Genetical genomic dissection of *Puccinia graminis* TTKS infection in barley: a systems biology approach to rapid development of durable resistance for barley and wheat

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To rapidly identify both breeding and biochemical targets that will mitigate rust diseases threatening barley and wheat worldwide, we are performing a large-scale genetical genomics experiment similar to those that recently elucidated genetic predispositions to obesity and cancer. This systems biology approach to disease defense leverages the complementary strengths of genetics and molecular biology to connect genetic loci that confer resistance with gene expression networks that are responsive to infection. The genetical genomics method is often called "eQTL mapping" because the phenotypes in question are the expression of individual genes. Affymetrix GeneChips are being used to profile the transcriptome of barley in inoculated vs. mock-inoculated leaves of the Q21861 x SM89010 doubled haploid population that segregates for reaction to *Puccinia graminis* TTKS, a stem rust isolate from East Africa that parasitizes both barley and wheat. Each RNA sample will be fluorescently labeled and hybridized to a Barley1 GeneChip, which will allow us to acquire genotype data for 4,000+ SFPs as well as gene expression data for 22,000 genes. In order to focus our eQTL mapping efforts on genes and gene networks relevant to disease defense, we will first identify the subset of the genes that show differential expression between TTKS-inoculated and mock-inoculated leaves. Mapping the eQTL that regulate the expression of these genes will generate a large dataset of eQTL (approximately 10,000). To identify the most important of these loci, we will perform hierarchical analyses to identify regulators of the networks that respond most dramatically to TTKS infection. A locus that regulates one or more significant disease resistance networks is an obvious target for immediate use in breeding.