

Dissecting Multiple Pathogen Recognition at the *Mla* locus in Barley

Adult Plant Resistance to Barley Yellow Rust

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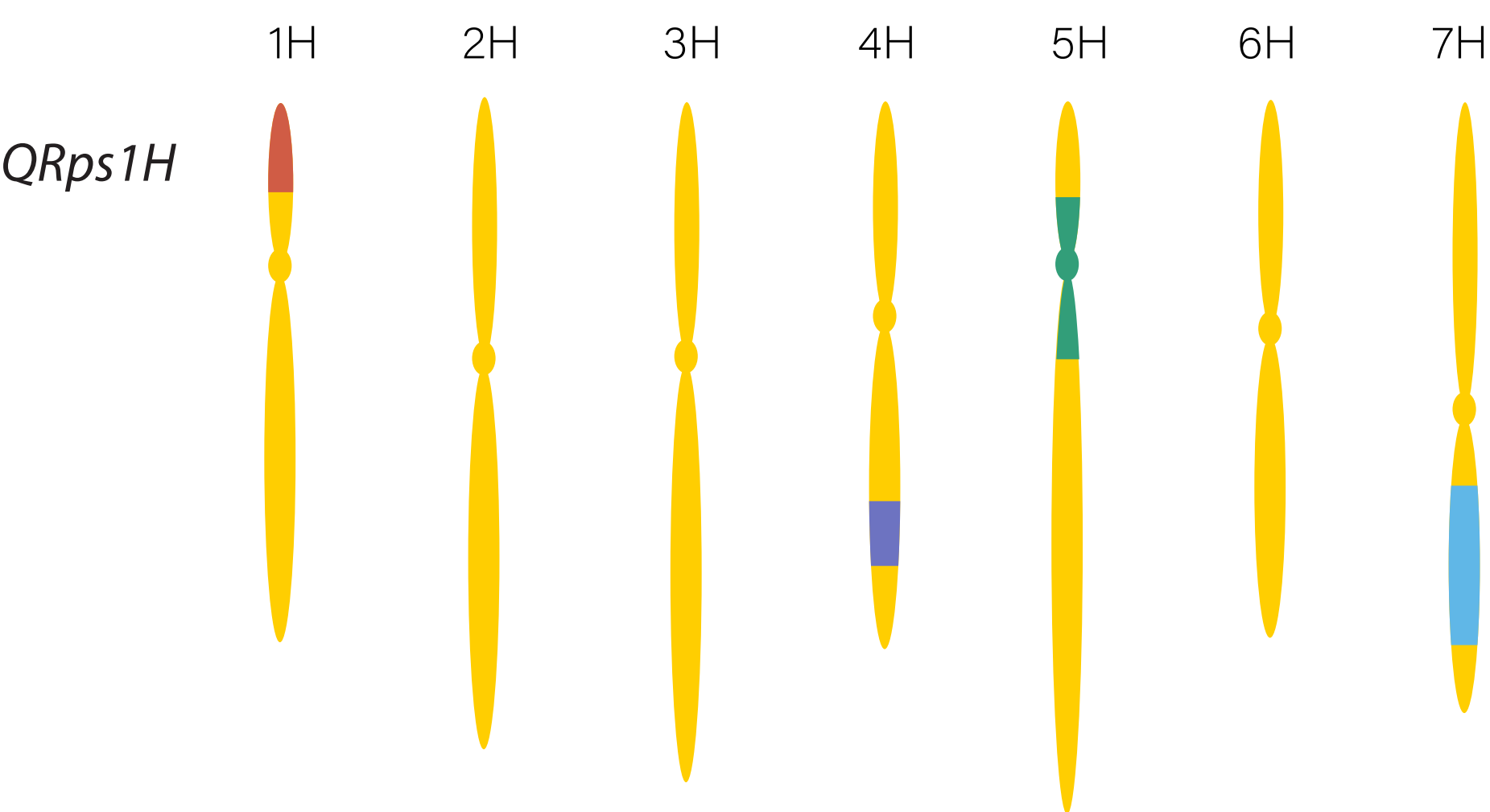


Barley yellow rust (*Puccinia striiformis* f. sp. *hordei*) has spread extensively throughout all worldwide barley growing regions and causes substantial agricultural loss.

