

## Genomic characterization of *DEP1* gene in the Triticinae species with compact, compactoid and normal spike shape

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**Motivation and Aim:** Spike shape of Triticinae species is one of the most important taxonomically characteristic of this tribe. There are four main variants of spike shape (spelt, compact, compactoid and normal), that widely distributed among wheat and *Aegilops* species. Several genes and loci associated with spike shape trait have been identified previously [1]. Nevertheless, there are practically no data about nucleotide sequences of this genes and loci. *DENSE AND ERECT PANICLE 1 (DEP1)* gene is related to several traits in rice (erect panicle, number of grains per panicle and panicle dense) [2]. In case of *T. aestivum* the experiments with the transgenic line showed that downregulation of *DEP1* homologue affects the length of the ear, ear density and number of spikelets [3]. The aim of this study was investigation and genomic characterization of *DEP1* gene in wheat and *Aegilops* species with compact, compactoid and normal spike shape.

**Methods and Algorithms:** A combination of bioinformatical tools and standard molecular biology methods was used.

**Results:** We determined the spike shape of several accessions of *Triticum* and *Aegilops* species (*T. antiquorum*, *T. macha*, *T. sphaerococcum* and *Ae. tauschii*) by calculation of Flaksberger's formula. The full-length sequences of *DEP1* gene were obtained for all accessions studied. Nucleotide sequences comparing revealed *DEP1* gene regions which distinguish analyzed wheat and *Aegilops* species with compact, compactoid and normal spike phenotypes. Phylogenetic analysis allowed to determined the origin of *DEP1* alleles and different Triticinae species.

**Conclusion:** *DEP1* gene variability could contribute to the spike shape formation in wheat and *Aegilops* species.

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### References

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