Using Genebank Accessions for Discovery Loci Determining Pre-harvest Sprouting and Dormancy in Wheat and Barley – An Association Mapping Approach

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Introduction

Pre-harvest sprouting (PHS) (fig. 1) is a phenomenon of cereal crops when germination of grains occurs in the spikes before harvest and therefore it is a big problem in wheat and barley production. It reduces crop yield to the point of a total damage of the harvest. Seed dormancy can prevent sprouting but can also for example delay the malting process in cultivated barley. Searching for dormancy and sprouting genes can help to prevent these effects. As complex traits with high genetic variation it can be assumed that both traits are controlled by multigenes or quantitative trait loci (QTLs).

Fig. 1: Pre-harvest sprouting in wheat

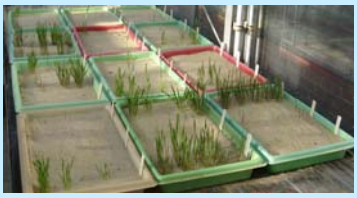

Fig. 2: PHS test

Fig. 3: Scoring of the PHS test
1 = no coleoptile visible
7 = all seeds germinated

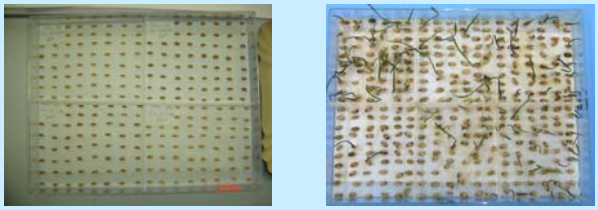

Fig. 4: Dormancy test at 20 °C, at the beginning (left), after 7 days (right)

Plant Material

Three wheat and two barley populations were used to study PHS and dormancy. For wheat two biparental populations (ITMI and D-genome introgression lines) and one multiparental population based on 183 genebank accessions were investigated. For barley two biparental populations (OWB and “Steptoe” x “Morex”) were studied. All material was cultivated in Gatersleben, Germany, on experimental fields, in greenhouses and/or in a foil tunnel in different years.

Tests

Pre-Harvest Sprouting Test

Five ears per line directly harvested at maturity are placed in a plate full of sand for 14 days (fig. 2). For the interpretation of the data a rating of seven score points is used (fig. 3).

Dormancy Test

60 seeds per line directly harvested at maturity are tested under two different temperature conditions: at 20°C for 7 d and at 10°C for 14 d under a light regime of 12 h light/12 h dark (fig. 4).

QTL analysis / marker trait associations

A classical quantitative trait loci analysis was combined with an association mapping approach. Many quantitative trait loci and marker trait associations (MTAs) could be detected on all seven chromosome groups of wheat and on the chromosomes 2H, 3H, 5H, 6H, and 7H of barley. Especially, the known regions on chromosome 3A and 4A (fig. 6) for wheat and 5H (fig. 5) for barley were confirmed. Via a candidate homologues search and via expressed sequence tag annotation putative functions could be found. On chromosome 3A the *viviparous1* gene is located which is associated to pre-harvest sprouting and dormancy. On chromosome 4A a protein is detected which belongs to the aquaporin family. Aquaporins are responsible for water flow through the cell membrane. In barley an association with the *aleurain* gene on chromosome 5H was found. The expression of *aleurain* is regulated by abscisic acid and gibberellic acid. From both hormones an influence on dormancy and pre-harvest sprouting is known. It can be concluded that dormancy and pre-harvest sprouting are very complex traits regulated by multigenes and/or quantitative trait loci (Lohwasser et al., Biol. Plant. in press).

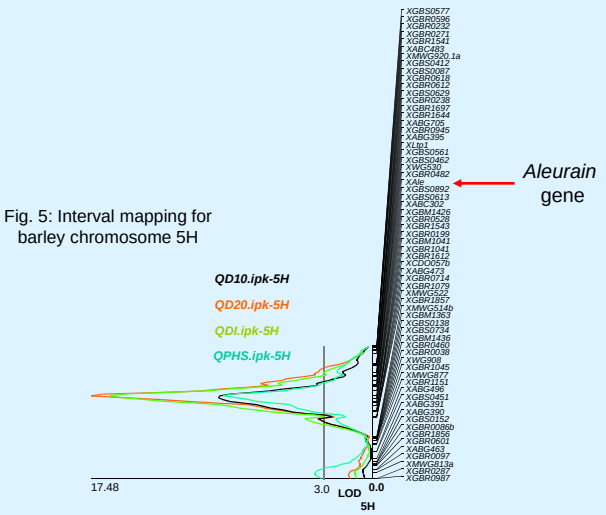

Fig. 5: Interval mapping for barley chromosome 5H

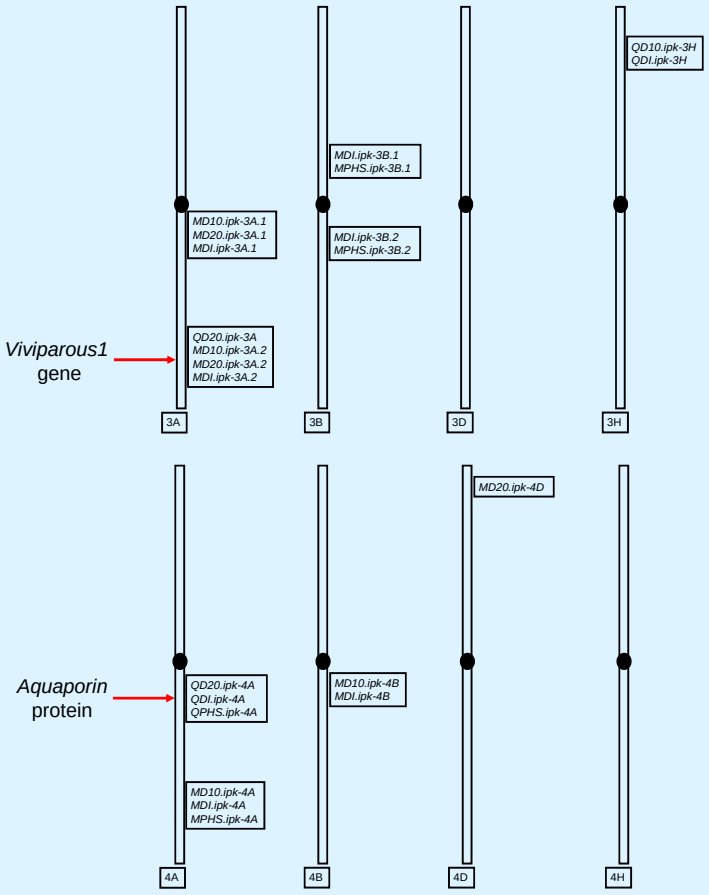

Fig. 6: Comparison of detected QTLs and MTAs in wheat and barley for chromosome groups 3 and 4

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