Few genes in barley (*Hordeum vulgare*) have been identified for resistance to yellow rust. This project sets out to fine-map an adult plant resistance (APR) QTL, *QRps1H*, and introduce this to elite cultivars.

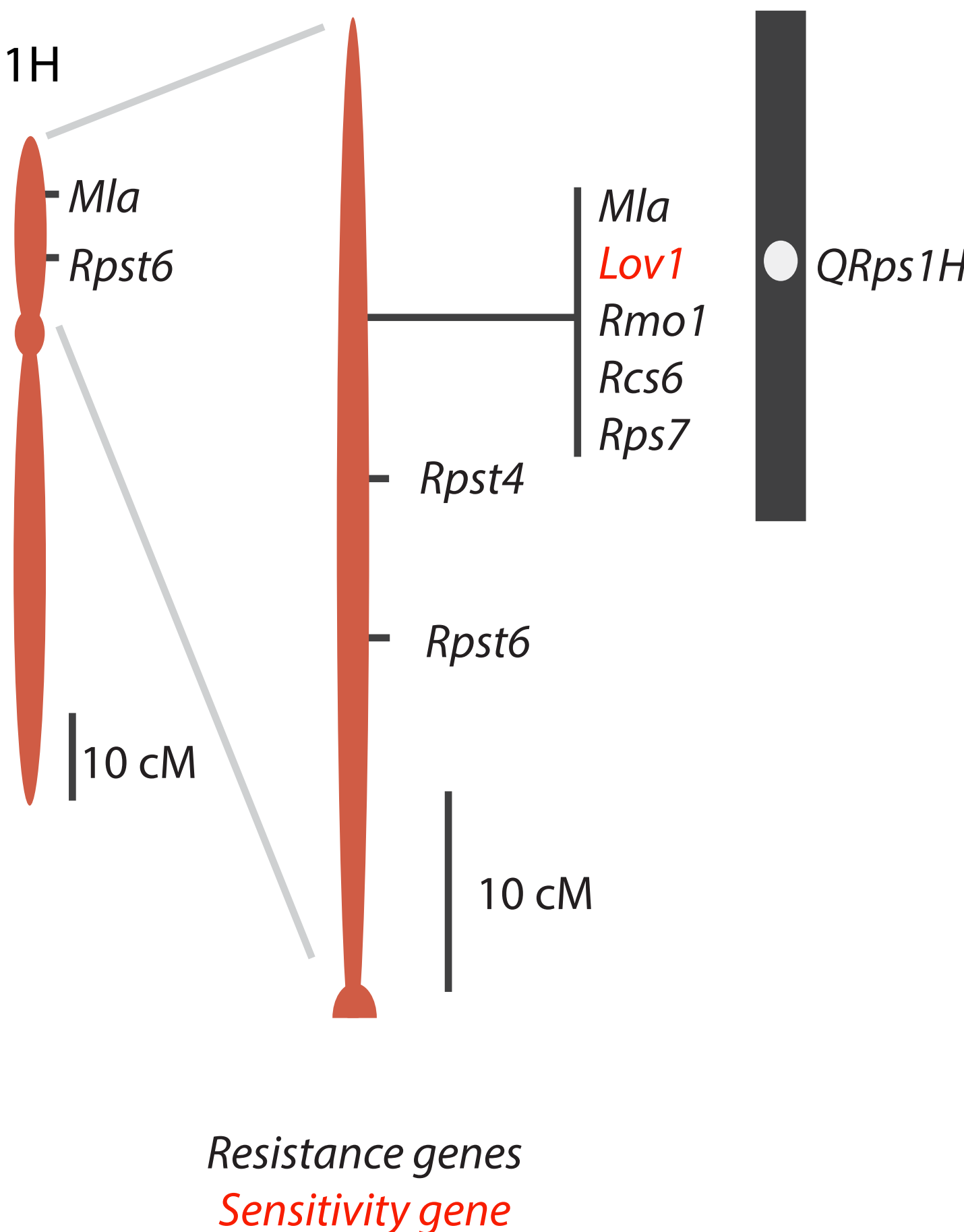


Multiple QTLs confer quantitative resistance



Plant disease epidemics occur following introduction of new plant pathogen isolates, or after existing field resistance has been overcome. It is critical to identify and introduce new novel sources of resistance to existing crops and breed cultivars for disease resistance. Multiple quantitative QTLs have been identified conferring resistance to barley yellow rust, these have been introgressed into near-isogenic barley lines (BISON).

