the case of *kg DM/ha*, *crude cellulose yield/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* The mean value of parent 2 showed significant differences with the means of only parents 4 and 5. Parents 4 and 5, as the only two parents that were at least significantly lower than the mean value of parent 2, also occurred in the case of *kg DM/ha*, *IVDOM yield/ha* and *ME yield/ha.* Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1, as in the case of *kg DM/ha*, *crude cellulose yield/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. This was in agreement with the findings in the case of *kg DM/ha*, *crude cellulose yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* Significant differences were shown with the means of 1*x*2, 2*x*5 and 3*x*6. Only in the case of *kg DM/ha*, *IVDOM yield/ha* and *ME yield/ha* were the means of all three these F_1 hybrids also identified as significantly lower than the mean of 2*x*6.

A few significant differences between means were shown in cut 2 when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 6 had the highest value of the parents in cut 2, as in the case of *kg DM/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* The mean value of parent 6 showed a significant difference with the mean of parent 4. No plant production character could identify parent 4 as the only parent with a significantly lower mean value than those of parent 6. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2, as in the case of *kg DM/ha*, *crude cellulose yield/ha*, *IVDOM yield/ha* and *ME yield/ha*. The mean value of 1*x*6 showed a highly significant difference with the mean of only 2*x*3. This was in agreement with the findings in the case of *kg DM/ha*, *IVDOM yield/ha* and *ME yield/ha.* Significant differences were shown with the means of 2*x*6, 3*x*4, 4*x*6 and 5*x*6. No plant production character could identify all four of these F_1 hybrids as having significantly lower mean values than those of 1*x*6.

The mean predicted *Live weight gain/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.28 before.

When the means for the predicted *Live weight gain/ha*, according to the *NRC* approach of each parent and F_1 hybrid in Table 4.38 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 showed significant differences with the means of parents 4 and 5, as in the case of the *Pienaar* approach. Amongst the F_1 hybrids, 2*x*6 had the highest mean value in cut 1, as in the case of the *Pienaar* approach. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*2 and 2*x*5. These results were in agreement with the *Pienaar* approach with regard to all the F_1 hybrids which showed highly significant differences with the mean of 2*x*6, but differ in the lack of a significance difference between the mean of 2x6 and 3*x*6.

Parent 6 had the highest value of the parents in cut 2, as in the case of the *Pienaar* approach. The mean value of parent 6 showed significant differences with the means of parents 2 and 4. These results differ from the *Pienaar* approach which failed to show a significant difference between the mean of parent 6 and parent 2. No plant production character could identify parents 2 and 4 as the only parents with significantly lower mean values than those of parent 6. Amongst the F_1 hybrids, 1*x*6 had the highest mean value in cut 2. The mean value of 1*x*6 showed a highly significant difference with the mean of 2*x*3 and significant differences with the means of 2*x*6, 3*x*4, 4*x*6 and 5*x*6 as in the case of the *Pienaar* approach.

The mean predicted *Live weight gain/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.28 before.

When the means for the predicted *Live weight gain/ha*, according to the *Cornell* approach of each parent and F1 hybrid in Table 4.38 were compared, the following were found: Parent 2 had the highest and therefore best value of the parents in cut 1. The mean value of parent 2 showed significant differences with the means of parents 4 and 5, as in the case of both the *Pienaar* and *NRC* approaches. Amongst the F1 hybrids, 2*x*6 had the highest mean value in cut 1. The mean value of 2*x*6 showed highly significant differences with the means of 1*x*4, 1*x*5, 1*x*6, 3*x*4, 4*x*5, 4*x*6 and 5*x*6, as in the case of both the *Pienaar* and *NRC* approaches. Significant differences were shown with the means of 1*x*2 and 2*x*5, as in the case of the *NRC* approach.

A few significant differences between means were shown in cut 2 when using the LSD test although the F-test failed to indicate any significant differences between genotypes. Parent 6 had the highest value of the parents in cut 2, as in the case of both the *Pienaar* and *NRC* approaches. The mean value of parent 6 showed significant differences with the means of parents 2 and 4, as in the case of the *NRC* approach. Amongst the F1 hybrids, 1*x*6 had the highest mean value in cut 2, as in the case of both the *Pienaar* and *NRC* approaches. The mean value of 1*x*6 showed a highly significant difference with the mean of 2*x*3 in agreement with both the *Pienaar* and *NRC* approaches. Significant differences were shown with the means of 1*x*5, 2*x*4, 2*x*6, 3*x*4, 4*x*6 and 5*x*6. These results were in agreement with both the *Pienaar* and *NRC* approaches with regard to 2*x*6, 3*x*4, 4*x*6 and 5*x*6, but differ with the additional significant differences that were shown between the mean of 1x6 and the means of 1*x*5 and 2*x*4.

The mean predicted *Live weight gain/ha* of cut 2 was highly significantly higher than the mean value in cut 1, as was indicated in Table 4.28 before.

Table 4.38 Means of treatment combinations for the predicted live weight gain of steers per ha for cut 1and cut 2 of the triticale vegetative material.

	Live weight gain/ha (kg/ha)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	244.1**	301.4	218.8**	327.8	215.6**	277.2
2	325.4*	230.1**	284.7	247.7**	294.8*	213.6**
3	239.9**	298.1	202.1**	320.9*	227.0**	293.6
4	152.1**	216.0**	133.4**	208.8**	145.4**	189.1**
5	167.0**	301.3	140.9**	287.8*	161.6**	283.0
6	288.7*	390.5	247.0*	405.3	268.3*	363.7
1 *x* **2**	319.9*	387.3	277.3*	412.5	295.7*	359.6
1 *x* **3**	361.1	402.6	315.0	434.1	336.7	361.5
1 *x* **4**	161.7**	400.3	137.6**	362.8	155.2**	312.6
1 *x* **5**	160.9**	349.4	133.7**	359.1	153.9**	260.7*
1 *x* **6**	260.8**	***464.5***	229.1**	***474.1***	255.8**	***413.8***
2 *x* **3**	347.2	193.0**	301.0	221.7**	319.0	193.6**
2 *x* **4**	398.2	313.9	358.7	332.2	360.3	237.7*
2 *x* **5**	309.4*	390.3	268.3*	406.1	298.5*	369.2
2 *x* **6**	***475.6***	280.2*	***406.0***	316.3*	***432.0***	253.1*
3 *x* **4**	260.2**	278.2*	225.6**	298.4*	249.0**	235.7*
3 *x* **5**	387.5	461.0	325.4	460.8	362.0	391.4
3 *x* **6**	316.7*	329.8	282.6	357.8	307.5	298.2
4 *x* **5**	211.3**	439.2	180.7**	420.2	206.3**	373.9
4 *x* **6**	171.1**	257.9*	142.0**	304.6*	158.6**	236.3*
5 *x* **6**	164.8**	275.5*	139.8**	292.7*	160.7**	261.4*
Mean	272.6	331.4	235.7	345.3	255.4	294.2
LSD$_{0.05}$	143.8	171.9	124.2	153.0	130.0	146.5
LSD$_{0.01}$	192.3	229.9	166.1	204.6	173.9	195.9
C.V.	31.96	31.42	31.92	26.84	30.83	30.16

When the means for the predicted total *Live weight gain/ha*, according to the *Pienaar* approach of each parent and F_1 hybrid in Table 4.39 were compared, the following were found: Parent 6 had the highest value of the parents when the total *Live weight gain/ha* across two cuts was considered. This agree with the results of *kg DM/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* The mean value of parent 6 showed a significant difference with the mean of parent 4.No plant production character could identify parent 4 as the only parent with a significantly lower mean value than those of parent 6. Amongst the F_1 hybrids, 3*x*5 had the highest total mean value across the two cuts, as in the case of *NSC yield/ha* and *ME yield/ha*. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*4, 2*x*3 and 3*x*4. The results of both *IVDOM yield/ha* as well as *ME yield/ha* also identified the means of all six these F_1 hybrids as having significantly lower values than the mean of the best performing F_1 hybrid, although the level of significance with which 1*x*4, 1*x*5 and 4*x*6 were identified differed.

When the means for the predicted total *Live weight gain/ha*, according to the *NRC* approach of each parent and F_1 hybrid in Table 4.39 were compared, the following were found: Parent 6 had the highest value of the parents when the total *Live weight gain/ha* across two cuts was considered. This agreed with the results of the *Pienaar* approach. The mean value of parent 6 showed a highly significant difference with the mean of parent 4 and a significant difference was shown with the mean of parent 5. These results differ from the *Pienaar* approach which failed to show a significant difference between the mean of parent 6 and parent 5. The level of significance with which parent 4 was identified also differed from the *Pienaar* approach. Amongst the F_1 hybrids, 3*x*5 had the highest total mean value across the two cuts, as in the case of the *Pienaar* approach. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 1*x*4, 2*x*3 and 3*x*4. These results were in agreement with the *Pienaar* approach with regard to the all the F_1 hybrids.

When the means for the predicted total *Live weight gain/ha*, according to the *Cornell* approach of each parent and F_1 hybrid in Table 4.39 were compared, the following were found: Parent 6 had the highest value of the parents when the total *Live weight gain/ha* across two cuts was considered. This result agreed with the results of both the *Pienaar* and *NRC* approaches. The mean value of parent 6 showed a highly significant difference with the mean of only parent 4. This result was in agreement with the *Pienaar* approach which showed a significant difference between the mean of parent 6 and the mean of only parent 4. The level of significance with which parent 4 was identified however, differed between the *Pienaar* and *NRC* approaches. Amongst the F_1 hybrids, 3*x*5 had the highest total mean value across the two cuts, as in the case of both the *Pienaar* and *NRC* approaches. The mean value of 3*x*5 showed highly significant differences with the means of 1*x*4, 1*x*5, 4*x*6 and 5*x*6. Significant differences were shown with the means of 2*x*3 and 3*x*4. These results were in agreement with both the *Pienaar* and *NRC* approaches with regard to the identification of all six the F_1 hybrids with significantly lower mean values than the mean of 3*x*5, but differ with regard to the level of significance with which the mean of 1*x*4 differed from the mean of 3*x*5.

The CV for the different predicted *Live weight gain/ha*, according to the *Pienaar*, *NRC* and *Cornell* approaches were very close to each other and 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.

The mean predicted values of the total *Live weight gain/ha* across two cuts were very similar between the three approaches. The *Pienaar* approach gave a result which was 4.1% higher than the result of the *NRC* approach. The result of the *Cornell* approach on the other hand was only 0.01% higher than those of the *NRC* approach.

Table 4.39 Means of treatment combinations for the total predicted live weight gain of steers per ha from the triticale vegetative material.

	Total live weight gain/ha (kg/ha)		
Genotypes	**Pienaar**	**NRC**	**Cornell**
1	545.5*	546.6*	521.4*
2	555.5*	532.5*	539.0*
3	538.0*	523.0*	533.4*
4	368.1**	342.1**	341.2**
5	468.3**	428.7**	450.0**
6	679.2	652.4	652.4
1 *x* **2**	707.2	689.8	655.3
1 *x* **3**	763.7	749.1	698.2
1 *x* **4**	562.0*	500.5*	467.8**
1 *x* **5**	510.2**	492.9**	414.6**
1 *x* **6**	725.3	703.2	669.5
2 *x* **3**	540.2*	522.7*	512.5*
2 *x* **4**	712.0	691.0	598.0
2 *x* **5**	699.7	674.4	667.7
2 *x* **6**	755.8	722.4	685.2
3 *x* **4**	538.4*	524.0*	484.6*
3 *x* **5**	***848.5***	***786.2***	***753.4***
3 *x* **6**	646.5	640.4	605.7
4 *x* **5**	650.5	600.9	580.2
4 *x* **6**	429.0**	446.6**	394.9**
5 *x* **6**	440.3**	432.5**	422.1**
Mean	604.0	581.0	554.6
$LSD_{0.05}$	236.9	217.0	210.9
$LSD_{0.01}$	316.9	290.3	282.2
C.V.	23.76	22.63	23.05

4.4 Conclusion

4.4.1 Plant quality characteristics

4.4.1.1 Plant quality characters relevant to the intake model of Cornell

Parents 3, 4, 5 and 6 looked to be the best for $\%NDF_{adj}$ because the means of all these parents were never significantly higher than the mean of the parent with the lowest $\%NDF_{adj}$, when viewed across both cutting treatments. These parents should show good *gca* for this character in a combining ability analysis. Parents 3, 4 and 5 were identified as the best parents for low *%NDF* values when *%NDF* was studied in isolation. It was interesting to note that the means of the same parents 3, 4 and 5 were never significantly lower in *%NSC* than the means of the parent with the highest respective *%NSC* values. Surprisingly the means of these three parents were highly significantly lower in *%EE* than the mean of the parent with the highest mean *%EE* in cut 1. The additive genetic correlations between these characters could prove to be worthwhile to look at as an aid for possible selection of parents for a breeding program.

Amongst the F_1 hybrids, the means of 1*x*6, 2*x*5, 3*x*5, 3*x*6, 4*x*5, 4*x*6 and 5*x*6 were never significantly different from the respective best performing genotype for $\%NDF_{adj}$ in the two different cuts. It could be worthwhile to look at the *sca* for this character in hybrid combinations 1*x*6 and 2*x*5 in a combining ability analysis, because parents 1 and 2 were not good for this character.

4.4.1.2 Plant quality characters relevant to the intake models of Pienaar and NRC

Parents 2, 4, 5 and 6 looked to be the best for *%IVDOM* because the means of these parents were never significantly lower than the mean of the best performing parent, when viewed across both cuts. These parents should show good *gca* for this character in a combining ability analysis. When *ME* and *MRT* which are to a large extent functions of *%IVDOM* were used for parent identification, parents 4 and 5 and parents 4, 5 and 6 were identified respectively as the parents with the best mean values. The use of these last two characters therefore tends to narrow the cultivar choice down compared to *%IVDOM*.

Amongst the F_1 hybrids, the means of 1*x*2, 1*x*4, 1*x*6, 3*x*5 and 4*x*5 were never significantly different from the respective best performing genotype for *%IVDOM* in the different cuts. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis, especially 1*x*2, 1*x*4 and 1*x*6 because the means of parent 1 were always significantly worse than those of the best respective parent for this character in the different cuts.

4.4.2 Plant production characteristics

4.4.2.1 DM yield/ha

Parents 1, 2, 3 and 6 looked to be the best for initial growth as well as for total *DM yield/ha* because the means of the other parents were significantly lower than the mean of the best parent in cut 1 as well as in total production. These parents should show good *gca* for this character in a combining ability analysis.

Parents 1, 3 and 6 looked to be the best for regrowth after cutting because the means of all the other parents were significantly lower than the mean of the best parent in cut 2. These parents should show good *gca* for this character in a combining ability analysis.

Amongst the F_1 hybrids, the means of 1*x*3, 2*x*4 and 2*x*6 were never significantly different from the respective best performing genotype in the different cuts. The hybrid combination of 2*x*4 may show above average *sca* for this character in a combining ability analysis, because the means of parent 4 were in all the cases highly significantly worse than the mean of the respective best performing genotype.

4.4.2.2 DM yield/ha in combination with plant quality characters

Parents 1, 3 and 6 were identified to be the best for *NSC yield/ha, IVDOM yield/ha* as well as *ME yield/ha* when viewed across both cuts as well as total production. This agree with the parents which were identified when *DM yield/ha* was used as criterion across both cuts as well as total production. These parents should show good *gca* for this character in a combining ability analysis.

Amongst the F_1 hybrids, the means of 1*x*3, 2*x*4, 2*x*6 and 3*x*5 were never significantly different from the respective best performing genotype in the different cuts when

ME yield/ha was considered. When *IVDOM yield/ha* was used for selection three out of these four of these F_1 hybrids were selected and 1*x*3 was omitted. When *NSC yield/ha* was considered, two out of the four F_1 hybrids were in agreement and 1*x*3 and 2*x*4 were not selected. In comparison, when *DM yield/ha* was used as criterion across both cuts as well as total production, three out of the four F_1 hybrids were in agreement and only 3*x*5 was not selected. The hybrid combination of 2*x*4 may show above average *sca* for this character in a combining ability analysis, because the means of parent 4 were in all the cases highly significantly worse than the mean of the respective best performing genotype.

The three plant quality characters in combination with *DM yield/ha* which are discussed in this conclusion are the three that had the best agreement in the selection of parents and F_1 hybrids. The best one to use for selection purposes will depends on the additive genetic correlation of these characters with the predicted animal production per hectare.

4.4.3 Animal production characteristics

4.4.3.1 Predicted DM- and ME intake per animal

It is suggested that the comparative discriminating method as described in 4.3.3.2 be used to identify the *DM intake* approach which use the first limiting factor that inhibit voluntary intake and therefore gives the lowest predicted *DM intake/steer/day* of the three. More research in Animal Science is needed to identify the most suitable *DM intake* models which can be used for selection between genotypes when only small quantities of vegetative material are available for analysis. Parents 2, 3, 4, 5 and 6 looked to be the best for predicted *DM intake/steer/day* because the mean of parent 1 was significantly lower than the mean of the respective best performing genotype when viewed across cuts and the respective animal production model most appropriate to each cut. The determination of *gca* for *DM intake/steer/day* in a combining ability analysis will indicate the parents with the best additive genetic component for this character.

Amongst the F_1 hybrids, the means of 1*x*2, 1*x*6 and 2*x*3 were never significantly different from the best performing genotype for this character when viewed across cuts and the respective animal production model most appropriate to each cut. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis. The hybrid combination of 1*x*2 and 1*x*6 may show above average *sca* for this character in a combining ability analysis, because the means of parent 1 were in all three approaches significantly worse than the mean of the respective best performing genotype.

Parents 3, 4, 5 and 6 looked to be the best for predicted *ME intake/steer/day* because the means of all the other parents were significantly lower than the mean of the respective best performing genotype when viewed across cuts and the respective animal production model most appropriate to each cut. The determination of *gca* for *ME intake/steer/day* in a combining ability analysis will indicate the parents with the best additive genetic component for this character.

Amongst the F_1 hybrids, the means of 1*x*4, 1*x*6, 2*x*5 and 4*x*5 were never significantly different from the best performing genotype for this character when viewed across cuts and the respective animal production model most appropriate to each cut. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis. The hybrid combinations 1*x*4, 1*x*6 and 2*x*5 may show above average *sca* for this character in a combining ability analysis, because the means of parents 1 and 2 were in all three approaches significantly worse than the mean of the respective best performing genotype.

4.4.3.2 Predicted production per animal

Parents 3, 4, 5 and 6 looked to be the best for predicted production per animal because the means of all the other parents were significantly lower than the mean of the respective best performing genotype when viewed across cuts and the respective animal production model most appropriate to each cut. The determination of *gca* for predicted production per animal in a combining ability analysis will indicate the parents with the best additive genetic component for this character.

Amongst the F_1 hybrids, the means of 1*x*4, 2*x*5 and 4*x*5 were never significantly different from the best performing genotype for this character when viewed across cuts and the respective animal production model most appropriate to each cut. It should be worthwhile to look at the *sca* of these hybrid combinations for this character in a combining ability analysis. The hybrid combination of 1*x*4 may show above average *sca* for this character in a combining ability analysis, because the means of parent 1 were in all three approaches significantly worse than the mean of the respective best performing genotype.

The parents and F_1 hybrids selected to be the best for predicted production per animal corresponds more closely with the genotypes selected for *ME intake/steer/day* than the genotypes selected for *DM intake/steer/day.*

4.4.3.3 Predicted animal production per hectare

Parents 1, 2, 3 and 6 looked to be the best for animal production per hectare from initial growth as well as for total animal production per hectare across the two cuts because the means of the other parents were significantly lower than the mean of the best parent in cut 1 as well as in total production.

Parents 1, 3, 5 and 6 looked to be the best for animal production from vegetative regrowth after cutting because the means of all the other parents were significantly lower than the mean of the best parent in cut 2. The determination of *gca* for predicted animal production per hectare in a combining ability analysis will indicate the parents with the best additive genetic component for this character in cut 1 and cut 2.

Amongst the F_1 hybrids, the means of 1*x*3, 3*x*5 and 3*x*6 were never significantly different from the best performing genotype for this character when viewed across cuts and the respective animal production model most appropriate to each cut. The hybrid combination of 3*x*5 may show above average *sca* for this character in a combining ability analysis, because the mean of parent 5 was in cut 1 significantly worse than the mean of the best performing parent.

These are all rough conclusions based upon the phenotypical performance of the parents and F_1 hybrid combinations across the different treatments. To know for certain the results of the different combining ability analyses must be studied.

Chapter 5

Combining ability for yield and nutritive quality characteristics in triticale.

5.1 Plant quality characteristics

5.1.1 Combining ability analysis

5.1.1.1 Results

The mean squares for the different plant quality characteristics of the triticale vegetative material in the combining ability analyses of variance are presented in Tables 5.1 to 5.4.

5.1.1.2 Discussion

No reference of a genetic study on any forage cereal where the combining ability for the different plant quality characteristics of vegetative material was investigate, could be found.

Ross, Bullis & Lin (1970) and Tan et al., (1978) did diallel studies on smooth bromegrass, Thaden, Ross & Akyurek (1975) did a diallel study on intermediate wheatgrass, while Nguyen et al. (1982), Soh, Frakes, Chilcote & Sleper (1984) and Annicchiarico & Romani (2005) did diallel studies on tall fescue. The plant quality characteristics studied were *%NDF*, *%ADF*, %*hemicellulose* as well as *in vitro* dry matter digestibility (IVDMD).

The analyses of variance in Table 5.1 showed the following:

In the combining ability analysis of variance for *%NDF* 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. These results were in agreement with the results of Nguyen et al. (1982) and Annicchiarico & Romani (2005) for cut 1, but differ from their results of cut 2. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. These results were in agreement with the results of the first two cuts of Nguyen et al. (1982) and Annicchiarico & Romani (2005) There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. This meant that the environment had a bigger effect in differences amongst the F_1 genotypes than either the gca or sca effects in cut 2. Based on the results of the F-test, it will be worthwhile to try to decrease the *%NDF* of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

In the combining ability analysis of variance for *%ADF* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects in cut 1, but no significant differences were shown in cut 2. The results of cut 1 were in agreement with the results of the first cut on tall fescue by Nguyen et al. (1982) and Annicchiarico & Romani (2005), while the results of the second cut were in agreement with the results of Tan et al. (1978) on the second cut of smooth bromegrass. The F-test showed no significant differences with regard to sca effects in either of the two cuts. This was in agreement with the results on tall fescue by Nguyen et al. (1982) and the results of the second cut by Tan et al. (1978) and Annicchiarico & Romani (2005). There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in both cut 1 and cut 2. This meant that the environment had a bigger effect in differences amongst the F_1 genotypes than either the gca or sca effects in cut 2. Based on the results of the F-test, it will be worthwhile to try to decrease the *%ADF* of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

In the combining ability analysis of variance for *%ADL* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects in cut 1, but no significant differences were shown in cut 2. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. No significant differences between blocks were detected with the F-test in the case of *%ADL* of the vegetative material. In this case selection for decreased *%ADL* 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 for any of the characters shown in Table 5.1.

Table 5.1 Mean squares for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material in the combining ability ANOVA's.

		Characters					
		%NDF		**%ADF**		**%ADL**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Blocks	2	12.907	120.256**	65.418**	67.993**	1.100	2.360
gca	5	13.303**	8.179	8.637*	6.241	1.171*	0.136
sca	9	4.173	9.860	3.702	3.947	0.896	0.502
Error	28	2.520	6.537	3.062	3.304	0.429	0.441

The analyses of variance in Table 5.2 showed the following:

The combining ability analysis of variance for %*hemicellulose* of the triticale vegetative material showed no significant differences with regard to both the gca and sca effects in either of the two cuts. This differ from the results of cut 2 on tall fescue by Nguyen et al. (1982), but was in agreement with their results on gca effects in cut 1 and their results on sca effects in all the cuts. There were also no significant differences between blocks according to the F-test of the normal randomised block analysis in either cut 1 or cut 2. Based on the results of the F-test, there is not enough genetic variation for %*hemicellulose* between the genotypes used in this study and therefore it will not be worthwhile to try to decrease the %*hemicellulose* of the vegetative material in the triticale genotypes used in this study through selection.

In the combining ability analysis of variance for %*crude cellulose* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects in cut 1, but no significant differences were shown in cut 2. The F-test showed no significant differences with regard to sca effects in either of the two cuts. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in both cut 1 and cut 2. This meant that the environment had a bigger effect in differences amongst the F_1 genotypes than either the gca or sca effects in cut 2. Based on the results of the F-test, it will be worthwhile to try to alter the %*crude cellulose* of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

In the combining ability analysis of variance for %*NDF*$_{adj}$ 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. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. This meant that the environment had a bigger effect in differences amongst the F$_1$ genotypes than either the gca or sca effects in cut 2. Based on the results of the F-test, it will be worthwhile to try to decrease the %*NDF*$_{adj}$ of the vegetative material in the triticale genotypes used in this study, through selection 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 for any of the characters shown in Table 5.2.

Table 5.2 Mean squares for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material in the combining ability ANOVA's.

