

Evaluation of the dominant dwarfing gene *Ddw1* with respect to its use in hybrid rye breeding

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Abstract

Winter rye (*Secale cereale* L.) is a traditional cereal in Austria and Germany with versatile uses for human and animal nutrition as well as a substrate for bioenergy production. Rye breeding aims to develop varieties with high yield potential, as well as high nutrient efficiency and robustness to environmental stresses to cope with the expected outcome of the ongoing climate change. These efforts are key to enhance the sustainability of rye growing and to keep rye competitive in modern agricultural production systems. Lodging resistance ranks among the major breeding goals to reduce yield losses in rye. The main approach to overcome lodging is a reduction of plant height by exploiting dwarfing genes. In wheat and rice the alteration of plant height by recessive dwarfing genes resulted in an increased harvest index (HI). The lesser growth of vegetative organs allowed for a differential partitioning of dry matter from non-reproductive to reproductive organs and, as a consequence, to a significant increase of grain yield. Although recessive dwarfing genes allowed to reduce plant height in rye as well (Geiger, pers. comm.), modern rye varieties do not yet reach a HI comparable to that of wheat. In Eastern European and Finnish breeding programmes the dominant dwarfing gene *Ddw1*, which has been discovered by V. D. Kobyljansky already in 1972 and which was originally named *H1* (*Humilus*) (KOBYLJANSKY 1972), has been used to improve lodging in population varieties. However, the potential of *Ddw1* to increase the HI in highly productive hybrid rye varieties has not yet been elucidated. Use of *Ddw1* in the development of homozygous dwarf inbred lines is hampered because an efficient and reliable method to distinguish homozygous and heterozygous dwarf genotypes is not available.

We have investigated *Ddw1*, which was previously mapped in a 17.1 cM interval on the long arm of chromosome 5R (KORZUN et al. 1996), in a comparative genetic approach using genome data of related grass species as a blueprint for marker development (HACKAUF and WEHLING 2005, HACKAUF et al. 2009, 2012). Intron-spanning primers were derived from rye ESTs (HASENEYER et al. 2011). An integrated map covering 27.6 cM on rye chromosome 5R was established based on 768 $F_{4:5}$ individuals segregating for *Ddw1*, which originated from the cross R1620 (tall)×R347/1 (dwarf).

We were able to delimit the location of the dwarfing gene to a 4.3 cM interval. The novel, co-dominant conserved orthologous set (COS) markers developed in this study enable an easy scoring and clear discrimination between homozygous and heterozygous dwarf genotypes and to predict *Ddw1* genotypes with a precision not feasible before. In addition, these molecular tools enable to identify recombination events, which allow for breaking up the linkage drag associated with *Ddw1* (BÖRNER et al. 2000).

In Germany, rye is mainly grown on marginal and drought-prone soils in the north German plain. The HI counts among the traits to improve yield in dry environments with plant height being a main factor to increase a drought-independent HI (RICHARDS et al. 2001). We started to evaluate semi-dwarf test hybrids in target environments located in the north German plain as well in the Marchfeld in Austria. $F_{4:5}$ near-isogenic elite inbred lines (NIL), which are homozygous either for the recessive (tall) or dominant (dwarf) allele at the *Ddw1* locus, were crossed to 6 male-sterile tester lines. The advanced NIL had been developed from a cross of a *Ddw1* donor with a tall elite inbred line and have a similar genetic background but differ in the 5RL segment carrying *Ddw1*. Performance of these test crosses will be evaluated in 8 environments (four locations, two years). In 2012, reduced precipitation from April 1 through May 31 resulted in drought stress during flower induction and inflorescence development at three experimental sites in Mecklenburg-Western Pomerania, Brandenburg and the Marchfeld. Plant height in test hybrids carrying *Ddw1* was reduced on average by 35% compared to tall test hybrids. Thus, *Ddw1* hybrids might allow for a cultivation of rye without a need of growth regulators, thus increasing the economic efficiency of rye production. Among the 36 semi-dwarf hybrids evaluated in all the 4 environments, 17 (47%) revealed no significant differences in grain yield compared to test-crosses with tall NIL. Interestingly, 5 of the semi-dwarf hybrids significantly outperformed their tall full-sibs with respect to grain yield in two of the drought-stressed environments. Given the complexity of the genetic control of grain yield and drought tolerance, the performance of semi-dwarf genotypes carrying *Ddw1* needs to be assessed in additional environments. The evaluation of semi-dwarf test hybrids is in progress.

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Keywords

Dominant dwarfing gene, drought stress, lodging, *Secale cereale*, testcross performance

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References

- BÖRNER A, KORZUN V, VOYLOKOV AV, WORLAND AJ, WEBER WE, 2000: Genetic mapping of quantitative trait loci in rye (*Secale cereale* L.). *Euphytica* 116, 203-209.
- HACKAUF B, WEHLING P, 2005: Approaching the self-incompatibility locus *Z* in rye (*Secale cereale* L.) via comparative genetics. *Theor Appl Genet* 110, 832-845.
- HACKAUF B, RUDD S, VAN DER VOORT JR, MIEDANER T, WEHLING P, 2009: Comparative mapping of DNA sequences in rye (*Secale cereale* L.) in relation to the rice genome. *Theor Appl Genet* 118, 371-384.
- HACKAUF B, KORZUN V, WORTMANN H, WILDE P, WEHLING P, 2012: Development of conserved ortholog set markers linked to the restorer gene *Rfp1* in rye. *Mol Breed* 30, 1507-1518.
- HASENEYER G, SCHMUTZER T, SEIDEL M, ZHOU R, MASCHER M, SCHÖN CC, TAUDIEN S, SCHOLZ U, STEIN N, MAYER KF, BAUER E, 2011: From RNA-seq to large-scale genotyping - genomics resources for rye (*Secale cereale* L.). *BMC Plant Biol* 11, 131.
- KOBYLJANSKY VD, 1972: On the genetics of the dominant factor of short-strawed rye. *Genetika* 8, 12-17.
- KORZUN V, MELZ G, BÖRNER A, 1996: RFLP mapping of the dwarfing (*Ddw1*) and hairy peduncle (*Hp*) genes on chromosome 5 of rye (*Secale cereale* L.). *Theor Appl Genet* 92, 1073-1077.
- RICHARDS RA, CONDON AG, REBETZKE GJ, 2001: Traits to improve yield in dry environments. In: Reynolds MP, Ortiz-Monasterio JI, McNab A (Eds.), *Application of physiology in wheat breeding*, 88-100. CIMMYT, Mexico, DF.