CALIFORNIA CROP IMPROVEMENT ASSOCIATION

COMPREHENSIVE ANNUAL RESEARCH REPORT
July 1, 2014 to June 30, 2015

PROJECT TITLE: Fine Mapping of CYDV in Barley

PRINCIPAL INVESTIGATORS: I.A. del Blanco and Jorge Dubcovsky

OTHER INVESTIGATORS: J. Hegarty, B. Falk, and L. Gallagher

LEVEL OF 2014-2015 FUNDING: U$S 5,000

OBJECTIVES:

Fine map individual QTL for resistance to CYDV in the Madreselva/Butta 12 mapping population. Increase density of markers in the QTL regions. Use QTL flanking markers to assist selection in the breeding program.

Previous work: A mapping population was developed by Lynn Gallagher crossing a moderately resistant malting barley cultivar (Butta 12), and a previously reported CYDV tolerant cultivar (Madreselva). Starting in F2, the population was derived by single seed descendence (SSD) to near-homozygosis; then, the 184 resulting lines, and parental genotypes, were genotyped using 384 SNPs. Simultaneously, lines and parents were phenotyped using virus (CYDV-RPV) infected aphids. About two weeks after infection, population and parents were scored for yellowing. Preliminary quantitative trait loci (QTL) analysis showed significant peaks on chromosome 2H (two peaks), 4H, and 7H.

SUMMARY OF 2014-2015 RESEARCH:

Cereal Yellow Dwarf Virus (CYDV) is a serious disease affecting small grain crops around the world. CYDV is transmitted by aphids, and it has been a major challenge to develop malting barley in California. Fine mapping of QTL for resistance/tolerance to CYDV has not previously
been done. Precise genome location of resistance/tolerance will allow the identification of markers to assist selection in breeding populations, accelerate the improvement of the populations and the advancement of resistant cultivars and to locate candidate genes contributing to the resistance.

During 2014-2015, approximately 500 F₂ plants from the high density (HD) mapping populations with the flanking markers for the two major QTL – 2Ha and 7H were screened. Sixty one and forty three recombinants were recovered for the 7H and 2H regions, respectively.

F₃ seeds, from F₂ families, have been planted. The plants homozygous for the desired recombination, selected by Kasp assays, will be inoculated with CYDV, in collaboration with Bryce Falk team, by using virus-infected aphids. Three weeks after inoculation, plants will be evaluated for symptom development. This data and the HD map will allow a more precise location of the two regions contributing the major QTL to CYDV tolerance.

Besides the fifty six additional SNP markers added during 2013/14 to the original map, with the assistance of the USDA small genotyping center, another eight Kasp assays were developed during 2014/15, and further markers will be added to saturate the regions of interest and refine the QTL regions.

**PUBLICATIONS OR REPORTS:**


**Previous year Publications:**


CONCISE GENERAL SUMMARY OF CURRENT YEAR’S RESULTS

Genotypes carrying individual QTL for resistance to CYDV were crossed to fully susceptible genotypes (none QTL) to create subpopulations for each QTL. All crosses have been completed. Progenies were advanced to F2 generation and are currently being genotyped and phenotyped by challenging them with virus infected aphids.
Eight additional Kasp assays were developed (besides the fifty six from the previous year) and further markers will be added to saturate the regions of interest and refine the QTL regions. Phenotype data of these subpopulations of recombinant lines and new marker data will allow a more precise location of the QTL.
The budget of $5,000 from the CCIA was used in part to hire a part time undergraduate, Saarah Kuzay, who did the planting and genotyping of the recombinants. The other part of the budget was used to develop KASP assays.

We thank the CCIA for last year support. Resistance to CYDV is essential to developing malting barley cultivars for California. The identification of resistance, and its precise location within the barley genome, will facilitate the use of marker assisted selection in our breeding program.

APPROVALS:

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