		Characters					
		%Hemi-cellulose		**%Crude cellulose**		**%NDF$_{adj}$**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Blocks	2	43.163	30.117	67.690**	88.791**	19.366	133.890**
gca	5	3.959	16.659	9.229*	7.229	17.304**	7.908
sca	9	4.940	13.766	1.648	2.655	3.240	9.194
Error	28	5.010	10.012	2.933	2.840	3.058	6.749

The analyses of variance in Table 5.3 showed the following:

In the combining ability analysis of variance for %*EE* of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1 and significant differences were shown in cut 2. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. There were significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and highly significant differences between blocks were shown in cut 2. Based on the results of the F-test, it will be better to try to increase the %*EE* of the vegetative material in the triticale genotypes used in this study, through selection at cut 1 than at cut 2.

In the combining ability analysis of variance for %*NSC* of the triticale vegetative material, the F-test showed no significant differences with regard to the gca effects in either cut 1 or cut 2. The F-test showed significant differences with regard to sca effects in cut 1. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1. This meant that the environment had a bigger effect in differences amongst the F_1 genotypes than the gca effects in cut 1. Based on the results of the F-test, there is not enough additive genetic variation for %*NSC* between the genotypes used in this study and therefore it will not be worthwhile to try to increase the %*NSC* of the vegetative material in the triticale genotypes used in this study through selection.

In the combining ability analysis of variance for %*IVDOM* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects in cut 2, but no significant differences were shown in cut 1. These results were in agreement with regard to the IVDMD results of cut 2 by Nguyen et al. (1982), but differ from the IVDMD results of cut 1 by Ross et al. (1970), Thaden et al. (1975) and Nguyen et al. (1982) on smooth bromegrass, intermediate wheatgrass and tall fescue respectively. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. These results were in agreement with the IVDMD results of Ross et al. (1970) and Nguyen et al. (1982) on smooth bromegrass and tall fescue respectively, but differ from the IVDMD results of Thaden et al. (1975) on intermediate wheatgrass. There were also no significant differences between blocks according to the F-test of the normal randomised block analysis in either cut 1 or cut 2. Based on the results of the F-test, there would definitely be an advantage to do a second cut and to do the selection on the second cut to increase the %*IVDOM* of the vegetative material in the triticale genotypes used in this study.

Table 5.3 **Mean squares for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material in the combining ability ANOVA's.**

		Characters					
		%EE		%NSC		%IVDOM	
	df	Cut1	Cut2	Cut1	Cut2	Cut1	Cut2
Blocks	2	0.724*	1.349**	151.242**	15.855	8.516	58.836
gca	5	0.453**	0.112*	10.045	12.440	0.710	16.850*
sca	9	0.088	0.028	13.735*	13.176	2.595	3.990
Error	28	0.064	0.037	4.859	8.780	5.367	6.037

The analyses of variance in Table 5.4 showed the following:

The combining ability analysis of variance for *ME* of the triticale vegetative material showed significant differences with regard to the gca effects in cut 2, but no significant differences were shown in cut 1. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. There were also no significant differences between blocks according to the F-test of the normal randomised block analysis in either cut 1 or cut 2. Based on the results of the F-test, it will be worthwhile to try to increase the *ME* of the vegetative material in the triticale genotypes used in this study, through selection at cut 2.

In the combining ability analysis of variance for *MRT* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects in cut 2, but no significant differences were shown in cut 1. The F-test showed no significant differences with regard to sca effects in either of the two cuts. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. Based on the results of the F-test, it will be worthwhile to try to shorten the *MRT* of the vegetative material in the triticale genotypes used in this study, through selection at cut 2.

Table 5.4 Mean squares for the metabolic energy value and mean retention time of the triticale vegetative material in the combining ability ANOVA's.

		Characters			
		ME (MJ/kg DM)		MRT (hour)	
	df	Cut1	Cut2	Cut1	Cut2
Blocks	2	1.652	1.327	9.307	18.780**
gca	5	0.244	0.370*	0.566	2.575*
sca	9	0.113	0.073	0.782	1.111
Error	28	0.173	0.136	1.451	0.818

5.1.2 General combining ability

5.1.2.1 Results

The most favourable gca value for each character per cut 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 α = 0.05 level of confidence or by a ** for a α = 0.01 level of confidence.

The estimates of mean general combining ability effects of parents for the different plant quality characteristics of the triticale vegetative material are presented in Tables 5.5 to 5.8.

5.1.2.2 Discussion

The estimates of mean general combining ability effects of parents in Table 5.5 showed the following:

In the case of estimated gca effects for %*NDF*, the F-test and LSD test were in agreement for cut 1. In cut 1, the estimated gca effect of parent 5 showed highly significant differences with the gca effects of parents 2, 3 and 4. A significant difference between gca effects for %*NDF* was shown in 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 2, the estimated gca effect of parent 6 showed a significant difference with the gca effect of parents 4. The strong gca effect for low %*NDF* levels of parent 6 in cut 1 was in contrast to expectations, because the mean phenotypic performance of parent 6 was significantly different from that of parent 5.

In the case of estimated gca effects for %*ADF*, the F-test and LSD test were in agreement for cut 1 in so far as to indicate that significant differences existed. In cut 1, the estimated gca effect of parent 6 showed a highly significant difference with the gca effect of parent 2 and significant differences were shown with the gca effects of parents 1, 3 and 4. A few significant differences between gca effects were shown in cut 2 when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. For %*ADF*, the estimated gca effect of parent 5 showed significant differences with the gca effects of parents 1 and 6. The strong gca effect of parent 6 for high %*ADF* in cut 2 was 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.

In the case of estimated gca effects for %*ADL*, the F-test and LSD test were in agreement for cut 1 as well as cut 2. In cut 1, the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 4. No significant differences between gca effects for %*ADL* were shown in cut 2 The strong gca effects for low %*ADL* of parents 2 and 3 in cut 1 were in contrast to the gca effects of these two parents for both %*NDF* and %*ADF*. This suggested that these two parents should have good gca effects for high %*hemicellulose* or %*crude cellulose* or both.

Table 5.5 Estimates of mean general combining ability effects of parents for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material.

	Characters					
	%NDF		**%ADF**		**%ADL**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	-0.454	0.863	0.360^{*}	1.327^{*}	0.262	-0.268
2	2.614^{**}	-0.540	1.800^{**}	-0.343	***-0.550***	0.192
3	0.862^{**}	-0.396	0.435^{*}	0.610	-0.334	0.099
4	0.790^{**}	2.349^{*}	0.812^{*}	-0.636	0.760^{**}	0.168
5	***-2.598***	-0.457	-1.083	***-2.010***	0.374	-0.044
6	-1.214	***-1.818***	***-2.324***	1.052^{*}	-0.512	-0.147
$LSD_{0.05}$	2.299	3.703	2.534	2.632	0.949	0.961
$LSD_{0.01}$	3.102	4.995	3.419	3.551	1.280	1.297

The estimates of mean general combining ability effects of parents in Table 5.6 showed the following:

A few significant differences between gca effects for %*hemicellulose* were shown in 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, no significant differences between gca effects were shown for %*hemicellulose*. In cut 2, the estimated gca effect of parent 6 showed a significant difference with the gca effect of parent 4. This was in contrast to expectations from the phenotypical performances for this character because no significant differences were shown between the parents in that respect.

In the case of estimated gca effects for %*crude cellulose*, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. In cut 1, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 5 and 6. A highly significant difference between gca effects was shown in cut 2, when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. The estimated gca effect of parent 1 showed a highly significant difference with the gca effect of parent 5. The good gca effects of parents 2 and 3 in cut 1 were in agreement with the expectations from the gca of %*ADL* as discussed earlier.

In the case of estimated gca effects for %NDF_{adj}, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. The estimated gca effect of parent 5 showed highly significant differences with the gca effects of parents 2 and 3 and a significant difference was shown with the gca effect of parent 4. In cut 2 a significant difference between gca effects for %NDF_{adj} was shown when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. The estimated gca effect of parent 6 showed a significant difference with the gca effect of parent 4. The strong gca effects for low %NDF_{adj} of parents 5 and 6 across both cut 1 and cut 2 suggested that these two parents might also have good estimated gca values for *DM intake/steer/day*, according to the *Cornell* approach.

Tabel 5.6 Estimates of mean general combining ability effects of parents for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material.

	Characters					
	%Hemi-cellulose		**%Crude cellulose**		**%NDF$_{adj}$**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	-0.824	-0.464	0.099	***1.594***	-0.728	1.081
2	0.804	-0.197	***2.351***	-0.535	3.164**	-0.709
3	0.417	-1.006	0.769	0.511	1.193**	-0.468
4	-0.003	2.984*	0.052	-0.803	0.096*	2.213*
5	-1.496	1.553	-1.458**	-1.966**	***-3.029***	-0.405
6	1.101	***-2.870***	-1.812**	1.199	-0.696	***-1.713***
LSD$_{0.05}$	3.241	4.582	2.480	2.440	2.533	3.762
LSD$_{0.01}$	4.373	6.182	3.346	3.292	3.417	5.076

The estimates of mean general combining ability effects of parents in Table 5.7 showed the following:

In the case of estimated gca effects for %*EE*, the F-test and LSD test were in agreement for cut 1 and cut 2 in so far as to indicate that significant differences existed. In cut 1, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 4 and 5. The estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 6 and significant differences were shown with the gca effects of parents 4 and 5.

In the case of %*NSC*, a few significant differences between gca effects were shown in both cut 1 and cut 2 when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 1, the estimated gca effect of parent 5 showed a highly significant difference with the gca effect of parent 2 and significant differences were shown with the gca effects of parents 1 and 6. In cut 2, the estimated gca effect of parent 6 showed a significant difference with the gca effect of parent 4.

In the case of estimated gca effects for %*IVDOM*, the F-test and LSD test were in agreement for cut 1 and cut 2 in so far as to indicate that significant differences existed. In cut 1, no significant differences between gca effects were shown for %*IVDOM*. In cut 2, the estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2, 3 and 6. The good gca effect of parent 1 in cut 2 was in contrast to expectations from the phenotypical performance of parent 1 in cut 2 for this character. This shows that the breeding value of an inbred parent cannot be deducted from its phenotypic performance.

Tabel 5.7 Estimates of mean general combining ability effects of parents for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material.

	Characters					
	%EE		%NSC		%IVDOM	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	0.253	0.163	-1.121*	-0.766	0.231	***2.128***
2	***0.342***	***0.212***	-1.697**	-0.074	-0.478	-1.806*
3	0.218	0.055	0.631	1.176	0.656	-1.547*
4	-0.432**	-0.133*	0.492	-2.947*	-0.061	1.694
5	-0.388**	-0.106*	***2.629***	0.445	0.064	1.753
6	0.007	-0.191**	-0.934*	***2.166***	-0.411	-2.222*
$LSD_{0.05}$	0.367	0.277	3.192	4.291	3.355	3.558
$LSD_{0.01}$	0.495	0.373	4.307	5.789	4.526	4.800

The estimates of mean general combining ability effects of parents in Table 5.8 showed the following:

In the case of *ME*, a few significant differences between gca effects were shown in cut 1 when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 1, the estimated gca effect of parent 3 showed a significant difference with the gca effect of parent 6. In cut 2, the estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2 and 6. The strong gca effects for high *ME* of parent 3 in cut 1 and parents 1, 4 and 5 in cut 2 suggested that these parents might also have good estimated gca values for *DM intake/steer/day*, according to the *NRC* approach. The good gca effect of parent 1 in cut 2 was again in contrast to expectations from the phenotypical performance of parent 1 in cut 2 for this character.

In the case of estimated gca effects for *MRT*, the F-test and LSD test were in agreement for cut 1 and cut 2 in so far as to indicate that significant differences existed. In cut 1, no significant differences between gca effects were shown for *MRT*.

In cut 2, the estimated gca effect of parent 5 showed significant differences with the gca effects of parents 2 and 6. The strong gca effects for a short *MRT* of parents 1, 4 and 5 in cut 2 suggested that these parents might also have good estimated gca values for *DM intake/steer/day*, according to the *Pienaar* approach*.* The good gca effect of parent 1 in cut 2 was once again in contrast to expectations from the phenotypical performance of parent 1 in cut 2 for this character. This shows that the breeding value of an inbred parent cannot be deducted from its phenotypic performance.

Tabel 5.8 Estimates of mean general combining ability effects of parents for metabolic energy value and mean retention time of the triticale vegetative material.

	Characters			
	ME (MJ/kg DM)		**MRT (hour)**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	0.090	***0.325***	-0.203	-0.711
2	0.116	-0.299*	0.206	0.872*
3	***0.343***	-0.174	-0.369	0.531
4	-0.031	0.237	0.189	-0.694
5	-0.135	0.253	-0.378	***-0.769***
6	-0.383*	-0.341*	0.556	0.772*
$LSD_{0.05}$	0.603	0.533	1.744	1.310
$LSD_{0.01}$	0.814	0.704	2.353	1.767

5.1.3 Specific combining ability

5.1.3.1 Results

The best 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 α = 0.05 level of confidence or by a ** for a α = 0.01 level of confidence.

The estimates of specific combining ability effects for the different plant quality characteristics of the triticale vegetative material are presented in Table 5.9 to 5.12.

5.1.3.2 Discussion

The estimates of specific combining ability effects for %*NDF*, %*ADF* and %*ADL* in Table 5.9 showed the following:

In both cut 1 and cut 2, a few significant differences between sca effects for %*NDF*, %*ADF* and %*ADL* were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects.

In the case of estimated sca effects for %*NDF*, the estimated sca effect of 1*x*4 showed a highly significant difference with the sca effect of 2*x*4 and a significant difference was shown with the sca effect of 1*x*3 in cut 1. In cut 2, the estimated sca effect of 1*x*4 showed significant differences with the sca effects of 1*x*5 and 2*x*4. These results were in agreement with the expectation from the phenotypical performance of 2*x*4 for this character.

In the case of estimated sca effects for %*ADF*, the estimated sca effect of 2*x*5 showed signficant differences with the sca effects of 2*x*6 and 4*x*5 in cut 1. In cut 2, the estimated sca effect of 5*x*6 showed a significant difference with the sca effect of 1*x*6. These results were in agreement with the expectation from the phenotypical performance of 5*x*6 for this character in cut 2.

In the case of estimated sca effects for %*ADL*, the estimated sca effect of 3*x*5 showed highly significant differences with the sca effects of 1*x*5 and 4*x*5 and significant differences were shown with the sca effects of 1*x*3, 2*x*3 and 2*x*6 in cut 1. In cut 2, the estimated sca effect of 2*x*6 showed a significant difference with the sca effect of 1*x*6. The good estimated sca effects of 3*x*5 and 2*x*6 for %*ADL* in cut 1 and cut 2 respectively were in agreement with the phenotypical performance of these crosses for this character.

Table 5.9 Estimates of specific combining ability effects for percentages neutral detergent fibre, acid detergent fibre and acid detergent lignin of the triticale vegetative material.

	Characters					
	%NDF		**%ADF**		**%ADL**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	-0.613	-2.514	0.267	-0.642	-0.673	-0.689
1 *x* **3**	2.475*	-0.388	1.197	-0.829	0.620*	-0.068
1 *x* **4**	***-2.684***	***-2.689***	-1.430	-1.742	-0.960	-0.625
1 *x* **5**	1.009	5.107*	0.876	-1.039	1.339**	0.048
1 *x* **6**	-0.186	0.484	-0.911	4.252*	-0.326	1.333*
2 *x* **3**	-1.651	-1.527	0.218	-0.238	0.530*	0.588
2 *x* **4**	3.636**	5.373*	-0.653	-0.105	0.258	0.789
2 *x* **5**	-2.129	-2.679	***-2.178***	1.664	-0.857	0.133
2 *x* **6**	0.757	1.347	2.346*	-0.678	0.741*	***-0.821***
3 *x* **4**	-0.405	0.598	0.071	1.806	0.005	-0.068
3 *x* **5**	0.094	0.869	-1.814	0.565	***-1.268***	-0.273
3 *x* **6**	-0.513	0.448	0.328	-1.305	0.113	-0.179
4 *x* **5**	0.268	-2.149	3.446*	0.561	1.005**	0.164
4 *x* **6**	-0.815	-1.132	-1.433	-0.520	-0.308	-0.260
5 *x* **6**	0.757	-1.148	-0.330	***-1.750***	-0.220	-0.073
LSD$_{0.05}$	3.982	6.413	4.389	4.559	1.643	1.665
LSD$_{0.01}$	5.372	8.652	5.921	6.151	2.217	2.246

The estimates of specific combining ability effects for %*hemicellulose*, %*crude cellulose* and %*NDF$_{adj}$* in Table 5.10 showed the following:

In both cut 1 and cut 2, a few significant differences between sca effects for %*hemicellulose* and %*NDF$_{adj}$* were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In cut 2, a significant difference between sca effects for %*crude cellulose* was shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects.

In the case of estimated sca effects for %*hemicellulose*, the estimated sca effect of 4*x*5 showed a significant difference with the sca effect of 2*x*4 in cut 1. In cut 2, the estimated sca effect of 2*x*5 showed significant differences with the sca effects of 1*x*5 and 2*x*4. These results were in agreement with the expectation from the phenotypical performance of 2*x*4 for this character.

In the case of estimated sca effects for %*crude cellulose*, no significant differences were shown between the estimated sca effect in cut 1. This was in agreement with the results of the F-test for cut 1. In cut 2, the estimated sca effect of 1*x*6 showed a significant difference with the sca effect of 5*x*6. This result in cut 2 was in agreement with the expectation from the phenotypical performance of 5*x*6 for this character in cut 2.

In the case of estimated sca effects for %NDF_{adj}, the estimated sca effect of 2*x*3 showed a significant difference with the sca effect of 2*x*4. In cut 2, the estimated sca effect of 2*x*5 showed significant differences with the sca effects of 1*x*5 and 2*x*4. These results were in agreement with the expectation from the poor phenotypical performance of 2*x*4 for this character. The good estimated sca effect of 2*x*5 in the combining ability analysis was in agreement with the expectation from the phenotypical performance of combination.

Table 5.10 Estimates of specific combining ability effects for percentages hemicellulose, crude cellulose and adjusted neutral detergent fibre of the triticale vegetative material.

	Characters					
	%Hemi-cellulose		%Crude cellulose		%NDF$_{adj}$	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	-0.870	-1.872	0.940	0.047	0.023	-1.901
1 *x* **3**	1.289	0.440	0.577	-0.761	1.915	-0.303
1 *x* **4**	-1.271	-0.947	-0.470	-1.117	-1.747	-2.117
1 *x* **5**	0.115	6.147*	-0.463	-1.088	-0.319	5.101*
1 *x* **6**	0.736	-3.768	-0.585	***2.919***	0.127	-0.780
2 *x* **3**	-1.857	-1.289	-0.313	-0.826	***-2.197***	-2.076
2 *x* **4**	4.272*	5.478*	-0.911	-0.894	3.411*	4.682*
2 *x* **5**	0.032	***-4.342***	-1.322	1.530	-1.286	***-2.808***
2 *x* **6**	-1.578	2.025	1.606	0.143	0.049	2.104
3 *x* **4**	-0.494	-1.209	0.067	1.874	-0.387	0.646
3 *x* **5**	1.891	0.304	-0.546	0.838	1.323	1.106
3 *x* **6**	-0.829	1.753	0.214	-1.125	-0.654	0.627
4 *x* **5**	***-3.109***	-2.710	2.440	0.396	-0.737	-2.329
4 *x* **6**	0.601	-0.612	-1.125	-0.259	-0.540	-0.881
5 *x* **6**	1.070	0.602	-0.110	-1.677*	1.018	-1.070
LSD$_{0.05}$	5.614	7.937	4.296	4.227	4.386	6.516
LSD$_{0.01}$	7.574	10.708	5.796	5.702	5.918	8.791

The estimates of specific combining ability effects for %*EE*, %*NSC* and %*IVDOM* in Table 5.11 showed the following:

In the case of estimated sca effects for %*NSC*, the F-test and LSD test were in agreement for cut 1 in so far as to indicate that significant differences existed. In cut 2, a few significant differences between sca effects for %*NSC* were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. A few significant differences between sca effects for %*EE* were shown in cut 1 and cut 2 when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In cut 2, a few significant differences between sca effects for %*NSC* were shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects. In the case of estimated sca effects for %*IVDOM*, the F-test and LSD test were in agreement for both cut 1 and cut 2 in so far as to indicate the absence of any significant differences between estimated sca effects.

In the case of estimated sca effects for %*EE*, the estimated sca effect of 1*x*2 showed significant differences with the sca effects of 1*x*4, 1*x*5, 1*x*6, 2*x*3 and 2*x*5 in cut 1. In cut 2, the estimated sca effect of 5*x*6 showed a significant difference with the sca effect of 3*x*6.

In the case of estimated sca effects for %*NSC*, the estimated sca effect of 1*x*4 showed highly signficant differences with the sca effects of 1*x*2, 1*x*3, 1*x*5, 2*x*4, 3*x*4, 4*x*6 and 5*x*6 and significant differences were shown with the sca effects of 2*x*6 and 3*x*5 in cut 1. In cut 2, the estimated sca effect of 2*x*5 showed significant differences with the sca effects of 1*x*5 and 2*x*4. These results were in agreement with the expectation from the poor phenotypical performances of 1*x*5 and 2*x*4 for this character in both cuts.

In the case of estimated sca effects for %*IVDOM*, no significant differences between sca effects were shown for %*IVDOM* in either of the two cuts.

Table 5.11 Estimates of specific combining ability effects for percentages ether extract, non structural carbohydrates and *in vitro* digestible organic matter of the triticale vegetative material.

	Characters					
	%EE		**%NSC**		**%IVDOM**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	***0.488***	-0.141	-1.445**	2.966	0.825	0.107
1 *x* **3**	0.158	0.130	-3.562**	0.743	0.358	-1.318
1 *x* **4**	-0.255*	0.098	***6.701***	2.769	0.208	2.940
1 *x* **5**	-0.203*	-0.060	-3.192**	-5.861*	-1.783	-2.618
1 *x* **6**	-0.188*	-0.028	1.498	-0.616	0.392	0.890
2 *x* **3**	-0.339*	0.133	2.488	0.455	0.300	-0.685
2 *x* **4**	0.114	0.039	-4.253**	-5.931*	-1.450	-0.227
2 *x* **5**	-0.246*	-0.040	3.053	***4.003***	-1.142	-0.452
2 *x* **6**	-0.017	0.010	0.157*	-1.492	1.467	1.257
3 *x* **4**	0.208	0.041	-1.934**	-1.440	-1.283	-0.785
3 *x* **5**	0.025	-0.057	0.875*	0.334	2.158	1.923
3 *x* **6**	-0.052	-0.247*	2.134	-0.091	-1.533	0.865
4 *x* **5**	0.050	-0.143	1.270	1.964	1.808	1.115
4 *x* **6**	-0.118	-0.034	-1.784**	2.639	0.717	-3.043
5 *x* **6**	0.374	***0.299***	-2.005**	-0.439	-1.042	0.032
LSD$_{0.05}$	0.636	0.479	5.529	7.432	5.811	6.163
LSD$_{0.01}$	0.857	0.647	7.459	10.027	7.840	8.315

The estimates of specific combining ability effects for *ME* and *MRT* in Table 5.12 showed the following:

In the case of estimated sca effects for *ME*, the F-test and LSD test were in agreement for both cut 1 and cut 2 in so far as to indicate the absence of any significant differences between estimated sca effects. In the case of estimated sca effects for *MRT*, the F-test and LSD test were in agreement for cut 1 in so far as to indicate the absence of any significant differences between estimated sca effects. In cut 2, a significant difference between sca effects for *MRT* was shown when using the LSD test, although the F-test failed to indicate any significant differences between sca effects.

In the case of estimated sca effects for *ME*, as with %*IVDOM*, no significant differences between sca effects were shown in either of the two cuts.

In the case of estimated sca effects for *MRT*, no significant differences between sca effects were shown in cut 1. In cut 2, the estimated sca effect of 1*x*4 showed a significant difference with the sca effect of 4*x*6. These results were in agreement with the expectation from the phenotypical performance of 1*x*4 for this character in cut 2.

Table 5.12 Estimates of specific combining ability effects for metabolic energy value and mean retention time of the triticale vegetative material.

	Characters			
	ME (MJ/kg DM)		**MRT (hour)**	
Genotypes				
1 *x* **2**	0.065	0.027	-0.125	0.357
1 *x* **3**	0.047	-0.069	0.450	0.698
1 *x* **4**	0.060	0.371	-0.308	***-1.843***
1 *x* **5**	-0.521	-0.445	-0.342	1.198
1 *x* **6**	0.349	0.116	0.325	-0.410
2 *x* **3**	-0.145	-0.146	-0.225	0.215
2 *x* **4**	-0.015	-0.028	0.950	0.207
2 *x* **5**	-0.129	0.003	0.317	-0.285
2 *x* **6**	0.224	0.145	-0.917	-0.493
3 *x* **4**	-0.213	-0.139	0.158	0.748
3 *x* **5**	0.448	0.256	-1.242	-0.877
3 *x* **6**	-0.136	0.097	0.858	-0.785
4 *x* **5**	0.404	0.170	0.367	-0.418
4 *x* **6**	-0.236	-0.374	-1.167	1.307^*
5 *x* **6**	-0.202	0.017	0.900	0.382
LSD$_{0.05}$	1.044	0.924	3.021	2.268
LSD$_{0.01}$	1.409	1.246	4.076	3.060

5.1.4 GCA/SCA Ratios

5.1.4.1 Results

The ratios of the gca variance to the sca variance for the different plant quality characteristics of the triticale vegetative material are presented in Table 5.13.

