



A new approach to reduce the risk of Take-all disease

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Take-all disease, caused by the soil-borne fungus, *Gaeumannomyces graminis* var. *tritici*, inflicts devastating stress to the roots of cereal crops worldwide and is a major disease problem in the UK. The effects of the disease are reduced grain yield, impaired grain quality (e.g. small shrivelled grains, Fig. 1) and an increased amount of residual soil mineral nitrogen left in the soil post-harvest (see RRA newsletter Issue 27, June 2008). Despite the use of chemical, biological and cultural control methods the take-all fungus is still one of the most difficult pathogens of wheat to control.

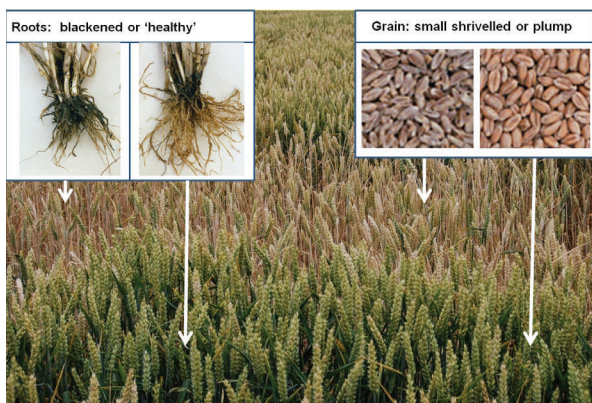


Fig 1. Below and above ground symptoms of take-all in the field and the effect of take-all on grain appearance.

Predicting the risk of severe disease in a crop is always problematic as many farm management practices, and also environmental conditions, can influence how an epidemic progresses.

The level of take-all inoculum in the soil and the associated risk of take-all disease can be indirectly measured using bait plants in a soil core bioassay. This bioassay measures the take-all infectivity of the soil, giving an indication of the amount of infective take-all inoculum present at any particular site. The percentage of bait plant roots infected in the bioassay gives a reliable indication of the risk of severe take-all occurring should a susceptible crop be grown in that soil, i.e. the more roots infected the greater the risk to the subsequent crop.

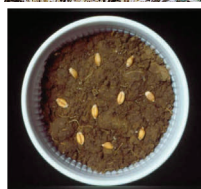
1. Soil core taken angled underneath row



2. Core inverted into plastic cup



3. Ten bait wheat seeds sown



4. Growth room for five weeks

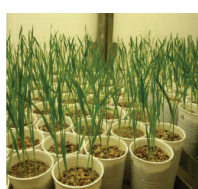


Fig 2. The bioassay method.

Previous work at Rothamsted in the 1980s had suggested that winter wheat cultivars may differ in their ability to build-up the take-all fungus when grown as a first wheat. This hypothesis was more rigorously tested in a series of field experiments between the years 2004 – 2008, which were part of the Wheat Genetic Improvement Network (WGIN; www.wgin.org.uk) designed to study the nitrogen use efficiency of different winter wheat cultivars. The experiments, all grown as first wheats, tested a number of cultivars (20-32 cultivars) at three or four nitrogen rates (0-350Kg/ha). The take-all infectivity of the soil (i.e. inoculum) after harvest was measured by a soil core bioassay (Fig. 2).

Results from these field trials showed that cultivars can differ in their ability to build-up the take-all fungus when grown as a first wheat (McMillan *et al.* (2011) Plant Pathology). The same nine sampled cultivars were common in each trial year and so it was possible to analyse differences between these cultivars over four years of experimentation. This revealed highly significant differences between these cultivars (Fig. 3).

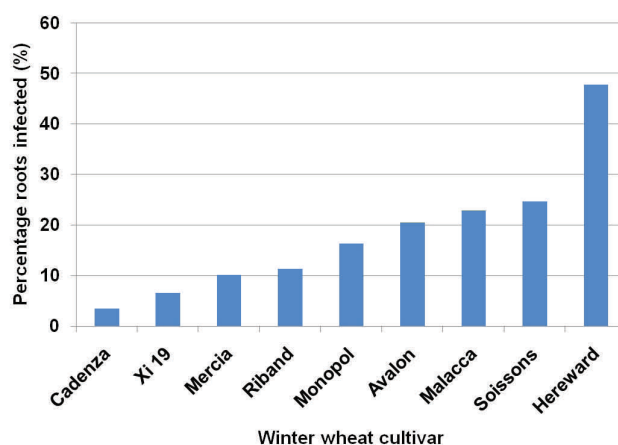


Fig 3. Percentage of roots infected in a bioassay using soil cores taken after harvest from plots containing different winter wheat cultivars - 4 year means.

The overall difference in the percentage of roots infected in the soil core bioassay between the lowest and the highest inoculum building cultivars (Cadenza and Hereward, respectively) was 44.4%. This demonstrates the potential of growing a low building cultivar, such as Cadenza, as a first wheat crop to manipulate take-all inoculum levels in the soil. This could provide farmers with a practical solution to reduce the risk of damaging take-all disease in second wheat crops.

