# *Investigating the resistance of UK oats to Fusarium langsethiae*

Joseph Crosby, Harper Adams University, Newport, Shropshire, TF10 8NB
Jcrosby@harper-adams.ac.uk

## Introduction

*Fusarium langsethiae* is a *Fusarium* species that has been identified as the main producer of HT2+T2 mycotoxin in UK oats (Edwards *et al*,. 2012). The current group tolerable daily intake for HT2+T2 and their associated phase I and II metabolites is recommended for humans as 0.02 µg $kg^{-1}$ body weight $day^{-1}$ (Knutsen *et al*,. 2016).

This project aims to measure the impact of various quantitative trait loci (QTL) on the resistance/susceptibility of winter oats to accumulation of HT2+T2. This poster specifically examines the effect of a QTL on chromosome Mrg04 which is associated with the height of the oat plant.

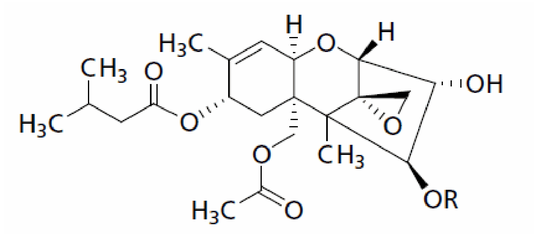



**Figure 1: Skeletal diagram of HT2 and T2 molecular structure, the R group represents the difference between the two molecules.**

## The Problem

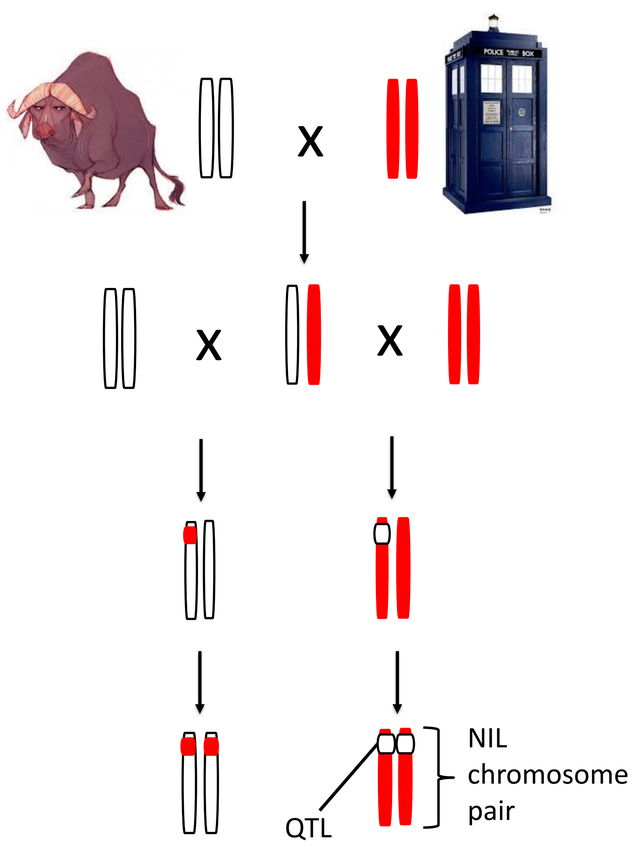
- *F. langsethiae* is the major producer of harmful HT2+T2 in UK winter oats
- Indicative levels of HT2+T2 have been set by the European Commission at 1000 µg $kg^{-1}$
- Each year between 1 and 30% (mean 16%) of UK oat samples exceeded 1000 µg $kg^{-1}$ (Edwards, 2017)
- *F. langsethiae* elicits few if no visible symptoms and its epidemiology is unknown
- Research on mitigating HT2+T2 accumulation currently relies on natural infection, which is unreliable

## Experimental Aims

- Measure the impact of the QTL on Mrg04 on the plant phenotype
- Measure impact of Mrg04 on HT2+T2 accumulation in near isogenic lines (NILs)

## Methods of Investigation

A mapping population was generated by Aberystwyth University from a cross between Buffalo (dwarf variety) and Tardis (regular height variety) and following replicated field trials, a QTL was identified on Mrg04 associated with plant height. To measure the impact of this QTL NILs have been developed from the mapping population. A NIL allows for one QTL from a donor parent to be examined in the background of the other parent so that its impact can be measured against the original background parent.




Initial cross of the parent cultivars

Backcross the $F_1$ generation with the parent several times using molecular markers to select the loci of interest

Plants are then selfed until homozygous

NILs are achieved when the genetic material from the donor parent has been introgressed into the background genome of the other parent and the plant is homozygous

**Figure 2: NILs from the Buffalo x Tardis mapping population are generated through successive backcrosses until one QTL of interest from one parent exists within the background genome of the other parent**

## Mrg04 QTL

Figure 2 below shows the Mrg04 QTL which when derived from Buffalo contains the dwarfing gene Dw6 which causes the shortening of the upper internode lengths, creating shorter plants. Using this mapping population Mrg04 has been associated with flowering time, HT2+T2 accumulation, *F. langsethiae* DNA accumulation, as well as height (Stančić, 2016)

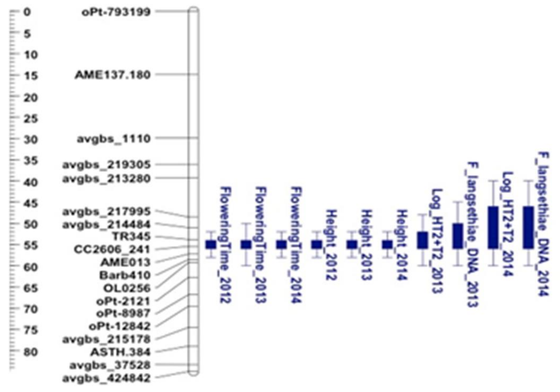



**Figure 3: Location of QTL on Mrg04 and the traits associated with this region**

Twenty five NILs were grown in a field with a cereal intense history, in a complete randomised block design with four replications. Plant heights were measured prior to harvest and HT2+T2 was measured in the harvested grain using an enzyme immunoassay (ELISA).