5.1.4.2 Discussion

Both the estimated gca effects and the sca effects of the same genotype changed between cuts when the same characteristic was considered, as was shown in Tables 5.5 to 5.12. When the ratio of $\sigma^2_{\mathbf{gca}}$ to σ^2_{sca} for each characteristic is viewed across cuts, the value obtained also changes between the two cuts. Each cut 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 higher than those for cut 2 for the various fibre characters considered. It must be remembered that *NDF* consists mainly of cellulose, hemicellulose and lignin and that the relative compositions of these components of *NDF* may vary from the first cut to the second cut. *ADF* consists also mainly of cellulose and lignin and the relative compositions of these components of *ADF* may vary from the first cut to the second cut as well. The phenotypic- and additive genetic correlations of these various components to *NDF* and *ADF* that will be shown in Chapter 7 may throw more light on these possibilities. The ratio for *%NSC* in cut 2 was higher than the ratio for cut 1, but both were very low.

The variance of gca played a bigger role than the variance of sca in the case of *NDF*, *ADF*, NDF_{adj} and *EE* for cut 1 and in the case of *ADF* and *MRT* for cut 2. These results give an indication that these quality characters will show high narrow sense heritabilities when evaluated in the respective cuts.

Table 5.13 Ratios of the gca variance to the sca variance for the different plant quality characteristics of the triticale vegetative material.

Characters	$\sigma^2_{gca}/\sigma^2_{sca}$ Ratio
NDF cut 1	1.631
NDF cut 2	0.124
ADF cut 1	2.178
ADF cut 2	1.142
ADL cut 1	0.397
ADL cut 2	-
Hemicellulose cut 1	-
Hemicellulose cut 2	0.443
Crude cellulose cut 1	-
Crude cellulose cut 2	-
NDF_{adj} cut 1	19.569
NDF_{adj} cut 2	0.119
EE cut 1	4.052
EE cut 2	-
NSC cut 1	0.146
NSC cut 2	0.208
IVDOM cut 1	-
IVDOM cut 2	-
ME cut 1	-
ME cut 2	-
MRT cut 1	-
MRT cut 2	1.499

5.2 Plant production characteristics

5.2.1 Combining ability analysis

5.2.1.1 Results

The mean squares for the different plant production characteristics of the triticale vegetative material in the combining ability analyses of variance are presented in Tables 5.14 to 5.19.

5.2.1.2 Discussion

No reference of a genetic study on any forage cereal where the combining ability for the different plant production characteristics of vegetative material was investigate, could be found.

Tan et al. (1978), Nguyen et al. (1982) and Annicchiarico & Romani (2005) did diallel studies on smooth bromegrass and tall fescue respectively, but the only plant production character studied was *kg DM/ha.*

The analyses of variance in Table 5.14 showed the following:

In the combining ability analysis of variance for *kg DM/ha* of the triticale vegetative material, the F-test showed that highly significant differences existed between estimated gca effects in cut 1. No significant differences were shown with regard to the gca effects in cut 2, or where the gca of the total *kg DM/ha* across the two cuts was considered. These results were in contrast with the results of Tan et al. (1978), Nguyen et al. (1982) as well as Annicchiarico & Romani (2005) who found significant differences between gca effects for *kg DM/ha* in all cuts. These studies were conducted on different species however and the timing of the cuts was different as well. The combining ability analysis of variance showed significant differences with regard to the sca effects in cut 1 and where the sca of the total *kg DM/ha* across the two cuts was considered. These results were in agreement with the results of Tan et al. (1978) with regard to the first cut, but in contrast with the results of Nguyen et al. (1982) who never found any significant differences between sca effects for *kg DM/ha* in any cut. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and significant differences between blocks were shown where the total *kg DM/ha* across the two cuts was considered. Based on the results of the F-test, meaningful selections can be made at cut 1 to improve the additive value of genotypes for this characteristic.

Table 5.14 Mean squares for the dry matter yield of the triticale vegetative material in the combining ability ANOVA's.

		kg DM/ha		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	1145742.134**	528181.308	2502175.924*
gca	5	333618.713**	104930.199	431378.671
sca	9	89069.826*	169816.954	420041.632*
Error	28	37291.860	93030.659	169293.377

The analyses of variance in Table 5.15 showed the following:

In the combining ability analysis of variance for *crude cellulose* yield/ha 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 cellulose* yield/ha across the two cuts was considered. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts or where the sca of the total *crude cellulose* yield/ha across the two cuts was considered. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and also where the total *crude cellulose* yield/ha across the two cuts was considered. Significant differences between blocks were shown in the case of cut 2. This meant that the environment had a bigger effect in differences amongst the F_1 genotypes than either the gca or sca effects in cut 2 or where the total *crude cellulose* yield/ha across the two cuts was considered. Based on the results of the F-test, it will be worthwhile to try to alter the *crude cellulose* yield/ha of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

Table 5.15 Mean squares for the crude cellulose yield of the triticale vegetative material in the combining ability ANOVA's.

		Crude cellulose yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	48017.213**	125188.997*	291861.574**
gca	5	14919.687**	15652.492	28790.500
sca	9	2676.899	13463.944	21537.891
Error	28	1686.506	8183.970	12832.753

The analyses of variance in Table 5.16 showed the following:

In the combining ability analysis of variance for *EE* yield/ha of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1 and where the gca of the total *EE* yield/ha across the two cuts was considered. Significant differences were shown with regard to the gca effects in cut 2. The F-test showed no significant differences with regard to sca effects in either of the two cuts but significant differences were shown where the sca of the total *EE* yield/ha across the two cuts was considered. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 only. Based on the results of the F-test, it will be worthwhile to try to increase the *EE* yield/ha of the vegetative material in the triticale genotypes used in this study, through selection at cut 1 and also to a lesser extend also at cut 2.

Table 5.16 Mean squares for the ether extract yield of the triticale vegetative material in the combining ability ANOVA's.

		EE yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	1550.407**	158.932	720.268
gca	5	711.650**	234.563*	1333.514**
sca	9	143.086	154.543	483.594*
Error	28	67.945	89.388	194.231

The analyses of variance in Table 5.17 showed the following:

In the combining ability analysis of variance for *NSC* yield/ha of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1 and where the gca of the total *NSC* yield/ha across the two cuts was considered. No significant differences were shown with regard to the gca effects in cut 2. The F-test showed significant differences with regard to sca effects in cut 2 and where the sca of the total *NSC* yield/ha across the two cuts was considered. No significant differences with regard to the sca effects were shown in cut 1. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and where the total *NSC* yield/ha across the two cuts was considered. Based on the results of the F-test, it will be worthwhile to try to increase the *NSC* yield/ha of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

Table 5.17 Mean squares for the non structural carbohydrate yield of the triticale vegetative material in the combining ability ANOVA's.

		NSC yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	266672.974**	14504.478	374771.827**
gca	5	34804.087**	23614.398	75330.036**
sca	9	7851.320	24659.781*	45896.468*
Error	28	4934.913	9736.996	19658.195

The analyses of variance in Table 5.18 showed the following:

In the combining ability analysis of variance for *IVDOM* yield/ha of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1. No significant differences were shown with regard to the gca effects in cut 2 or where the gca of the total *IVDOM* yield/ha across the two cuts was considered. The F-test showed significant differences with regard to sca effects in cut 1 and where the sca of the total *IVDOM* yield/ha across the two cuts was considered. No significant differences with regard to the sca effects were shown in cut 2. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and where the total *IVDOM* yield/ha across the two cuts was considered. Based on the results of the F-test, it will be worthwhile to try to increase the *IVDOM* yield/ha of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

Table 5.18 Mean squares for the *in vitro* digestible organic matter yield of the triticale vegetative material in the combining ability ANOVA's.

		IVDOM yield/ha (kg/ha)		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	951901.707**	326933.526	2208872.377**
gca	5	253986.107**	69949.009	244378.958
sca	9	72059.037*	108451.365	299895.537*
Error	28	28634.315	63870.318	117112.612

The analyses of variance in Table 5.19 showed the following:

In the combining ability analysis of variance for *ME* yield/ha of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects in cut 1. No significant differences were shown with regard to the gca effects in cut 2 or where the gca of the total *ME* yield/ha across the two cuts was considered. The F-test showed significant differences with regard to sca effects in cut 1 and where the sca of the total *ME* yield/ha across the two cuts was considered. No significant differences with regard to the sca effects were shown in cut 2. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1 and where the total *ME* yield/ha across the two cuts was considered. Based on the results of the F-test, it will be worthwhile to try to increase the *ME* yield/ha of the vegetative material in the triticale genotypes used in this study, through selection at cut 1.

Table 5.19 Mean squares for the metabolic energy yield of the triticale vegetative material in the combining ability ANOVA's.

		ME yield/ha (MJ/ha)		
	df	**Cut1**	**Cut2**	**Total**
Blocks	2	222078838.200**	72905775.000	515035443.200**
gca	5	55132361.800**	15054718.300	52769978.200
sca	9	15252205.300*	23407149.100	64305948.300*
Error	28	6344235.348	13449889.348	24552969.816

5.2.2 General combining ability

5.2.2.1 Results

The highest gca value for each character per cut 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 α = 0.05 level of confidence or by a ** for a α = 0.01 level of confidence.

The estimates of mean general combining ability effects of parents for the different plant production characteristics of the triticale vegetative material are presented in Tables 5.20 to 5.23.

5.2.2.2 Discussion

The estimates of mean general combining ability effects of parents in Table 5.20 showed the following:

In the case of estimated gca effects for *kg DM/ha*, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. 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. A few significant differences between gca effects for *kg DM/ha* were shown in cut 2 and for the total *kg DM/ha* across the two cuts when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of cut 2, the estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 4. In the case where the total *kg DM/ha* across the two cuts was considered, the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 4 and a significant difference with the gca effect of parent 5. The strong gca effect of parent 1 in cut 2 was in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 1 in cut 1.

Table 5.20 Estimates of mean general combining ability effects of parents for dry matter yield of the triticale vegetative material.

	kg DM/ha		
Genotypes	**Cut1**	**Cut2**	**Total**
1	-208.185**	***195.541***	-12.644
2	***468.322***	-55.020	***413.302***
3	199.934	3.704	203.638
4	-241.350**	-280.020*	-521.370**
5	-236.274**	34.325	-201.949*
6	17.553**	101.470	119.023
$LSD_{0.05}$	279.655	441.701	595.847
$LSD_{0.01}$	377.288	595.908	803.870

The estimates of mean general combining ability effects of parents in Table 5.21 showed the following:

In the case of estimated gca effects for *crude cellulose* yield/ha, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. In cut 1, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 1, 4, 5, 6 and a significant difference with the gca effect of parent 3. A few significant differences between gca effects for *crude cellulose* yield/ha were shown in cut 2 and for the total *crude cellulose* yield/ha across the two cuts when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of cut 2, the estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 4. In the case where the total *crude cellulose* yield/ha across the two cuts was considered, the estimated gca effect of parent 2 showed significant differences with the gca effects of parents 4 and 5. The strong gca effect of parent 1 in cut 2 was once again in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 1 in cut 1.

In the case of estimated gca effects for *EE* yield/ha, the F-test and LSD tests were in agreement for both cuts and for the total *EE* yield/ha across the two cuts in so far as to indicate that significant differences existed. 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 cut 2, the estimated gca effect of parent 1 showed a highly significant difference with the gca effect of parent 4. In the case where the total *EE* yield/ha across the two cuts was considered, the estimated gca effect of parent 2 showed highly significant differences with the gca effects of parents 4 and 5 and a significant difference with the gca effect of parent 6. The strong gca effect of parent 1 in cut 2 was once again in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 1 in cut 1.

Table 5.21 Estimates of mean general combining ability effects of parents for crude cellulose yield and ether extract yield of the triticale vegetative material.

	Characters					
	Cr. cellulose yield/ha (kg/ha)			EE yield/ha (kg/ha)		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1	-32.141**	***86.928***	54.787	-3.228**	***11.034***	7.805
2	***106.950***	-29.475	***77.475***	***19.918***	3.318	***23.236***
3	34.571*	7.153	41.725	9.385	1.126	10.511
4	-37.687**	-80.202*	-117.889*	-13.806**	-12.388**	-26.194**
5	-58.128**	-39.822	-97.949*	-14.149**	-2.234	-16.383**
6	-13.565**	55.417	41.852	1.881**	-0.855	1.025*
LSD$_{0.05}$	59.472	131.008	164.050	11.937	13.692	20.183
LSD$_{0.01}$	80.234	176.745	221.323	16.104	18.472	27.229

The estimates of mean general combining ability effects of parents in Table 5.22 showed the following:

In the case of estimated gca effects for *NSC* yield/ha *crude cellulose* yield/ha, the F-test and LSD tests were in agreement for cut 1 and for the total *NSC* yield/ha across the two cuts in so far as to indicate that significant differences existed. 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. A highly significant difference between gca effects for *NSC* yield/ha was shown in 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 2, the estimated gca effect of parent 6 showed a significant difference with the gca effect of parent 4. In the case where the total *NSC* yield/ha across the two cuts was considered, the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 4. The strong gca effect of parent 6 in cut 2 was in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 6 in cut 1.

In the case of estimated gca effects for *IVDOM* yield/ha, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. 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. A few significant differences between gca effects for *IVDOM* yield/ha were shown in cut 2 and for the total *IVDOM* yield/ha across the two cuts when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of cut 2, the estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 4. In the case where the total *IVDOM* yield/ha across the two cuts was considered, the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 4. The strong gca effect of parent 1 in cut 2 was in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 1 in cut 1.

Table 5.22 Estimates of mean general combining ability effects of parents for non structural carbohydrate yield and *in vitro* digestible organic matter yield of the triticale vegetative material.

	Characters					
	NSC yield/ha (kg/ha)			**IVDOM yield/ha (kg/ha)**		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1	-95.235**	29.512	-65.724	-180.625**	***200.757***	20.131
2	***135.038***	-8.465	***126.573***	***403.073***	-83.018	***320.055***
3	86.910	34.055	120.965	182.750	-30.082	152.668
4	-86.537**	-148.579**	-235.116**	-218.198**	-183.055*	-401.253**
5	-33.336**	24.705	-8.631	-202.809**	72.966	-129.844
6	-6.840**	***68.773***	61.933	15.810**	22.432	38.242
LSD$_{0.05}$	101.731	142.898	203.042	245.052	365.986	495.583
LSD$_{0.01}$	137.248	192.787	273.929	330.605	493.760	668.602

The estimates of mean general combining ability effects of parents in Table 5.23 showed the following:

In the case of estimated gca effects for *ME* yield/ha, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed. 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. A few significant differences between gca effects for *ME* yield/ha were shown in cut 2 and for the total *ME* yield/ha across the two cuts when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In the case of cut 2, the estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 4. In the case where the total *ME* yield/ha across the two cuts was considered, the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 4. The strong gca effect of parent 1 in cut 2 was once again in contrast to expectations, because the estimated gca effect of parent 2 showed a highly significant difference with the gca effect of parent 1 in cut 1.

Table 5.23 Estimates of mean general combining ability effects of parents for metabolic energy yield of the triticale vegetative material.

	ME yield/ha (MJ/ha)		
Genotypes	**Cut1**	**Cut2**	**Total**
1	-2532.663**	***2943.207***	410.544
2	***5927.678***	-1289.298	4638.380
3	2907.057	-294.859	2612.197
4	-3112.372**	-2683.077*	-5795.449**
5	-3033.387**	1069.001	-1964.386
6	-156.312**	255.027	98.714
LSD$_{0.05}$	3647.578	5310.976	7175.745
LSD$_{0.01}$	4921.025	7165.149	9680.948

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 α = 0.05 level of confidence or by a ** for a α = 0.01 level of confidence.

The estimates of specific combining ability effects for the different plant production characteristics of the triticale vegetative material are presented in Table 5.24 to 5.27.

5.2.3.2 Discussion

The estimates of specific combining ability effects for *kg DM/ha* in Table 5.24 showed the following:

In the case of estimated sca effects for *kg DM/ha*, the F-test and LSD test were in agreement for cut 1 and the total *kg DM/ha* in so far as to indicate that significant differences existed. A few significant differences between sca effects for *kg DM/ha* 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 1, the estimated sca effect of 2*x*4 showed a highly significant difference with the sca effect of 2*x*3. In cut 2, the estimated sca effect of 3*x*5 showed a highly significant difference with the sca effect of 2*x*3 and significant differences were shown with the sca effects of 1*x*4 and 5*x*6. In the case of the total *kg DM/ha*, the estimated sca effect of 3*x*5 showed highly significant differences with the sca effects of 2*x*3 and 5*x*6 and significant differences were shown with the sca effects of 1*x*4 and 1*x*5.

Table 5.24 Estimates of specific combining ability effects for dry matter yield of the triticale vegetative material.

	kg DM/ha		
Genotypes	**Cut1**	**Cut2**	**Total**
1 *x* **2**	-148.9	136.9	-12.0
1 *x* **3**	276.1	247.1	523.1
1 *x* **4**	-148.6	-365.9*	-514.5*
1 *x* **5**	-66.6	-328.0	-394.6*
1 *x* **6**	88.0	309.9	397.9
2 *x* **3**	-478.6**	-640.7**	-1119.3**
2 *x* **4**	***363.3***	180.2	543.5
2 *x* **5**	-78.6	327.9	249.3
2 *x* **6**	342.8	-4.3	338.5
3 *x* **4**	-78.3	-123.7	-202.0
3 *x* **5**	291.7	***405.4***	***697.1***
3 *x* **6**	-10.9	111.9	101.1
4 *x* **5**	68.5	160.9	229.4
4 *x* **6**	-204.9	148.5	-56.4
5 *x* **6**	-215.0	-566.1*	-781.1**
LSD$_{0.05}$	484.4	765.0	1032.0
LSD$_{0.01}$	653.5	1032.1	1392.3

The estimates of specific combining ability effects for *crude cellulose* yield/ha and *EE* yield/ha in Table 5.25 showed the following:

In the case of estimated sca effects for *crude cellulose* yield/ha, a few significant differences between sca effects for *crude cellulose* yield/ha were shown in cut 1, cut 2 and total *crude cellulose* yield/ha 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 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 2*x*5 and 4*x*6. In cut 2, the estimated sca effect of 1*x*6 showed a highly significant difference with the sca effect of 5*x*6 and significant differences with the sca effects of 1*x*4, 1*x*5 and 2*x*3. In the case of the total *crude cellulose* yield/ha, the estimated sca effect of 3*x*5 showed significant differences with the sca effects of 1*x*4, 2*x*3 and 5*x*6.

In the case of estimated sca effects for *EE* yield/ha, the F-test and LSD test were in agreement for the total *EE* yield/ha across two cuts in so far as to indicate that significant differences existed. A few significant differences between sca effects for *EE* yield/ha were shown in cut 1 and cut 2 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 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*4, 2*x*5 and 4*x*6. In cut 2, the estimated sca effect of 1*x*3 showed a highly significant difference with the sca effect of 2*x*3 and a significant difference with the sca effect of 1*x*5. In the case of the total *EE* yield/ha, the estimated sca effect of 1*x*3 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*4, 1*x*5 and 5*x*6.

Table 5.25 Estimates of specific combining ability effects for crude cellulose yield and ether extract yield of the triticale vegetative material.

	Characters					
	Cr. cellulose yield/ha (kg/ha)			**EE yield/ha (kg/ha)**		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1 *x* **2**	-11.0	23.9	12.9	1.0	0.5	1.5
1 *x* **3**	49.7	38.8	88.5	12.1	***13.0***	***25.2***
1 *x* **4**	-30.8	-115.0^{*}	-145.8^{*}	-7.6^{*}	-9.3	-16.9^{*}
1 *x* **5**	-5.3	-92.8^{*}	-98.1	-3.4	-13.3^{*}	-16.8^{*}
1 *x* **6**	-2.7	***145.1***	142.4	-2.0	9.0	7.0
2 *x* **3**	-79.1^{**}	-151.9^{*}	-231.0^{*}	-20.9^{**}	-20.0^{**}	-40.9^{**}
2 *x* **4**	54.9	27.5	82.4	13.4	7.2	20.6
2 *x* **5**	-34.9^{*}	100.5	65.6	-7.1^{*}	11.0	3.9
2 *x* **6**	***70.1***	0	70.1	***13.7***	1.2	14.9
3 *x* **4**	-11.5	10.6	-0.9	-1.9	-2.1	-4.0
3 *x* **5**	37.0	105.9	***142.9***	9.5	12.6	22.0
3 *x* **6**	3.9	-3.4	0.4	1.2	-3.5	-2.3
4 *x* **5**	30.9	52.5	83.4	5.1	0.3	5.4
4 *x* **6**	-43.5^{*}	24.4	-19.1	-8.9^{*}	3.8	-5.1
5 *x* **6**	-27.8	-166.1^{**}	-193.8^{*}	-3.9	-10.6	-14.5^{*}
LSD$_{0.05}$	103.0	226.9	284.1	20.7	23.7	35.0
LSD$_{0.01}$	139.0	306.1	383.3	27.9	32.0	47.2

The estimates of specific combining ability effects for *NSC* yield/ha and *IVDOM* yield/ha in Table 5.26 showed the following:

In the case of estimated sca effects for *NSC* yield/ha, the F-test and LSD test were in agreement for cut 2 and the total *NSC* yield/ha in so far as to indicate that significant differences existed. A few significant differences between sca effects for *NSC* yield/ha were shown in cut 1 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 3*x*5 showed significant differences with the sca effects of 2*x*3, 4*x*6 and 5*x*6.

In cut 2, the estimated sca effect of 2*x*5 showed highly significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6 and a significant difference with the sca effect of 2*x*4. In the case of the total *NSC* yield/ha, the estimated sca effect of 3*x*5 showed highly significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6.

In the case of estimated sca effects for *IVDOM* yield/ha, the F-test and LSD test were in agreement for cut 1 and the total *IVDOM* yield/ha across two cuts in so far as to indicate that significant differences existed. A few significant differences between sca effects for *IVDOM* yield/ha 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 1, the estimated sca effect of 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*2, 1*x*4, 4*x*6 and 5*x*6. In cut 2, the estimated sca effect of 3*x*5 showed significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6. In the case of the total *IVDOM* yield/ha, the estimated sca effect of 3*x*5 showed highly significant differences with the sca effects of 2*x*3 and 5*x*6 and significant differences with the sca effects of 1*x*4 and 1*x*5.

Table 5.26 Estimates of specific combining ability effects for non structural carbohydrate yield and *in vitro* digestible organic matter yield of the triticale vegetative material.

	Characters					
	NSC yield/ha (kg/ha)			**IVDOM yield/ha (kg/ha)**		
Genotypes	**Cut1**	**Cut2**	**Total**	**Cut1**	**Cut2**	**Total**
1 *x* **2**	-56.0	116.3	60.3	-120.7*	110.9	-9.7
1 *x* **3**	33.3	87.7	121.0	243.7	148.3	391.9
1 *x* **4**	23.5	-54.6	-31.1	-123.2*	-229.0	-352.1*
1 *x* **5**	-62.4	-229.3**	-291.8**	-78.0	-324.4*	-402.4*
1 *x* **6**	61.6	79.9	141.5	78.1	294.2	372.3
2 *x* **3**	-119.9*	-180.5**	-300.4**	-416.9**	-495.7*	-912.6**
2 *x* **4**	46.5	-79.8*	-33.4	293.9	136.5	430.4
2 *x* **5**	23.6	***186.9***	210.5	-88.4	235.7	147.4
2 *x* **6**	105.8	-42.8	63.0	***332.0***	12.5	344.6
3 *x* **4**	-30.7	-55.9	-86.6	-82.0	-113.3	-195.2
3 *x* **5**	***110.5***	112.0	***222.6***	284.1	***355.1***	***639.3***
3 *x* **6**	6.7	36.7	43.5	-29.0	105.6	76.6
4 *x* **5**	31.6	97.3	128.9	87.3	175.8	263.1
4 *x* **6**	-70.9*	93.1	22.2	-176.1*	29.9	-146.2
5 *x* **6**	-103.3*	-166.9**	-270.2**	-205.1*	-442.3*	-647.3**
LSD$_{0.05}$	176.2	247.5	351.7	424.4	633.9	858.4
LSD$_{0.01}$	237.7	333.9	474.5	572.6	855.2	1158.1

The estimates of specific combining ability effects for *ME* yield/ha in Table 5.27 showed the following:

In the case of estimated sca effects for *ME* yield/ha, the F-test and LSD test were in agreement for cut 1 and the total *ME* yield/ha across two cuts in so far as to indicate that significant differences existed. A few significant differences between sca effects for *ME* yield/ha 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 1, the estimated sca effect of 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*2, 1*x*4, 4*x*6 and 5*x*6. In cut 2, the estimated sca effect of 3*x*5 showed significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6. In the case of the total *ME* yield/ha, the estimated sca effect of 3*x*5 showed highly significant differences with the sca effects of 2*x*3 and 5*x*6 and significant differences with the sca effects of 1*x*4 and 1*x*5.

Table 5.27 Estimates of specific combining ability effects for metabolic energy yield of the triticale vegetative material.

