

Genetic diversity and heterosis in perennial ryegrass

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Introduction Plant breeders are concerned with the diversity among and within breeding populations, because it largely determines the future prospects of success in breeding programs. DNA markers provide a powerful tool for the assessment of genetic diversity. The relationship between genetic diversity and heterosis has been investigated in several species (Melchinger, 1999). In hybrid breeding programs divergent gene pools have been established in the past, according to heterotic patterns based on testcross information. In the last decade it has been shown, that new breeding materials can be assigned to already existing gene pools using molecular markers. The phenomenon of heterosis has been of interest in grass breeding research for a long time, and the occurrence of heterosis has been demonstrated for particular crosses (review in Posselt, 2003). However, no attempts have been made to group perennial ryegrass populations according to diversity measures. So far, breeders have mostly combined diverse materials into a base population and applied intra-population improvement. Accidentally, heterosis was captured in the new variety. For more reliable exploitation of heterosis in grasses, divergent gene pools have to be established.

Materials and methods In a previous diversity study (Bolaric *et al.*, 2004), ecotypes and cultivars have been investigated using a RAPD marker. Genetic distance (GD) among all populations was calculated, and eight populations (6 ecotypes and 2 cultivars) with GDs from 0.21 to 0.42 were selected as parents for diallel mating. The 8 parents and their 28 hybrids were investigated in performance trials for 2 years in 2 testing sites.

Results On average the parents yielded 10.7 t ADMY (annual dry matter yield) while the hybrids performed only slightly better (10.9 t ADMY). Average heterosis (expressed as midparent heterosis MPH) across all crosses was only 2 %. Highest MPH was 7.6 % for hybrid P4 x P5 (Table 1). Compared to total ADMY, MPH in the first cut was much more pronounced (14.6 %).

Table 1 Annual dry matter yield (t/ha) of hybrids (above diagonal) and their parents (italics), and midparent heterosis in % (below diagonal)

P	1	2	3	4	5	6	7	8
1	<i>11.1</i>	11.1	10.9	10.6	11.8	10.5	10.9	11.6
2	0.5	<i>10.8</i>	11.1	10.1	11.2	10.2	10.4	11.1
3	2.7	5.6	<i>10.2</i>	10.7	11.5	10.2	10.9	11.4
4	0.3	-2.5	6.2	<i>9.9</i>	11.4	10.6	10.7	10.9
5	5.4	1.9	6.6	7.6	<i>11.3</i>	11.1	11.1	12.1
6	0.1	0.9	1.6	6.8	5.4	<i>9.8</i>	10.7	11.3
7	-1.0	-3.8	3.9	3.0	0.6	3.9	<i>10.8</i>	11.9
8	1.1	-2.2	2.9	0.7	4.6	3.9	5.1	<i>11.8</i>

The average association between GD and MPH was rather low ($r = 0.10$), but higher (Figure 1) for GD vs. Hybrid performance ($r = 0.27$). For in-dividual parents and their hybrids, much closer associations ($r = 0.48$) could be identified.

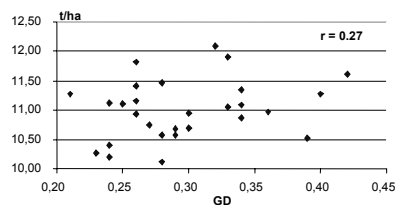


Figure 1 Hybrid performance (ADMY in t/ha) vs. genetic distance (GD)

Conclusions The results of the present study demonstrate, that parents can be pre-selected according to genetic similarity based on molecular markers. Thus, the number of cross combinations to be produced and tested can be reduced. The most promising cross combination to identify heterotic potential is hybrid 5 x 8. The former is the best performing ecotype, while the latter is the highest yielding cultivar among the parents. Thus, parents P5 and P8 could be assigned to divergent gene pools. To broaden the respective pools, P7 could join the pool of P5, since it is also heterotic with P8.

References

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