Investigating a potential link between take-all disease progression and root system phenotypes in two important elite winter wheat cultivars

Take-all root disease in wheat can be responsible for > 50% yield loss, posing challenges for future food security. Take-all is caused by the ascomycete fungus *Gaeumannomyces graminis* var. *tritici* (*Ggt*) which infects roots penetrating the inner cortex and preventing flow of water and nutrients. The fungus has little impact on first wheat yields because during this period take-all inoculum builds in the rhizosphere but is not highly infective. Without rotation subsequent wheat crops suffer from the accumulated soil inoculum resulting in higher levels of root infection. By a fifth wheat rotation, changes in soil microbiota mean *Ggt* is outcompeted causing a decline in disease. When grown as first wheats, cultivars differ in the amount of take-all inoculum which accumulates in the rhizosphere. A cultivar with low accumulation of inoculum is referred to as a LowTAB (low take-all build-up) cultivar. My project focussed on comparing a LowTAB cultivar to a HighTAB (high take-all build-up) cultivar in order to understand their root architecture phenotypes and its potential contribution to the LowTAB trait.

Field trials on the Rothamsted Research Farm in Hertfordshire, UK were used to assess take-all build-up using a soil core bioassay method. Monthly soil cores were taken from a first wheat site and baited with seeds of wheat cultivar Hereward (highly susceptible to take-all). After 5 weeks in a controlled environment seedlings were visually assessed for take-all lesions. Infection levels in pot bioassay seedlings have been proven to correlate well with levels of take-all that occur if second wheat is sown. In 2015, in the field site selected the LowTAB trait behaved differently to expected, with similar levels of take-all build up between the LowTAB and HighTAB cultivars ($p = 0.364$). This is likely to result from overall low levels of inoculum accumulating in the soil (in LowTAB 6.8% roots infected in bioassay compared to 6.1% in HighTAB).

To investigate root architecture I assessed roots from whole plant samples. To achieve this I utilised both a first wheat and a third wheat field trial, with a higher take-all infection level expected in the third wheat. Comparing current commercial cultivars in these trials revealed no significant difference in the susceptibility to take-all or total number of crown and seminal roots. However, we found a significant difference (two-way ANOVA, $p<0.05$) in root dry mass with mass lower in the LowTAB cultivar for samples taken for April, May and June. In light of these findings one key question arose: What is the cause of the lower dry mass? To answer this we examined root architecture in more detail, focusing on the June sample, as a previous BSPP Summer Student, Joseph Earley in 2014, also found a significant difference in dry root mass at this time. To deepen our study we used a WinRHIZO scanner. The analysis showed no difference in root length or diameter between cultivars. However, there was a significant interaction effect between rotation position and cultivar in one of the other parameters measured. Due to the low level of take-all build-up the correlation of differences in root architecture found with the LowTAB trait would be unreliable.

At Rothamsted Research, under guidance from Joseph Moughan, I designed my own experiment to understand the role of root exudates in take-all infection. The experiment consisted of an agar filled petri-dish centrally inoculated with one of four *Ggt* isolates, then measurements of the average growth of hyphae from the central inoculum towards the four equidistant squares of filter paper. One piece of filter paper on each plate was infiltrated with: water, take-all active fungicide, LowTAB cultivar root exudates and HighTAB root exudates. The results of the experiment showed significantly reduced hyphal growth towards the fungicide and significantly increased towards the water relative to the other four treatments. There was no significant difference between growth of hyphae towards the two cultivars.

My summer studentship has challenged me to question further the causes of food insecurity. Whilst also providing me with an understanding of new tools, techniques and approaches, namely experimental design, disease assessment, statistical analysis, culturing and linking laboratory and field methodologies. Such skills will help in my endeavour to answer questions on improving food security in my pursuit of a PhD. I would like to thank Rothamsted Research, specifically Dr Vanessa McMillan, Prof. Kim Hammond-Kosack and Joseph Moughan for his day-to-day supervision.

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Erin checking take-all isolate growth in a root exudate chemotaxis assay

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