	ME yield/ha (MJ/ha)		
Genotypes	**Cut1**	**Cut2**	**Total**
1 *x* **2**	-1798.0*	1650.1	-147.9
1 *x* **3**	3428.8	2470.8	5899.6
1 *x* **4**	-1728.5*	-3478.4	-5206.9*
1 *x* **5**	-1310.5	-4861.7*	-6172.1*
1 *x* **6**	1408.3	4219.2	5627.4
2 *x* **3**	-5987.6**	-7278.7*	-13266.3**
2 *x* **4**	4461.5	1985.0	6446.5
2 *x* **5**	-1269.0	3564.6	2295.5
2 *x* **6**	***4593.2***	79.0	4672.2
3 *x* **4**	-1298.1	-1724.0	-3022.1
3 *x* **5**	4159.0	***5088.5***	***9247.4***
3 *x* **6**	-302.0	1443.4	1141.3
4 *x* **5**	1342.6	2583.8	3926.4
4 *x* **6**	-2777.4*	633.6	-2143.8
5 *x* **6**	-2922.0*	-6375.2*	-9297.2**
LSD$_{0.05}$	6317.8	9198.9	12428.8
LSD$_{0.01}$	8523.5	12410.4	16767.9

5.2.4 GCA/SCA Ratios

5.2.4.1 Results

The ratios of the gca variance to the sca variance for the different plant production characteristics of the triticale vegetative material are presented in Table 5.28.

5.2.4.2 Discussion

Both the estimated gca effects and the sca effects of the same genotype changed once again between cuts when the same characteristic was considered, as was shown in Tables 5.20 to 5.27. When the ratio of $\sigma^2_{\mathbf{gca}}$ to σ^2_{sca} for each characteristic is viewed across cuts, the value obtained also change between the different cuts. Each cut was almost like a different environment for these genotypes as explained in 5.1.4.2.

The ratios for cut 1 were higher than those for cut 2 or the total value across cuts for all the plant production characters considered. All these ratios in cut 1 were higher than 1, indicating that the variance of gca played a bigger role than the variance of sca. These results give an indication that these production characters will show high narrow sense heritabilities when evaluated in cut 1.

Table 5.28 Ratios of the gca variance to the sca variance for the different plant production characteristics of the triticale vegetative material.

Characters	$\sigma^2_{gca}/\sigma^2_{sca}$ **Ratio**
kgDM/ha cut 1	1.431
kgDM/ha cut 2	0.039
kgDM/ha total	0.261
Crude cellulose yield/ha cut 1	3.340
Crude cellulose yield/ha cut 2	0.354
Crude cellulose yield/ha total	0.458
EE yield/ha cut 1	2.141
EE yield/ha cut 2	0.557
EE yield/ha total	0.984
NSC yield/ha cut 1	2.560
NSC yield/ha cut 2	0.232
NSC yield/ha total	0.530
IVDOM yield/ha cut 1	1.297
IVDOM yield/ha cut 2	0.034
IVDOM yield/ha total	0.174
ME yield/ha cut 1	1.369
ME yield/ha cut 2	0.040
ME yield/ha total	0.177

5.3 Animal production characteristics

5.3.1 Combining ability analysis

5.3.1.1 Results

The mean squares for the different animal production characteristics of the triticale vegetative material in the combining ability analyses of variance are presented in Tables 5.29 to 5 34.

5.3.1.2 Discussion

No reference of a genetic study on any forage cereal where the combining ability for the different animal production characteristics of vegetative material was investigate, could be found.

The analyses of variance in Table 5.29 showed the following:

In the combining ability analysis of variance for the predicted *DM intake/steer/day* of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects of the *Cornell* approach in cut 1, but no significant differences were shown in cut 2. Significant differences with regard to the gca effects of the *Pienaar* and *NRC* approaches were shown in cut 2, but no significant differences were shown in cut 1. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. This was the case for the *Pienaar*, *NRC* as well as the *Cornell* approaches. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. This was the case for both the *Pienaar* and *Cornell* approaches. Significant differences between blocks were shown in cut 2 for the *NRC* approach. Based on the results of the F-test, there is no unanimity between the different approaches at which cut to select for increased *DM intake/steer/day* of the vegetative material in the triticale genotypes used in this study.

Table 5.29 Mean squares for the predicted dry matter intake per steer per day of the triticale vegetative material in the combining ability ANOVA's.

		DM Intake (kg/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Blocks	2	0.752	2.759**	0.167	0.118*	1.007	2.437**
gca	5	0.362	0.382*	0.024	0.028*	1.006**	0.137
sca	9	0.421	0.205	0.013	0.007	0.167	0.127
Error	28	0.797	0.112	0.019	0.010	0.193	0.105

The analyses of variance in Table 5.30 showed the following:

In the combining ability analysis of variance for the predicted *ME intake/steer/day* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects of the *Cornell* approach in cut 1, but no significant differences were shown in cut 2. Significant differences with regard to the gca effects of the *Pienaar* and *NRC* approaches were shown in cut 2, but no significant differences were shown in cut 1. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. This was the case for the *Pienaar*, *NRC* as well as the *Cornell* approaches. There were significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. This was the case for both the *Pienaar* and *Cornell* approaches. Significant differences between blocks were shown in cut 1 for the *NRC* approach. Based on the results of the F-test, there is no unanimity between the different approaches at which cut to select for increased *ME intake/steer/day* of the vegetative material in the triticale genotypes used in this study.

Table 5.30 Mean squares for the predicted metabolic energy intake per steer per day of the triticale vegetative material in the combining ability ANOVA's.

		ME Intake (MJ/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Blocks	2	554.122	542.649*	24.545*	26.443	8.794	409.519*
gca	5	91.026	136.199*	3.810	7.781*	115.411*	10.802
sca	9	79.587	52.958	1.350	1.359	27.057	23.497
Error	28	203.533	38.323	2.231	3.030	33.650	25.933

The analyses of variance in Table 5.31 showed the following:

In the combining ability analysis of variance for the predicted *LWG/steer/day* of the triticale vegetative material, the F-test showed significant differences with regard to the gca effects of the *Pienaar* and *NRC* approaches in cut 2, but no significant differences were shown in cut 1. No significant differences with regard to the gca effects of the *Cornell* approach were shown in either of the two cuts. The combining ability analysis of variance showed no significant differences with regard to the sca effects in either of the two cuts. This was the case for the *Pienaar*, *NRC* as well as the *Cornell* approaches. There were significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2 for the *Pienaar* approach. Significant differences between blocks were shown in cut 1 for the *NRC* approach. Based on the results of the F-test, there is no unanimity between the different approaches at which cut to select for increased *LWG/steer/day* of the vegetative material in the triticale genotypes used in this study.

Table 5.31 Mean squares for the predicted live weight gain per steer per day from the triticale vegetative material in the combining ability ANOVA's.

		LWG/steer/day (kg/steer/day)					
		Pienaar		**NRC**		**Cornell**	
	df	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
Blocks	2	0.590	0.433*	0.077*	0.075	0.038	0.312
gca	5	0.079	0.124*	0.012	0.022*	0.066	0.013
sca	9	0.058	0.042	0.004	0.004	0.023	0.019
Error	28	0.153	0.036	0.007	0.008	0.030	0.024

The analyses of variance in Table 5.32 showed the following:

In the combining ability analysis of variance for the predicted *Live weight gain/ha* of the triticale vegetative material, the F-test showed highly significant differences with regard to the gca effects of the *Pienaar, NRC* and *Cornell* approaches in cut 1. The combining ability analysis of variance showed no significant differences with regard to the sca effects in any of the three different animal production approaches. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis in cut 1. This was the case for the *Pienaar*, *NRC* as well as the *Cornell* approaches. Based on the results of the F-test, all three the different approaches showed that selection at cut 1 would be advisable to increase *Live weight gain/ha* of the vegetative material in the triticale genotypes used in this study.

Table 5.32 Mean squares for the predicted live weight gain of steers per ha for cut 1 of the triticale vegetative material in the combining ability ANOVA's.

		Live weight gain/ha (Cut1) (kg/ha)		
	df	Pienaar	NRC	Cornell
Blocks	2	94644.618**	67728.487**	72780.415**
gca	5	17737.201**	14012.750**	13916.116**
sca	9	5335.675	4056.970	4302.717
Error	28	2522.404	1855.272	1953.279

The analyses of variance in Table 5.33 showed the following:

In the combining ability analysis of variance for the predicted *Live weight gain/ha* of the triticale vegetative material, the F-test showed no significant differences with regard to the gca effects of the *Pienaar, NRC* and *Cornell* approaches in cut 2. The combining ability analysis of variance showed no significant differences with regard to the sca effects in any of the three different animal production approaches. There were also no significant differences between blocks according to the F-test of the normal randomised block analysis in cut 2. This was the case for the *Pienaar*, *NRC* as well as the *Cornell* approaches. Based on the results of the F-test, no selection at cut 2 would be advisable in any of the three the different approaches in order to increase *Live weight gain/ha* of the vegetative material in the triticale genotypes used in this study.

Table 5.33 Mean squares for the predicted live weight gain of steers per ha for cut 2 of the triticale vegetative material in the combining ability ANOVA's.

		Live weight gain/ha (Cut2) (kg/ha)		
	df	Pienaar	NRC	Cornell
Blocks	2	20187.111	22442.522	13312.968
gca	5	7850.456	4952.365	4281.868
sca	9	5873.217	5049.442	5116.056
Error	28	4549.901	3498.713	3345.096

The analyses of variance in Table 5.34 showed the following:

In the combining ability analysis of variance for the predicted total *Live weight gain/ha* of the triticale vegetative material, the F-test showed no significant differences with regard to the gca effects of the *Pienaar, NRC* and *Cornell* approaches. The combining ability analysis of variance showed significant differences with regard to the sca effects for every one of the three different animal production approaches. There were highly significant differences between blocks according to the F-test of the normal randomised block analysis for all the three different animal production approaches. Based on the results of the F-test, no selection to increase *Live weight gain/ha* would be advisable when the yields of *Live weight gain/ha* are combined between cut 1 and cut 2.

Table 5.34 Mean squares for the total predicted live weight gain of steers per ha from the triticale vegetative material in the combining ability ANOVA's.

		Total live weight gain/ha (kg/ha)		
	df	**Pienaar**	**NRC**	**Cornell**
Blocks	2	187228.259**	167876.925**	133452.534**
gca	5	10258.326	9831.139	11268.197
sca	9	18762.679*	15503.784*	14817.286*
Error	28	6897.383	5690.506	5462.789

5.3.2 General combining ability

5.3.2.1 Results

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

The estimates of mean general combining ability effects of parents for the different animal production characteristics of the triticale vegetative material are presented in Tables 5.35 to 5.39.

5.3.2.2 Discussion

The estimates of mean general combining ability effects of parents in Table 5.35 showed the following:

In the case of estimated gca effects for *DM intake/steer/day*, the F-test and LSD tests were in agreement for cut 1 of the *Cornell* approach, cut 1 and cut 2 of the *Pienaar* approach and cut 2 of the *NRC* approach in so far as to indicate that significant differences existed. A significant difference between gca effects were shown in cut 1 for the *NRC* approach and in cut 2 for the *Cornell* approach when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 1, no significant differences were shown between the estimated gca effects of the parents for the *Pienaar* approach. The estimated gca effect of parent 3 showed a significant difference with the gca effect of parent 6 for the *NRC* approach. The estimated gca effect of parent 5 showed highly significant differences with the gca effects of parents 2 and 3 for the *Cornell* approach. In cut 2, the estimated gca effect of parent 4 showed significant differences with the gca effects of parents 2, 3 and 6 for the *Pienaar* approach. The estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2 and 6 for the *NRC* approach. The estimated gca effect of parent 6 showed a significant difference with the gca effect of parent 4 for the *Cornell* approach. The good gca effect of parent 1 in cut 2 of the *NRC* approach was in contrast to expectations from the phenotypical performance of parent 1 in cut 2 for this character.

Table 5.35 Estimates of mean general combining ability effects of parents for the predicted dry matter intake per steer per day of the triticale vegetative material.

	DM Intake (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	0.047	0.260	-0.021	***-0.088***	0.172	-0.131
2	-0.447	-0.333*	-0.032	0.086*	-0.754**	0.064
3	0.158	-0.247*	***-0.116***	0.053	-0.314**	0.019
4	-0.148	***0.309***	0.018	-0.074	0.016	-0.288*
5	0.447	0.272	0.038	-0.066	***0.734***	0.096
6	-0.058	-0.261*	0.113*	0.089*	0.145	***0.240***
LSD$_{0.05}$	1.293	0.484	0.200	0.148	0.637	0.469
LSD$_{0.01}$	1.744	0.652	0.270	0.200	0.859	0.632

The estimates of mean general combining ability effects of parents in Table 5.36 showed the following:

In the case of estimated gca effects for *ME intake/steer/day*, the F-test and LSD tests were in agreement for cut 1 and cut 2 of the *Pienaar* and *Cornell* approaches and cut 2 of the *NRC* approach in so far as to indicate that significant differences existed. A significant difference between gca effects were shown in cut 1 for the *NRC* approach when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 1, no significant differences were shown between the estimated gca effects of the parents for the *Pienaar* approach. The estimated gca effect of parent 3 showed a significant difference with the gca effect of parent 6 for the *NRC* approach. The estimated gca effect of parent 5 showed a highly significant difference with the gca effect of parent 2 and a significant difference was shown with the gca effect of parent 6 for the *Cornell* approach. In cut 2, the estimated gca effect of parent 4 showed significant differences with the gca effects of parents 2, 3 and 6 for the *Pienaar* approach. The estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2 and 6 for the *NRC* approach. No significant differences were shown between the estimated gca effects of the parents for the *Cornell* approach in cut 2. The good gca effect of parent 1 in cut 2 of the *NRC* approach was again in contrast to expectations from the phenotypical performance of parent 1 in cut 2 for this character.

Table 5.36 Estimates of mean general combining ability effects of parents for the predicted metabolic energy intake per steer per day of the triticale vegetative material.

	ME Intake (MJ/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	1.461	5.422	0.492	***1.521***	3.146	0.392
2	-4.764	-6.190*	0.569	-1.310*	-8.309**	-1.264
3	6.286	-4.269*	***1.094***	-0.702	-0.578	-0.936
4	-2.504	***5.570***	0.077	0.914	0.003	-1.691
5	4.401	4.889	-0.613	1.251	***7.795***	2.722
6	-4.879	-5.421*	-1.619*	-1.674*	-2.056*	0.778
LSD$_{0.05}$	20.660	8.965	2.163	2.521	8.401	7.375
LSD$_{0.01}$	27.873	12.095	2.918	3.401	11.333	9.949

The estimates of mean general combining ability effects of parents in Table 5.37 showed the following:

In the case of estimated gca effects for *LWG/steer/day*, the F-test and LSD tests were in agreement for cut 1 and cut 2 of the *Pienaar* approach and cut 2 of the *NRC* and *Cornell* approaches in so far as to indicate that significant differences existed. Significant differences between gca effects were shown in cut 1 for the *NRC* and *Cornell* approaches when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 1, no significant differences were shown between the estimated gca effects of the parents for the *Pienaar* approach. The estimated gca effect of parent 3 showed a significant difference with the gca effect of parent 6 for the *NRC* approach. The estimated gca effect of parent 5 showed a highly significant difference with the gca effect of parent 2 and a significant difference was shown with the gca effect of parent 6 for the *Cornell* approach. In cut 2, the estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2, 3 and 6 for the *Pienaar* approach. The estimated gca effect of parent 1 showed significant differences with the gca effects of parents 2 and 6 for the *NRC* approach. No significant differences were shown between the estimated gca effects of the parents for the *Cornell* approach in cut 2. The good gca effects of parent 1 in cut 2 of the *Pienaar* and *NRC* approaches was again in contrast to expectations from the phenotypical performances of parent 1 in cut 2 for these characters.

Table 5.37 Estimates of mean general combining ability effects of parents for the predicted live weight gain per steer per day from the triticale vegetative material.

	LWG/steer/day (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	0.0505	***0.169***	0.025	***0.080***	0.092	0.042
2	-0.094	-0.185*	0.030	-0.070*	-0.181**	-0.063
3	0.209	-0.124*	***0.065***	-0.039	0.037	-0.041
4	-0.067	0.163	0.001	0.051	-0.003	-0.014
5	0.083	0.146	-0.032	0.064	***0.165***	0.092
6	-0.181	-0.170*	-0.088*	-0.086*	-0.110*	-0.016
LSD$_{0.05}$	0.566	0.274	0.123	0.131	0.253	0.223
LSD$_{0.01}$	0.763	0.370	0.166	0.177	0.341	0.301

The estimates of mean general combining ability effects of parents in Table 5.38 showed the following:

In the case of estimated gca effects for predicted *Live weight gain/ha*, the F-test and LSD tests were in agreement for cut 1 in so far as to indicate that significant differences existed for all three approaches. In cut 1, highly significant differences were shown between the estimated gca effect of parent 2 and parents 1, 4, 5 and 6 for the *Pienaar*, *NRC*, as well as *Cornell* approaches. The similarity in patterns of significant differences between the gca effects for the three approaches in cut 2 mirrored the similarity found in the phenotypical performances of parents for these characters.

In the case of estimated gca effects for predicted *Live weight gain/ha*, the F-test and LSD tests were in agreement for cut 2 in so far as to indicate the absence of significant differences between estimated gca effects of parents for the *Cornell* approach. A few significant differences between gca effects were shown in cut 2 for the *Pienaar* and *NRC* approaches when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. In cut 2, significant differences were shown between the estimated gca effect of parent 1 and parents 2 and 6 for the *Pienaar* approach. The estimated gca effect of parent 1 showed a significant difference with the gca effect of parent 2 for the *NRC* approach. No significant differences were shown between the estimated gca effects of the parents for the *Cornell* approach in cut 2. The good gca effects of parent 1 in cut 2 for both the *Pienaar* and *NRC* approaches and was in contrast to expectations, because the estimated gca effects of parent 2 showed highly significant differences with the gca effects of parent 1 in cut 1 for all three approaches.

Table 5.38 Estimates of mean general combining ability effects of parents for the predicted live weight gain of steers per ha for cut 1and cut 2 of the triticale vegetative material.

	Live weight gain/ha (kg/ha)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1	-42.785**	***65.796***	-37.050**	***56.217***	-38.282**	47.147
2	***103.695***	-44.093*	***92.603***	-32.257*	***88.794***	-26.592
3	59.340	-19.104	52.161	-11.259	55.923	-9.794
4	-58.236**	-12.893	-49.094**	-24.901	-55.256**	-30.831
5	-50.408**	43.589	-48.269**	30.269	-42.246**	34.268
6	-11.607**	-33.295*	-10.351**	-18.069	-8.933**	-14.197
LSD$_{0.05}$	72.732	97.682	62.376	85.658	64.003	83.757
LSD$_{0.01}$	98.124	131.785	84.153	115.563	86.347	112.998

The estimates of mean general combining ability effects of parents in Table 5.39 showed the following:

In the case of estimated gca effects for predicted total *Live weight gain/ha* across two cuts, a few significant differences between gca effects were shown for the *Pienaar*, *NRC* and *Cornell* approaches when using the LSD test, although the F-test failed to indicate any significant differences between gca effects. The estimated gca effect of parent 2 showed a significant difference with the gca effect of parent 4 for the *Pienaar, NRC* and *Cornell* approaches. The similarity in patterns of significant differences between the gca effects for the three approaches in this case mirrored the similarity found in the phenotypical performances of parents for these characters.

Table 5.39 Estimates of mean general combining ability effects of parents for the total predicted live weight gain of steers per ha from the triticale vegetative material.

	Total live weight gain/ha (kg/ha)		
Genotypes	**Pienaar**	**NRC**	**Cornell**
1	23.012	19.168	8.865
2	***59.602***	***60.345***	***62.202***
3	40.236	40.902	46.129
4	-71.129*	-73.995*	-86.087**
5	-6.819	-18.000	-7.979
6	-44.903	-28.420	-23.130
$LSD_{0.05}$	120.270	109.242	107.034
$LSD_{0.01}$	162.259	147.381	144.402

5.3.3 Specific combining ability

5.3.3.1 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 α = 0.05 level of confidence or by a ** for a α = 0.01 level of confidence.

The estimates of specific combining ability effects for the different animal production characteristics of the triticale vegetative material are presented in Tables 5.40 to 5.44.

5.3.3.2 Discussion

The estimates of specific combining ability effects for predicted *DM intake/steer/day* in Table 5.40 showed the following:

In the case of estimated sca effects for *DM intake/steer/day*, the F-test and LSD test were in agreement for cut 1 of the *Pienaar* approach and cut 1 and cut 2 of the *NRC* approach in so far as to indicate the absence of any significant differences. A few significant differences between sca effects for *DM intake/steer/day* were shown in cut 2 for the *Pienaar* approach and cut 1 and cut 2 of the *Cornell* approach 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 2*x*3 showed a significant difference with the sca effect of 2*x*4 for the *Cornell* approach. In cut 2, the estimated sca effect of 1*x*4 showed highly significant differences with the sca effects of 1*x*3, 1*x*5, 3*x*4 and 4*x*6 and significant differences with the sca effects of 1*x*2, 2*x*4 and 5*x*6 for the *Pienaar* approach. The estimated sca effect of 2*x*5 showed significant differences with the sca effects of 1*x*5 and 2*x*4 for the *Cornell* approach in cut 2.

Table 5.40 Estimates of specific combining ability effects for the predicted dry matter intake per steer per day of the triticale vegetative material.

	DM Intake (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	0.151	-0.175*	-0.028	0.006	-0.057	0.207
1 *x* **3**	-0.324	-0.354**	-0.029	0.028	-0.426	0.009
1 *x* **4**	0.168	***0.841***	-0.025	-0.128	0.368	0.242
1 *x* **5**	0.323	-0.453**	0.183	0.127	0.186	-0.541*
1 *x* **6**	-0.318	0.141	-0.100	-0.033	-0.072	0.082
2 *x* **3**	0.313	0.049	0.047	0.012	***0.533***	0.313
2 *x* **4**	-0.698	-0.160*	0.004	0.020	-0.723*	-0.541*
2 *x* **5**	-0.333	0.036	0.059	0.011	0.234	**0.337**
2 *x* **6**	0.566	0.250	-0.081	-0.049	0.012	-0.317
3 *x* **4**	-0.093	-0.343**	0.076	0.060	0.083	-0.064
3 *x* **5**	0.816	0.371	-0.154	-0.081	-0.380	-0.184
3 *x* **6**	-0.713	0.277	0.061	-0.020	0.191	-0.075
4 *x* **5**	-0.325	0.188	-0.132	-0.055	0.181	0.220
4 *x* **6**	0.947	-0.525**	0.077	0.104	0.091	0.142
5 *x* **6**	-0.482	-0.142*	0.044	-0.003	-0.222	0.167
LSD$_{0.05}$	2.240	0.838	0.347	0.256	1.103	0.812
LSD$_{0.01}$	3.022	1.130	0.468	0.346	1.488	1.095

The estimates of specific combining ability effects for predicted *ME intake/steer/day* in Table 5.41 showed the following:

In the case of estimated sca effects for *ME intake/steer/day*, the F-test and LSD test were in agreement for cut 1 of the *Pienaar* approach and cut 1 and cut 2 of the *NRC* approach in so far as to indicate the absence of any significant differences. A few significant differences between sca effects for *ME intake/steer/day* were shown in cut 2 for the *Pienaar* approach and cut 1 and cut 2 of the *Cornell* approach 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 4*x*5 showed a significant difference with the sca effect of 2*x*4 for the *Cornell* approach. In cut 2, the estimated sca effect of 1*x*4 showed highly significant differences with the sca effects of 1*x*5 and 4*x*6 and significant differences were shown with the sca effects of 1*x*3, 2*x*4 and 3*x*4 for the *Pienaar* approach. The estimated sca effect of 1*x*4 showed a significant difference with the sca effect of 1*x*5 for the *Cornell* approach in cut 2.

Table 5.41 Estimates of specific combining ability effects for the predicted metabolic energy intake per steer per day of the triticale vegetative material.

	ME Intake (MJ/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	2.65	-2.07	0.10	0.38	-0.17	2.75
1 *x* **3**	-3.45	-4.77*	-0.16	-0.14	-4.63	-0.11
1 *x* **4**	3.00	**13.18**	0.11	1.20	5.06	***4.98***
1 *x* **5**	-2.44	-8.62**	-1.62	-1.99	-3.00	-9.33*
1 *x* **6**	0.25	2.28	1.56	0.54	2.73	1.71
2 *x* **3**	2.17	0.11	-0.51	-1.17	5.13	2.53
2 *x* **4**	-8.46	-2.44*	-0.08	0.08	-8.98*	-6.29
2 *x* **5**	-5.73	0.31	-0.10	0.20	2.02	3.81
2 *x* **6**	9.37	4.09	0.58	0.51	2.00	-2.79
3 *x* **4**	-3.51	-5.42*	-0.59	-0.25	-1.11	-1.59
3 *x* **5**	15.27	6.30	1.40	1.01	-0.55	-0.26
3 *x* **6**	-10.49	3.78	-0.14	0.55	1.16	-0.56
4 *x* **5**	0.51	3.43	1.44	0.67	***6.22***	3.52
4 *x* **6**	8.47	-8.75**	-0.88	-1.70	-1.19	-0.62
5 *x* **6**	-7.60	-1.41	-1.12	0.11	-4.70	2.26
LSD$_{0.05}$	35.78	15.53	3.75	4.37	14.55	12.77
LSD$_{0.01}$	48.28	20.95	5.05	5.89	19.63	17.23

The estimates of specific combining ability effects for predicted *LWG/steer/day* in Table 5.42 showed the following:

In the case of estimated sca effects for *LWG/steer/day*, the F-test and LSD test were in agreement for cut 1 of the *Pienaar* and *Cornell* approaches and cut 1 and cut 2 of the *NRC* approach in so far as to indicate the absence of any significant differences. A few significant differences between sca effects for *LWG/steer/day* were shown in cut 2 for the *Pienaar* and *Cornell* approaches 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 1*x*4 showed significant differences with the sca effects of 1*x*3, 1*x*5, 3*x*4 and 4*x*6 for the *Pienaar* approach. The estimated sca effect of 1*x*4 showed a significant difference with the sca effect of 1*x*5 for the *Cornell* approach in cut 2.

