

The study of the localization, structure and expression of the genes regulating the development of the ligular region of the tribe Triticeae

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Leaves of Poaceae have a unique morphological feature: they consist of a proximal sheath and a distal blade separated by a ligular region. The sheath provides structural support and protects young developing leaves, whereas the main function of the blade is photosynthesis. The auricles allow the blade to tilt back for optimal photosynthesis and determine the angle of a leaf, whereas the ligule protects the stem from the entry of water, microorganisms, and pests. Research on liguleless mutants of maize and other cereals has led to identification of genes that are involved in leaf patterning and differentiation. A liguleless line of *Ae. tauschii* is an induced mutant (*Lgt*-mutant), whose phenotype is under control of the dominant gene *Lg^t*. Using 3933 polymorphic DArTseq markers, a high-throughput genotyping of F2 population from the cross *Lgt*-mutant/KU-2126 was performed; highly saturated molecular-genetic maps of *Ae. tauschii* were constructed. The *Lg^t* gene was placed on the short arm of chromosome 5D by molecular-genetic mapping. *In silico* mapping of the DArTseq markers on *Ae. tauschii* physical map allowed to establish the coordinates of *Lg^t* on 5D pseudomolecule and to determine the list of the *Lg^t* candidate genes. *Lg^t* gene is not an orthologue of the previously studied *Lg4*, *Lgn1* and *Knox1* cereal genes, whose dominant mutations cause the liguleless phenotype, and presents a new cereal gene, involved in the genetic control of the development of the ligular region and the formation of the distal-proximal axis of differentiation. SNP and SSR markers help us to shorten the list of candidate genes for *Lg^t*.

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