

## **SCREENING WHEAT VARIETIES FOR RESISTANCE WITH PURIFIED VIRULENCE RACES OF COMMON BUNT (*TILLETIA CARIES*)**

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### **Introduction**

Trials screening wheat for resistance to common bunt sometimes suffers from inconsistent results because spores used often are diverse, and contains a variable mixture of virulent and avirulent races to certain resistance genes. An attempt has in this study been made to screen varieties using spores purified with specific virulence.

### **Methods**

From 2012 and onwards, resistant varieties were infected with spores collected from the same varieties if infected spikes were found. In this way, a collection of 98 virulence races were build up specific to the 98 wheat varieties, including differential varieties with known resistance genes. In 2013-14 and in 2014-15, spores from 7 selected varieties were used to infect the other varieties. The varieties were sown in 0.5 rows without replication with 5g seed per row.

### **Results**

Some of the varieties that had low infection in previous trials, and therefore earlier were recorded as almost fully resistant, could indeed be infected if they were re-inoculated with the spores from the few infected plants of the variety. For example, varieties with the resistance gene *Bt10* had no or low infection when infected with the diverse spore collection,

and it was concluded that Danish spores were avirulent to *Bt10*. However, when varieties with *Bt10* were inoculated with spores from varieties with *Bt10*, they turned out to be highly susceptible. The spore collection is therefore a mixture of virulent and avirulent spores against *Bt10*. The same is the case for *Bt2*, *Bt7*, *Bt13* and *BtZ*. When varieties were inoculated with spores that had been purified on other varieties, they were normally either more resistant or more susceptible compared with inoculation with the spores mixture. It is likely that varieties that react in a similar way to different origins of spores may have the same resistance genes. However, this is not always the case. Some (or maybe most) varieties carry more than one gene affecting the susceptibility, and certainly most virulence races of the pathogen are virulent to more than one resistance gene. For example, all spores virulent to *Bt10* are in this study also virulent to *BtZ*, and I have been unable to distinguish between these two genes. Some varieties have so far been resistant in all studies, and even if a few plants were infected, spores from these plants have been unable to create a high infection level. Some of these varieties may have a resistance gene to which no virulence have been found, and some varieties may have a combination of pyramided genes. I have been unable to develop virulence races specific to the resistance genes *Bt3*, *Bt4*, *Bt5*, *Bt6*, *Bt8*, *Bt9*, *Bt11*, *Bt12*. It is possible that the varieties NGB9014, NGB-9015, Tambor, Kuban, Begra, Maribos, Fold, Monopol, Tarso, Torrild, Cardos, Kranich, Türkis, Gluten, Folke have *Bt7*, since they react in a similar way to the 7 different sources of spores used in 2014-15. It is possible that the varieties Format, Curier, Complet, Solstice, Bussard, Paroli, Dream, Butaro, Ochre, PG3540 and Hereward have *Bt2*. The varieties Korrund, Aron, Karat, Tulsa, Xenos, Tataros, Erbachshofer Braun and Indigo have in some trials shown resistance, but in 2014-15, they have been susceptible to most or all virulence races. Spores harvested on the variety Tommi in Sweden in 2014 were able to give a high infection in the Tommi, Globus and Segor, and a medium infection was achieved with spores from Austria, even though these varieties have so far been resistant or shown low susceptibility to spores from Denmark. The spores from Sweden were unable to infect differential lines resistant to all the Danish spores. The variety Quebon could be infected by spores collected in Czech Republic, but was resistant to all other spores tested on other varieties. This indicates that Tommi, Globus and Segor may carry the same resistance gene, which is different to the gene in Quebon, and different to the known *Bt*-genes.