Table 5.42 Estimates of specific combining ability effects for the predicted live weight gain per steer per day from the triticale vegetative material.

	LWG/steer/day (kg/steer/day)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	0.07	-0.05	0.01	0.02	0	0.07
1 *x* **3**	-0.07	-0.12*	0	-0.01	-0.11	-0.01
1 *x* **4**	0.08	***0.36***	0.01	0.07	0.13	***0.16***
1 *x* **5**	-0.15	-0.26*	-0.10	-0.11	-0.15	-0.28*
1 *x* **6**	0.07	0.07	0.08	0.03	0.12	0.06
2 *x* **3**	0.03	-0.01	-0.03	-0.05	0.10	0.04
2 *x* **4**	-0.20	-0.06	0	0	-0.22	-0.15
2 *x* **5**	-0.15	0.01	-0.01	0.01	0.04	0.09
2 *x* **6**	0.26	0.12	0.04	0.03	0.08	-0.05
3 *x* **4**	-0.12	-0.15*	-0.04	-0.02	-0.06	-0.05
3 *x* **5**	0.43	0.18	0.08	0.06	0.05	0.03
3 *x* **6**	-0.27	0.10	-0.02	0.03	0.01	-0.01
4 *x* **5**	0.08	0.10	0.08	0.04	0.21	0.10
4 *x* **6**	0.15	-0.25*	-0.05	-0.09	-0.06	-0.05
5 *x* **6**	-0.21	-0.03	-0.06	0.01	-0.15	0.06
$LSD_{0.05}$	0.980	0.48	0.21	0.23	0.44	0.39
$LSD_{0.01}$	1.322	1.31	0.29	0.31	0.59	0.52

The estimates of specific combining ability effects for predicted *Live weight gain/ha* in Table 5.43 showed the following:

In the case of estimated sca effects for predicted *Live weight gain/ha*, a few significant differences between sca effects were shown in cut 1 and cut 2 for the *Pienaar*, NRC and *Cornell* approaches 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 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*5, 2*x*5, 4*x*6 and 5*x*6 for the *Pienaar* approach. The estimated sca effect of 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 4*x*6 and 5*x*6 for the *NRC* approach. The estimated sca effect of 2*x*6 showed a highly significant difference with the sca effect of 2*x*3 and significant differences with the sca effects of 1*x*5, 4*x*6 and 5*x*6 for the *Cornell* approach. In cut 2, the estimated sca effect of 3*x*5 showed significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6 for the *Pienaar* approach. The estimated sca effect of 3*x*5 showed significant differences with the sca effects of 1*x*5, 2*x*3 and 5*x*6 for the *NRC* approach. The estimated sca effect of 1*x*6 showed a highly significant difference with the sca effect of 1*x*5 and a significant difference with the sca effect of 2*x*3 for the *Cornell* approach in cut 2.

Table 5.43 Estimates of specific combining ability effects for the predicted live weight gain of steers per ha for cut 1and cut 2 of the triticale vegetative material.

	Live weight gain/ha (kg/ha)					
	Pienaar		**NRC**		**Cornell**	
Genotypes	**Cut1**	**Cut2**	**Cut1**	**Cut2**	**Cut1**	**Cut2**
1 *x* **2**	-28.1	17.4	-26.5	25.0	-24.8	35.1
1 *x* **3**	57.5	7.8	51.7	25.6	48.9	20.3
1 *x* **4**	-24.4	-0.8	-24.4	-32.0	-21.4	-7.6
1 *x* **5**	-33.0*	-108.2*	-29.1	-90.9*	-35.6*	-124.6**
1 *x* **6**	28.1	83.8	28.3	72.4	32.9	***76.9***
2 *x* **3**	-102.9**	-92.0*	-91.9**	-98.4*	-95.8**	-74.0*
2 *x* **4**	65.6	22.6	67.0	25.8	56.7	-8.7
2 *x* **5**	-31.0*	42.6	-24.2	44.5	-18.1	57.6
2 *x* **6**	***96.4***	9.4	***75.6***	3.07	***82.1***	-10.0
3 *x* **4**	-27.9	-38.0	-25.7	-29.0	-21.8	-27.6
3 *x* **5**	91.5	***88.3***	73.3	**78.2**	78.2	63.1
3 *x* **6**	-18.1	34.0	-7.4	23.6	-9.5	18.3
4 *x* **5**	32.9	60.3	29.8	51.2	33.8	66.6
4 *x* **6**	-46.1*	-44.2	-46.7*	-16.0	-47.3*	-22.6
5 *x* **6**	-60.3*	-83.0*	-49.8*	-83.1*	-58.2*	-62.6
$LSD_{0.05}$	126.0	169.2	108.0	148.4	110.9	145.1
$LSD_{0.01}$	170.0	228.3	145.8	200.2	149.6	195.7

The estimates of specific combining ability effects for predicted *Live weight gain/ha* in Table 5.44 showed the following:

In the case of estimated sca effects for total *Live weight gain/ha*, the F-test and LSD test were in agreement for the *Pienaar*, *NRC* and *Cornell* approaches in so far as to indicate that significant differences existed. The estimated sca effect of 3*x*5 showed highly significant differences with the sca effect of 1*x*5, 2*x*3 and 5*x*6 and significant differences with the sca effects of 3*x*4 and 4*x*6 for the *Pienaar* approach. The estimated sca effect of 3*x*5 showed highly significant differences with the sca effect of 1*x*5, 2*x*3 and 5*x*6 and significant differences with the sca effects of 1*x*4, 3*x*4 and 4*x*6 for the *NRC* approach. The estimated sca effect of 3*x*5 showed highly significant differences with the sca effect of 1*x*5, 2*x*3 and 5*x*6 and significant differences with the sca effects of 3*x*4 and 4*x*6 for the *Cornell* approach.

Table 5.44 Estimates of specific combining ability effects for the total predicted live weight gain of steers per ha from the triticale vegetative material.

	Total live weight gain/ha (kg/ha)		
Genotypes	**Pienaar**	**NRC**	**Cornell**
1 *x* **2**	-10.7	-1.5	10.3
1 *x* **3**	65.2	77.3	69.2
1 *x* **4**	-25.2	-56.5*	-29.0
1 *x* **5**	-141.2**	-120.1**	-160.3**
1 *x* **6**	111.9	100.7	109.8
2 *x* **3**	-194.9**	-190.3**	-169.8**
2 *x* **4**	88.3	92.8	47.9
2 *x* **5**	11.6	20.3	39.5
2 *x* **6**	105.8	78.7	72.1
3 *x* **4**	-65.9*	-54.7*	-49.4*
3 *x* **5**	***179.8***	***151.5***	***141.2***
3 *x* **6**	15.9	16.2	8.7
4 *x* **5**	93.1	81.1	100.3
4 *x* **6**	-90.3*	-62.7*	-69.9*
5 *x* **6**	-143.3**	-132.8**	-120.8**
LSD$_{0.05}$	208.3	189.2	185.4
LSD$_{0.01}$	281.0	255.3	250.1

5.3.4 GCA/SCA Ratio

5.3.4.1 Results

The ratios of the gca variance to the sca variance for the different animal production characteristics of the triticale vegetative material are presented in Table 5.45.

5.3.4.2 Discussion

Both the estimated gca effects and the sca effects of the same genotype changed once again between cuts when the same characteristic was considered, as was shown in Tables 5.35 to 5.37 and Tables 5.40 to 5.42. When the ratio of $\sigma^2_{\mathbf{gca}}$ to σ^2_{sca} for each characteristic is viewed across cuts, there were not enough values to make conclusions about changes in ratios between cuts.

When the ratios of $\sigma^2_{\mathbf{gca}}$ to σ^2_{sca} for the different predicted animal production per hectare were considered, as were shown in Tables 5.38, 5.39 and Tables 5.43, 5.44, clear differences between cuts emerged. The ratios for predicted *Live weight gain/ha* of all three the different approaches showed a higher value in cut 1 than in cut 2. All three the ratios were close to each other and all three were higher than 1, indicating that the variance of gca played a bigger role than the variance of sca. These results give an indication that these production characters will show high narrow sense heritabilities when evaluated in cut 1.

Table 5.45 **Ratios of the gca variance to the sca variance for the different animal production characteristics of the triticale vegetative material.**

Characters	$\sigma^2_{gca}/\sigma^2_{sca}$ **Ratio**
DM intake/steer/day; *Pienaar* (1)	-
DM intake/steer/day; *Pienaar* (2)	0.726
DM intake/steer/day; *NRC* (1)	-
DM intake/steer/day; *NRC* (2)	-
DM intake/steer/day; *Cornell* (1)	-
DM intake/steer/day; *Cornell* (2)	0.364
ME intake/steer/day; *Pienaar* (1)	-
ME intake/steer/day; *Pienaar* (2)	1.672
ME intake/steer/day; *NRC* (1)	-
ME intake/steer/day; *NRC* (2)	-
ME intake/steer/day; *Cornell* (1)	-
ME intake/steer/day; *Cornell* (2)	-
LWG/steer/day; *Pienaar* (1)	-
LWG/steer/day; *Pienaar* (2)	3.667
LWG/steer/day; *NRC* (1)	-
LWG/steer/day; *NRC* (2)	-
LWG/steer/day; *Cornell* (1)	-
LWG/steer/day; *Cornell* (2)	-
LWG/ha; *Pienaar* (1)	1.352
LWG/ha; *Pienaar* (2)	0.624
LWG/ha; *Pienaar* (T)	0.071
LWG/ha; *NRC* (1)	1.381
LWG/ha; *NRC* (2)	0.234
LWG/ha; *NRC* (T)	0.106
LWG/ha; *Cornell* (1)	1.273
LWG/ha; *Cornell* (2)	0.132
LWG/ha; *Cornell* (T)	0.155

5.4 Conclusion

With the aim of evaluating the combining ability effects to select parents for a triticale with better plant quality as well as plant- and animal production characteristics and to identify possible good hybrid combinations in mind, the following conclusions can be made.

5.4.1 Plant quality characteristics

5.4.1.1 Plant quality characters relevant to the intake model of Cornell

When the gca and sca results for $\%NDF_{adj}$ are compared, the gca effects of parents 1, 5 and 6 were the best for this character in cut 1. As discussed previously in 4.3.3.2, the intake model of *Cornell* will only be the preferred approach in cut 2. In cut 2, the gca effects of parents 1, 2, 3, 5 and 6 were not significantly different from the gca effect of the best parent. It was however already shown in Table 5.2 that selection for lower $\%NDF_{adj}$ will be more effective in cut 1 than in cut 2. Selection for parents with good gca values for low $\%NDF_{adj}$ in cut 1 will therefore only be partially successful to select the correct parents for low $\%NDF_{adj}$ in cut 2. Only the gca effects of parents 1, 5 and 6 were not significantly different from the gca effect of the best parent in both cuts. This was only in partial agreement with the prediction made in 4.4.1.1 when conclusions were made based on phenotypic performances for $\%NDF_{adj}$. If a hybrid triticale is the aim, then the combinations to be considered for this character in cut 2 are 1*x*2, 1*x*4, 2*x*3, 2*x*5 and 4*x*5. The hybrid combinations that were also significantly better than the worst sca in cut 1, were 1*x*4, 2*x*3 and 2*x*5. Preference would therefore be given to these three hybrid combinations when breeding a hybrid triticale for low $\%NDF_{adj}$.

The same parents would be selected for *%NDF* based on the gca effects of the parents across the two cuts. More than the three selected hybrid combinations discussed above would be used if lower *%NDF* was taken as the aim.

5.4.1.2 Plant quality characters relevant to the intake models of Pienaar and NRC

When the gca and sca results for *%IVDOM*, *ME* and *MRT* are compared, it becomes clear that these characters must be selected in cut 2, where possible. The gca effects of parents 1, 4 and 5 emerged as the best for all three these related characters in cut 2. As discussed previously in 4.3.3.2, the intake model of *NRC* will only be the preferred approach in cut 1. The situation is here again that selection is recommended in the cut where the specific intake approach is not the preferred one to use. It would be recommended to look at the phenotypic and additive genetic correlations of these intake approaches with the predicted animal production per hectare to see if it is worthwhile to select for these characters at all. No significant differences between any sca effects for either *%IVDOM* or *ME* in any one of the two cuts means that it would not be possible to select a combination for a possible triticale hybrid with better qualities for these quality characters.

The *%IVDOM* and *MRT* values of the material in this study were never the limiting factors and therefore the *Pienaar* approach was never the preferred intake model in any of the two cuts.

5.4.2 Plant production characteristics

5.4.2.1 DM yield/ha

When the gca results for *DM yield/ha* are compared, more emphasis would normally be placed on the results of cut 1 because this was the only cut where the F-test found significant differences between gca effects. The gca effects of parents 2 and 3 were not significantly different from the gca effect of the best parent for this character in cut 1. Parents 2 and 3 looked therefore to be the obvious choice for a combination to breed for better *DM yield/ha.* When one look at the sca results in the cuts where the F-test showed significant differences between sca effects however, a different picture emerged. The specific combination of parent 2 with parent 3 was the worst combination in cut 1 as well as where the total *DM yield/ha* across two cuts was considered. When the results of significant differences between gca effects as indicated by the LSD test were also brought into consideration, parents 1, 2, 3, 5 and 6 emerged in cut 2 as possible parents to use. Only the gca effects of parents 1, 2, 3 and 6 did not show significant differences with the gca effect of the best parent when the total *DM yield/ha* across two cuts was considered. These four parents would therefore be recommended to be used instead of just parents 2 and 3 as originally identified. When the sca results for total *DM yield/ha* are compared, the combinations to be considered if a hybrid triticale is the aim are 1*x*3, 1*x*6, 2*x*4, 2*x*6 and 3*x*5. The inclusion of combination 2*x*4 was in agreement with the conclusion made in 4.4.2.1, before.

5.4.2.2 DM yield/ha in combination with plant quality characters

When the gca results for *NSC yield/ha, IVDOM yield/ha* as well as *ME yield/ha* are compared, the situation is much the same as in the case of *DM yield/ha.* The same parents would be selected for improvement of all three these characters in each of the two cuts. The gca effects of parents 1, 2, 3, 5 and 6 did not show significant differences with the gca effect of the best parent when the total yield across two cuts was considered. These five parents would therefore be recommended to be used instead of just parents 2 and 3 as identified in cut 1. When the sca results for these three characters are compared, the inclusion of the performance of a combination in cuts where only the LSD test showed significant differences, would also be recommended. If a hybrid triticale is the aim, then the combinations to be considered for total *NSC yield/ha* are 1*x*2, 1*x*3, 1*x*6, 2*x*5, 2*x*6, 3*x*5, and 4*x*5. The combinations to be considered for both total *IVDOM yield/ha* and total *ME yield/ha* are 1*x*3, 1*x*6, 2*x*4, 2*x*5, 2*x*6, 3*x*5, 3*x*6 and 4*x*5. The inclusion of combination 2*x*4 in the case of total *IVDOM yield/ha* and *ME yield/ha* was in agreement with the conclusion made in 4.4.2.2, before.

5.4.3 Animal production characteristics

5.4.3.1 Predicted DM and ME intake per animal

When the gca and sca results for the relevant approach, identified by the comparative discriminating method as described in 4.3.3.2 are compared, the following conclusions can be made:

Parents 1, 2, 3, 4 and 5 looked to be the best for both predicted *DM intake/steer/day* and *ME intake/steer/day* in cut 1 because the gca effects of these parents were never significantly worse than the gca effect of the best parent in each case. Parents 1, 2, 3, 5 and 6 looked to be the best for predicted *DM intake/steer/day* in cut 2. No choice of parents could be made in cut 2 for improvement of *ME intake/steer/day*, because of the lack of any significant differences between gca effects. When viewed across both cuts, parents 1, 2, 3 and 5 would be used in a breeding program for the improvement of these two characters. If a hybrid triticale with improved *DM intake/steer/day* is the aim, then the combinations to be considered for this character are 2*x*3 and 2*x*5. More important, if a hybrid triticale with improved *ME intake/steer/day* is the aim, then the combinations to be considered for this character are 1*x*4, 2*x*5 and 4*x*5. These hybrid combinations performed in cut 2 for the preferred *Cornell* approach significantly better than the worst combination in each case. No selection of a hybrid combination is possible for the preferred *NRC* approach in cut 1, because of the lack of any significant differences between sca effects in this cut.

5.4.3.2 Predicted production per animal

When the gca and sca results for the relevant approach, identified by the comparative discriminating method as described in 4.3.3.2 are compared, the following conclusions can be made:

As in the case of *ME intake/steer/day*, parents 1, 2, 3, 4 and 5 looked to be the best for predicted *LWG/steer/day* in cut 1 because the gca effects of these parents were never significantly worse than the gca effect of the best parent. No choice of parents could be made in cut 2 for improvement of *LWG/steer/day*, because of the lack of any significant differences between gca effects. If a hybrid triticale with improved *LWG/steer/day* is the aim, then the combination to be considered for this character is 1*x*4. This hybrid combination performed in cut 2 for the preferred *Cornell* approach significantly better than the worst combination. No selection of a hybrid combination is possible for the preferred *NRC* approach in cut 1, because of the lack of any significant differences between sca effects in this cut.

5.4.3.3 Predicted animal production per hectare

When the gca results for *Live weight gain/ha* are compared, the situation is much the same as in the case of *NSC yield/ha, IVDOM yield/ha* as well as *ME yield/ha.* The same parents would be selected for improvement of all four these characters when the total yield across two cuts was considered. The gca effects of parents 1, 2, 3, 5 and 6 did not show significant differences with the gca effect of the best parent when the total *Live weight gain/ha* across two cuts was considered. The same five parents would be selected while using any one of the three animal production approaches. The same five parents was selected for total *DM yield/ha*, total *IVDOM yield/ha* as well as total *ME yield/ha*. These five parents would be recommended to be used instead of just parents 2 and 3 as identified in cut 1. If a hybrid triticale is the aim, then the combinations to be considered for improved total *Live weight gain/ha* are 1*x*3, 1*x*6, 2*x*4, 2*x*6, 3*x*5 and 4*x*5. These six combinations were identified by each of the three animal production approaches. These six hybrid combinations can be evaluated more intensively over several environments in order to identify the best hybrid.

The selected hybrid combinations were in close agreement with the combinations 1*x*3, 1*x*6, 2*x*4, 2*x*6 and 3*x*5 that were selected for improvement of total *DM yield/ha* and with the combinations 1*x*3, 1*x*6, 2*x*4, 2*x*5, 2*x*6, 3*x*5, 3*x*6 and 4*x*5 that were selected for improvement of total *IVDOM yield/ha* as well as total *ME yield/ha*. The best one of these characters use for selection purposes instead of total *Live weight gain/ha* will depend on the additive genetic correlation of these characters with the predicted animal production per hectare.

Chapter 6

Heterosis for yield and nutritive quality characteristics in triticale.

6.1 Plant quality characteristics

6.1.1 Relative mid-parent and high-parent heterosis

6.1.1.1 Results

The mean percentages *relative mid-* and *high-parent heterosis* for the different characters measured, were determined between the replications and the 15 F_1 hybrid combinations.

All cases where significant differences occurred between the heterosis values of the 15 F_1 hybrid combinations are indicated by a * for a $\alpha = 0.05$ level of confidence or by a ** for a $\alpha = 0.01$ level of confidence.

The mean percentages *relative mid-parent heterosis* (MPH%) as well as *relative high-parent heterosis* (HPH%) for the different plant quality characteristics of the triticale vegetative material are presented in Table 6.1.

6.1.1.2 Discussion

No reference of a genetic study to investigate the level of heterosis for the different plant quality characteristics of vegetative material on any forage cereal or pasture species, could be found in literature.

When the mean MPH% and HPH% for the different plant quality characteristics amongst the 15 F_1 hybrid combinations in Table 6.1 were compared, the following were found:

With the exception of the mean MPH% for *%ADL* in cut 1 and for *%hemicellulose* in both cuts, all the mean MPH% values were lower than ten percent. Both *%ADL* and *%hemicellulose* are quality characters which aught to be minimized for optimum quality and the positive heterosis for these characters are therefore not desirable.

The mean MPH% for valuable quality characters like *%NSC*, *%IVDOM*, *ME* and *MRT* were negative or less than two percent in both cuts. There were highly significant differences in MPH% between hybrids for *%NSC* in cut 1 and significant differences in MPH% between hybrids for *%NDF*, *%ADL* and $\%NDF_{adj}$ in cut 1 and for *MRT* in cut 2 were shown.

The mean HPH% value for *%ADL* in cut 1 was the only value from all the quality characters which exceeded ten percent positive. Not one plant production character showed a mean HPH% of ten percent positive and more in cut 2. There were highly significant differences in HPH% between hybrids for *%NDF*, $\%NDF_{adj}$ and *%NSC* in cut 1 and significant differences in HPH% between hybrids for *%EE* in cut 1 and for *MRT* in cut 2 were shown. In all the cases where highly significant and significant differences occurred, the mean HPH% values were negative.

Table 6.1 **Mean percentages relative mid- and high-parent heterosis for the different plant quality characteristics of the triticale vegetative material.**

	Mid Parent Heterosis		High Parent Heterosis	
	Cut 1	**Cut 2**	**Cut 1**	**Cut 2**
%NDF	-1.610* ±13.802	6.995 ±17.780	-7.595** ±14.591	3.374 ±19.161
%ADF	7.719 ±33.047	3.615 ±23.696	-0.418 ±30.036	-3.699 ±24.876
%ADL	35.225* ±90.301	7.383 ±72.584	21.521 ±80.606	-5.562 ±63.969
%Hemicell.	15.562 ±26.816	11.719 ±48.243	8.719 ±28.263	5.717 ±40.311
%Crude cellulose	3.651 ±39.125	3.651 ±23.076	-6.500 ±34.442	-4.323 ±23.321
%NDF$_{adj}$	-3.470* ±13.224	-4.337 ±51.369	-9.199** ±13.412	-5.506 ±47.858
%EE	-2.385 ±21.957	-3.034 ±16.851	-12.524* ±21.03	-7.155 ±16.472
%NSC	-0.813** ±20.908	-8.081 ±32.225	-12.952** ±18.93	-15.465 ±27.657
%IVDOM	-1.277 ±8.750	-1.951 ±8.249	-3.592 ±8.494	-4.241 ±8.808
ME	-2.805 ±10.346	-1.794 ±8.313	-5.413 ±9.882	-4.508 ±8.891
MRT	1.584 ±25.825	1.449* ±11.919	-4.561 ±25.744	-2.812* ±11.870

6.2 Plant production characteristics

6.2 1 Relative mid-parent and high-parent heterosis

6.2.1.1 Results

The mean percentages *relative mid-* and *high-parent heterosis* for the different characters measured, were determined between the replications and the 15 F_1 hybrid combinations.

All cases where significant differences occurred between the heterosis values of the 15 F_1 hybrid combinations are indicated by a * for a $\alpha = 0.05$ level of confidence or by a ** for a $\alpha = 0.01$ level of confidence.

The mean percentages *relative mid-parent heterosis* (MPH%) as well as *relative high-parent heterosis* (HPH%) for the different plant production characteristics of the triticale vegetative material are presented in Table 6.2.

6.2.1.2 Discussion

Only one reference of a genetic study to investigate the level of heterosis for the different plant production characteristics of vegetative material on a forage cereal, could be found in literature. Pfeiffer, Sayre & Mergoum (1998) did a genetic study on the heterosis in spring triticale hybrids. The only plant production characteristic studied was *kg DM/ha* at harvesting stage.

When the mean MPH% and HPH% for the different plant production characteristics amongst the 15 F_1 hybrid combinations in Table 6.2 were compared, the following were found:

All the mean MPH% values in cut 1 were higher than thirty percent. All the mean MPH% values in cut 2, with the exception of *NSC* yield/ha were higher than twenty percent. When the mean MPH% values for the various total plant production characters were considered, all were higher than twenty percent. The mean MPH% value of 9.1 percent for total *kg DM/ha* at harvesting stage obtained by Pfeiffer et al. (1998) was lower than the values obtained in this study, but the phenologic stage at which they measured plant production was different from this study.

There were highly significant differences in MPH% between hybrids for *EE* yield/ha and significant differences in MPH% between hybrids for *kg DM/ha*, *crude cellulose* yield/ha, *IVDOM* yield/ha and *ME* yield/ha were shown in cut 1. No significant differences between hybrids were found in cut 2 for any one of the plant production characters. Significant differences between hybrids in the case of the total plant production across two cuts were only shown for total *EE* yield/ha.

The mean HPH% value for *NSC* yield/ha was the only value from all the plant production characters which exceeded ten percent in cut 1. The mean HPH% value for *crude cellulose* yield/ha was the only value from all the plant production characters which exceeded ten percent in cut 2. There were however no significant differences between hybrids for any of these two characters in the relevant cuts where good HPH% values were shown. None of the plant production characters showed mean HPH% values higher than ten percent when the total plant production across both cuts was considered.

