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CHARACTERISATION OF MAJOR GENES MEDIATING RESISTANCE TO SEPTORIA TRITICI BLOTCH DISEASE IN WHEAT

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INTRODUCTION

Zymoseptoria tritici is a highly destructive wheat pathogen, that can cause crop losses of up to 50% in high risk climates. Traditionally Z. tritici has been controlled with resistance (Stb) genes and fungicides, but the high selection pressures placed on the fungi result in these protections being broken (e.g. the Stb6 resistance gene present in most European wheat cultivars is now ineffective in the UK). New diverse sources of resistance are needed - many wheat lines with durable resistance contain multiple Stb genes, suggesting that pyramiding resistances may be a viable method for enhancing their longevity.

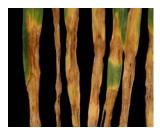


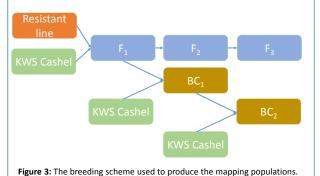
Figure 1: The damage symptoms of a severe Septoria tritici blotch infection in wheat. Leaf necrosis (causing a reduction in leaf photosynthetic capacity) and black pycnidia (enabling fungal reproduction) are both visible.

OBJECTIVES

- Identify a combination of Stb genes providing broad spectrum STB resistance in the UK, by screening a panel of most promising exotic or synthetic wheat genotypes (Table 1) against >100 current UK Z. tritici isolates.
- Isolates found to be avirulent against effective Stb genes will be used to map and trace these genes in segregating populations using linked KASP markers, enabling breeders easily integrate them into elite lines.
- In light of the recent identification of the Stb6 gene as a wall-associated receptor-like kinase (WAK) (Saintenac et al., 2018), WAK genes in the chromosome regions identified will be treated as Stb gene gene candidates as functionally analysed using Virus-induced gene silencing.

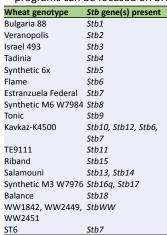
KASP MARKER DEVELOPMENT

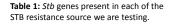
- Backcrossed lines produced using KWS Cashel as the recurring susceptible parent.
- F₃ populations derived from the first backcross generation will also be phenotyped and genotyped to analyse effectiveness of KASP markers used to follow resistances in the BC populations.



KNOWN STB GENES

- More than 20 Stb genes are currently known (Table 1 and Figure 2), but only a few have been used in elite cultivars.
- Some Stb genes have been found in landraces, synthetic varieties and wild ancestors effective markers will be vital for moving these into elite lines.
- Few systematic studies have been conducted on the effectiveness of each Stb gene in field conditions – in most studies resistances are only tested against small numbers of lab strains of Z. tritici. More research is necessary to identify Stb genes that are still effective under field conditions, so that the limited resources available in breeding programs can be focused on breeding these into elite lines.





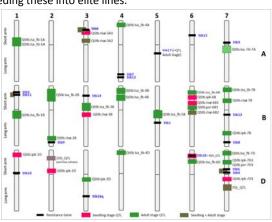


Figure 2: Chromosomal locations of each of the genetically mapped Stb genes (shown in blue) and resistance QTLs (shown in pink, green, and patterns of pink and green)

RESISTANCE SCREENING

- 54 isolates virulent on Stb6 wheat have up so far been tested against six selected wheat genotypes.
- Two genotypes show acceptable level of resistance to the UK Z. tritici, suggesting it is possible to identify a set of resistances that together protect from most isolates.

Wheat	Resistance gene		Average leaf coverage by chlorosis/ necrosis (%)
Taichung 29	none known	2.28	100
KWS Cashel	none known	3.92	82
Riband	Stb15	4.14	90
Estanzuela Federal	Stb7	2.04	96
Israel 493	Stb3, Stb6	0.52	70
TE9111	Stb6, Stb7, Stb11	0.32	43

Table 2: The reproductive success and damage caused by UK Z. tritici isolates on leaves of six wheat cultivars tested so far. Green cells indicate a resistant phenotype

WIDER RESEARCH APPLICATIONS

- Development of KASP markers will be directly useful to breeding efforts for resistances.
- Knowledge of field effectiveness of each resistances will help to target UK breeding efforts to useful end goals and avoid wasting resources on resistances that are already ineffective.
- Developing a list of resistances that together are effective against most or all UK Z. tritici isolates will provide breeders with options for effectively pyramiding resistances, potentially reducing breakdown rates.
- If further resistance genes can be identified and cloned, this will shed more light on the emerging role of WAK genes in plant disease resistance and may help to target further gene discovery efforts.

Acknowledgments.

References

Thanks to Bart Fraaije for providing the Septoria isolates utilised in the resistance screens, and to RAGT Seeds for providing mapping populations and genotyping data.