Understanding populations to inform Potato Cyst Nematode control

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We have identified genomic regions of *G. pallida* that are under selection when exposed to both H3 and Gpa5 resistance sources. Characterisation of PCN populations on a large scale using high-throughput sequencing and the development of avirulence diagnostics based on this genomic analysis will allow the development of high-throughput diagnostics for virulent populations of PCN. This work links with project B1-1 on identification of resistance against PCN with the overall aim of improving deployment of resistance in Scotland and with the KE activities in the Plant Health Centre PCN project increasing awareness of the importance of resistance in managing PCN.

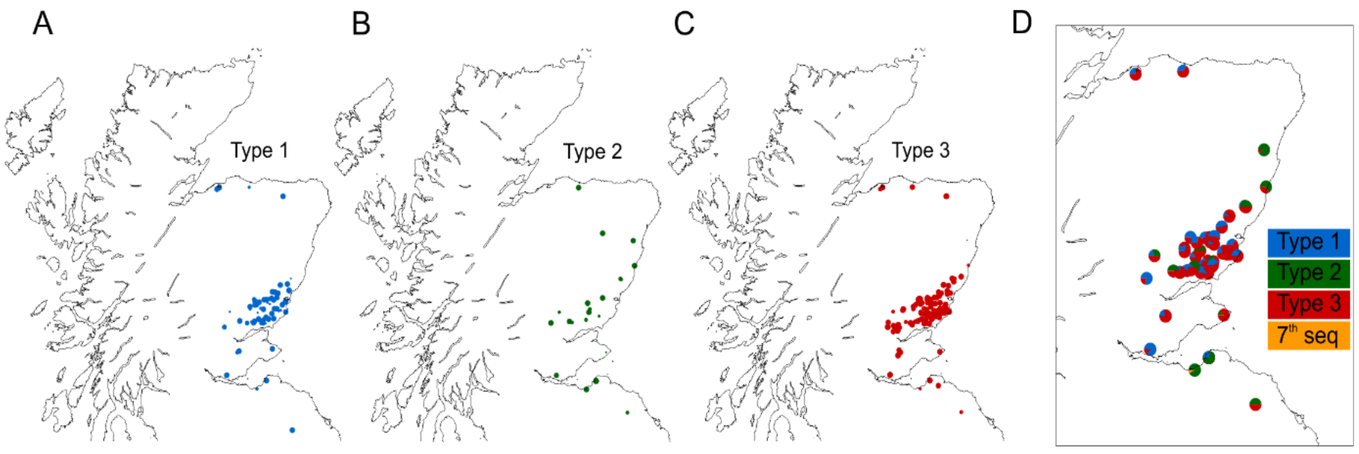


Figure 1 – Distribution of the three main *G. pallida* mitotypes in Scotland.

Where is the problem?

There are 3 main types of *G. pallida* in Scotland as described by a single mitochondrial gene. Using samples collected by SASA, the location of these "mitotypes" can be resolved at the farm level (figure 1).

Why is this a problem?

Different mitotypes represent different pathotypes which differ in virulence. If *G. pallida* is continuously exposed to a source of resistance, it can adapt to overcome that resistance (figure 2). Characterisation of the genomes of these selected lines has identified certain regions of the genome that have become changed in response to selection (figure 3). If adapted populations of *G. pallida* spread throughout Scotland, certain sources of resistance will become ineffectual.

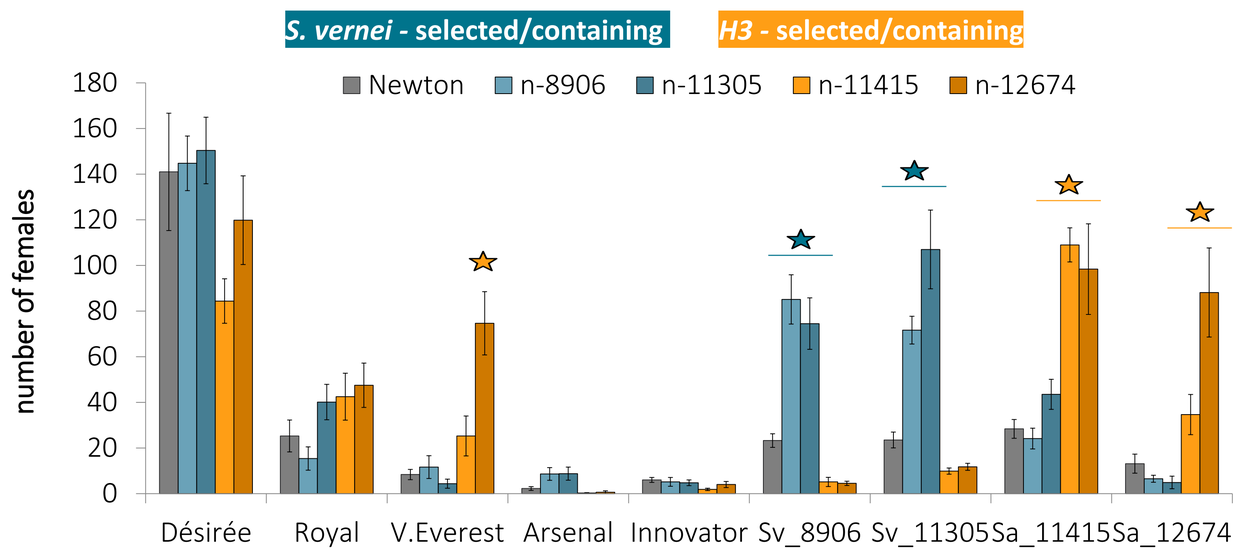


Figure 2 – *G. pallida* populations continuously exposed to resistance overcome that resistance.