There were significant differences in HPH% between hybrids for *crude cellulose* yield/ha and *EE* yield/ha in cut 1 and highly significant differences for *EE* yield/ha in cut 2 and where the total production across both cuts was considered.

Table 6.2 Mean percentages relative mid- and high-parent heterosis for the different plant production characteristics of the triticale vegetative material.

	Mid Parent Heterosis		High Parent Heterosis	
	Cut 1	**Cut 2**	**Cut 1**	**Cut 2**
kg DM/ha	35.169* ±84.859	29.182 ±58.039	7.824 ±85.392	7.980 ±43.973
Cr.cellulose yield/ha	37.501* ±96.035	33.800 ±75.989	4.510* ±83.148	10.446 ±63.436
EE yield/ha	30.890** ±82.548	22.512 ±52.754	0.374* ±73.417	1.435** ±34.933
NSC yield/ha	5.237 ±91.330	18.754 ±69.033	11.783 ±93.671	0.906 ±55.560
IVDOM yield/ha	33.032* ±80.094	26.672 ±58.834	6.575 ±79.885	7.202 ±44.230
ME yield/ha	31.230* ±80.234	27.067 ±59.396	5.180 ±79.877	7.786 ±44.885
	Total		**Total**	
kg DM/ha	30.511 ±56.671		7.979 ±47.847	
Cr.cellulose yield/ha	33.616 ±70.527		8.221 ±57.372	
EE yield/ha	23.832* ±51.535		0.514** ±38.922	
NSC yield/ha	23.278 ±60.812		6.613 ±55.005	
IVDOM yield/ha	27.952 ±55.862		7.275 ±46.188	
ME yield/ha	27.623 ±56.064		7.316 ±46.600	

6.3 Animal production characteristics

6.3.1 Relative mid-parent and high-parent heterosis

6.3.1.1 Results

The mean percentages *relative mid-* and *high-parent heterosis* for the different characters measured, were determined between the replications and the 15 F_1 hybrid combinations.

All cases where significant differences occurred between the heterosis values of the 15 F_1 hybrid combinations are indicated by a * for a $\alpha = 0.05$ level of confidence or by a ** for a $\alpha = 0.01$ level of confidence.

The mean percentages *relative mid-parent heterosis* (MPH%) as well as *relative high-parent heterosis* (HPH%) for the different animal production characteristics of the triticale vegetative material are presented in Table 6.3.

6.3.1.2 Discussion

No reference of a genetic study to investigate the level of heterosis for the different animal production characteristics of vegetative material on any forage cereal or pasture species could be found in literature.

When the mean MPH% and HPH% for the different animal production characteristics amongst the 15 F_1 hybrid combinations in Table 6.3 were compared, the following were found:

The relative heterosis of the animal production characters where the intake or LWG were stated as units per animal followed the values of relative heterosis for the desirable plant quality characters and mostly negative or very low positive values were obtained. The relative heterosis of the animal production characters where the productions were stated as units per hectare followed the values of relative heterosis for the plant production characters and higher positive values were generally obtained. The mean MPH% values of *Live weight gain/ha* (LWG/ha) according to the *Pienaar*, *NRC* as well as the *Cornell* approaches were all higher than twenty five percent in cut 1. Only the mean MPH% values of *Live weight gain/ha* according to the *Pienaar* and *NRC* approaches were higher than twenty percent in cut 2 and where the total production across both cuts was considered.

There were highly significant differences in MPH% between hybrids for *ME intake/steer/day* and *LWG/steer/day* according to the *Cornell* approach and significant differences in MPH% between hybrids for *DM intake/steer/day* according to the *Cornell* approach and *Live weight gain/ha* according to the *Pienaar* and *NRC* approaches in cut 1. Significant differences in MPH% between hybrids were shown for *DM intake/steer/day* and *ME intake/steer/day* according to the *Pienaar* approach in cut 2. No significant differences in MPH% between hybrids were shown for any one of the three approaches where the total animal production across both cuts was considered.

No mean HPH% for any of the animal production characters exceeded a value of even four percent positive in cut 1. The mean HPH% values for *Live weight gain/ha* according to the *Pienaar* and *NRC* approaches were the only values from all the animal production characters which exceeded six percent positive in cut 2. Both had mean HPH% values lower than seven percent however. These two characters were the only two of all the animal production characters which showed positive values for mean HPH% in both cuts. There were however no significant differences between hybrids for any of these two characters in the relevant cuts where positive HPH% values were shown. The mean HPH% values for *Live weight gain/ha* according to the *Pienaar* and *NRC* approaches exceeded five percent when the total animal production across both cuts was considered, but both were lower than six percent positive however.

There were no significant differences in HPH% between hybrids for any of the animal production characters in cut 1. Significant differences in HPH% between hybrids were shown for *DM intake/steer/day* according to the *Pienaar* approach in cut 2 and for *Live weight gain/ha* according to the *Pienaar* and *NRC* approaches where the total production across both cuts was considered.

Table 6.3 Mean percentages relative mid- and high-parent heterosis for the different animal production characteristics of the triticale vegetative material.

	Mid Parent Heterosis		High Parent Heterosis	
	Cut 1	**Cut 2**	**Cut 1**	**Cut 2**
DMI/steer/day Pienaar	1.482 ±28.103	-1.145* ±11.373	-4.392 ±27.007	-5.040* ±11.374
DMI/steer/day NRC	1.681 ±6.102	0.693 ±3.425	0.020 ±6.554	-0.650 ±3.379
DMI/steer/day Cornell	3.961* ±14.231	-5.499 ±13.890	-2.396 ±14.261	-8.766 ±14.390
ME Intake Pienaar	-1.141 ±36.452	-2.745* ±17.981	-8.830 ±33.485	-8.754 ±17.838
ME Intake NRC	-1.296 ±4.684	-1.167 ±5.251	-2.350 ±4.590	-2.663 ±5.579
ME Intake Cornell	0.895** ±14.080	-7.154 ±17.818	-6.436 ±14.730	-11.812 ±17.613
LWG/steer/day Pienaar	-3.067 ±56.362	-6.873 ±41.251	-14.315 ±48.182	-18.287 ±37.667
LWG/steer/day NRC	-4.785 ±17.740	-4.286 ±19.716	-8.772 ±16.595	-9.624 ±19.877
LWG/steer/day Cornell	-0.850** ±25.656	-15.704 ±42.869	-12.273 ±24.871	-25.397 ±39.222
LWG/ha Pienaar	27.316* ±81.606	22.968 ±70.822	1.796 ±76.016	6.443 ±59.998
LWG/ha NRC	26.796* ±79.284	24.365 ±63.393	1.643 ±75.697	6.614 ±50.155
LWG/ha Cornell	28.970 ±81.565	15.209 ±66.395	3.975 ±78.671	-0.752 ±55.879
	Total		**Total**	
LWG/ha Pienaar	24.162 ±56.732		5.424* ±47.026	
LWG/ha NRC	24.680 ±55.229		5.613* ±45.606	
LWG/ha Cornell	16.497 ±51.797		-0.607 ±43.299	

6.4 Conclusion

6.4.1 Plant quality characteristics

Hybridisation will not improve any of the desirable plant quality characters because all of these characters showed negative or very low positive levels of relative MPH% and HPH%. The levels of these plant quality characters must be determined by additive genetic inheritance. The relatively high relative heterosis levels of *%ADL* in cut 1 may be linked to a probable good additive genetic correlation with *kg DM/ha.*

6.4.2 Plant production characteristics

Although the relative MPH% showed promising levels of heterosis, the low levels of relative HPH% do not justify the use of hybrid breeding to improve these characters. Most of these characters with the exception of *EE* yield/ha did not show any significant differences between hybrids in the case of the total plant production across two cuts as already discussed under *6.2.1.2.* The relative HPH% of only 0.514 for the total *EE* yield/ha does not justify hybrid breeding to improve this character in any case.

6.4.3 Animal production characteristics

The conclusion for the animal production characters where the intake or LWG were stated as units per animal is the same as those made for the desirable plant quality characters in *6.4.1.* The conclusion for the animal production characters where the productions were stated as units per hectare is also the same as those made for the plant production characters in *6.4.2.* In both of these cases the low levels of relative HPH% as well as the extra expense and possible problems with hybrid seed production in a harsh climatic environment do not justify the production of hybrids in order to improve the animal production potential from the triticale genotypes used in this study. The very high LSD values for all the means of the heterosis values also make any possible gains in heterosis very uncertain.

Tams, Bauer, Oettler, Melchinger & Schön (2006) came to the conclusion that no distinct heterotic subgroups like in maize existed in available triticale germplasm after studying parental genetical distances with the help of 93 polymorphic simple sequence repeat (SSR) marker loci and 10 amplified fragment length polymorphism

(AFLP) primer-enzyme combinations (PEC). This fact may explain the disappointingly low HPH% values obtained in this study and the conclusions made on the facts.

Chapter 7

Variance components, heritabilities, phenotypic- and additive genetic correlations for yield and nutritive quality characteristics in triticale*.*

7.1 Variance components and heritabilities

7.1.1 Plant quality characteristics

7.1.1.1 Results

The variance components and heritabilities for the different plant quality characteristics of the triticale vegetative material are presented in Table 7.1. Calculated variance components which resulted in negative values were indicated with minus (-) signs.

7.1.1.2 Discussion

No reference of a genetic study to investigate the variance components and heritabilities for different plant quality characteristics of vegetative material from any forage cereal, could be found in literature.

Tan et al. (1978) did a diallel study on smooth bromegrass, while Nguyen et al. (1982) and Annicchiarico & Romani (2005) did diallel studies on tall fescue. The plant quality characters for which heritabilities were determined, were *%NDF*, *%ADF*, *%hemicellulose* as well as *in vitro* dry matter digestibility (IVDMD).

When the variance components and heritabilities for the different plant quality characteristics amongst the 15 F_1 hybrid combinations in Table 7.1 were compared, the following were found:

The additive genetic variance for *%NDF*, *%ADF* and $\%NDF_{adj}$ in cut 1 were relatively more than the respective non-additive genetic variances and environmental variance (σ^2_e) and resulted in relatively higher narrow sense heritabilities for these characters in cut 1 compared to cut 2. The ratios of narrow sense heritabilities to broad sense heritabilities for these characters in cut 1 were high. This corresponded with the higher $\sigma^2_{\mathbf{gca}}/\sigma^2_{sca}$ values obtained for cut 1 relative to cut 2 for these characters in Chapter 5.

The broad sense heritability for *%NDF* in cut 1 of this study was lower than the range found by Nguyen et al. (1982) in tall fescue. However, the broad sense heritability for *NDF* in cut 2 of this study was lower than the lowest value found by Nguyen et al. (1982). The narrow sense heritability for *%NDF* found in cut 1 of this study was similar to the lowest values found by Annicchiarico & Romani (2005) in their diallel study on tall fescue, but lower than the values found by Nguyen et al. (1982). The narrow sense heritability for *%NDF* found in cut 2 of this study was lower than the lowest values found by Nguyen et al. (1982) or Annicchiarico & Romani (2005).

The broad sense heritabilities for *%ADF* found in the two cuts of this study were lower than the values found by Tan et al. (1978) and Nguyen et al. (1982) in smooth bromegrass and tall fescue respectively. The narrow sense heritability for *%ADF* in cut 1 of this study was lower than the values found by Nguyen et al. (1982) and Annicchiarico & Romani (2005) in their diallel studies on tall fescue. The narrow sense heritability for *%ADF* found in cut 2 of this study was lower than the lowest values found by Nguyen et al. (1982) and Annicchiarico & Romani (2005), but higher than the narrow sense heritability found by Tan et al. (1978) for the regrowth of smooth bromegrass.

There was a wide ratio of broad sense heritability to narrow sense heritability for *%ADL* in cut 1, indicating strong non-additive genetic variances. This corresponded with the low $\sigma^2_{\mathbf{gca}}/\sigma^2_{sca}$ value of 0.397 obtained in cut 1 for this character in Chapter 5. The narrow sense heritability for *%ADL* in cut 1 had a low value of 0.175 ±0.060. No estimates for heritability could unfortunately be made for *%ADL* in cut 2 because of a negative value for the calculated additive genetic variance.

Wherever it was possible to compare the heritabilities of the above mentioned plant fibre quality characteristics between cut 1 and cut 2, the heritabilities in cut 1 were always much higher than in the case of the regrowth in cut 2. The *%hemicellulose* in particular showed a very high σ^2_e in relation to the additive genetic variance and non-additive genetic variance values, resulting in a very low narrow sense heritability value of 0.090 ±0.076 in cut 2. In the case of *%hemicellulose* in cut 1, there were negative values for both the calculated additive genetic variance and the non-additive genetic variance and no heritabilities could unfortunately be calculated. The broad sense- as well as narrow sense heritabilities for *%hemicellulose* in cut 2 of this study were both lower than the values found by Nguyen et al. (1982) in their diallel study on tall fescue.

The additive genetic variance for *%EE* in cut 1 was relatively more than the non-additive genetic variance and σ^2_e and this resulted in a moderately high narrow sense heritability for this character in cut 1. The ratio of narrow sense heritability to broad sense heritability for this character in cut 1 was therefore also high. This corresponded with the high $\sigma^2_{gca}/\sigma^2_{sca}$ value obtained in cut 1 for this character in Chapter 5. No estimates for heritability could unfortunately be made for *%EE* in cut 2 because of a negative value for the calculated non-additive genetic variance.

The ratios of narrow sense heritability to broad sense heritability for *%NSC* in both cut 1 and cut 2 were low, indicating strong non-additive genetic variances. This corresponded with the low $\sigma^2_{gca}/\sigma^2_{sca}$ values of 0.146 and 0.208 obtained in cut 1 and cut 2 for this character in Chapter 5. The estimated narrow sense heritabilities for *%NSC* in cut 1 and cut 2 were disappointingly low at 0.100 ±0.068 and 0.056 ±0.066 respectively.

No estimates for heritability could unfortunately be made for *%IVDOM* or *ME* in either cut 1 or cut 2 because of negative values for calculated non-additive genetic variances. In the case of *MRT* in cut 1, there were negative values for both the calculated additive genetic variance and the non-additive genetic variance and no heritabilities could unfortunately be calculated. The additive genetic variance for *MRT* in cut 2 was relatively more than the non-additive genetic variance and σ^2_e and this resulted in a moderate narrow sense heritability of 0.243 ±0.037 for this character. The ratio of narrow sense heritability to broad sense heritability for this character in cut 2 was moderately high**.** This corresponded with the moderately high $\sigma^2_{gca}/\sigma^2_{sca}$

value obtained in cut 2 for this character in Chapter 5. The narrow sense heritability for *MRT* in cut 2 was comparable to the lowest values found by Nguyen et al. (1982) for IVDMD.

Table 7.1 Variance components and heritabilities for plant quality characteristics of triticale vegetative material.

	σ^2_A	σ^2_{D+I}	σ^2_G	σ^2_e	σ^2_P	h^2_b	h^2_n
%NDF(1)	5.392 ±2.341	1.653 ±0.746	7.045 ±2.493	7.560	14.605 ±2.493	0.482 ±0.101	0.369 ±0.108
%NDF(2)	0.821 ±1.655	3.323 ±1.837	4.144 ±2.641	19.611	23.755 ±2.168	0.174 ±0.113	0.035 ±0.063
%ADF(1)	2.788 ±1.568	0.640 ±0.593	3.428 ±1.663	9.186	12.614 ±1.663	0.272 ±0.125	0.221 ±0.099
%ADF(2)	1.469 ±1.097	0.643 ±0.846	2.112 ±1.488	9.912	12.024 ±1.986	0.176 ±0.119	0.122 ±0.078
%ADL(1)	0.371 ±0.139	0.467 ±0.142	0.838 ±0.147	1.287	2.125 ±0.147	0.394 ±0.050	0.175 ±0.06
%ADL(2)	-	0.061 ±0.102	-	1.323	-	-	-
%Hemi-cellulose(1)	-	-	-	15.030	-	-	-
%Hemi-cellulose(2)	3.324 ±3.015	3.754 ±2.138	7.078 ±3.106	30.036	37.114 ±3.106	0.191 ±0.095	0.090 ±0.076
%Crude cellulose(1)	3.148 ±1.633	-	-	8.799	-	-	-
%Crude cellulose(2)	2.195 ±1.087	-	-	8.520	-	-	-
%NDF$_{adj}$(1)	7.123 ±3.478	0.182 ±.589	7.305 ±3.688	9.174	16.479 ±3.688	0.443 ±0.150	0.432 ±0.132
%NDF$_{adj}$(2)	0.580 ±1.791	2.445 ±1.531	3.025 ±2.282	20.247	23.272 ±2.282	0.130 ±0.098	0.025 ±0.061
%EE(1)	0.195 ±0.052	0.024 ±0.011	0.219 ±0.052	0.192	0.411 ±0.052	0.533 ±0.114	0.474 ±0.109
%EE(2)	0.038 ±0.012	-	-	0.111	-	-	-

	σ^2_A	σ^2_{D+I}	σ^2_G	σ^2_e	σ^2_P	h^2_b	h^2_n
%NSC(1)	2.593 ±1.895	8.876 ±2.303	11.469 ±2.449	14.577	26.046 ±2.449	0.440 ±0.084	0.100 ±0.068
%NSC(2)	1.830 ±2.570	4.396 ±2.424	6.226 ±3.376	26.340	32.566 ±3.376	0.191 ±0.095	0.056 ±0.066
%IVDOM(1)	-	-	-	16.101	-	-	-
%IVDOM(2)	5.407 ±0.744	-	-	18.111	-	-	-
ME(1)	0.036 ±0.048	-	-	0.519	-	-	-
ME(2)	0.117 ±0.024	-	-	0.408	-	-	-
MRT(1)	-	-	-	4.353 .	-	-	-
MRT(2)	0.879 ±0.118	0.293 ±0.191	1.172 ±0.177	2.454	3.622 ±0.177	0.324 ±0.040	0.243 ±0.037

7.1.2 Plant production characteristics

7.1.2.1 Results

The variance components and heritabilities for *kg DM/ha* and *IVDOM yield/ha* of the different plant production characteristics of the triticale vegetative material are presented in Table 7.2. This was done because both characters play an important part when correlations with animal production per hectare are considered, as will be shown later in this chapter. These two plant production characters can also be determined without any formulas using assumptions, by means of direct weighing and laboratory analysis as in the case of *IVDOM yield/ha*. Calculated variance components which resulted in negative values were indicated with minus (-) signs.

7.1.2.2 Discussion

No reference of a genetic study to investigate the variance components and heritabilities for different plant production characteristics of vegetative material from any forage cereal, could be found in literature.

Tan et al. (1978), Nguyen et al. (1982) and Annicchiarico & Romani (2005) did diallel studies on smooth bromegrass and tall fescue respectively, but the only plant production character of which heritability estimates was determined, was *kg DM/ha.*

When the variance components and heritabilities for the selected plant production characteristics amongst the 15 F_1 hybrid combinations in Table 7.2 were compared, the following were found:

The additive genetic variances for both *kg DM/ha* and *IVDOM yield/ha* in cut 1 were relatively more than the non-additive genetic variances and σ^2_e and resulted in relatively higher narrow sense heritabilities for these characters in cut 1 compared to cut 2 or where the total productions across both cuts were considered. This corresponded with the higher $\sigma^2_{gca}/\sigma^2_{sca}$ values obtained for cut 1 relative to cut 2 or the total of the two cuts, in Chapter 5. The ratio of narrow sense heritabilities to broad sense heritabilities for these characters in cut 1 were also moderately high, indicating strong additive genetic action in the initial growth up to cut 1. Moderately high estimated narrow sense heritabilities of 0.475 ±0.098 and 0.466 ±0.100 respectively were found in cut 1 for these two plant production characters. The broad sense heritability for *kg DM/ha* in cut 1 of this study was within the range found by Tan et al. (1978) and Nguyen et al. (1982) in smooth bromegrass and tall fescue respectively. The narrow sense heritability for *kg DM/ha* in cut 1 of this study was within the range found by Nguyen et al. (1982), higher than the values found by Tan et al. (1978) on smooth bromegrass and lower than the values found by Annicchiarico & Romani (2005) in their diallel study of tall fescue. The broad sense heritability for *kg DM/ha* in cut 2 of this study was within the range of values found by Nguyen et al. (1982), but lower than the value found by Tan et al. (1978) for the regrowth of smooth bromegrass. The narrow sense heritability for *kg DM/ha* in cut 2 of this study was lower than the lowest values found by Tan et al. (1978), Nguyen et al. (1982) and Annicchiarico & Romani (2005) in their diallel studies on smooth bromegrass and tall fescue. It must be remembered that the studies of Tan et al. (1978), Nguyen et al. (1982) as well as Annicchiarico & Romani (2005) were conducted on different species however and the timing of the cuts was different as well.

The ratio of narrow sense heritabilities to broad sense heritabilities for both of these characters in cut 2 were very low, indicating strong non-additive genetic action in the regrowth from cut 1 to cut 2. Very low estimated narrow sense heritabilities of 0.016 ±0.063 and 0.013 ±0.056 respectively were found in cut 2 for these two plant production characters.

The variance components and heritabilities for the total *kg DM/ha* and total *IVDOM yield/ha* are not considered important for discussion, because it is products of the combination of two cuts.

Table 7.2 Variance components and heritabilities for plant production characteristics of triticale vegetative material.

	σ^2_A	σ^2_{D+I}	σ^2_G	σ^2_e	σ^2_P	h^2_b	h^2_n
kgDM/ha(1)	148163.4	51778.0	199941.4	111875.7	311817.1	0.641	0.475
	±56870.0	±14029.0	±67734.8		±67734.8	±0.09	±0.10
kgDM/ha(2)	5949.8	76786.3	82736.1	279092.1	361828.2	0.229	0.016
	±23237.0	±16894.4	±10648.5		±10648.5	±0.02	±0.06
kgDM/ha(T)	131042.6	250748.3	381790.9	507880.2	889671.1	0.429	0.147
	±80410.1	±51629.2	±87649.3		±87652.6	±0.08	±0.08
IVDOM yield/ha(1)	112675.9	43424.7	156100.6	85902.9	242003.5	0.645	0.466
	±41813.0	±7971.5	±45612.1		±49421.5	±0.08	±0.10
IVDOM yield/ha(2)	3039.3	44581.0	47620.4	191610.9	239231.3	0.199	0.013
	±13123.1	±12573.9	±10666.1		±10666.1	±0.04	±0.06
IVDOM yield/ha(T)	63633.2	182782.9	246416.1	351337.8	597753.9	0.412	0.106
	±49094.7	±35983.1	±52907.9		±52907.9	±0.07	±0.08

7.1.3 Animal production characteristics

7.1.3.1 Results

The variance components and heritabilities for the different animal production characteristics of the triticale vegetative material are presented in Table 7.3.

Calculated variance components which resulted in negative values were indicated with minus (-) signs.

7.1.3.2 Discussion

No reference of a genetic study to investigate the variance components and heritabilities for different animal production characteristics of vegetative material from any forage cereal or pasture species, could be found in literature.

When the variance components and heritabilities for the different animal production characteristics amongst the 15 F_1 hybrid combinations in Table 7.3 were compared, the following were found:

Calculated additive genetic variances and heritabilities of *DM intake/steer/day*, *ME intake/steer/day* and *LWG/steer/day* for the relevant approach, identified by the comparative discriminating method as described in 4.3.3.2 were moderately low to very low.

The heritabilities of *Live weight gain/ha* for the different approaches in cut 1, cut 2 and where the total production across the two cuts are concerned, followed the patterns of heritabilities found for *kg DM/ha* and *IVDOM yield/ha.*

The additive genetic variances for *Live weight gain/ha* according to the different approaches in cut 1 were relatively more than the respective non-additive genetic variances and σ^2_e and resulted in relatively higher narrow sense heritabilities for these characters in cut 1 compared to cut 2 or where the total productions across both cuts were considered. This corresponded with the higher $\sigma^2_{\mathbf{gca}}/\sigma^2_{sca}$ values obtained for cut 1 relative to cut 2 or the total of the two cuts, in Chapter 5. The ratio of narrow sense heritabilities to broad sense heritabilities for *Live weight gain/ha* according the different approaches in cut 1 were also high, indicating strong additive genetic action in the initial growth up to cut 1. Similar moderate estimated narrow sense heritabilities of 0.423 ±0.087, 0.439 ±0.089 and 0.422 ±0.089 respectively were found in cut 1 for the *Pienaar*, *NRC* and *Cornell* approaches.

The ratio of narrow sense heritabilities to broad sense heritabilities for *Live weight gain/ha* according to all three approaches in cut 2 were low, indicating strong non-additive genetic action in the regrowth from cut 1 to cut 2. Very low estimated narrow sense heritabilities of 0.099 ±0.061, 0.053 ±0.050 and 0.038 ±0.044 respectively were found in cut 2 for the *Pienaar*, *NRC* and *Cornell* approaches.

The variance components and heritabilities for the total *Live weight gain/ha* according to the three different approaches are not considered important for discussion, because it is products of the combination of two cuts.

Table 7.3 Variance components and heritabilities for animal production characteristics of triticale vegetative material.

