

Identification of molecular markers associated with QTLs in rye

Dörthe Musmann¹, Matthias Enders², Eike Lornsen¹, Barbara Kusterer³, F. Joachim Fromme³, Regine Dieterich⁴, Frank Ordon², Peter Wehling¹, Bernd Hackauf¹

¹Julius Kühn-Institut, Institute for Breeding Research on Agricultural Crops

²Julius Kühn-Institut Institute for Resistance Research and Stress Tolerance

³HYBRO Saatzucht GmbH & Co. KG

⁴Saatzucht Steinach GmbH&Co KG

doerthe.musmann@jki.bund.de

Winter rye (*Secale cereale* L.) is a traditional cereal in Middle and Eastern Europe with versatile uses. Rye bread is particularly appreciated due to the high nutritional value of the rye grain. Rye is also used for feeding purposes and as a source for renewable energy to supplement and mix up biomass crop rotations.

Highly productive hybrid varieties keep rye growing competitive in modern agricultural production systems. Because of the complexity of hybrid performance, breeders take much effort to identify best performing cross progenies between inbred lines originating from heterotic pools. Up to now, no markers for quantitative inherited trait loci (QTLs) governing grain yield, thousand-grain weight, plant height or days to heading have been described for rye. Markers associated with QTLs could be used to improve these complex inherited traits more efficiently in practical rye breeding programs.

Recent progress in marker technology renders association mapping in rye on a genome-wide scale a feasible task. We have fingerprinted elite lines representing a successful hybrid rye breeding program with SSR as well as high-throughput, microarray-based DNA markers. Furthermore, candidate gene sequences for selected traits were included. Marker analysis enabled us to assess the genetic diversity in elite inbred lines of rye and to clearly distinguish both heterotic groups 'Petkus' and 'Carsten' at the molecular level. Correlation analysis identified markers with significant effects on the analysed traits. Sequence information on associated markers allowed for comparative QTL mapping between rye and rice. This approach revealed that orthologs of some of these markers coincide with QTLs that have been reported in rice. Results obtained in this study contribute to elucidate the molecular basics of agronomic important, complex inherited traits in rye.