Identification of quantitative trait loci for flowering time in a field-grown *Lolium perenne x Lolium multiflorum* mapping population

R.N. Brown[1], R.E. Barker[2], S.E. Warnke[3], L.A. Brilman[4], M.A.R. Mian[5], S.C. Sim[6] and G. Jung[6]
[1]University of Rhode Island, Kingston RI 02881 USA; [2]National Forage Seed Production Research Center, USDA-ARS, Corvallis OR 97331 USA; [3]National Arboretum, USDA-ARS, Washington DC 20002 USA; [4]Seed Research Oregon, 27630 Llewellyn Rd., Corvallis OR 97333 USA; [5]USDA-ARS, Wooster OH 44691 USA; [6]University of Wisconsin, Madison WI 53706 USA Email: brownreb@onid.orst.edu

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Introduction Perennial ryegrass (*L. perenne*) and annual, or Italian, ryegrass (*L. multiflorum*) are considered to be separate species by the seed trade, and are used and bred for distinct purposes. However, the two species are cross-fertile. Seed producers rely on the different flowering times of the two species to produce pure seed. Flowering times can overlap, leading to genetic mixing. Contamination of perennial ryegrass seed lots with annual types is an expensive problem for grass seed producers in western Oregon, USA.

Materials and methods The mapping population is a pseudo-F_2 derived from *L. perenne* 'Manhattan' and *L. multiflorum* 'Floregon' The population of 186 individuals was planted in two replications in each of two sites near Corvallis, Oregon, USA, (OSU and SRO) in March 2000. Four replications were planted in Ardmore, Oklahoma, USA (NF) in October 2000. Days to anthesis, defined as three tillers shedding pollen, was recorded for each plant. Plants were also scored on whether they flowered each year. Data was collected in 2000 and 2001 in Oregon, and in 2001 in Oklahoma. None of the plants were vernalised before being transplanted to the field in 2000. QTLs were mapped using both non-parametric analysis and interval analysis. Only those QTLs which were significant (LOD $\geq$ 3.0, $\alpha \leq .005$) in both analyses are reported. The two or four replications were pooled for a given year and location.

Results In 2000 58% of the plants flowered and 42% remained vegetative. In 2001 all of the plants flowered at all three locations. The locations and LOD scores for the significant QTLs are given in Table 1. The wheat vernalisation genes *Vrn1* and *Vrn2* are located on chromosomes syntenic to *Lolium* linkage group (LG) 4 (Sim *et al*., 2005), and a homologue of the wheat *Vrn1* gene has been mapped to LG4 in *L. perenne* (Jensen *et al*., 2005). Growth chamber studies with this population identified vernalisation and photoperiod QTLs on LG1 and LG7. Genes on these linkage groups account for much of the variation among plants whose vernalisation needs have been met. The QTLs on LG3 and LG6 may reflect genes for earliness *per se*, or they may reflect stress response genes.

Conclusions Linkage groups four and seven are most important in determining flowering time in this population. Additional mapping efforts focused on these linkage groups would be useful to generate accurate markers for distinguishing between annual and perennial types in *Lolium*, and for developing cultivars with more defined flowering periods.

Table 1 QTL data for flowering time and vernalisation requirement

Trait	LG	Peak Marker	LOD	Position	Variation
Flower in	4	CDO1196	3.9	54 cM	15%
2000	4	TF45-420MFB	3.1	87 cM	16%
SRO 2000	4	CDO1387	3.0	25 cM	28%
	7	CDO595	3.4	76 cM	30%
OSU 2000	1	CDO105.2	7.0	27 cM	66%
SRO 2001	2	CDO1376	3.5	38 cM	14%
	3	CDO281	3.35	46 cM	15%
OSU 2001	7	CDO464	3.4	53 cM	27%
	7	BCD938	3.5	71 cM	18%
NF 2001	1	CDO105.1	3.7	54 cM	17%
	3	CDO460	3.6	89 cM	16%
	4	CDO541	3.3	35 cM	21%
	6	CDO1380	3.9	69 cM	15%
	7	TF58-292MFA	7.2	22 cM	37%

References

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