Yielding potential of perennial ryegrass (*Lolium perenne* L.) in a current variety selection- Effect of genotype and ploidy level

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Introduction

The proceeding liberalization of trade, the eastward extension of the European Union, as well as the EU Agricultural Policy reform lead to an increasing pricing pressure on the dairy production. Additional pressure on soil rental rates results from intensive biogas production in several regions. Consequently, the reduction of the fodder costs through increasing the yielding potential is nowadays an important target for forage grass breeding. A significant genotypic variation in yielding potential of perennial ryegrass is documented (e.g. SMIT et al., 2005). However, the evaluation of this variation is hampered by genotype-environment interaction, or heading variation within maturity groups (WILKINS and HUMPHREYS, 2003). The ploidy effect on the yielding performance and forage quality is until now unambiguously defined, in spite of all the deducted studies (KUTOVA et al., 1998; GILLILAND et al., 2002; JAFARI et al., 2003). Therefore, the main objective of the current project is a systematic screening of perennial ryegrass genotypes in terms of its yielding potential, as well as a process-oriented assessment of the protein and carbohydrates quality. In this paper the results of the first growing season regarding the yielding potential will be presented.

Materials and Methods

Two field experiments were conducted at three different experimental sites in northern Germany during the 2006 growing season. Twenty *Lolium perenne* L. genotypes belonging to the intermediate heading group were tested in a Randomized Complete Block Design with three replicates in the first experiment. Swards were cut at the early ear emergence in each regrowth. Five, three and four cuts were achieved at the end of the growing season from the three sites, respectively.

A Lattice Design was used in the second experiment to evaluate the yielding performance of 25 genotypes subjected to two cutting regimes A and B. These 25 genotypes (20 *L. perenne*, 3 *L. multiflorum*, and 2 *Festuca pratense*) were classified according to the ploidy level to 9 ploidy families, each consisting of one diploid genotype and the tetraploid genotype(s) derived from it. Cutting regime A was applied at ear emergence of the earliest genotype, with a subsequent cutting interval of 5 weeks. Cutting regime B began 2 weeks later than regime A with a cutting interval of 6-7 weeks. Applying these 2 cutting regimes resulted in 4 cuts from each regime in the first site, 3 cuts from each regime in the second site, while in the third site 5 and 4 cuts were achieved from regimes A and B, respectively.

Fresh herbage mass per plot was determined using a Haldrup plot harvester cutting at 5 cm above ground level. A representative sub sample of 400 g for each plot was dried at 58°C for 24 hours and used to determine the dry matter yields (DMY). The developmental stage of the tested genotypes was recorded only in site 3 by determining Mean Stage by Count (MSC) of 50 tillers from each plot in each cut. Assessment of phenological development was based on the code suggested by Park (1980). Data were statistically analyzed using the mixed procedure of SAS analysis. The least significant difference (L.S.D) procedure was used for mean comparison. The probabilities were adjusted according to Bonferroni-Holm Test.

Results and Discussion

Experiment 1

Results obtained in the 2006 growing season indicated that DMY varied significantly among the 20 tested genotypes and between the three experimental sites (Table 1). Differences among the 20 tested genotypes were significant concerning both annual and 1st cut DMYs, with a maximum difference of 18.2 (1st cut) and 20.1 dt DM ha^{-1} (annual DMY), see Table 2. Consistently, genotype 6 gave the highest DMY. Yields on site 1, with mean values of 147.9 and 64.6 dt DM ha^{-1} for annual and 1st cut DMY, were significantly superior to the other two sites (site 2: 99.1 and 51.9 dt DM ha^{-1}; site 3: 117.9 and 43.1 dt DM ha^{-1}). This variation could be mainly attributed to the environmental influence. The temperature during the first growth period varied substantially among the three sites and reached its lowest values in the third site, which clarifies the very low 1st cut DMY obtained from this site.

Tab. 1: Analysis of variance for annual and first cut dry matter yields (dt DM ha^{-1}) of the twenty genotypes in the three sites.

S.O.V	D.F	F value		*Pr*>F	
		Annual DMY	1st Cut DMY	Annual DMY	1st Cut DMY
Site (S)	2	129.89	32.36	<0.0001	0.0006
Genotype (G)	19	3.70	4.21	<0.0001	<0.0001
S*G	38	1.46	1.23	0.0657	0.2041

MSC values, determined for the 20 genotypes in site 3, varied substantially, ranging between 4.7 and 7.5 in the 1st cut and between 4.2 and 5.7 for annual DMY. The relationship quantified between MSC and yield assumes that the genotype effect found in the analysis of variance can to some extent be attributed to differences in developmental stage at cutting:

1st cut DMY = 7.44 MSC – 0.3508 (r^2 = 0.29)

Annual DMY = 12.52 MSC + 56.33 (r^2 = 0.30)

Tab. 2: Mean values for annual and first cut dry matter yields (dt DM ha^{-1}) for the twenty genotypes over three sites. Means followed by the same letter within the same column are not significantly different according to LSD test at 0.01 level of probability.