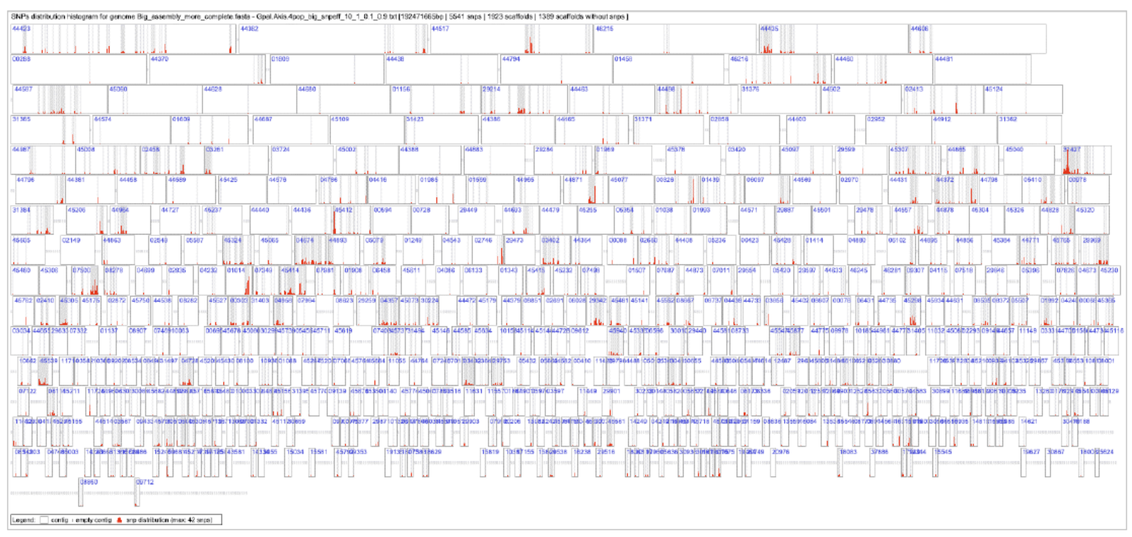
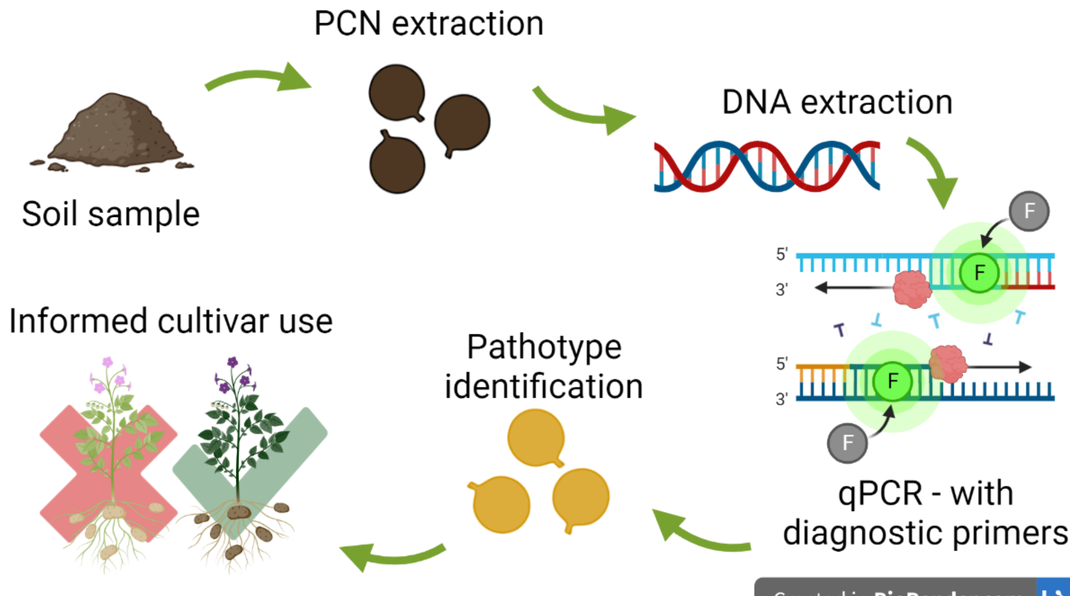


Figure 3 – Regions within the genome of a *G. pallida* population raised in the presence of resistance. Polymorphisms localise to regions of the genome (red bars)

What are we doing?

New diagnostic primers for amplifying pathotype-specific regions of DNA have been created and tested. Illumina sequencing will be used to confirm differences in SNPs between amplicons from different pathotypes. Incorporating these diagnostics tests into current statutory testing will inform varietal choice for growers, avoiding breakdown of resistance, reducing PCN populations and increasing yields.



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