

Positive effect of increased AFLP diversity among parental plants on yield of polycross progenies in perennial ryegrass (*Lolium perenne* L.)

R. Kölliker, B. Boller and F. Widmer

Agroscope FAL Reckenholz, Swiss Federal Research Station for Agroecology and Agriculture, 8046 Zurich, Switzerland, Email:roland.koelliker@fal.admin.ch

Keywords: heterosis, molecular markers, polycross breeding, yield

Introduction In outbreeding forage crops such as perennial ryegrass (*Lolium perenne* L.), genetic diversity among parental plants may greatly influence the success of a cultivar through mechanisms such as heterosis and inbreeding depression. The aim of this study was to evaluate the use of amplified fragment length polymorphism (AFLP) markers to select polycross parents with contrasting levels of genetic diversity and to analyse genetic diversity and agronomic performance of first and second generation synthetic progenies (Syn1, Syn2).

Materials and methods Genetic diversity among 98 plants from advanced breeding germplasm including three maturity groups was analysed using 184 AFLP markers. Based on Euclidean squared distances, two polycrosses (PC) with contrasting levels of genetic diversity (PC narrow with low diversity, PC wide with large diversity), consisting of six parental plants each, were composed for three maturity groups. Genetic diversity within Syn1 progenies of all six PC was analysed using the same 184 AFLP markers scored in parental plants. Agronomic performance of Syn1 and Syn2 progenies was assessed by measuring dry matter yield of three cuts in the field and uniformity was assessed by comparing coefficients of variation for heading date.

Results Genetic diversity, expressed as average Euclidean squared distance, among parental plants selected to form narrow polycrosses was on average 36 % lower than the genetic diversity among plants selected for wide polycrosses. The differences between Syn1 progenies were less pronounced, with Syn1 progenies from narrow polycrosses showing 16 % lower genetic diversity when compared to Syn1 progenies from wide polycrosses. In general, diversity within Syn1 progenies derived from narrow polycrosses was comparable to the diversity among the respective parental plants while diversity within Syn1 progenies from wide polycrosses was considerably lower when compared to the respective parents. Syn1 and Syn2 progenies derived from wide polycrosses showed consistently higher dry matter yields when compared to progenies derived from narrow polycrosses. Averaged across both generations and all maturity groups, this difference reached 3.7 % and was highly significant (Figure 1 A). While there was no significant difference for the coefficients of variation for heading date between narrow and wide polycrosses of the early and intermediate maturity groups, Syn1 and Syn2 progenies from narrow polycrosses of the late maturity group showed significantly higher variation when compared to progenies from wide polycrosses (Figure 1 B). However, all progenies still showed coefficients of variation comparable to standard cultivars assessed in the same experiment.

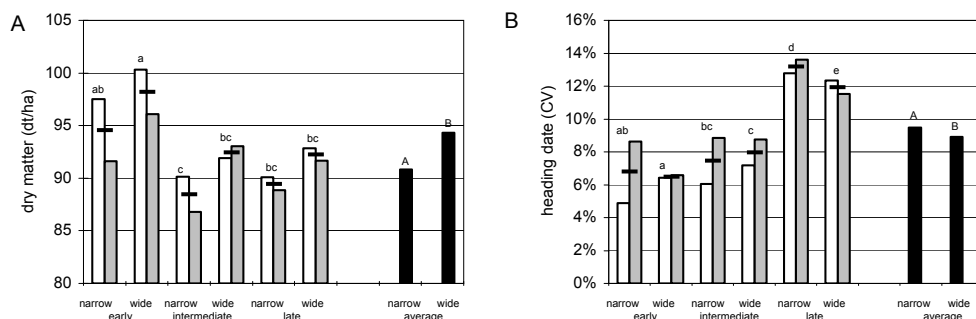


Figure 1 Dry matter yield of three subsequent cuts (A) and coefficients of variation for heading date (B) for first (Syn1; white columns) and second generation synthetic progenies (Syn2; grey columns) derived from polycrosses with contrasting levels of genetic diversity (narrow, wide) of three maturity groups (early, intermediate, late). Bars indicate average values of Syn1 and Syn2, black columns indicate average values across maturity groups. Different letters indicate significant differences ($P < 0.05$).

Conclusions Our results provide evidence for an effective application of molecular markers to select genetically diverse parents in a polycross breeding program in order to increase agronomic performance of synthetic progenies without compromising phenotypic uniformity.