Genome Wide Association Study for Common Bunt Resistance in Wheat and Creation of Common Bunt Resistant Composite Cross Populations

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Common bunt remains a major challenge to organic wheat production in Denmark. In order to increase our understanding of the genetic components involved in common bunt resistance a genome wide association study involving 250 wheat lines was conducted. Lines were grown in two replications per year in Mariager, Denmark. Infection was recorded as the percentage infected ears of all ears per line and replication.

Wheat lines were genotyped with DArT markers (Diversity Arrays Technology, Australia), yielding 1824 polymorphic marker. A compressed mixed linear model accounting for both population structure and familial relatedness was used to estimate marker effects on common bunt resistance score. In total, 3 QTL for common bunt resistance could be identified, 1 QTL located on chromosome 2B and the others on chromosome 7A.

Wheat composite cross populations are created by the inter crossing of varieties and the subsequent bulking of the offspring, creating highly diverse populations with an increased resilience towards environmental impacts. Such a buffering is anticipated to be of great benefit in organic farming systems with a reduced impact of agrochemicals.

A number of 22 winter wheat varieties with different degrees of common bunt resistances was used in 33 crosses. The offspring was bulked in two different ways: 'Population 1' was created by bulking equal amounts of F_2 seeds from each cross. In order to build the second population 160 head rows, from seed of the F_2 of the crosses, with less than 2% infection were selected to form “Population shr” (selected hear rows). Both populations were grown both under heavy common bunt inoculum pressure in order to select for resistance among its plants, and without common bunt disease pressure as a control. Disease incidence was recorded in both populations in generations F_4 and F_5, and the populations grown without disease pressure were compared to their parents in a two location yield trial.

Infection levels between “Population 1” and “Population shr” differed significantly with disease incidences of 14% and 4% for “Population 1” and “Population shr”, respectively. In a two location yield trial the population yield did not differ significantly from the mean parental yield. We believe that it is possible to use such wheat composite cross populations as a germplasm source for organic breeding, and it should also be possible to give improved populations directly to farmers for commercial wheat production. The resistance development in the populations will be continued for 3 more years.