

Annual Project Report October 2019 to September 2020

Project title	Identification of fusarium resistance within UK oat breeding lines (PhD)		
Project number	21130012		
Start date	October 2016	End date	September 2021

Project aim and objectives

To develop an inoculation method for the infection of oats with *Fusarium langsethiae*
To identify quantitative trait loci (QTL) for resistance/susceptibility to *Fusarium* spp. through the analysis of mapping populations and near-isogenic lines (NILs).

Key messages emerging from the project

Significant differences in fusarium mycotoxins exist in the NILs generated from a Buffalo x Tardis cross. In the lines grown, there is a negative association between mycotoxin concentration and height.

Summary of results from the reporting year

Near-isogenic lines (NILs)

Figure 1 shows the results of the 2017, 2018 and 2019 NIL collection, across autumn and spring sowings. 2019 had a very low infection level. Samples from 2020 are being processed, with data on height and flowering time collected.

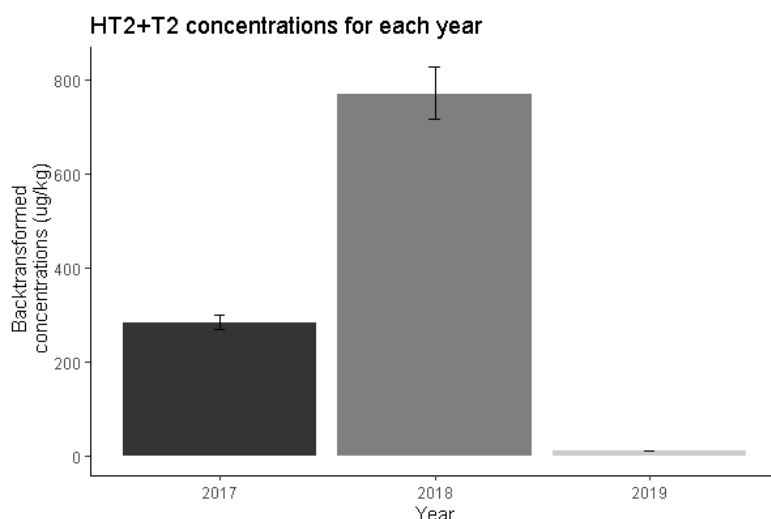


Figure 1: HT2+T2 concentrations in the harvested grain from the NIL experiments (2017–19). Error bars represent the standard error of the mean.

The results described in this summary report are interim and relate to one year. In all cases, the reports refer to projects that extend over a number of years.

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Figure 2 shows that across all three years (2017–19) there is only a small difference between the sowing seasons, and that spring sowing currently generates higher HT2+T2 concentrations.

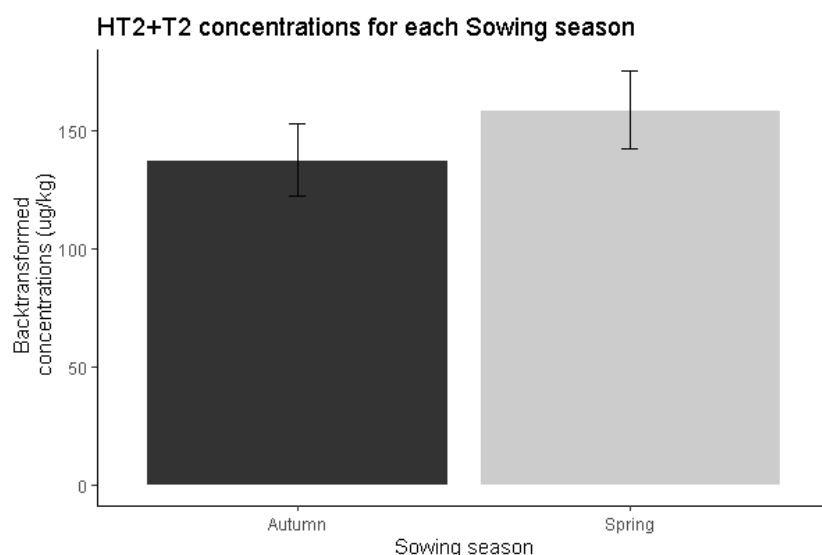


Figure 2: HT2+T2 concentrations in the harvested grain from the NIL experiments (2017–20) for each sowing season. Error bars represent the standard error of the mean.