However, the majority of the cultivars used in the above mentioned study are not currently grown and information is required on the inoculum build-up of those cultivars on the current HGCA recommended winter wheat cultivar list. This activity is currently underway and forms part of Vanessa McMillan's PhD project sponsored by HGCA and BBSRC (2008 – 2011).

Over four years of WGIN trials, Avalon and Cadenza have shown consistent contrasting abilities to build-up the take-all fungus when grown in a first wheat situation (Fig. 4).

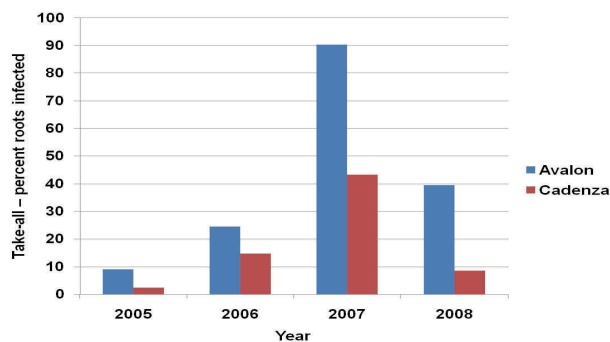


Fig 4. Percentage of bait plant roots infected with take-all in a soil core bioassay from Avalon (A) and Cadenza (C) 2005 - 2008 WGIN Diversity trial plots.

These two cultivars are the parents of a large mapping population of doubled haploid (DH) lines which had already been investigated for other traits within the WGIN programme. This was a fortuitous cross from a take-all perspective as by assessing this DH population for inoculum build-up we could explore the genetic basis for this new trait.



Fig 5. Take-all patch scores and yield of two contrasting over-sown A×C DH lines.

On the Rothamsted farm in 2007, 62 Avalon × Cadenza (A×C) DH lines along with two plots of each parent were grown on large well spaced plots for seed multiplication. In autumn 2008 these plots and plot margins were over-sown with winter wheat cv. Oakley. In early July 2009 rectangular take-all patches were evident over this site, and these clearly corresponded to the location of the A×C DH line multiplication plots grown in the previous year. The percentage area of each over-sown original plot was scored for take-all patches on 7th July

2009 and grain yields of Oakley for each original plot were taken in August (Fig. 5).

There were distinct differences between the parent cultivars. The percentage areas affected by take-all patches for the two original Cadenza plots were 5% and 10% and yielded 9.9 t/ha and 9.4 t/ha, respectively. For the over-sown Avalon the take-all scores were 50% and 70% with yields of 7.8 t/ha and 6.6 t/ha, respectively. Overall there was a significant correlation between the take-all patch score and yield (Fig. 6).

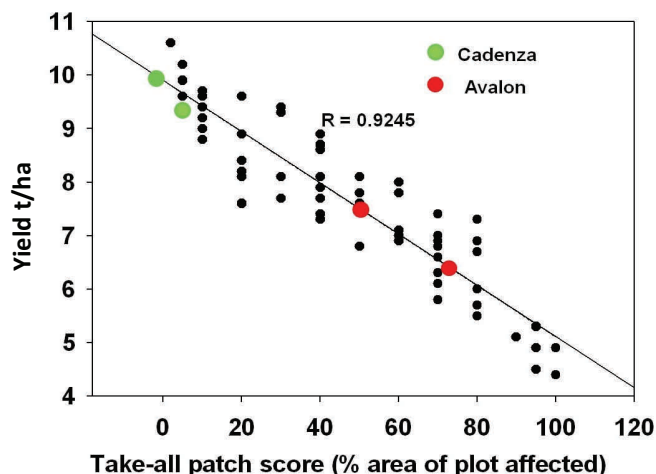


Fig 6. A×C DH lines in 2008, over-sown with winter wheat cv. Oakley in 2009. Relationship between take-all patch score and yield.

Other studies have shown a correlation between the severity of the disease and the amount of take-all inoculum in the soil at the time of sowing. Therefore, it is likely that the differences observed in 2009 were a result of the differential build up of take-all soil inoculum in 2008. A molecular mapping analysis of this A×C DH population has shown two possible major quantitative trait loci (QTLs) controlling the take-all inoculum build-up (TAB) trait.

Further field and molecular work on this trait is ongoing within the WGIN project. In addition, the Technology Strategy Board has agreed to co-fund further research and development work. The new project entitled 'Protecting Second Wheat through the Reduction of Take-All Inoculum Build Up', acronym LowTAB aims to identify and track the presence of this newly discovered trait in the pedigrees of the current elite wheat breeding germplasm pool used by the UK breeders. This new knowledge on the trait in current and future wheat cultivars should help farmers and farm advisors to reduce the risk of take-all by selecting a Low TAB first wheat cultivar when deciding to grow consecutive wheat crops.

Reference:- McMillan VE, et al., 2011. Plant Pathology 60, 200-206.



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