Poster abstract

Association Mapping for Common Bunt Resistance in Wheat

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Key words: Common bunt (*Tilletia caries*), Wheat (*Triticum aestivum*), Association mapping, Organic farming

Abstract

Common bunt, caused by *Tilletia caries* and *T. foetida*, is a fungal disease of wheat world wide. Infection, occurring via seed borne teliospores, is generally controlled by the application of seed treatments prior to sowing. Farming systems like organic agriculture with a very limited range of organic seed treatments available rely heavily on common bunt resistance genes within wheat. In the framework of the BIOBREED project an association study in winter wheat was conducted, aiming at the identification of genetic loci linked to resistance towards common bunt in wheat.

152 European wheat cultivars were phenotyped for their resistance reaction for the two consecutive years 2011/12 at Agrologica research station at Mariager. Infection was scored as percent infected ears. The scorings were log-transformed to fit a disease scoring scale ranging from 1 to 9. The association analysis was performed for each year separately as well as for the mean scoring of the two years. The wheat cultivars were genotyped with DArT markers, yielding 1832 polymorphic loci. The association analysis was conducted using the computer program Genstat, with the ASReml module. Minimun allele frequency for the association analysis was set to 0.07.

13 out of the total of1832 marker in our study were linked to common bunt resistance in wheat (-log10(*P*) >3). These marker are located on 8 out of the 21 wheat chromosomes. Comparisons of these findings with other published results are difficult since only very little is known about the chromosomal location of common bunt resistance genes/QTL in wheat. Chromosome 2B was previously reported to carry gene(s) for common bunt resistance. Findings of our analysis are in accordance with this: 4 of the linked marker resided on this chromosome. Further, another two linked marker were found on chromosome 2D, another chromosome previously reported to carry common bunt resistance genes.

Our study shows the possibilities of finding makers linked to common bunt resistance in wheat, and of using these markers for marker assisted selection of wheat cultivars tailored for the needs of organic agriculture.

Acknowledgments

BIOBREED is supported by The Danish Food Industry Agency, Ministry of Food, Agriculture and Fishery 2010-14.

References

Jaccoud D, Peng K, Feinstein D, Kilian A (2001) Diversity Arrays: a solid state technology for sequence information independent genotyping. Nucleic Acids Research 29: e25.