Höhere Bundeslehr- und Forschungsanstalt
Raumberg-Gumpenstein

65. Tagung der Vereinigung der Pflanzenzüchter und Saatgutkaufleute Österreichs 2014, 123 – 124
ISBN: 978-3-902849-22-9

Mapping dwarf bunt resistance in winter wheat

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Abstract

During the last two decades, bunt diseases have re-emerged in organic winter wheat throughout Europe. Currently, no bunt resistant and adapted varieties are available for organic farming in Austria. Whereas the predominantly seed-borne disease common bunt (*Tilletia tritici, T. laevis*) can be managed by careful seed hygiene, control of the soil-borne dwarf bunt (*T. controversa*) is more challenging: Dwarf bunt teliospores are long-lived and contaminated soils cannot be used for organic winter wheat production for a minimum of 10 years. Host resistance therefore constitutes the most important tool for bunt control in organic farming. Breeding for bunt resistance is time and cost intensive and molecular marker technology could greatly facilitate the development of resistant winter wheat varieties. Knowledge regarding the genetic basis of bunt resistance, however, is limited and little is known about the interaction between dwarf and common bunt resistance. Monogenic, race specific bunt resistance in winter wheat is conferred by 13 to date identified bunt resistance genes *Bt1* to *Bt13*, of which seven have been allocated to individual wheat chromosomes. Molecular markers are available for *Bt10* only. Quantitative, non-race specific bunt resistance has also been described in winter wheat.

Ten mapping populations, based on crosses between bunt resistant exotic material (Turkish landraces and North American cultivars) and susceptible but adapted winter wheat cultivars were developed; these will be tested for bunt resistance in field trials at multiple sites for three years from 2014 to 2016. In contrast to common bunt, dwarf bunt disease development depends on favourable weather conditions during winter: multiple years of testing are therefore required to assess the resistance phenotype. In 2014, the mapping populations were tested at two sites in Austria for dwarf bunt resistance but overall infection levels were too low to gain informative results. A subset of the populations was tested for common bunt resistance and highly informative results were collected already in the first year of testing. All parental lines were tested at additional sites in the Czech Republic and Germany for dwarf bunt and in Sweden for common bunt resistance, i.e. resistant parental lines, representing monogenic (*Bt11*, *Bt12*) as well as complex sources of resistance, conferred durable protection against a broad spectrum of bunt races across locations. The set of bunt differential lines - of which each contains one of the 13 *Bt* genes - was tested at all trial sites for dwarf bunt and common bunt resistance. Of these, only *Bt11* and *Bt12* conferred stable resistance against dwarf bunt and common bunt at the same time. In 2015 and 2016 all mapping populations will be tested for dwarf bunt and common bunt resistance in field trials located in Austria. In addition, populations will be tested for dwarf bunt resistance in Utah (Logan, USA). The most promising populations with regard to differentiation of the resistance trait will be genetically fingerprinted using genotyping by sequencing (GBS). Combined statistical analysis of phenotypic and genotypic data will identify genes (QTL) for durable bunt resistance in winter wheat, and will allow the development of molecular markers for application in organic wheat breeding.

Keywords

Breeding, disease resistance, marker assisted selection, *Tilletia* sp., *Triticum aestivum*

Acknowledgments

The project *COBRA Austria* is funded within the framework of the ERA-Net project Core Organic 2 by the Austrian Federal Ministry of Agriculture, Forestry, Environment and Water Management (project number 100898). We highly appreciate ongoing collaboration with the following COBRA partners regarding bunt resistance field trials: Veronika Dumalasova (Crop Research Institute, CZ), Robert Bauer, Berta Killermann, Benno Voit (LFL Bayern, DE), Inger Ahman (Swedish University of Agricultural Sciences, SE). We are grateful for excellent technical support at experimental stations in Tulln (Matthias Fidesser, Lisa-Maria Schmid, IFA Tulln), Schönfeld (Ferdinand Klinger, Christian Auer-Wallisch, AGES) and Lambach (Manfred Pamminger, Angelika Schneider, HBLFA Raumberg-Gumpenstein).

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