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QTL analysis of vernalisation requirement and heading traits in *Festuca pratensis* Huds.

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Introduction The transition from the vegetative phase to the reproductive phase occurs as a result of environmental and endogenous stimuli. In *Festuca pratensis*, low temperature and/or short days over a certain period (primary induction) followed by long days (secondary induction) will lead to heading and flowering (Heide, 1988). We present results from QTL mapping of vernalisation requirement and heading traits and mapping of the Vrn-1 ortholog in *F. pratensis*.

Materials and methods A mapping family of *F. pratensis* consisting of 138 progeny from a cross between Norwegian genotype HF2/7 and Yugoslavian genotype BF14/16 were characterized for vernalisation requirement and heading traits. In a greenhouse experiment, plants were vernalized at 6 °C and 8h photoperiod for 12, 9, 6 or 0 weeks and then transferred to warmer temperatures and long days to stimulate heading. Vernalisation requirement was recorded, together with heading date, final number of panicles and final number of panicles per tiller after 12 weeks of vernalisation. In a field experiment, non-vernalized plants were planted at two locations in the spring and the number of panicles produced during the summer season was recorded. The data was subjected to QTL analysis using previously obtained genotype data (Alm *et al.*, 2003) and the MapQTL software (van Ooijen and Maliapaard, 1996). The presence of cereal anchor probes on the map allows the comparison with genes and QTLs for similar traits mapped in other species. A segment of a gene with high similarity to the homoeoallelic series of Vrn-1 genes controlling vernalization requirement in cereals (Snape *et al.*, 2001; Yan *et al.*, 2003) was PCR-amplified and sequenced. A single nucleotide polymorphism identified two different alleles in the mapping population. Individuals in the mapping population were characterized for these alleles and coupling analysis was performed to determine the position of the Vrn-1 gene.

Results A large portion of linkage group (LG) 4 was strongly associated with vernalisation requirement in both greenhouse and field experiments. The upper half of LG4 had the strongest effect on the phenotype, however, to our knowledge no genes or QTLs relating to vernalisation requirement or heading time are reported in comparable regions of other genomes. Strong QTLs were also found in the lower part of the LG, as well as near Xwg644, a marker which is closely linked to several interesting genes; the Vrn-1-series in cereals and grasses, Tack2a/Hd6 (casein kinase 2 α) in wheat/rice and Phytochrome C in barley. The sequence of the *F. pratensis* Vrn-1 gene segment (most of its MADS-box domain) was 100% identical to that of Vrn-1 in wheat and ryegrass species at the amino acid level and it was closely linked to Xwg644. It therefore represents a member of the Vrn-1-series and is likely to affect vernalisation requirement in *F. pratensis*. QTLs for heading time were found on LG1 and LG5, whereas QTLs for number of panicles were found on LG1, LG4, LG5, LG6 and LG7. The QTL for heading time on LG5 is located in a region comparable to that containing the rice flowering time QTL FLT2 and the QTL for number of panicles on the same LG is located near Xwg364a, which is linked to the barley cold-binding factor Hvcbf3. The QTLs on LG7 were found in a region known to contain genes in rice, barley and ryegrass with similarity to CONSTANS, an important gene in the photoperiod pathway in arabidopsis.

References

- Alm, V., Fang, C., Busso, C.S., Devos, K.M., Vollan, K., Grieg, Z., and Rognli, O.A. (2003). A linkage map of meadow fescue (*Festuca pratensis* Huds.) and comparative mapping with other Poaceae species. *Theoretical and Applied Genetics* 108, 25-40.
- Heide, O.M. (1988). Flowering requirements of Scandinavian *Festuca pratensis*. *Physiologia Plantarum* 74, 487-492.
- Snape, J.W., Butterworth, K., Whitechurch, E. and Worland, A.J. (2001) Waiting for fine times: genetics of flowering time in wheat. *Euphytica* 119, 185-190.
- Van Ooijen, J.W. and Maliapaard, C. (1996). MapQTL (tm) version 3.0: Software for the calculation of QTL positions on genetic maps. CPRO-DLO, Wageningen.
- Yan, L., Loukoianov, A., Tranquili, G., Helguera, M., Fahima, T. and Dubcovsky, J. (2003). Positional cloning of the wheat vernalization gene VRN1. *Proceedings of the National Academy of Sciences* 100, 6263-6268.