

## Wheat target genes for CRISPR/Cas9 editing in the post-genomic era

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CRISPR/Cas9 editing has been developing most intensively for the genomes of agricultural plants in the last 10 years. This is primarily due to overcoming barriers such as genotype-dependent plant regeneration, as well as the expansion of the number of genes associated with agricultural traits. Significant progress in the identification and cloning of target genes of common wheat has been noted since 2018, i.e. since the construction of the first reference map of this genome. The number of isolated genes increased by more than 2 times during this period and reached 172 by the end of 2024, which stimulated the development of work on genomic editing [1]. From the point of view of practical results, it remains important to maintain a balance between genomic editing of the target gene and wheat yield. In this regard, it is interesting to combine knockouts genes, which result in semi-dwarf and high-yielding plants [2].

Plant height is a key agronomic trait in wheat, influencing plant architecture and yield potential. The most widely used alleles in modern breeding are those of the *Rht-1* genes, which are involved in the gibberellin (GA) signaling pathway. Although the semi-dwarf phenotype resulting from the introduction of *Rht-B1b* and *Rht-D1b* alleles reduces lodging, these alleles are also associated with decreased biomass, smaller spikes and grain size, reduced nitrogen use efficiency, and consequently require higher fertilizer inputs to achieve high yields. Recently, *ZnF* genes have been described that function in the signaling pathway of another class of phytohormones, brassinosteroids, and are also associated with plant height regulation. It has been shown that combining knockouts of *Rht-1* and *ZnF* genes can produce semi-dwarf yet high-yielding wheat plants [2].

We used genome editing to create knockouts of *Rht-1* and *ZnF* genes on all three homoeologous chromosomes in the tall common wheat breeding line. More than 200 T0 plants were obtained. A selection is currently underway to identify plants carrying combinations of knockouts in the target genes on different chromosomes, with the goal of evaluating their effects on plant growth and productivity.

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### References

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