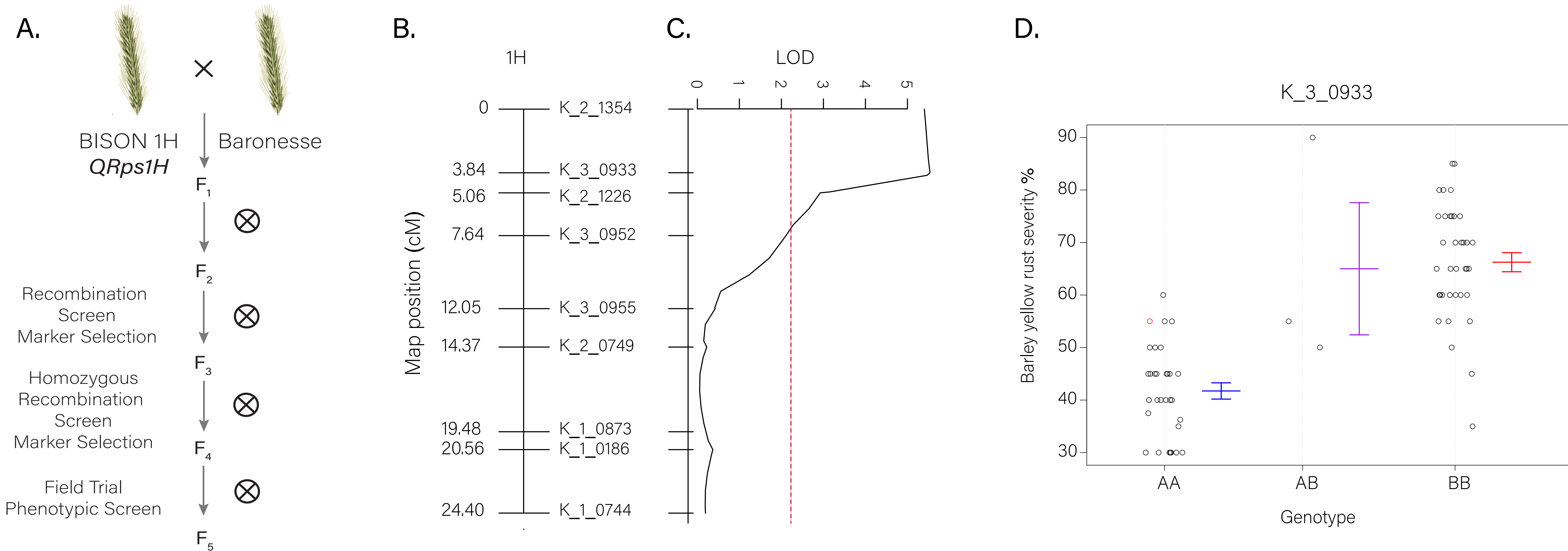
QRps1H maps to the *Mla* locus



The *Mla* locus of barley has been associated with resistance to multiple pathogens. The locus contains three resistance gene families, and is highly divergent across haplotypes.

Allelic variants of *Mla* confer isolate-specific disease resistance against the host pathogen barley powdery mildew (*Blumeria graminis* f. sp. *hordei*). The relationship of *QRps1H* and *Mla* will be investigated.

A mapping population underwent field trials in Mexico, Oregon, and the UK to map *QRps1H*



QTL analysis of *QRps1H* in the BISON1H x Baronesse $F_{4:5}$ mapping population using phenotypic data from Oregon and Mexico field trails 2018. **A.** Genetic linkage map for the short arm of chromosome 1H. **B.** LOD scan of *QRps1H* for barley yellow rust severity with a 5% LOD threshold of 2.27 based on 1,000 permutations (dashed red line). **C.** Phenotype by genotype plot of marker K_3_0933 located at the peak of the *QRps1H*, where genotype A = *QRps1H* from resistant parent BCD12, B = susceptible parent Baronesse.