Genotype	Mean DMY (dt ha^{-1})		Genotype	Mean DMY (dt ha^{-1})	
	Annual DMY	1st cut DMY		Annual DMY	1st cut DMY
1	120.1 ab	52.5 abc	11	117.1 ab	49.0 abc
2	127.3 ab	60.5 ab	12	113.5 b	47.5 bc
3	119.4 ab	53.3 abc	13	120.7 ab	55.6 abc
4	115.6 ab	45.7 bc	14	126.8 ab	55.9 abc
5	130.2 a	60.3 ab	15	121.8 ab	52.6 abc
6	131.1 a	63.7 a	16	128.5 ab	59.7 ab
7	113.6 b	43.4 c	17	127.2 ab	54.1 abc
8	112.8 b	46.3 bc	18	117.4 ab	46.7 bc
9	117.3 ab	48.1 abc	19	127.7 ab	57.9 abc
10	118.1 ab	50.6 abc	20	126.1 ab	60.7 ab

Experiment 2

Analysis of variance presented in Tab. 3 revealed a significant influence of all the studied factors on the annual and 1st cut DMYs. Due to place restrictions, only the ploidy families that showed significant variations as influenced by the interaction between site and cutting regime will be presented. In case of 1st cut DMY (Fig. 1) the tetraploid genotypes in families C, D and I showed significant superiority over the diploid genotypes on site 2 in cutting regime A with a DMY difference of around 15 dt DM ha^{-1}. On the contrary, in family F the diploid genotype produced significantly higher DMY than the tetraploid genotype. Concerning the annual DMY, Fig. 2 reveals that the diploid genotypes in families E and H gave around 21 and 24 dt DM ha^{-1}, respectively, more than their tetraploid derivatives. On the other hand, the situation was reversed for family D. Again, MSC values recorded on site 3 indicate an impact of maturity behaviour on the assessment of yield performance, although MSC values did not differ significantly.

Our results on the effect of ploidy level on yield performance reflect the inconsistent findings in literature, where KUTOVA et al. (1998), GILILAND et al. (2002), and JAFARI et al. (2003) reported tetraploid genotypes to show better yielding performance compared to diploid ones, while LAIDLAW (2004) found no significant differences in DMY.

Tab. 3: Analysis of variance for the annual and 1st cut DMYs (dt DM ha^{-1}) for the twenty genotypes as affected by the two cutting regimes in the three sites.

S.O.V.	D.F	F value		Pr>F	
		1st cut DMY	Annual DMY	1st cut DMY	Annual DMY
Site (S)	2	32.22	29.85	0.0006	0.0008
Cutting Regime (CR)	1	17.39	111.06	0.0005	<0.0001
S*CR	2	17.26	48.1	0.0032	0.0002
Genotype (G)	24	11.22	15.34	<0.0001	<0.0001
S*G	48	5.56	4.68	<0.0001	<0.0001
CR*G	24	1.63	1.69	0.0524	0.0499
S*CR*G	48	2.34	2.47	0.0003	0.0004

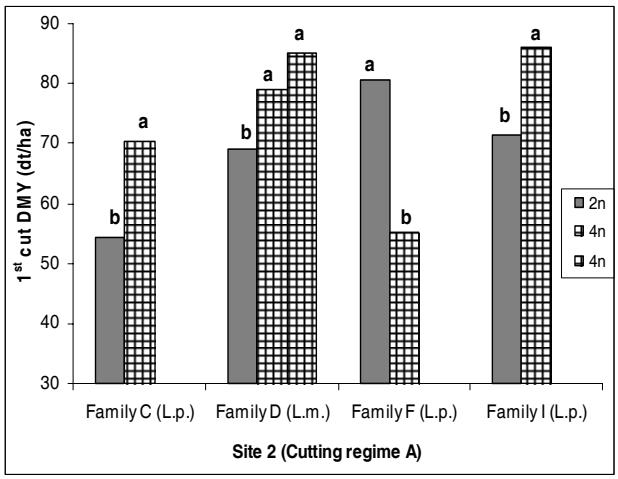

Fig. 1. Differences in 1st cut DMY (dt DM ha^{-1}) between diploids and tetraploids within the same ploidy family as affected by the three way interaction

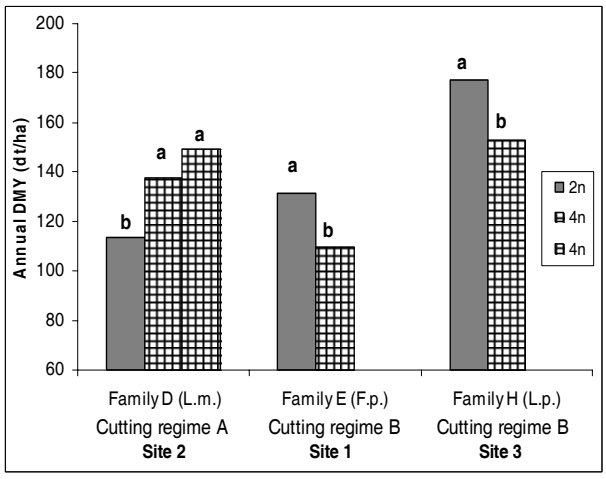

Fig. 2. Differences in annual DMY (dt DM ha^{-1}) between diploids and tetraploids within the same ploidy family as affected by the three way interaction

Conclusions

The results achieved from both experiments show a significant variation in yielding performance among the tested genotypes and within some ploidy families. These variations could be partially explained in terms of the different maturity behaviour of the different genotypes. This work will be repeated in the second growing season to confirm the results and to investigate forage quality parameters.

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