Effect of Genotype and ploidy levels on the digestibility and fibre fractions of perennial ryegrass (Lolium perenne L.)

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Introduction

In temperate environments, perennial ryegrass is the most widely used species in grassland because of its high palatability, digestibility and persistence. For a more sophisticated evaluation of forage quality, parameters should be considered, which allow a better assessment of the carbohydrate degradation processes in the rumen. The main target of the current project is to screen systematically a set of perennial ryegrass genotypes in terms of its yielding potential, as well as a process-oriented assessment of their carbohydrate contents in order to quantify the impact of genotype and ploidy level. In this paper, results of the first growing season regarding fiber fractions, digestible organic matter (DOM), and metabolizable energy (ME) content are presented and discussed.

Materials and methods

Two field trials were conducted at three sites in northern Germany during the growing season of 2006. In the first trial, 20 diploid intermediate heading genotypes were screened in a Randomized Complete Block Design with three replicates in a 4-cut system. A Lattice Design was used in the second trial to evaluate 25 genotypes under two cutting regimes A and B. These 25 genotypes (20 *Lolium perenne*, 3 *L. multiflorum*, and 2 *Festuca pratense*) belonged to 9 ploidy families, each consisting of one diploid (2n) genotype and the tetraploid (4n) near isogenic line(s) derived from it. The *L. multiflorum* and *F. pratense* genotypes were mainly used for the purpose of comparison. Cutting regime A was applied at ear emergence of the earliest genotype, with a cutting interval of 5 weeks. Cutting regime B began 2 weeks later than regime A with an interval of 6-7 weeks. Forage quality was estimated by NIRS, based on the following wet chemical analysis: Neutral Detergent Fiber (NDF) and Acid Detergent Fiber (ADF) using the semiautomatic ANKOM apparatus (Van Soest *et al*., 1991). DOM (g kg^{-1} DM) and ME (MJ kg^{-1} DM) were calculated according to Weißbach *et al*. (1999) based on the cellulase method (De Boever et al., 1988). Data were statistically analyzed using the mixed procedure of SAS, with the least significant difference procedure for mean comparison, and probabilities being adjusted by Tukey test (main effects) and Bonferroni-Holm test (interactions).

Results and Discussion

Trial 1: NDF, ADF, ME values varied significantly among the 20 tested genotypes and also among the 3 sites in both the 1st cut and the annual average. The DOM showed significant variations among the 20 genotypes in the 1st cut, the annual average and among the 3 sites only in the 1st cut. A significant difference of about 63 and 44 g NDF kg^{-1} DM was obtained between the highest and lowest values from the 1st cut and annual average, respectively. Similarly, a difference of 51 and 38 g ADF kg^{-1} DM, 68 and 33 g DOM kg^{-1} DM, 0.98 and 0.58 MJ ME kg^{-1} were achieved from the 1st cut and the annual average, respectively.

Trial 2: Analysis of variance (Table 1) revealed significant main effects of the sites, genotypes and cutting regimes on the studied quality parameters in the 1st cut, while the 3-way interaction didn't show any significant effect. However, the 3-way interaction exerted a significant influence on all the four quality parameters in the annual average.

Table 1: Analysis of variance for 1st cut and annual averages (A.A.) for NDF, ADF, DOM and ME for the genotypes in the three sites under the two cutting regimes.

Effect	D.F	Pr>F							
		NDF		ADF		DOM		ME	
		1st cut	A.A.	1st cut	A.A.	1st cut	A.A.	1st cut	A.A.
Site (S)	2	0.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001
Cutting Regime (R)	1	0.9324	<.0001	0.0321	0.0150	0.0018	<.0001	<.0001	<.0001
S*R	2	0.0847	<.0001	0.2446	0.0002	0.0132	<.0001	0.0004	<.0001
Genotype (G)	24	0.0001	<.0001	<.0001	<.0001	<.0001	<.0001	<.0001	0.0002
S*G	48	0.0023*	0.0016	<.0001	<.0001	<.0001	0.0053	0.2153	0.0106
R*G	24	0.1130	<.0001	0.0508	<.0001	0.1965	0.0002	0.7208	<.0001
S*R*G	48	0.3265	0.0007	0.5035	0.021	0.5142	<.0001	0.9972	0.0001

* non significant after applying Bonferroni-Holm test

Since the main target of trial 2 is to highlight the impact of ploidy level, only the significant interactions including genotypes will be clarified and discussed. Figure 1 points out the significant differences between 2n and 4n in the 1st cut. The 2n genotypes in families A, E and I gave significantly higher values than their 4n derivatives with regard to NDF and ADF. The situation was totally reversed in case of DOM, where the 4n of the families A, E and F showed higher values than the 2n of the same families. The trend was not clear in the amount of ME produced, the 4n of family D were better than the 2n of the same family, while the 2n of family H produced higher amount of ME than the 4n. Concerning the annual average, the significant influence of the 3-way interaction was clear only in few ploidy families. In NDF the 2n genotypes of families E, F and I were higher than their 4n derivatives. The same trend was observed in family I for the ADF (Fig.2.a). For DOM, a significant interaction was observed only in two ploidy families, where in family A the highest values were in favour of the 4n genotype; on the contrary, in family F the 2n genotype showed higher DOM (Fig.2.b). In families E and F the 2n genotypes gave higher values than the 4n ones in the amount of ME produced, while the situation was reversed in the Family A (Fig.2.c).