Analysis has been conducted on the data collected to date. A summary of the variance accounted for when HT2+T2 concentration is modelled by year, height, and QTL is presented in table 1. So far, it looks like height has a small impact but the QTL present in the plant has a much larger impact. Year is the most influential factor.

Table 1: Output from the linear model examining year, height and QTL

	DF	Sum of squares	Mean sq	F value	Pr(F)	% variation
Year	2	387.8	193.9	456.4	***	43.1
QTL	8	187.6	23.5	55.2	***	20.9
Height	1	3.1	3.1	7.4	**	0.4
QTL*Height	8	21.6	2.7	6.3	***	2.4
Year*Height	2	18.4	9.2	21.7	***	2.0
Residual	662	281.2	0.4			

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Artificial inoculation

Several artificial inoculation experiments have been conducted, including two at outdoor inoculations, neither of which succeeded in raising the HT2+T2 concentration above background levels. A third field inoculation, in addition to a glasshouse experiment, was planned in 2020. However, coronavirus restrictions prevented lab access and it was not possible to produce the required inoculum. Previous glasshouse experiments were more successful. In 2017, Gerald oats were successfully infected in the glasshouse, the analysis showed that the inoculation was successful in causing a statistically significant ($P < 0.001$) increase in the concentration of HT2+T2 in the inoculated plant panicles. Furthermore, the application of inoculum to plants at the earlier growth stage of GS59 resulted in significantly ($P < 0.001$) greater concentrations of HT2+T2 in the harvested panicles. The inclusion of the potato dextrose broth (PDB) in the applied spore suspension of 2.4g/L, and 0.24g/L did not have a statistically significant effect on the end concentration of HT2+T2.

