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Molecular breeding for virus resistance in cereals - present state and future perspectives

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Abstract

Soil-borne viruses, i.e. *Barley yellow mosaic virus* (BaYMV) and *Barley mild mosaic virus* (BaMMV), with respect to barley and *Soil-borne cereal mosaic virus* (SBCMV) in wheat, have gained evident importance in Europe during the last decades. The same holds true for insect transmitted viruses like the aphid transmitted *Barley yellow dwarf virus* (BYDV) and *Cereal yellow dwarf virus* (CYDV), or the leafhopper transmitted *Wheat dwarf virus* (WDV, for review cf. ORDON et al. 2009).

With respect to BaMMV/BaYMV several resistance genes have been mapped in the barley genome (ORDON et al. 2009, KAI et al. 2012) and molecular markers are available facilitating efficient marker based selection procedures (PALLOIX and ORDON 2011) and pyramiding of resistance genes (WERNER et al. 2005). Out of these, the *Rym4/Rym5* locus comprising the translation initiation factor 4E (*Hv-eIF4E*) has been isolated (STEIN et al. 2005) and several alleles were identified at this locus (STRACKE et al. 2007, HOFINGER et al. 2011). The isolation of additional resistance genes is in progress and using genomic resources and tools available today, e.g. the genome-zipper (MAYER et al. 2011), markers co-segregating with *rym11* on a high resolution mapping population have been developed (LÜPKEN et al. 2013).

While BaMMV/BaYMV are of prime importance in Europe, SBCMV is mostly a threat to wheat cultivation in France and Italy up to now. Using DH-lines and field testing in France the resistance gene *Sbm1* was located on chromosome 5DL5 and a diagnostic marker was developed facilitating efficient marker based selection and quarantine breeding (PEROVIC et al. 2009).

On the world wide level barley yellow dwarf is the most important viral disease of cereals. Besides the resistance gene *Ryd4*^{Hb}, which confers complete resistance to BYDV but cannot be used in barley breeding due to linkage drag up to now (SCHOLZ et al. 2009), *Ryd2* (COLLINS et al. 1996), *Ryd3* (NIKS et al. 2004) and several QTL (TOOJINDA et al. 2000, SCHEURER et al. 2001) are known conferring tolerance to BYDV. Marker based pyramiding of these genes in doubled haploid lines revealed that a combination of *Ryd2* and *Ryd3* leads to a significantly reduced virus titre, i.e. quantitative resistance to BYDV (RIEDEL et al. 2011). Analyses based on the electrical penetration graph (EPG) technique revealed that *R. padi* - one of the main vectors of BYDV - shows a significantly reduced time of phloem salivation on genotypes carrying *Ryd4*^{Hb,} giving hint that this fact maybe involved in BYDV resistance (SCHLIEPHAKE et al. 2013).

In summary, molecular markers facilitate already today efficient selection procedures to improve virus resistance in cereals. The availability of dense marker maps, high throughput genotyping platforms, physical maps and genome sequences of cereals itself and related species will facilitate an enhanced isolation of resistance genes in the future thereby leading to a deeper understanding of virus resistance and the transfer of marker based selection to the allele level. This together with new selection strategies, e.g. genomic selection procedures, will lead to an enhanced breeding of virus resistant cultivars.

Keywords

BaMMV, BaYMV, BYDV, cereals, molecular breeding, molecular markers, SBCMV, virus resistance

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