

viduals and are therefore of limited use to wheat breeders carrying out commercial scale breeding programs. To identify co-dominant SNP-based markers, which are capable of distinguishing between heterozygotes and homozygotes, we have used targeted re-sequencing of the wheat exome to generate large amounts of genic sequences from eight varieties. Using a bioinformatics approach, these sequences have been used to identify 95,266 putative, gene-based, single nucleotide polymorphisms, of which 10,251 were classified as being suitable markers for the discrimination of homozygote and heterozygote individuals. Validation of a sample of these markers confirmed that 81% could easily discriminate between heterozygous and homozygous individuals. Comparison of these co-dominant markers with dominant markers indicated that both marker types were distributed similarly across genetic maps. In addition, the use of both marker types across two U.K. mapping populations revealed that the two populations had different levels of polymorphism across the A, B, and D genomes. The new co-dominant markers described here are capable of complete genotypic classification of a segregating locus in polyploid wheat and can be used on a variety of genotyping platforms; as such they represent a powerful tool for wheat breeders. The markers and related information described here have been made publically available on an interactive web-based database in order to facilitate their use in genotyping programs worldwide.

Molecular adaptation to cooler climates and ecological diversification of Pooideae.

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Adaptation to temperate environments is a common feature in the grass subfamily Pooideae, suggesting an ancestral origin of low temperature stress tolerance dating back to the beginning of Pooideae taxonomic divergence. It also has been suggested that climate cooling during the Eocene-Oligocene transition (~34MYA) was important for cold climate adaptation in the core Pooideae clade, in which the Triticeae species is contained. Here we analyze the molecular evolution of genes involved in low-temperature stress response and present evidence for the importance these genes in the evolution of the Pooideae lineage.

Maximum likelihood-based phylogenetic methods were used to estimate substitution rates in Pooideae species relative to rice and test the hypothesis that cold induced loci were under positive selection during radiation of the Pooideae lineage. In addition we carried out in depth studies of the evolution of three Pooideae-specific gene families, *CBF*, *FST*, and *IRIP* genes, known to be central in core Pooideae low temperature stress responses.

Phylogenies of 4330 orthologous loci were produced, of which 388 loci were defined as low-temperature induced in Pooideae. A general increase in substitution rates was observed for all genes in the Pooideae lineage relative to rice, and this rate increase was higher for nonsynonymous substitutions (+7–20%) compared to synonymous substitutions (+0–7%). However, the nonsynonymous substitution rate increase in Pooideae was significantly higher in those loci defined as low-temperature induced. Tests for positive selection on the basal Pooideae branch showed a 3.3-fold increase in significant tests for low temperature induced loci compared to all loci. Analyses of Pooideae-specific gene families involved in low temperature stress responses identified both ancient evolutionary innovations (basal Pooideae), as well as more recent innovations in carbohydrate metabolism specific for core Pooideae.

The Pooideae lineage evolved from a tropical/subtropical ancestor to become a taxonomic group with ecological dominance in temperate ecosystems. Our results suggest that adaptive evolution of low temperature responses was of importance in the basal Pooideae, possibly enabling the ecological radiation into cooler ecosystems.