

Approaching the dominant dwarfing gene *Ddw1* in rye by comparative genetics

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Winter rye (*Secale cereale* L.) is a traditional cereal in Germany with versatile uses for human and animal nutrition as well as a substrate for bioenergy production. Rye displays higher stability in yield compared to wheat and barley on marginal-gain soils due to its pronounced abiotic stress tolerance. Rye breeding aims to develop new high yielding varieties which are, in view of the global climate change, more robust and less demanding in water and fertilizer. These efforts are directed to enhance the sustainability of rye production and to keep rye competitive in modern agricultural production systems.

Lodging resistance ranks among the major breeding goals in rye. Improved lodging resistance will reduce the application of growth regulators and, thus, increase the efficiency of rye production. The main approach to overcome lodging is a reduction of plant height by exploiting dwarfing mutants. In wheat and rice the alteration of

plant height by recessive dwarfing genes resulted in a dramatic increase of crop yield. In rye, particularly the dominant dwarfing gene *Ddw1* has been used in Eastern European and Finnish breeding programs to improve lodging in population varieties. The potential of *Ddw1* for breeding highly productive hybrid rye varieties has yet not been elucidated. The implementation of *Ddw1* in the development of homozygous dwarf inbred lines is hampered, as an efficient and reliable method to distinguish homo- and heterozygous dwarf genotypes is currently not available. In this study, we are approaching *Ddw1* located on the long arm of rye chromosome 5R by comparative genetics. We have identified the *Ddw1*-orthologous regions in rice, *Brachypodium*, and *Sorghum*, and were able to use the gene models of these grasses to develop conserved orthologous sequence (COS) markers for *Ddw1*. Results will be presented on mapping the novel COS markers relative to *Ddw1*.