**Pan-genomic variation of *Pisum* immune receptors enabled identification of novel downy mildew resistances**

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Downy mildew in pea, caused by the oomycete *Peronospora viciae* f. sp. *pisi* (*Pvp*), is a significant disease of peas and has been reported to cause annual yield loss of upto 30%1. Beyond the immediate impact, the pathogen’s oospores can persist in the soil for up to 8 years, thus limiting available land for pea cultivation. This issue is further exacerbated by the diverse distribution of pathogen races and recent restrictions on seed treatments. To identify new sources of resistance, we screened 230 lines from the pea diversity panel with two recently emerged *Pvp* races reported at multiple sites in the UK. Phenotype screening revealed that 20% of the lines exhibited high resistance to both the races. To identify the molecular basis of this resistance, we sequenced and assembled a repertoire of disease resistance genes from the diversity panel using R gene enrichment sequencing2, and their pan-genome variation was exploited using association genetics. We discovered a novel locus on chromosome 5 and a previously reported locus on chromosome 2. For the chromosome 2 locus, we implemented *k*-mers based haplotype analysis that reduced the mapping interval to a 300 kb region harbouring three R-genes. Using RNA sequencing of the host tisuse 48 hours post-inoculation with the pathogen, we found that one of the R-gene doesn’t have any expression, while the other two R-genes have significantly different expression and sequence structure between resistant and susceptible lines. Future work will involve validation of these candidates using gene silencing and editing approaches.

***References:***

[1] https://www.fwi.co.uk/arable/crop-management/disease-management/downy-mildew-warning-for-pulse-crop-growers

[2] Arora S. et al, Resistance gene cloning from a wild crop relative by sequence capture and association genetics, Nat Biotechnol, **37**(2): 139-143, 2019.