

Gene postulation based on phenotyping wheat varieties with a differential set of virulence races of common bunt (*Tilletia caries*)

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Abstract

Knowledge about the resistance genes in wheat varieties is crucial for predicting the actual field resistance against plant diseases, and also as a basic knowledge for development of genetic markers. As a basis for development of genetic markers for resistance to common bunt (*Tilletia caries* and *T. leavis*), and as a screening trial for breeding lines, a field trial was set up to evaluate wheat germplasm.

Based on a design described in Borgen *et al* (2018), a trial was set up using 8 races of common bunt (*Tilletia caries*) to infect 850 wheat varieties and breeding lines.

Approximately 50 seed of each line was applied with dry spores in a paper bag and shaken. Enough spores were applied to cover the seed surface and leave a few spores in surplus in the bottom of the bag. Seed was hand sown in rows directly from the seed bag to avoid mixtures of spores in sowing equipment. Symptoms of infection was done by visual assessment 4-5 weeks after heading.

Breeding lines and approved varieties for the experiment was supplied by Dottenfelder Hof, Cultivari, Saatzücht Donau and Agrológica. Genebank accessions was supplied by NordGen, John Innes Institute and USDA National Small Grain Collection.

Goates (2012) described 16 resistance genes denominated Bt1-15 plus BtP. Additional resistance genes BtZ (Blažková and Bartoš 2002), Trintella-resistance (Dumalasová *et al* 2012) and Blizzard-resistance (Wang *et al* 2009) has been described.

The races used in the experiment was:

- Vr-2 Virulent to Bt1, Bt2 and Bt7
- Vr10 Virulent to Bt7, Bt10 and BtZ
- VrZ Virulent to Bt4, Bt6, and Bt10
- Vr-5 Virulent to Bt5 and low infection in Bt7 and Bt4,
- Vr-3 Virulent to Bt2 and Bt3,
- Vr-DOT Virulent to Bt2 and low infection in Bt7 and Bt1,
- Vr-0 Not virulent to any Bt-genes,
- Vr-13 Low infection in Bt13,

None of the races were virulent to Bt8, Bt9, Bt11, Bt12, Blizzard or BtP. Also, no virulence was found against *Erythrospermum* 5221, which has a resistance gene translocated from *Agropyron* (Baranovskaya *et al.* 2003 cited in: Babayants 2006). Germplasm containing any of these genes came out as being resistant to all races.

There seems to be no additive effect of gene combinations. In contrast, the resistance of a variety is governed by the most effective gene, and if a bunt race is virulent to all the genes in a variety, then

the variety will be susceptible to the race. This confirms that the Bt-genes follows the gene-to-gene relationship (Flor 1942).

Based on the phenotyping, it was possible to postulate the Bt-resistance genes in most lines having a single or a combination of few genes to which virulence was present. Some two-gene combination were resistant to all races, and the resistance genes can therefore not be determined by this experiment alone. However, if the parents and the resistance of the parents are known, then phenotyping combined with parental information can often predict the resistance.

Based on parental information in combination with this experiment, and in combination with genotyping of the involved germplasm, it has been possible to perform GWAS and develop a range of genetic markers associated with the Bt-genes (Christensen and Borgen 2023A-F, Borgen and Christensen 2023).

Keywords

winter wheat, common bunt, breeding resistance, plant diseases.

Acknowledgments

Phenotyping was funded by BOOST funded by Organic RDD and DIVERSILIENCE funded by CoreOrganic Cofund.

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