In Figure 4, the Buffalo allele at the Mrg04 QTL is present in lines 2012-137/5/5 and 2012-137/5/1 (red squares) in a Tardis background and this has caused these plants to be shorter. In contrast lines 2012-139/6/25 and 2012-125/1/27 (green squares) have the Tardis derived allele at Mrg04 in a Buffalo background and are the two tallest lines in the experiment. The other lines in orange also contain the Tardis allele on Mrg04 but in a Tardis background and are also taller than the Buffalo parent. The NILs are ordered in terms of their HT2+T2 accumulation and it can be seen that the background genome has a large effect but that when the alleles on Mrg04 are swapped the resulting plants are present on the opposite end of the mycotoxin spectrum.

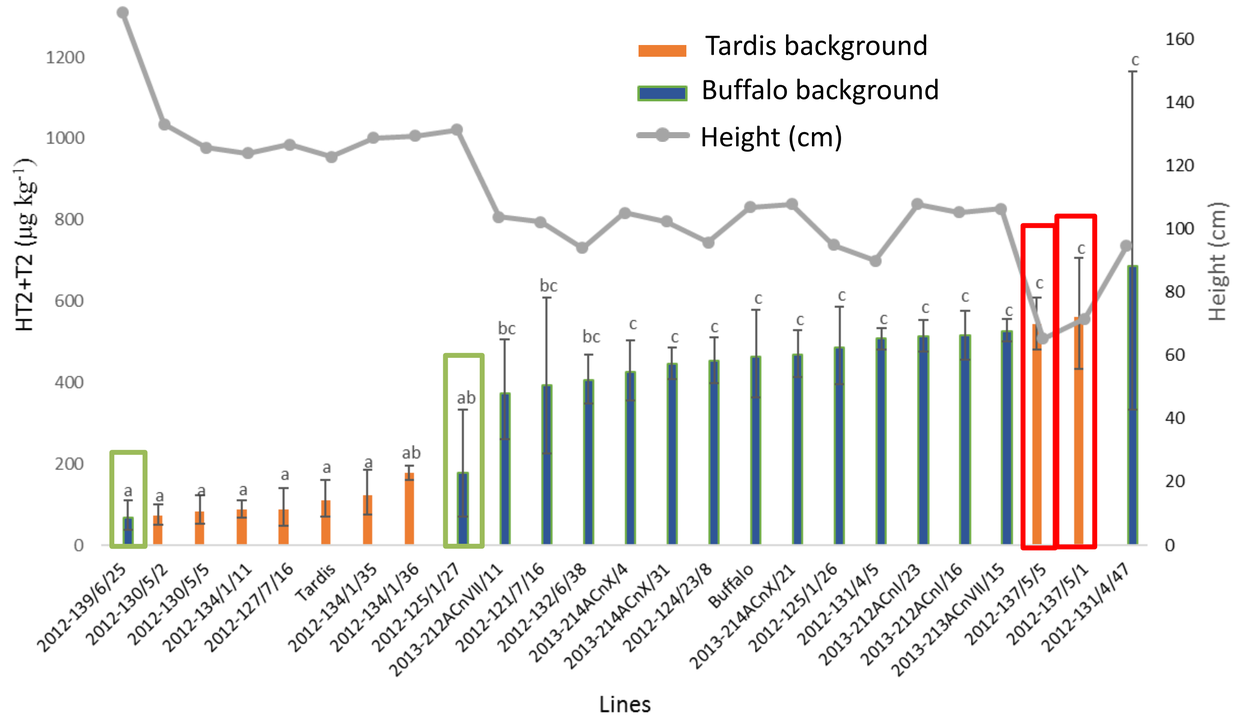



**Figure 4: Plant height and accumulation of T2 + HT2 in NILs and the parental lines, Buffalo and Tardis, columns headed with the same letters are not statistically distinct (P<0.05), error bars represent twice the standard error of the mean**

## Conclusion

Figure 4 suggests that HT2+T2 accumulation is reduced in the taller oat plants and that there is an association with the dwarfing gene Dw6. A linear regression model (not shown) supports this conclusion with a significant regression within which plant height at harvest explained 20% of the variation and background genome accounted for a further 30%. Only one season's data has been presented above and further conclusions will be drawn after multiple seasons.

## References

Edwards, S. G., Imathiu, S. M., Ray, R. V., Back, M. and Hare, M. C. 2012. Molecular studies to identify the fusarium species responsible for HT-2 and T-2 mycotoxins in UK oats. *International Journal of Food Microbiology,* 156, pp. 168-175.

Edwards, S. G. 2017. Impact of agronomic and climatic factors on the mycotoxin content of harvested oats in the UK. *Food Additives and Contaminants: Part A, 34*, pp. 2230-2241.

Knutsen *et al*., 2016. Appropriateness to set group health based guidance value for T2 and HT2 toxin and its modified forms . *EFSA Journal,* www.efsa.Europa.eu/efsajournal.

Stančić, 2016. *Fusarium* resistance in UK oat varieties: A thesis submitted in partial fulfilment of the requirements of Harper Adams University for the degree of Doctor of Philosophy. Newport: Harper Adams University.