	σ^2_A	σ^2_{D+I}	σ^2_G	σ^2_e	σ^2_P	h^2_b	h^2_n
DMI/steer/day Pienaar(1)	-	-	-	2.391	-	-	-
DMI/steer/day Pienaar(2)	0.135 ±0.014	0.093 ±0.039	0.228 ±0.039	0.336	0.564 ±0.039	0.404 ±0.044	0.239 ±0.031
DMI/steer/day NRC(1)	0.003 ±0.005	-	-	0.057	-	-	-
DMI/steer/day NRC(2)	0.009 ±0.002	-	-	0.030	-	-	-
DMI/steer/day Cornell(1)	0.407 ±0.201	-	-	0.579	-	-	-
DMI/steer/day Cornell(2)	0.016 ±0.025	0.022 ±0.014	0.038 ±0.029	0.315	0.353 ±0.029	0.108 ±0.087	0.045 ±0.068
ME Int./steer/ day P(1)	-	-	-	610.599	-	-	-
ME Int./steer/ day P(2)	48.938 ±5.066	14.635 ±9.942	63.573 ±10.919	114.969	178.542 ±10.919	0.356 ±0.044	0.274 ±0.031
ME Int./steer/ day N(1)	0.790 ±0.732	-	-	6.693	-	-	-
ME Int./steer/ day N(2)	2.376 ±0.648	-	-	9.090	-	-	-
ME Int./steer/ day C(1)	40.881 ±23.819	-	-	100.950	-	-	-
ME Int./steer/ day C(2)	-	-	-	77.799	-	-	-
LWG/steer/ day P(1)	-	-	-	0.459	-	-	-
LWG/steer/ day P(2)	0.044 ±0.005	0.006 ±0.008	0.050 ±0.009	0.108	0.158 ±0.009	0.316 ±0.045	0.278 ±0.032
LWG/steer/ day N(1)	0.003 ±0.002	-	-	0.021	-	-	-
LWG/steer/ day N(2)	0.007 ±0.002	-	-	0.024	-	-	-

	σ^2_{A}	σ^2_{D+I}	σ^2_{G}	σ^2_{e}	σ^2_{P}	h^2_{b}	h^2_{n}
LWG/steer/ day C(1)	0.018 ±0.010	-	-	0.090	-	-	-
LWG/steer/ day C(2)	-	-	-	0.072	-	-	-
LWG/ha Pienaar(1)	7607.40 ±2736.92	2813.27 ±713.69	10420.67 ±3235.94	7567.2	17987.87 ±3235.94	0.579 ±0.08	0.423 ±0.09
LWG/ha Pienaar(2)	1650.28 ±1128.99	1323.32 ±778.86	2973.59 ±1553.56	13649.7	16623.29 ±1554.29	0.179 ±0.09	0.099 ±0.06
LWG/ha Pienaar(T)	1680.47 ±1405.55	11865.30 ±1974.22	13545.77 ±1672.45	20692.1	34237.87 ±1672.45	0.396 ±0.04	0.049 ±0.05
LWG/ha NRC(1)	6078.74 ±2184.18	2201.70 ±501.58	8280.44 ±2578.93	5565.8	13846.24 ±2578.93	0.598 ±0.09	0.439 ±0.09
LWG/ha NRC(2)	726.83 ±818.56	1550.73 ±628.52	2277.56 ±1075.16	11396.1	13673.66 ±1075.15	0.167 ±0.07	0.053 ±0.05
LWG/ha NRC(T)	2070.32 ±1554.97	9813.28 ±1573.31	11883.59 ±1733.93	51214.5	63098.09 ±1733.93	0.188 ±0.05	0.033 ±0.06
LWG/ha Cornell(1)	5981.42 ±2004.85	2349.44 ±527.21	8330.86 ±2356.92	5859.8	14190.66 ±2356.92	0.587 ±0.08	0.422 ±0.09
LWG/ha Cornell(2)	468.39 ±577.25	1770.96 ±901.66	2239.35 ±1324.36	10035.3	12274.65 ±1324.36	0.182 ±0.09	0.038 ±0.04
LWG/ha Cornell(T)	2902.70 ±2151.27	9354.50 ±1645.32	12257.20 ±1527.38	16388.3	28645.50 ±1527.38	0.428 ±0.04	0.101 ±0.08

7.2 Phenotypic- and additive genetic correlations

7.2.1 Results

The phenotypic- and additive genetic correlations between the different plant quality-, plant production- and animal production characteristics of the triticale vegetative material are presented in Tables 7.4 to 7.9. The phenotypic correlation values are typed in Italic type, while the values of the additive genetic correlations are typed in bold type. Significant correlation values are indicated by a * for a $\alpha = 0.05$ level of confidence or by a ** for a $\alpha = 0.01$ level of confidence.

In this study it was refrained from calculating the usual correlations of *%ADF* and *%NDF* with each other and with *kg* DM/ha or IVDMD. This was done because *%ADF* and *%NDF* are interdependent characters. Each one of them is also made up of several components which may vary in relative composition. It was decided therefore to rather use the components *%hemicellulose*, *%crude cellulose* and *%ADL* in the correlations wherever possible. The character $\%NDF_{adj}$ was used in correlations however, because this character is the major determinant in the intake approach of *Cornell.*

7.2.2 Discussion

Of the various applicable diallel studies sourced, the study of Annicchiarico & Romani (2005) was the only one where genetic correlations was calculated. The diallel studies of Tan et al. (1978), Nguyen et al. (1982) and Soh et al. (1984) only listed the phenotypical correlations between the characters studied.

When the phenotypic- and additive genetic correlations between the different plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material in cut 1 and cut 2 were compared in Table 7.4 and Table 7.5 respectively, the following were found:

Significant positive additive genetic correlations were shown between *%crude cellulose* and $\%NDF_{adj}$ and between $\%NDF_{adj}$ and *kg DM/ha* in cut 1. A significant negative additive genetic correlation was shown between *%ADL* and *kg DM/ha* in cut 1. No significant phenotypic correlation between any of the different plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material was found in cut 1.

Table 7.4 Phenotypic- and additive genetic correlations for plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material in cut 1.

Independent variables	**Dependent variables**						
	%ADL	%Cr. cell.	$\%NDF_{adj}$	%EE	%NSC	ME	kgDM/ha
%ADL	-	*-0.064*	*-0.358*	*-0.276*	*-0.020*	*-0.058*	*-0.485*
%Crude cell.	**-0.268**	-	*0.409*	*0.093*	*0.050*	*0.246*	*0.338*
$\%NDF_{adj}$	**-0.539**	**0.884***	-	*0.463*	*-0.337*	*0.355*	*0.682*
%EE	**-0.739**	**0.597**	**0.654**	-	*-0.622*	*0.147*	*0.367*
%NSC	**0.529**	**-0.476**	**-0.671**	**-0.738**	-	*0.328*	*-0.062*
ME	**-0.049**	**0.764**	**0.538**	**0.482**	**-0.047**	-	*0.289*
kgDM/ha	**-0.845***	**0.699**	**0.850***	**0.714**	**-0.521**	**0.384**	-

Highly significant positive additive genetic- as well as phenotypic correlations were shown in cut 2 between *%IVDOM* and *ME* as seen in Table 7.5*.* Highly significant negative additive genetic correlations were shown between *%NSC* and $\%NDF_{adj}$, between *%IVDOM* and *MRT* and between *ME* and *MRT.* Significant negative phenotypic correlations were shown between *%NSC* and $\%NDF_{adj}$ and between *%IVDOM* and *MRT.* The significant phenotypic correlations between *%IVDOM* and *ME* as well as *%IVDOM* and *MRT* were expected, because of known relationships as described by Mann & Dugmore (2004) and Pienaar & Roux (1989a). The fact that these characters also showed highly significant additive genetic correlations is important when selection for better forage quality is the aim.

The additive genetic correlations of -0.671 between *%NSC* and $\%NDF_{adj}$, in cut 1 and -0.947 in cut 2 suggested a consisted negative genetic correlation between these two characters.

The difference in additive genetic correlations of 0.884 between *%crude cellulose* and $\%NDF_{adj}$ in cut 1 and -0.124 in cut 2 suggested that $\%NDF_{adj}$ is not a stable character in the sense that the relative contribution of *%crude cellulose* to $\%NDF_{adj}$ may vary genetically between cut 1 and cut 2.

The very low and non significant phenotypic correlation of *%hemicellulose* with *%IVDOM* in cut 2 of this study was within the range of correlations for hemicellulose with IVDMD found by Nguyen et al. (1982) and Soh et al. (1984) in their diallel studies of tall fescue.

Table 7.5 Phenotypic- and additive genetic correlations for plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material in cut 2.

Independent variables	**Dependent variables**								
	% Hemi.	% Cr.cell.	% NDF$_{adj}$	% EE	% NSC	% IVDOM	ME	MRT	kgDM/ ha
%Hemi-cellulose	-	*-0.485*	*0.790*	*-0.071*	*-0.803*	*0.041*	*-0.001*	*0.093*	*-0.121*
%Crude cellulose	**-0.732**	-	*0.153*	*-0.360*	*0.050*	*-0.114*	*-0.089*	*0.244*	*0.519*
%NDF$_{adj}$	**0.767**	**-0.124**	-	*-0.334*	*-0.875**	*-0.038*	*-0.067*	*0.281*	*0.228*
%EE	**-0.110**	**0.232**	**0.063**	-	*0.008*	*-0.108*	*-0.143*	*-0.105*	*-0.380*
%NSC	**-0.841***	**0.296**	**-0.947****	**-0.097**	-	*0.076*	*0.155*	*-0.179*	*0.009*
%IVDOM	**0.720**	**-0.283**	**0.773**	**-0.064**	**-0.682**	-	*0.985***	*-0.818**	*0.023*
ME	**0.697**	**-0.248**	**0.773**	**-0.052**	**-0.655**	**0.995****	-	*-0.798*	*0.053*
MRT	**-0.716**	**0.309**	**-0.742**	**0.187**	**0.633**	**-0.990****	**-0.990****	-	*0.092*
kg DM/ ha	**-0.700**	**0.571**	**-0.491**	**0.256**	**0.644**	**-0.078**	**-0.052**	**-0.094**	-

When the phenotypic- and additive genetic correlations between the different plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material in cut 1 versus the same character in cut 2 were compared in Table 7.6, the following were found:

The strong but not significant additive genetic correlation for *%EE* between cut1 and cut 2 suggest that selection for a genotype with a high *%EE* in cut 1, may result to have a high *%EE* in cut 2 as well.

No additive genetic correlations exist between cut 1 and cut 2 for the plant quality characteristics *%cellulose*, *%NDF$_{adj}$*, *%NSC* or *ME* or for the plant production character *kg DM/ha.* This indicated that genetic factors apart from plant growth type play a role in the regrowth of the plant material between cut 1 and cut 2 and that selection for any of these characters in cut 1 will have no influence on how the performance for the character will be in cut 2.

Table 7.6 Phenotypic- and additive genetic correlations for plant quality characteristics and kilogram dry matter production per hectare of the triticale vegetative material in cut 1 versus the same character in cut 2.

Independent variables	**Dependent variables**					
	kgDM/ha(2)	%Crude cellulose(2)	% NDF$_{adj}$(2)	% EE(2)	% NSC(2)	ME(2)
kgDM/ha(1)	*0.330* **-0.019**					
%Crude cellulose(1)		*0.404* **-0.005**				
%NDF$_{adj}$(1)			*0.226* **-0.066**			
%EE(1)				*0.372* **0.793**		
%NSC(1)					*0.005* **-0.041**	
ME(1)						*-0.133* **0.065**

When the phenotypic- and additive genetic correlations of plant quality characteristics with animal production characteristics in the same cut, were compared in Table 7.7, the following were found:

Highly significant negative phenotypic correlations were shown in cut 1 between *MRT* and the predicted *DM intake/steer/day* and *LWG/steer/day*, according to the *Pienaar* approach. Highly significant negative additive genetic- as well as phenotypic correlations were shown in cut 2 between *MRT* and the same two characters. A significant- and highly significant positive phenotypic correlation was shown in cut 1 between *%IVDOM* and the predicted *DM intake/steer/day* and *LWG/steer/day*, according to the *Pienaar* approach, respectively. Highly significant positive additive genetic correlations were shown in cut 2 between *%IVDOM* as well as *ME* and the same two characters. A strong- and highly significant positive phenotypic correlation of 0.794 and 0.950 was shown in cut 2 between *%IVDOM* and these two characters respectively. The phenotypic correlation between *ME* and the same two characters followed the same pattern with a strong- and highly significant positive phenotypic correlation of 0.751 and 0.935 that was shown in cut 2 between *ME* and these two characters respectively.

The significant additive genetic correlations of *MRT*, *%IVDOM* and *ME* with predicted *DM intake/steer/day*, according to the *Pienaar* approach in cut 2 were expected, because of a known phenotypic relationship between *MRT* and predicted *DM intake/steer/day*, as described by Pienaar & Roux (1989a) as well as the highly significant additive genetic correlations between *MRT* and *%IVDOM*, *MRT* and *ME*, *%IVDOM* and *ME* that was shown in Table 7.5 for cut 2, and discussed previously.

The significant additive genetic correlations of *MRT*, *%IVDOM* and *ME* with predicted *LWG/steer/day*, according to the *Pienaar* approach in cut 2, were new findings however, and can be used for indirect selection in cases where the analysis of the vegetative material made the *Pienaar* approach the preferred *DM intake* approach to use as discussed in 4.3.3.2.

Highly significant negative phenotypic- and additive genetic correlations were shown in cut 1 and cut 2 between *ME* and the predicted *DM intake/steer/day*, according to the *NRC* approach. A significant- and highly significant negative phenotypic correlation was shown between *%IVDOM* and the predicted *DM intake/steer/day*, according to the *NRC* approach in cut 1 and cut 2, respectively. A highly significant negative- and highly significant positive additive genetic correlation was shown in cut 2 between *%IVDOM*, *MRT* and the predicted *DM intake/steer/day*, according to the *NRC* approach, respectively. Highly significant positive phenotypic- and additive genetic correlations were shown in cut 1 and cut 2 between *ME* and the predicted *LWG/steer/day*, according to the *NRC* approach. A strong positive- and highly significant positive phenotypic correlation of 0.718 and 0.978 was shown between *%IVDOM* and the predicted *LWG/steer/day*, according to the *NRC* approach in cut 1 and cut 2, respectively. A highly significant positive- and highly significant negative additive genetic correlation was shown in cut 2 between *%IVDOM*, *MRT* and the predicted *LWG/steer/day*, according to the *NRC* approach, respectively. A highly significant phenotypic correlation was also shown in cut 2 between *MRT* and the predicted *LWG/steer/day*, according to the *NRC* approach.

The significant additive genetic correlations of *ME* with predicted *DM intake/steer/day*, according to the *NRC* approach in both cut 1 and cut 2, and of *%IVDOM* and *MRT* with the same character in cut 2 were expected, because of a known phenotypic relationship between *ME* and predicted *DM intake/steer/day*, as described by NRC (1996) as well as the highly significant additive genetic correlations between *ME* and *%IVDOM*, *ME* and *MRT*, *%IVDOM* and *MRT* that was shown in Table 7.5 for cut 2, and discussed previously.

The significant additive genetic correlations of *ME*, *%IVDOM* and *MRT* with predicted *LWG/steer/day*, according to the *NRC* approach in cut 2, and of *ME* with the same character in cut 1 were new findings however, and can be used for indirect selection in cases where the analysis of the vegetative material made the *NRC* approach the preferred *DM intake* approach to use as discussed in 4.3.3.2.

Highly significant negative phenotypic- and additive genetic correlations were shown in cut 1 and cut 2 between $\%NDF_{adj}$ and the predicted *DM intake/steer/day*, according to the *Cornell* approach. A moderately strong positive- and highly significant positive additive genetic correlation of 0.677 and 0.937 was shown between *%NSC* and the predicted *DM intake/steer/day*, according to the *Cornell* approach in cut 1 and cut 2, respectively. A significant positive phenotypic correlation was shown in cut 2 between *%NSC* and the same character. A highly significant negative additive genetic correlation was shown in cut 1 between *%crude cellulose* and the predicted *DM intake/steer/day*, according to the *Cornell* approach, but an additive genetic correlation of only 0.077 was shown between these two characters in cut 2. A strong negative additive genetic correlation of -0.766 was shown in cut 1 between $\%NDF_{adj}$ and the predicted *LWG/steer/day*, according to the *Cornell* approach. A strong negative phenotypic correlation of -0.721 was shown in cut 2 between the same two characters. A strong positive additive genetic correlation of 0.752 was shown in cut 1 between *%NSC* and the predicted *LWG/steer/day*, according to the *Cornell* approach, while a moderately strong positive phenotypic correlation of 0.680 was shown in cut 2 between these two characters. Strong positive phenotypic correlations of 0.693 and 0.703 for cut 1 and cut 2 respectively, were shown between *%IVDOM* and the predicted *LWG/steer/day*, according to the *Cornell* approach.

The significant additive genetic correlations of *%NDF*$_{adj}$, with predicted *DM intake/steer/day*, according to the *Cornell* approach in both cut 1 and cut 2 were expected, because of a known phenotypic relationship between *%NDF*$_{adj}$ and predicted *DM intake/steer/day*, as described by Williams et al. (1989). The significant additive genetic correlation between *%NDF*$_{adj}$ and *%crude cellulose* in cut 1 and the highly significant additive genetic correlation between *%NDF*$_{adj}$ and *%NSC* in cut 2 that was shown in Table 7.4 and Table 7.5 for cut 1 and cut 2 respectively, explain the additive genetic correlations found between these two characters and the predicted *DM intake/steer/day*, according to the *Cornell* approach.

The strong positive phenotypic correlations between *%IVDOM* and predicted *LWG/steer/day*, according to the *Cornell* approach in cut 1 and cut 2 respectively, suggested that the plant production character *IVDOM yield/ha* may have a good additive genetic correlation with predicted *Live weight gain/ha*, according to the *Cornell* approach.

Table 7.7 Phenotypic- and additive genetic correlations of plant quality characteristics with animal production characteristics of the triticale vegetative material in the same respective cut.

Independent variables	**Dependent variables**					
	DMI/ steer/day (Pienaar)	DMI/ steer/day (NRC)	DMI/ steer/day (Cornell)	LWG/ steer/day (Pienaar)	LWG/ steer/day (NRC)	LWG/ steer/day (Cornell)
%ADL(1)	*-0.032* **-**	*0.060* **0.099**	*0.400* **0.573**	*-0.053* **-**	*-0.058* **0.011**	*0.299* **0.657**
%ADL(2)	*0.044* **-**	*0.082* **-**	*0.149* **-**	*-0.021* **-**	*-0.096* **-**	*0.047* **-**
%Hemicellulose(1)	*-0.218* **-**	*-0.110* **-**	*-0.595* **-**	*-0.084* **-**	*0.125* **-**	*-0.417* **-**
%Hemicellulose(2)	*-0.061* **0.726**	*-0.015* **-0.704**	*-0.746* **-0.725**	*-0.027* **0.715**	*-0.015* **0.689**	*-0.512* **-**
%Crude cellulose(1)	*-0.061* **-**	*-0.232* **-0.728**	*-0.388* **-0.874***	*0.084* **-**	*0.260* **0.803**	*-0.124* **-0.443**
%Crude cellulose(2)	*-0.250* **-0.304**	*0.055* **0.238**	*-0.201* **0.077**	*-0.173* **-0.268**	*-0.113* **-0.256**	*-0.199* **-**
%NDF$_{adj}$(1)	*-0.285* **-**	*-0.336* **-0.519**	*-0.994*** **-0.999****	*-0.007* **-**	*0.377* **0.559**	*-0.556* **-0.766**
%NDF$_{adj}$(2)	*-0.249* **0.761**	*0.025* **-0.792**	*-0.984*** **-0.986****	*-0.156* **0.779**	*-0.100* **0.753**	*-0.721* **-**
%EE(1)	*-0.190* **-**	*-0.158* **-0.489**	*-0.476* **-0.680**	*-0.044* **-**	*0.133* **0.467**	*-0.287* **-0.438**
%EE(2)	*0.112* **-0.241**	*0.179* **0.094**	*0.340* **-0.158**	*-0.028* **-0.158**	*-0.111* **-0.019**	*0.133* **-**
%NSC(1)	*0.194* **-**	*-0.311* **0.012**	*0.324* **0.677**	*0.297* **-**	*0.341* **-0.093**	*0.588* **0.752**
%NSC(2)	*0.118* **-0.668**	*-0.134* **0.678**	*0.838** **0.937****	*0.139* **-0.673**	*0.169* **-0.633**	*0.680* **-**
%IVDOM(1)	*0.812** **-**	*-0.817** **-**	*-0.001* **-**	*0.947*** **-**	*0.718* **-**	*0.693* **-**
%IVDOM(2)	*0.794* **0.983****	*-0.973*** **-0.996****	*0.093* **-0.672**	*0.950*** **0.997****	*0.978*** **0.991****	*0.703* **-**

Independent variables	Dependent variables					
	DMI/ steer/day (Pienaar)	DMI/ steer/day (NRC)	DMI/ steer/day (Cornell)	LWG/ steer/day (Pienaar)	LWG/ steer/day (NRC)	LWG/ steer/day (Cornell)
ME(1)	*0.406* **-**	*-0.993*** **-0.995****	*-0.384* **-0.540**	*0.795* **-**	*0.989*** **0.993****	*0.575* **0.125**
ME(2)	*0.751* **0.976****	*-0.988*** **-0.998****	*0.113* **-0.677**	*0.935*** **0.992****	*0.993*** **0.999****	*0.729* **-**
MRT(1)	*-0.936*** **-**	*0.651* **-**	*-0.082* **-**	*-0.943*** **-**	*-0.589* **-**	*-0.627* **-**
MRT(2)	*-0.981*** **-0.994****	*0.759* **0.993****	*-0.332* **0.633**	*-0.942*** **-0.997****	*-0.815** **-0.984****	*-0.750* **-**

When the phenotypic- and additive genetic correlations of plant production characteristics with the predicted animal production per hectare in the same respective cut, were compared in Table 7.8, the following were found:

A highly significant positive phenotypic- and additive genetic correlation was shown in cut 1 between *kg DM/ha* and the predicted *Live weight gain/ha*, according to the *NRC* approach which was the preferred *DM intake* approach to use in cut 1 as discussed in 4.3.3.2. A positive phenotypic- and additive genetic correlation of 0.661 and 0.718 respectively, was shown in cut 2 between *kg DM/ha* and the predicted *Live weight gain/ha*, according to the *Cornell* approach which was the preferred *DM intake* approach to use in cut 2 as discussed in 4.3.3.2. These correlation values were taken as the standard against which the correlations of the other plant production characters were measured. Preference was given to a good additive genetic correlation ahead of phenotypic correlation, in the selection of the most appropriate plant production character to use. However, the selected plant production character to use had to have a stronger phenotypic correlation with the predicted *Live weight gain/ha*, according to the preferred *DM intake* approach to use in the relevant cut, than was the case for *kg DM/ha.*

The additive genetic correlations of *crude cellulose yield/ha*, *EE yield/ha* and *NSC yield/ha* with the predicted *Live weight gain/ha* were always lower than the standard set by the correlations of *kg DM/ha* as discussed in the previous paragraph, irrespective of the *DM intake* approach used in the correlations. The additive genetic correlations of these three plant production characteristics with the predicted animal production per hectare in cut 2 were even lower than those of *%IVDOM* with the predicted *Live weight gain/ha* values of all three different *DM intake* approaches in cut 2.

The additive genetic- as well as phenotypic correlations of *ME yield/ha* with the predicted *Live weight gain/ha* were always higher than the standard set by the correlations of *kg DM/ha* as discussed previously, irrespective of the *DM intake* approach used in the correlations. The correlations of *IVDOM yield/ha* with the predicted *Live weight gain/ha* followed those obtained from *ME yield/ha* closely in second place and the additive genetic- as well as phenotypic correlations obtained for the preferred *DM intake* approach in each cut, were always higher than the standard set by the correlations of *kg DM/ha* as discussed previously.

Both *ME yield/ha* and *IVDOM yield/ha* showed the highest additive genetic correlations with the predicted *Live weight gain/ha* in the case of the preferred *DM intake* approach for each respective cut.

Both of these plant production characters showed highly significant positive additive genetic- as well as phenotypic correlations with the predicted *Live weight gain/ha* in cut 1, irrespective of the *DM intake* approach used in the correlations. A highly significant- and significant positive additive genetic correlation, respectively was shown in cut 2 between *ME yield/ha*, *IVDOM yield/ha* and the predicted *Live weight gain/ha*, according to the preferred *Cornell* approach. Strong phenotypic correlations of 0.810 and 0.804 respectively were shown in cut 2 between *ME yield/ha*, *IVDOM yield/ha* and the predicted *Live weight gain/ha*, according to the preferred *Cornell* approach.

Table 7.8 Phenotypic- and additive genetic correlations of plant production characteristics and percentage *in vitro* digestible organic matter with the predicted animal production per hectare of the triticale vegetative material in the same respective cut.

