

Plant Genomics 2018- The genetic basis of resistance in barley to diverse *Puccinia striiformis* isolates- Rouja Haghdoost- The University of Sydney, Australia

Rouja Haghdoost

The University of Sydney, Australia

The genetic basis of resistance to stripe rust caused by *P. striiformis* in barley is not well understood. Therefore studies are required to determine the inheritance of resistance to this pathogen species in barley. Should such studies identify genes that are pleiotropic (effective to multiple pathogens); they could be transferred between cereal crops to increase the diversity of genetic resistance in disease control. Barley is infected by the adapted pathogen *Puccinia striiformis* f. sp. *hordei* (Psh) and is an intermediate or near nonhost to the formae speciales (ff. spp.) adapted to wheat [f. sp. *tritici* (Pst)] and to barley grass [f. sp. *pseudo-hordei* (Psph)]. The aims of this study were to determine the genetic basis of resistance in barley to diverse isolates of *P. striiformis* and to conclude whether or not the adult plant leaf rust resistance gene *Rph20* confers pleiotropic resistance to *P. striiformis*. To determine the genetic basis of resistance to *P. striiformis* in barley, we developed a Recombinant Inbred Line (RIL) population using a *P. striiformis*-susceptible accession (Biosaline-19) and the immune cultivar Pompadour, which carries *Rph20*. The immunity in Pompadour at the seedling stage to four diverse *P. striiformis* isolates was due to resistance Quantitative Trait Loci (QTL) on chromosomes 1H, 2H, 4H, 5H and 7H with both overlapping and distinct specificities that were confirmed through histology assessment.

In the field, RILs that were seedling-susceptible to Psph were resistant, indicating the presence of APR which was mapped to chromosome 7H and co-locate with the leaf rust APR gene *Rph23*, suggesting either pleiotropic resistance or the involvement of a gene closely linked to or allelic with *Rph23*. Unlike many pleiotropic APR genes identified and isolated in wheat, our data suggest that the leaf rust APR gene *Rph20* does not confer resistance to the *P. striiformis* isolates used in this study. Identifying and utilizing rust resistance genes in wheat has been hampered by the continuous and rapid emergence of new pathogen races. A major focus of many wheat breeding programs is achieving durable adult plant resistance (APR) to yellow (stripe) rust (YR) and leaf (brown) rust (LR), caused by *Puccinia striiformis* and *P. triticina*, respectively. This study aimed to determine the genetic basis of resistance to YR and LR in the common spring wheat 'Quaiu 3'. To that end, we evaluated 198 F5 recombinant inbred lines (RILs), derived from a cross of susceptible 'Avocet-YrA' with Quaiu 3, for APR to LR and YR in artificially inoculated field trials conducted in

Mexico during the 2009 and 2010 growing seasons. High narrow-sense heritability (h^2) estimates, ranging between 0.91 and 0.95, were obtained for both LR and YR disease severities for both years. The quantitative and qualitative approaches used to estimate gene numbers showed that, in addition to known resistance genes, there are at least two to three APR genes associated with LR and YR resistance in the RIL population. The moderately effective race-specific resistance gene *Lr42* and the pleiotropic slow-rusting APR gene *Lr46/Yr29* were found to interact with additional unidentified APR genes. The unidentified APR genes should be of particular interest for further characterization through molecular mapping, and for utilization by wheat breeding programs.