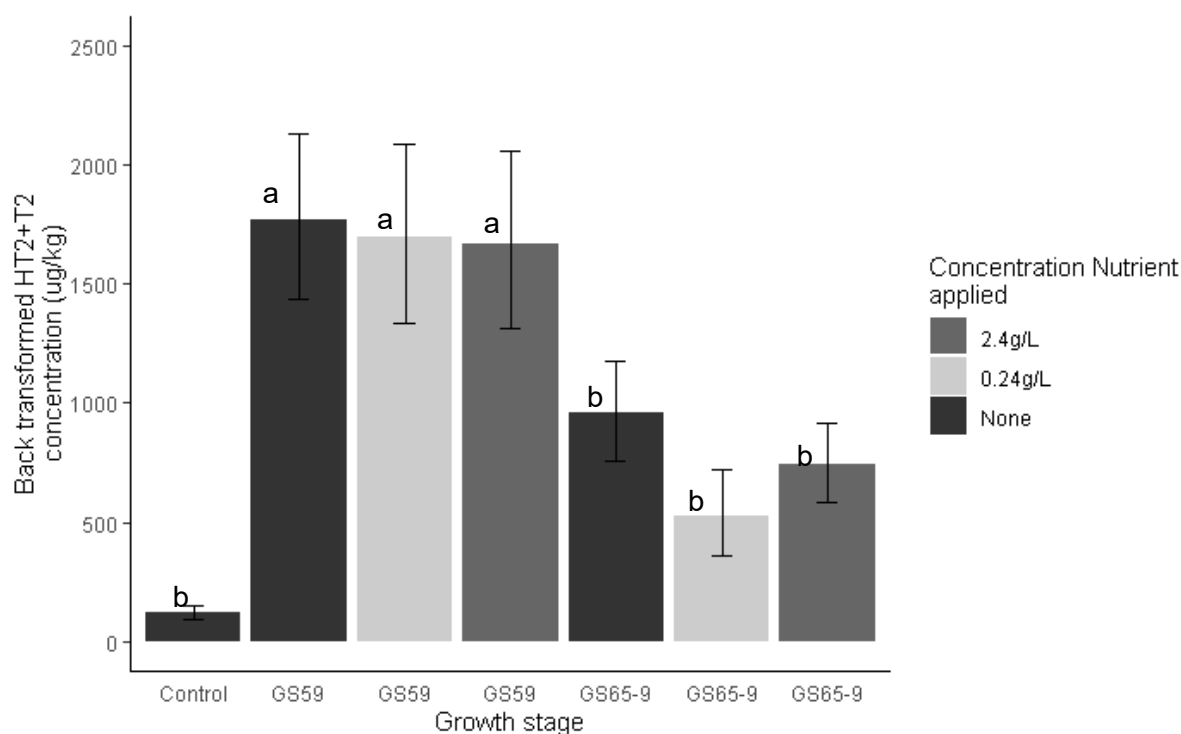


Figure 3: Back-transformed concentration of HT+T2 ($\mu\text{g kg}^{-1}$) for the control, GS59, and GS65-9 inoculated treatments. Error bars represent one standard error of the mean. Columns topped with the same letters are not statistically significant ($P < 0.05$).

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A similar experiment was repeated in 2018 looking at earlier growth stages in Balado oats (a more susceptible dwarf oat), the concentrations were less than the previous experiment. Once again, PDB was added to the inoculum to see if adding a nutrient encouraged greater infection and, again, the inoculated panicles with inoculum were not statistically distinct from those without.

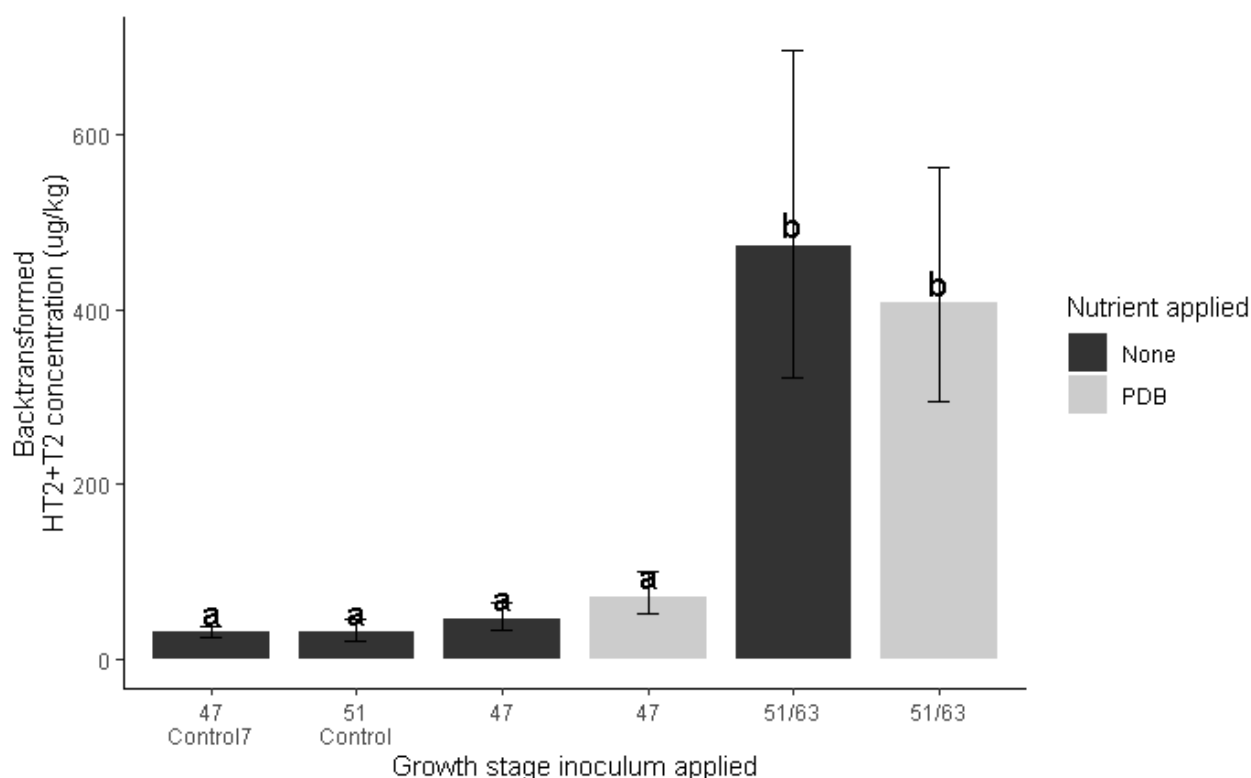


Figure 4: Back-transformed concentration of HT+T2 ($\mu\text{g kg}^{-1}$) for 2018 Balado inoculation. Error bars represent one standard error of the mean. Columns topped with the same letters are not statistically significant ($P < 0.05$).

