The Investigation of Flowering Control in Late/Rare Flowering Lolium Perenne

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The investigation of flowering control in late/rare flowering *Lolium perenne*

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Introduction Flowering in *Lolium perenne* (perennial ryegrass) results in reduced digestibility and its inhibition would enhance forage quality. Flowering regulation has been well studied in *Arabidopsis thaliana* (Simpson and Dean, 2002) and orthologs of *Arabidopsis* flowering genes underlying heading date Quantitative Trait Loci (QTL) have been identified in rice (Yano, M *et al.,* 2000). However it is not clear yet how universally applicable such studies are to *Lolium*. The project goals are to characterise the gene expression profiles of late/rare flowering *L. perenne* plants to determine factors affecting flowering and to map the genes involved in the flowering process. Initial studies, reported here, have focussed on the ability of 6 plant lines from the Oak Park breeding programme, previously identified as rare or non-flowering under natural day length conditions, to flower in controlled environments.

Materials and methods The 6 lines, representing 3 families, together with controls from each family (plants with normal heading pattern) and an early flowering variety (Moy) were vernalised. 5 tillered plants from each line were then transferred to growth chambers at 18^0C with continuous light for 21 days, after which they were monitored under greenhouse conditions for days to heading with day 0 taken as the start of secondary induction (Table 1). A large number of plants from each line was also observed in pots under outdoor conditions (Data not shown).

Results All 6 test lines headed under controlled conditions in 2004 except X15 (Table 1). The severely stunted X15 line did produce immature inflorescence in 2004 but they did not fully emerge. This was also observed in outdoor pot conditions (data not shown) in direct contrast to previous years. The 3 controls and Moy headed at the same time under controlled conditions, a situation not seen under natural day length conditions (controls headed as much as 18 days apart). This indicates saturation of the long day requirement. The J family plant lines, flowered as many as 8 days later than other families under controlled conditions, indicating a greater long day requirement. Within the J family, J43(c)and the later flowering J51 had the greatest difference in days to heading in both controlled conditions (8 days) and outdoor pot conditions (25 days).

Table 1 Average days to heading in controlled environments (c) = controls

L. perenne Line	Days to heading
X15	No Heading
X19 (c)	21
J74	28.6
J51	29.2
J54	26
J47	26.4
J43 (c)	21.2
V16	22.6
V13 (c)	21
Moy	21

Conclusion On the basis of these results J43 (c) and J51 will have their shoot apical meristem gene expression profiles compared. The comparison will be made after vernalisation and during secondary induction using Suppression Subtractive Hybridisation PCR, which allows the identification of differentially expressed genes. The expression of selected flowering genes that have been identified in other monocots will also be investigated in the subtracted library. J43(c) and J51 have been cross pollinated and a genetic linkage map will be constructed from the resulting population to identify possible heading date QTL .

References

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