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Identification and study on Lg^t – a new cereal gene for liguleless leaf phenotype

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Motivation and Aim: The leaf of family Poaceae has a ligule and auricle between its distal and proximal parts. The formation of the distal-proximal axis of differentiation and the development of the organs of the ligule region occurs at the early stages of leaf development. A study of the developing and genetic regulation of the formation of the distal-proximal axis of leaf differentiation in the liguleless mutant *Zea mays L.* made it possible to identify new genes that controlled the development processes-*Lg1*, *Lg2*, *Lg3*/*Lg4*, *Lgn*, etc. A liguleless line of *Ae. tauschii* is an induced mutant (Lgt-mutant), whose phenotype is under control of the dominant gene *Lgt.*
Methods and Algorithms: Using 3933 polymorphic DArTseq markers, a high-throughput genotyping of F2 population from the cross Lgt-mutant/KU-2126 (KU-2126 is an accession with the wild-type leaf phenotype) was performed; highly saturated molecular-genetic maps of *Ae. Tauschii* were constructed.
Results: The *Lgt* gene was placed on the short arm of chromosome 5D by molecular-genetic mapping. The *Lgt* gene locates in the region of conserved synteny with bread wheat 5DS, rice *Os12*, sorghum *Sb2* and Brachypodium *Bd4* chromosomes. in silico mapping of the DArTseq markers, flanking the gene of interest – *Lgt*, on *Ae. tauschii* physical map allowed to establish the coordinates of *Lgt* on 5D pseudomolecule and to determine the list of the *Lgt* candidate genes. It was shown that the orthologs of genes *LIGULELESS 4*, *LIGULELESS NARROW 1* and *KNOX1*, whose dominant mutations cause the liguleless phenotype in cereals, locate on *Ae. tauschii* chromosomes 1D, 4D and 7D, respectively, and they cannot be considered as candidate genes for Lgt (5DS).
Conclusion: Thus, the *Lgt* 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, previously unexplored cereal gene, involved in the genetic control of the development of the ligule region and the formation of the distal-proximal axis of differentiation. Using novel genetic models: near isogenic lines marked with the *Lgt* gene and recombinant lines at the next stage of research will help to shorten the list of candidate genes for *Lgt* and allow further isolation of this gene, to study its structural and functional organization.
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