Glasshouse work from 2019 was conducted but full analysis is not complete.

Window-pane analysis

Data from all the NIL experiments will be used in window-pane analysis examining the weather windows pre- and post-panicle emergence. Preliminary results, again, look like year will be the most significant factor. Figure 5 shows the different spreads of panicle emergence for each year and sowing season.

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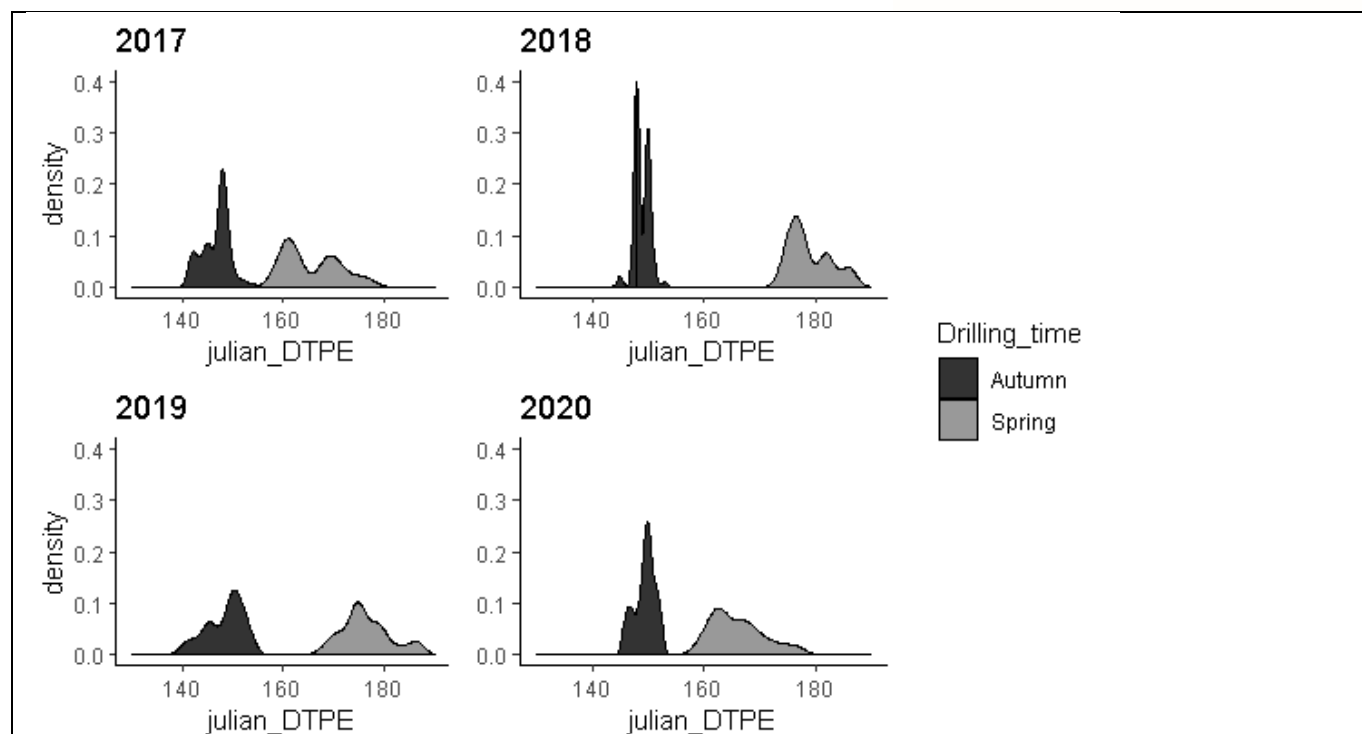


Figure 5: Density plots describing the variation in the durations of panicle emergence for each year in spring and winter from 2017–20, only genotypes that appeared in every year are included.

