



P 212 - Topic: Genetics and Genomics of Biotic and Abiotic Stress Resistance

The exploitation of wheat/*Amblyopyrum muticum* introgression lines carrying inter-genomic rearrangements, involving the D genome with the A and B genome of wheat, for durum wheat improvement to STB disease

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Key message: The effect of the D genome introgression in durum wheat on *Septoria tritici* blotch resistance and other traits for durum wheat improvement.

Septoria tritici blotch (STB), is an important foliar blight disease of wheat worldwide. Genetic resistance is the most effective and economical method of controlling STB. The aim of this study is to improve genetic resistance of two susceptible durum wheat varieties to STB disease through the exploitation of the D genome effect on the durum wheat specific strains. Forty plants coming from nine different introgression lines of wheat/*Amblyopyrum muticum* containing AD, BD and ABD chromosomal translocations were crossed in glasshouse conditions to the two durum wheat genotypes in an attempt to transfer the chromosomes carrying these intergenomic translocations involving the D genome into durum wheat. Five of those introgression lines were shown to also carry one or two segments of *Am. muticum* (King et al. 2017). Sixty crosses were made between these nine lines and two durum wheats to produce 488 F₁ seed. The presence of D genome translocations was assessed in 120 F₁ plants using multi-colour genomic *in situ* hybridisation technique. Only 40 plants were shown to carry the D genome translocations. Most of the D genome introgressions identified were located on the A genome especially in the telomeric regions, indicating that frequent associations of the A-D type occur in hybrid lines between wheat and the alien species *Am. muticum*. The F₁ plants selected will be back-crossed to the recurrent durum wheat parent and the BC₁ seed showing the presence of the D genome translocations will be selfed until they reach the tetraploid chromosome number with a potential homozygous introgression of the D genome. At this stage the selected plants will then be phenotyped in field conditions for STB disease resistance and other traits in two different environments. This will be achieved through a shuttle-breeding programme between Tunisia, a hot spot for STB disease, where the pathogen is durum wheat specific, and Mexico (CIMMYT). Phenotyping at these two locations will also enable selection for other traits in advanced generations. The aim is to map any potential STB resistance loci using genotyping with the 820K Axiom array SNP markers to identify D-genome specific contribution to such disease resistance.

Reference

King J, Grewal S, Yang CY, Hubbart S, Scholefield D, Ashling S, Edwards KJ, Allen AM, BurrIDGE A, Bloor C, Davassi A, da Silva GJ, Chalmers K King IP (2017) A step change in the transfer of interspecific variation into wheat from *Amblyopyrum muticum*. *Plant Biotechnol J* 15: 217-226.