Strategic use of virulence pattern to develop genetic markers for resistance to common bunt (*Tilletia caries*) in wheat

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When assesssing races of common bunt for virulens pattern within a region, it is important to take into account that collected spores may represent a diverse population of different virulence races. When screening spores on a differential set of wheat lines with known resistance genes, a low infection rate on a resistant wheat variety does not necessarily demonstrate that virulence is absent in the spore collection, but could be a sign that virulence is present, but only present in a low frequency among the spores. If just a few spores within a spore sample are indeed virulent, they may infect some plants and from there multiply the virulence quite rapidly next years. Previous studies have shown that virulence against most resistance genes were present in Denmark after purifying races of common bunt (*Tilletia caries*) on resistant varieties. So far, only wheat differential varieties with Bt4, Bt6, Bt9, Bt11 and Bt12 cannot be infected with bunt races purified from Danish collections [1, and later own unpublished data]. Virulence against Bt4, Bt6 and Bt9 has been found in other European studies [2], and Bt11 may not be only one gene but a combination of at least two genes [3]. Therefore, Bt12 seems to be the only gene for which virulence have not been found in European population of common bunt. This leads to the conclusion that if resistance breeding shall safely control common bunt in wheat, we need not only one effective gene, but a combination of pyramided genes. Since it is very difficult to test if a resistant line has only one gene or more genes, the most effective tool to achieve this at present is genetic markers.

Using Genome Wide Association Studies (GWAS) to find QTLs and markers for the major resistance genes in wheat have so far led to only few commercial useful markers. Till now, only markers for Bt9 [6] and Bt10 are used in practice, but a marker for Bt12 [4] and Blizzard [7] have also been found. One of the problems in developing markers for bunt resistance have been that spores used in GWAS trials have been divers or unknown in virulence, and that phenotypic results not distinguishs between different resistance genes. Therefore, the most successful studies have used segregating populations of single crosses where the resistance gene is known on before hand [5].

In the LIVESEED project, we have the ambition to develop genetic markers on several different resistance genes at the same time. We will do so by testing segregating populations of several different crosses between varieties with 7 different resistance genes, and infect them with 7-11 different virulence races of common bunt able to distinguish between the resistance genes. A total of 300 varieties will be pheno- and genotyped. Using this experimental design, we attempt during 2018 and ‘19 to develop markers for Bt1, Bt2, Bt5, Bt7, Bt13, BtZ and Quebon-resistance, and hopefully also a couple of minor QTLs.

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