Independent variables	Dependent variables		
	kg LWG/ha (Pienaar)	kg LWG/ha (NRC)	kg LWG/ha (Cornell)
kg DM/ha(1)	*0.943*** **0.989****	*0.960*** **0.990****	*0.952*** **0.985****
kg DM/ha(2)	*0.680* **0.472**	*0.824** **0.663**	*0.661* **0.718**
kg DM/ha(Tot.)	*0.870** **0.790**	*0.925*** **0.883***	*0.872** **0.903***
Crude cellulose yield/ha(1)	*0.909** **0.974****	*0.925*** **0.979****	*0.904** **0.962****
Crude cellulose yield/ha(2)	*0.582* **0.313**	*0.730* **0.504**	*0.578* **0.502**
Crude cellulose yield/ha(Tot.)	*0.769* **0.686**	*0.837** **0.795**	*0.768* **0.764**
EE yield/ha(1)	*0.884** **0.958****	*0.903** **0.961****	*0.887** **0.956****
EE yield/ha(2)	*0.519* **0.383**	*0.625* **0.562**	*0.520* **0.590**
EE yield/ha(Tot.)	*0.752* **0.847***	*0.795* **0.925****	*0.771* **0.900***
NSC yield/ha(1)	*0.920*** **0.967****	*0.928*** **0.960****	*0.941*** **0.972****
NSC yield/ha(2)	*0.597* **0.139**	*0.702* **0.352**	*0.747* **0.456**
NSCyield/ha(Tot.)	*0.806* **0.717**	*0.846** **0.797**	*0.887** **0.872***
%IVDOM(1)	*0.088* **-**	*0.150* **-**	*0.057* **-**
%IVDOM(2)	*0.729* **0.831***	*0.565* **0.682**	*0.662* **0.604**

Independent variables	**Dependent variables**		
	kg LWG/ha (Pienaar)	kg LWG/ha (NRC)	kg LWG/ha (Cornell)
IVDOM yield/ha(1)	*0.969*** **0.991****	*0.979*** **0.991****	*0.974*** **0.988****
IVDOM yield/ha(2)	*0.838** **0.759**	*0.937*** **0.888***	*0.804* **0.915***
IVDOM yield/ha(Tot.)	*0.936*** **0.853***	*0.971*** **0.928****	*0.929*** **0.943****
ME yield/ha(1)	*0.978*** **0.996****	*0.989*** **0.997****	*0.983*** **0.993****
ME yield/ha(2)	*0.837** **0.765**	*0.939*** **0.893***	*0.810* **0.919****
ME yield/ha(Tot.)	*0.938*** **0.883***	*0.975*** **0.951****	*0.932*** **0.960****

When the phenotypic- and additive genetic correlations for plant quality- and plant production characteristics in cut 2, versus plant production characteristics in cut 1 and cut 2 and animal production characteristics in cut 1 were compared in Table 7.9, the following were found:

Significant negative additive genetic correlations were shown between *%IVDOM* in cut 2 and *kg DM/ha* as well as *IVDOM yield/ha* in cut 1. The additive genetic correlations of *ME* in cut 2 with *kg DM/ha* as well as *IVDOM yield/ha* in cut 1, followed the same pattern and significant negative additive genetic correlations were shown as well. Significant positive genetic correlations were shown between *MRT* in cut 2 with *kg DM/ha*, *IVDOM yield/ha*, *ME yield/ha*, the predicted *Live weight gain/ha*, according to the *Pienaar*, *NRC* and *Cornell* approaches in cut 1. This last series of correlations is just as undesirable as the first two series of correlations, because a positive additive genetic correlation with *MRT* means that the *MRT* will get longer, which means slower vegetative material digestion with the result of lower predicted *DM intake* and lower predicted *LWG/steer/day.*

There were practically no additive genetic correlation between *%IVDOM*, *ME*, *MRT* with *kg DM/ha* in cut 2 and correlation values of -0.078, -0.052 and 0.094 respectively were found.

Highly significant positive phenotypic- and additive genetic correlations were shown in cut 2 between *kg DM/ha* and *IVDOM yield/ha* as well as *ME yield/ha.*

Table 7.9 Phenotypic- and additive genetic correlations for plant quality- and plant production characteristics of the triticale vegetative material in cut 2 versus plant production characteristics in cut 1 and cut 2 and animal production characteristics in cut 1.

Independent variables	**Dependent variables**						
	kgDM/ha (1)	kgDM/ha (2)	IVDOM y/ha(1)	ME y/ha(1)	LWG/ha Pien.(1)	LWG/ha NRC(1)	LWG/ha Corn.(1)
% IVDOM(2)	*-0.200* **-0.830***	*0.023* **-0.078**	*-0.206* **-0.833***	*-0.211* **-0.809**	*-0.221* **-0.776**	*-0.219* **-0.778**	*-0.207* **-0.787**
ME(2)	*-0.195* **-0.833***	*0.053* **-0.052**	*-0.204* **-0.834***	*-0.209* **-0.807**	*-0.224* **-0.769**	*-0.221* **-0.768**	*-0.209* **-0.775**
MRT(2)	*0.392* **0.885***	*0.092* **0.094**	*0.410* **0.887***	*0.419* **0.865***	*0.456* **0.833***	*0.442* **0.834***	*0.431* **0.838***
IVDOM y/ha(2)	*0.279* **-0.311**	*0.969*** **0.931****	*0.297* **-0.298**	*0.294* **-0.303**	*0.311* **-0.279**	*0.305* **-0.293**	*0.335* **-0.254**
ME y/ha(2)	*0.278* **-0.313**	*0.969*** **0.929****	*0.295* **-0.250**	*0.292* **-0.302**	*0.308* **-0.275**	*0.302* **-0.290**	*0.332* **-0.250**

7.3 Conclusion

With the aim of evaluating the heredity- and additive genetic correlation values to select characters for selection of a triticale with better plant quality as well as plant- and animal production characteristics, the following conclusions can be made:

The narrow sense heritabilities for *%NDF*$_{adj}$ of the vegetative material in cut 1 and of *MRT* in cut 2, were moderately high to moderate respectively. It will therefore be worthwhile to consider selection for these two plant quality characters directly in the selected, fixed population of genotypes used for this study.

The narrow sense heritabilities for *kg DM/ha* and *IVDOM yield/ha* of the vegetative material in cut 1 were moderalety high. Direct selection for these two plant production characters in the selected, fixed population of genotypes used for this study should have therefore positive results.

The narrow sense heritability for the predicted *Live weight gain/ha*, according to the preferred *NRC* approach of the vegetative material in cut 1 was moderately high. Selection for this predicted animal production character in cut 1 can therefore be considered in the selected, fixed population of genotypes used for this study. There are however highly significant positive additive genetic correlations of *kg DM/ha*, *IVDOM yield/ha* and *ME yield/ha* in cut 1 with the predicted *Live weight gain/ha* in the same cut, according to all three different approaches. Selection can therefore be done on the simplest directly measurable character in cut 1, namely *kg DM/ha* in order to improve the predicted *Live weight gain/ha* in this cut. The combining ability analyses in Chapter 5 showed that significant differences existed amongst the gca effects for *kg DM/ha* and *IVDOM yield/ha* in cut 1. The LSD values also showed that accurate identification of possible parents for a breeding program can be made for these characters in cut 1. The narrow sense heritabilities for these characters in cut 1 were also at acceptable levels for selection purposes as already stated earlier in this conclusion.

Direct selection against the moderately high heritable plant quality character $\%NDF_{adj}$ in cut 1 will have a significant negative consequence for *kg DM/ha* in cut 1 however, while selection for a shorter *MRT* in cut 2, will have significant negative consequences for the desirable characters discussed in the paragraph above, as discussed in 7.2.2.

These significant additive genetic correlations necessitate a careful consideration of selection strategy not to increase the *kg DM/ha* production in cut 1 at the expense of *%IVDOM*, *ME* and *MRT* duration in the regrowth of cut 2.

Recommendations

8.1 Identification of breeding parents

The rank of parent gca effects and parent mean values for dry matter yield, *in vitro* digestible organic matter yield, predicted live weight gain of steers per hectare, percentage *in vitro* digestible organic matter and metabolic energy value of the triticale vegetable material are presented in Table 8.1. These ranks were obtained from the parent mean values in Tables 4.11, 4.12, 4.21, 4.23, 4.38, 4.39 and the parent gca effects in Tables 5.7, 5.8, 5.20, 5.22, 5.38 and 5.39.

When the rank of parent gca effects were studied in Table 8.1, it became clear that it is not necessary to go all the way to predicted *Live weight gain/ha* for the different approaches in order to identify the breeding parents to use in a breeding program to increase the live weight gain of steers per hectare. The same potential parents were identified in cut 1, cut 2 as well as in the total of the two cuts when the top third of parents were selected for *IVDOM yield/ha* and predicted *Live weight gain/ha* for the three different approaches. Parents 2 and 3 were the clear favourites to be used because these two parents showed the best gca effects for both cut 1 as well as the total *IVDOM yield/ha.*

When the sca effects of this specific combination were studied in Tables 5.24, 5.26, 5.27, 5.43 and 5.44, it became clear that the combination of these two parents had the worst sca effects of all combinations for *kg DM/ha*, *IVDOM yield/ha* and *ME yield/ha* in cut 1, cut 2 as well as in the total of the two cuts. The same was the case for the combination of these two parents for *Live weight gain/ha* for all three different approaches in both cut 1 and in the total of the two cuts.

It is therefore recommended to proceed as follows to select parents for a breeding program:

Cut twice at the phenological growth stages as was done in this study.

Select the top third of parents on gca effects for *IVDOM yield/ha* in cut 1 as shown in the top part of Table 8.1, because this character is highly heritable in cut 1 according to Table 7.2 and also highly significantly correlated genetically with *Live weight gain/ha* for all three different approaches in cut 1 as shown in Table 7.8.

Parents 2 and 3 are identified at this stage.

Select the top third of parents for *%IVDOM* in cut 2 as shown in Table 8.1, because the highly correlated character *MRT* (Table 7.5) is moderately heritable in cut 2 as shown in Table 7.1.

Parents 1 and 5 are identified at this stage. The same parents are identified by both *%IVDOM* and *MRT*, but *%IVDOM* is easier and less expensive to determine.

Table 8.1 Rank of parent gca effects and parent mean values for dry matter yield, *in vitro* digestible organic matter yield, predicted live weight gain of steers per hectare, percentage *in vitro* digestible organic matter and metabolic energy value of the triticale vegetative material.

	kg DM/ha			**IVDOM yield/ha**			**Live weight gain/ha**									**% IVDOM**		**ME**	
							Pienaar			**NRC**			**Cornell**						
	C_1	C_2	T	C_1	C_2	T	C_1	C_2	T	C_1	C_2	T	C_1	C_2	T	C_1	C_2	C_1	C_2
Rank of parent gca effects	2	1	2	2	1	2	2	1	2	2	1	2	2	1	2	3	1	3	1
	3	6	3	3	5	3	3	5	3	3	5	3	3	5	3	1	5	2	5
	6	5	6	6	6	6	6	4	1	6	3	1	6	3	1	5	4	1	4
	1	3	1	1	3	1	1	3	5	1	6	5	1	6	5	4	3	4	3
	5	2	5	5	2	5	5	6	6	5	4	6	5	2	6	6	2	5	2
	4	4	4	4	4	4	4	2	4	4	2	4	4	4	4	2	6	6	6
Rank of parent means	2	6	6	2	6	6	2	6	6	2	6	6	2	6	6	3	4	3	4
	1	1	1	6	1	1	6	1	2	6	1	1	6	3	2	5	5	4	5
	6	3	2	1	3	2	1	5	1	1	3	2	3	5	3	6	6	2	6
	3	2	3	3	5	3	3	3	3	3	5	3	1	1	1	2	2	5	3
	5	5	5	5	2	5	5	2	5	5	2	5	5	2	5	4	1	6	2
	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	1	3	1	1

Look then at the performances of the different combinations of 2, 3, 1 and 5 for *IVDOM yield/ha* in cut 1 as shown in Table 5.26 and for *%IVDOM* in cut 2 as shown in Table 5.11. Select the combinations of these four parents which show positive sca effects.

The combinations 3*x*5, 1*x*3 and 1*x*2 are identified with this procedure. It is interesting to note that crosses within groups of parents identified for either *IVDOM yield/ha* in cut 1, or for *%IVDOM* in cut 2, performed poor. It is the cross combinations between parents identified for each character that really show up with good sca effects.

Parents 1, 2, 3 and 5 will therefore be chosen as parents and it is recommended that they are crossed only in combinations 1*x*2, 1*x*3 and 3*x*5. It is recommended that the amount of crossing combinations be limited as suggested, but that as many pollinations in these combinations as possible be done, in order to get as large F_1 populations as possible.

8.2 Selection in early generations

It is recommended to do two cuts at the phenological growth stages as was done in this study, in order to do proper selection in the early generations of the breeding program. The recommended procedure is outlined below:

It is not necessary to go all the way to predicted *Live weight gain/ha* for the different approaches in the selection procedure to increase the live weight gain of steers per hectare. The same phenotype was identified as the best individual in cut 1 when *kg DM/ha* was used instead of predicted *Live weight gain/ha* for the three different approaches, as can be seen in the phenotypic rankings in the bottom half of Table 8.1. The character *kg DM/ha* is simple to determine in a selection program, this character has moderately high heritability in cut 1 according to Table 7.2 and is also genetically highly significantly correlated with *Live weight gain/ha* for all three different approaches in cut 1 as shown in Table 7.8.

It is therefore recommended that *kg DM/ha* be used as the character for selection in cut 1.

Selection for improved *kg DM/ha* in cut 1 will have the following consequences due to additive genetic correlations as shown in Table 7.4: The *%ADL* in cut 1 will decline significantly, while the %NDF_{adj} in cut 1 will increase significantly. With the exception of parent 1 in cut 1 however, %NDF_{adj} was never the limiting factor for predicted *DM intake/steer/day* in cut 1 as discussed in 4.3.3.2 and shown in Table 4.35. The correlated increase in %NDF_{adj} in cut 1 due to selection for improved *kg DM/ha* in cut 1 will have practically no influence on the %NDF_{adj} in cut 2, because of an additive genetic correlation of r = -0.066 as shown in Table 7.6. Selection for improved *kg DM/ha* in cut 1 may also cause a small, but not significant increase in *ME* in cut 1 as shown in Table 7.4, while there will be practically no effect on the *kg DM/ha* in cut 2, due to an additive genetic correlation of r = -0.019 as shown in Table 7.6.

It is recommended that *%IVDOM* be used as the character for selection in cut 2. The plant quality character *MRT* has a moderate narrow sense heritability of 0.243 (Table 7.1), but is difficult and expensive to determine for selection purposes. Although the narrow sense heritability of *%IVDOM* in cut 2 could not be determined due to a negative calculated σ^2_{D+I} value, this character has highly significant additive genetic correlations of r = -0.990 with *MRT* and r = 0.995 with *ME* as shown in Table 7.5. Selecting for higher *%IVDOM* in cut 2 will therefore shorten *MRT* and increase *ME* in cut 2. The character *%IVDOM* is relatively simple to determine, this character is not only genetically highly correlated to both *MRT* and *ME* in cut 2 as discussed already, but is also genetically significantly correlated with *Live weight gain/ha* according to the *Pienaar* approach in cut 2 as shown in Table 7.8. The non significant additive genetic correlations of *%IVDOM* with *Live weight gain/ha* according to the *NRC* and *Cornell* approaches of r = 0.682 and r = 0.604 respectively in cut 2 (Table 7.8), show that selection for improved *%IVDOM* in cut 2, may also have a positive effect on the preferred *Cornell* approach to estimate *Live weight gain/ha.*

Selection for improved *%IVDOM* in cut 2 will have the following additional consequences due to additive genetic correlations as shown in Tables 7.5, 7.6 and 7.9: Selection for improved *%IVDOM* in cut 2 will have practically no effect on the *kg DM/ha* in cut 2, due to an additive genetic correlation of r = -0.078 (Table 7.5). The correspondent increase in *ME* in cut 2 on selection for improved *%IVDOM* will have practically no effect on the *ME* in cut 1, due to an additive genetic correlation of r = 0.065 (Table 7.6). The significant negative additive genetic correlation of -0.830 between improved *%IVDOM* in cut 2 and *kg DM/ha* in cut 1 (Table 7.9), necessitate a two step approach to selection with the two selected characters.

It is therefore recommended to proceed as follows with the selection in early generations in a breeding program:

Select all segregating plants in cut 1 with a *kg DM/ha* yield equal to or better than the yield of the plants of the control cultivar in a spaced plant nursery.

Determine the *%IVDOM* of the regrowth of the selected segregating plants and plants of the control cultivar in cut 2 and apply a threshold value of *%IVDOM* in the selection procedure. It is recommended that the *%IVDOM* of plants of the control cultivar in the spaced plant nursery be used as the threshold value. Select then all the plants with the same or better *%IVDOM* values than the threshold value in cut 2.

The end result of this selection is to select plants with better *kg DM/ha* yield, but the same *%IVDOM*, or alternatively with the same *kg DM/ha* yield, but improved *%IVDOM* compared to those of the control cultivar which want to be improved upon.

8.3 Final evaluation in order to select a new cultivar for registration

The recommended procedure to do a proper evaluation in order to select a new cultivar for registration is outlined below:

Plant the seed of selected lines as well as those of the control cultivar in plots at recommended planting rates for the area. Ensure to have at least three replications in each trial site.

Include as many locations as logistically possible to include the effects of genotype *x* environment interactions on *kg DM/ha* yield.

Do two cuts at the phenological growth stages as was done in this study at each location.

Measure the *kg DM/ha* yield and determine the *%IVDOM* of each plot in each cut at each location.

Calculate then the *IVDOM yield/ha* for cut 1 and cut 2 and summarise it to get the total *IVDOM yield/ha* of each plot at each location.

Calculate the means, C.V. and $LSD_{0.05}$ values for the total *IVDOM yield/ha* of each line as well as those of the control cultivar at each location. It is the simplest way to select at this stage on total *IVDOM yield/ha* because it can be determined directly and relatively cheaply. Although there are highly significant phenotypic correlations between total *IVDOM yield/ha* and total *Live weight gain/ha* according to all three different approaches (Table 7.8), the rank of the phenotypes for total *IVDOM yield/ha* is not exactly the same as for the three approaches as shown in Table 8.1. The same intake approach is also not necessarily the preferred approach in each cut as discussed previously in 4.3.3.2 and the phenotypic rankings of the total *Live weight gain/ha* according to each of the three different approaches could therefore contain some bias. When the comparative discriminating method as discussed in 4.3.3.2 is proved as valid by further research in animal nutrition, then it is suggested that total *IVDOM yield/ha* be used as an initial screening method to eliminate the lower half of the lines at each locality.

The comparative discriminating method would then be used for the remaining few lines as well as the control cultivar to determine the preferred intake method most suitable for each plot in each cut at each location. The predicted *Live weight gain/ha* according to the preferred intake approach for each cut would then be summarised per plot and the results given as predicted total *Live weight gain/ha* for each plot. The means, C.V. and $LSD_{0.05}$ values for the predicted total *Live weight gain/ha* of each line as well as those of the control cultivar at each location would then be calculated, and the results used to identify the line in the remaining group which performs most consistently better than the control cultivar across localities.

Summary / Opsomming

The objective of this study was to study the combining ability, heritability and additive genetic correlation of various nutritive quality, forage yield and animal production characteristics in a selected fixed population of triticale genotypes.

The vegetative matter obtained from two sequential cuts per plot was used for chemical analyses and the calculation of plant production and animal production. The trial was a split-plot in time experiment planted in a randomised block design. Three replications were planted and the plots were made up of three rows each.

Characters measured for forage quality in both cuts were *NDF*, *ADF*, *ADL*, *hemicellulose*, *crude cellulose*, NDF_{adj}, *EE*, *NSC*, *IVDOM*, *ME* and *MRT.* Characters used for plant production were *kg DM/ha*, *crude cellulose yield/ha*, *EE yield/ha*, *NSC yield/ha*, *IVDOM yield/ha* and *ME yield/ha.* Characters used for animal production were *DM Intake/steer/day*, *ME Intake/steer/day*, *LWG/steer/day* and *Live weight gain/ha*. Each one of the animal production characters were calculated according to three different feed intake models.

Significant differences were shown in cut 1 between genotypes for *NSC*, *EE and* all fibre characters except *hemicellulose* and *crude cellulose*. Significant differences were shown in cut 2 for *NSC*, *ME* and *MRT.* Significant differences were shown in both cuts for all the plant production characters. Highly significant differences were shown in cut 1 for *Live weight gain/ha* according to all three different intake models.

The F_1 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 (1956*b*), because only one reading per plot was obtainable for each of the characteristics measured.

In the combining ability analyses of the F_1 progeny, significant differences were shown in cut 1 for gca effects of *EE* and all fibre characters except *hemicellulose*. Significant differences were shown in cut 2 for *EE*, *IVDOM*, *ME* and *MRT.* Significant differences were only shown in cut 1 for all the plant production characters. Highly significant differences were shown in cut 1 for *Live weight gain/ha* according to all three different intake models.

The levels of relative high parent heterosis did not warrant the forming of hybrids in an effort to increase *Live weight gain/ha.*

The $\sigma^2_{\mathbf{gca}}/\sigma^2_{sca}$ and h^2_n were moderately high for NDF_{adj}, *kg DM/ha* and *Live weight gain/ha* in cut 1 and moderate for *MRT* in cut 2. Highly significant additive correlations were found between *IVDOM yield/ha* and *Live weight gain/ha* according to all three different intake models in cut 1. A significant negative additive genetic correlation was found between *kg DM/ha* in cut 1 and *IVDOM* in cut 2.

Recommendations were given for the identification of breeding parents, selection in the early generations as well as the final evaluation in order to select a new cultivar for registration.

Key words: triticale, diallel, fixed, nutritive quality, animal production, combining, heritability, correlation.

Die doel van hierdie studie was om die kombineervermoë, oorerflikhede en additiewe genetiese korrelasie van verskeie voedingswaarde-, voeropbrengs- en diereproduksie eienskappe in ‘n geselekteerde korog populasie te bepaal.

Die plantmateriaal verkry vanaf twee opeenvolgende snysels per perseel is gebruik vir die chemise ontledings en die daaropvolgende berekenings van plantproduksie- en diereproduksie eienskappe. Die proef was ‘n verdeelde perseel-in-tyd eksperiment wat geplant is volgens ‘n ewekansige blokontwerp. Drie herhalings is gebruik en elke perseel het uit drie rye bestaan.

Voedingswaarde eienskappe wat in albei snysels bepaal is, was ‘*NDF*’, ‘*ADF*’, ‘*ADL*’, hemi-sellulose, ru-sellulose, ‘NDF_{adj}’, ‘*EE*’, ‘*NSC*’, ‘*IVDOM*’, ‘*ME*’ en ‘*MRT*’. Eienskappe wat vir plantproduksie gebruik is, was *kg DM/ha*, ru-sellulose opbrengs/ha, ‘*EE*’ opbrengs/ha, ‘*NSC*’ opbrengs/ha, ‘*IVDOM*’ opbrengs/ha en ‘*ME*’ opbrengs/ha. Eienskappe wat vir diereproduksie gebruik is, was *DM* inname/dier/dag, ‘*ME*’ inname/dier/dag, lewende massatoename/dier/dag en lewende massatoename/ha. Elkeen van die diereproduksie eienskappe is volgens drie verskillende voedingsinname modelle bereken.

Daar was betekenisvolle verskille tussen genotipes by snysel 1 vir '*NSC*', '*EE*' en al die veseleienskappe behalwe hemi-sellulose en ru-sellulose. Daar was ook betekenisvolle verskille by snysel 2 vir '*NSC*', '*ME*' en '*MRT*'*.* Betekenisvolle verskille het in beide snysels voorgekom vir al die plantproduksie eienskappe. Daar is hoogs betekenisvolle verskille tussen genotipes by snysel 1 getoon vir lewende massatoename/ha volgens al drie inname modelle.

Die F_1 nageslag van 'n 6 x 6 halfdialleel kruising is d.m.v. *Metode 4, gemengde model B* van Griffing (1956*b*) vir kombineervermoë ontleed, omdat daar slegs een waarde per perseel vir elke eienskap beskikbaar was.

By die ontleding van kombineervermoë vir voedingswaarde eienskappe in die F_1 nageslag, is betekenisvolle verskille t.o.v. algemene kombineervermoë effekte vir '*EE*' en al die veseleienskappe behalwe hemi-sellulose en ru-sellulose by snysel 1 getoon. Betekenisvolle verskille is vir '*EE*', '*IVDOM*', '*ME*' en '*MRT*' by snysel 2 getoon. Betekenisvolle verskille het slegs by snysel 1 vir al die plantproduksie eienskappe voorgekom. Hoogs betekenisvolle verskille is in die geval van snysel 1 getoon vir lewende massatoename/ha volgens al drie inname modelle.

Die waardes wat verkry is vir heterose volgens die beter ouer ontledingsmetode was nie goed genoeg om die vorming van basters te regverdig om sodoende lewende massatoename/ha te probeer verhoog nie.

Die verhouding tussen die variansie van die algemene kombineervermoë tot die variansie van die spesifieke kombineervermoë asook 'h^2_n' was matig hoog vir 'NDF_{adj}', *kg DM/ha* en lewende massatoename/ha by snysel 1 en matig vir '*MRT*' by snysel 2. Hoogs betekenisvolle additiewe genetiese korrelasies is getoon tussen '*IVDOM*' opbrengs/ha en lewende massatoename/ha volgens al drie inname modelle in die geval van snysel 1 Daar was 'n betekenisvol negatiewe additiewe genetiese korrelasie tussen *kg DM/ha* by snysel 1 en '*IVDOM*' by snysel 2.

Aanbevelings is gegee vir die identifikasie van teelouers, die seleksieproses in vroeë generasies asook die finale evaluering om 'n nuwe kultivar te selekteer vir registrasie.

Sleutelwoorde: triticale, dialleel, vaste, voedingswaarde, diereproduksie, kombineervermoë, oorerflikheid, korrelasie.

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