Several studies reported a slight superiority of the 4n genotypes when compared to the 2n genotypes with respect to the DOM and the different quality aspects (Gilliland *et al*., 2002; Boller, 1999). In contrast, Nekrosas (2002) observed no significant differences between both 4n and 2n genotypes. However, the unclear trend of 2n and 4n observed in this study may be attributed to the genetic makeup of the near isogenic lines incorporated in the study, as the effect of ploidy on quality parameters is dependent on the genetic background of the genotypes (Smith *et al.,* 2001).

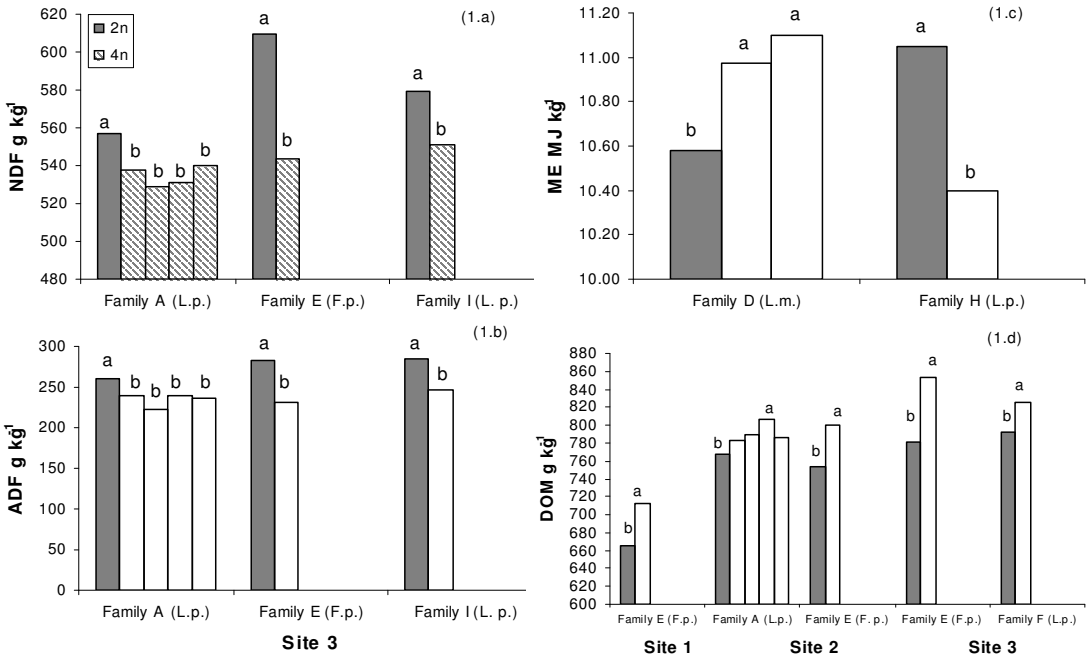

Fig.1: Differences in 1st cut NDF g kg^{-1} DM (1.a), ME MJ kg $^{-1}$ (1.b), ADF g kg^{-1} DM (1.c) and DOM g kg^{-1} DM (1.d) between diploids and tetraploids within the same ploidy family.

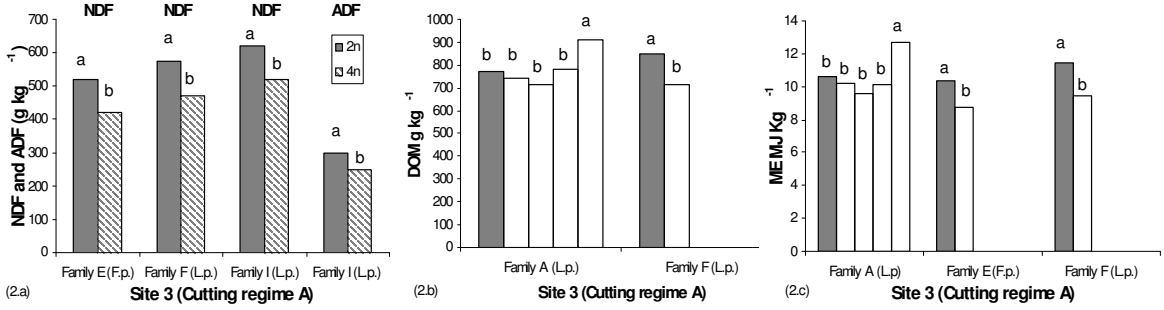

Fig 2: Differences in annual NDF, ADF g kg^{-1} DM (2.a), DOM g kg^{-1} DM (2.b) and ME MJ kg $^{-1}$ (2.c) between diploids and tetraploids within the same ploidy family as affected by the three way interaction.

Conclusion

Results obtained from this investigation indicated relevant differences in the tested quality parameters within the intermediate heading genotypes. With respect to ploidy level, an unclear trend of superiority is observed between the 2n and 4n genotypes, which maybe attributed to the genetic makeup of the near isogenic lines. This does not allow to draw any final conclusion. More attention should be paid to the genetic constitution of the genotypes under comparison. Work will be completed by investigating further quality parameters, and the same will be done for the second experimental year.

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