Panicle distribution

For two panicles from the 2018 autumn sown NIL experiment, the length of each individual branch was measured, and the position of each spikelet was recorded. One panicle was from the tallest line in the collection, which has shown consistent resistance to HT2+T2 accumulation, and the other the shortest line, which is among the most susceptible. Every spike of both panicles will be analysed by qPCR to determine the concentration of *F. langsethiae*, this will give some insight into the distribution of the pathogen across a panicle in a high-infection and low-infection scenario. So far, only the analysis of the first panicle of the taller plant has been completed and is shown in figure 6.

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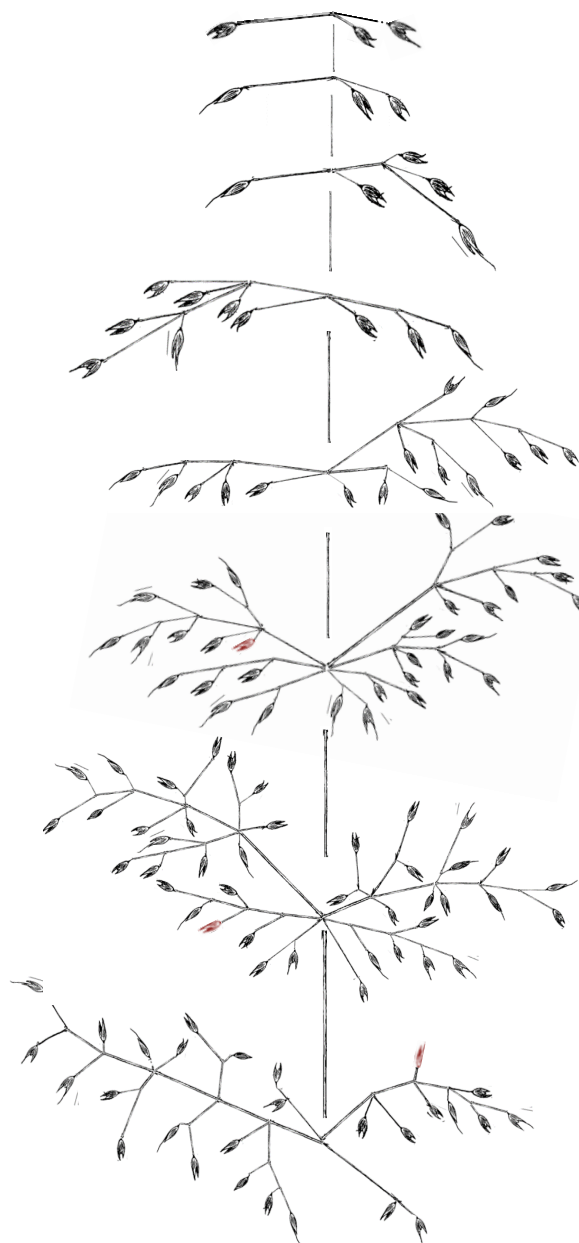


Figure 6: Mapped panicle of Buffalo + T Mrg04, the tallest genotype in the collection. Red spikes showed quantifiable concentrations of *F. langsethiae* DNA. The panicle has been drawn so that no branches overlap for clarity.

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Key issues to be addressed in the next year
Mycotoxin analysis of the 2020 harvest material, including final NIL experiment and grid samples from the field.
Analyse remaining mapped plant panicle experiment samples for <i>F. langsethiae</i> DNA
Complete window-pane analysis for all four growing years.
Complete written thesis.

Lead partner	Prof Simon Edwards, Harper Adams University
Scientific partners	Dr Catherine Howarth, Aberystwyth University
Industry partners	Felix Cobbold Trust Perry Foundation
Government sponsor	

Has your project featured in any of the following in the last year?	
Events	Press articles
None	None
Conference presentations, papers or posters	Scientific papers
Presented at the Nordic-Baltic Fusarium Seminar in March 2019 AFCP poster presentation April	None
Other	
None	

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