

High throughput analysis of grain quality parameters for hybrid rye breeding

Dörthe Musmann¹, Gisela Jansen², Hans-Ulrich Jürgens²,
Barbara Kusterer³, Franz Joachim Fromme³ and Bernd Hackauf^{1*}

Abstract

Rye (*Secale cereale* L.) is an invaluable part of crop rotation systems and contributes to increase crop species diversity mainly in European agroecosystems. This small grain cereal is a multi-purpose crop traditionally used in the production of bread or mixed animal feeds and is established as a renewable resource for bioenergy production. Regarding grain quality parameters, these versatile uses of rye require very diverging breeding goals. However, an efficient phenotyping of grain quality parameters, particularly with respect to the content of arabinoxylans as the predominant dietary fibre in the rye grain, is currently the limiting factor in rye breeding.

We have used a near infrared spectroscopy (NIRS) calibration to predict grain quality parameters in experimental rye hybrids. This NIRS calibration was adjusted by a set of 63 selected grain samples from 320 experimental hybrids, which were cultivated in 2011 in two replicates and five environments located in Germany and Poland. After non-destructive NIRS scans of the 3200 samples with two replicates each, the concentration of crude proteins (CP), starch (STC), water-extractable arabinoxylans (WEAX) as well as total arabinoxylans (TAX) was assayed as recently described. Thousand grain weight (TGW) of these samples was included in our analysis as an additional parameter.

The cross-validated NIRS calibration allowed to predict the content of CP, STC, WEAX and TAX in rye grains with unprecedented accuracy. The experimental hybrids revealed significant phenotypic variation for each of the assessed traits. All phenotypic data did not significantly deviate from normal distribution. Coefficients

of phenotypic correlation among traits were significant ($P < 0.05$) for every trait combination. A strong negative correlation ($r = -0.95$) could be observed between grain protein and starch content. The intensive phenotyping led to high heritability estimates for all traits including water-extractable arabinoxylan content.

We have applied an association mapping approach to unravel the genetic architecture of grain quality parameters in rye. For this purpose, we have tested 1511 DArT markers with an allele frequency $> 5\%$ in the 320 experimental hybrids for associations with quality traits. The squared correlation of allele frequencies (r^2) representing linkage disequilibrium (LD) were assessed for 483 DArT markers, which we were able to integrate in the recently published transcript map of rye. A critical value of r^2 , beyond which LD is likely to be caused by genetic linkage, was estimated at 0.13 for all experimental hybrids. Average LD was observed to decay below the critical level within a map distance of 5-7 cM. We have identified 502 significant ($P < 0.05$) marker trait associations of which 159 (32%) have known map positions. QTL for CP (31), STC (26), WEAX (27), TAX (27) and TGW (48) are located on each of the seven rye chromosomes. In total 18 QTL for CP and STC are co-localized, which is consistent with the observed strong negative phenotypic correlation between both parameters. The identified marker/trait associations provide a first step towards a targeted molecular characterization and utilization of genetic resources for precision breeding of hybrid rye varieties with defined grain qualities.

Keywords

Arabinoxylan, DArT marker, NIRS, *Secale cereale*

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¹ Julius Kühn-Institut, Institute for Breeding Research on Agricultural Crops, Rudolf-Schick-Platz 3, OT Groß Lüsewitz, 18190 SANITZ, Germany

² Julius Kühn-Institut, Institute for Resistance Research and Stress Tolerance, Rudolf-Schick-Platz 3, OT Groß Lüsewitz, 18190 SANITZ, Germany

³ HYBRO Saatzucht GmbH & Co. KG, Kleptow 53, 17291 SCHENKENBERG, Germany

* Corresponding author: Bernd HACKAUF, bernd.hackauf@jki.bund.de

