Genomic Regions that Underlie Barley Yellow Dwarf Tolerance in Cultivated Oat. (C07-kaeppler165322-Poster)

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Abstract:

Barley yellow dwarf (BYD) is one of the most important viral diseases in small grains. Characterization of major sources of tolerance and identification of marker and the trait associations will directly benefit breeding for BYD tolerance. Genomic regions underlying BYD tolerance were mapped and characterized in an oat population derived from the cross of 'Ogle' (tolerant) / MAM17-5 (sensitive). Tolerance was evaluated in replicated field trials across two years under artificial inoculation with viruliferous aphids harboring BYD virus isolate PAV-IL. Composite interval mapping was used for quantitative trait loci (QTL) analysis with a framework map of 272 molecular markers. Four QTL, BYDq1, BYDq2, BYDq3, and BYDq4, for BYD tolerance were identified on linkage groups OM1, 5, 7 and 24, respectively. The final model including the epistatic effect explained 50.3 to 58.2% of the total phenotypic variation for BYD tolerance. Some QTL for BYD tolerance were closely linked to QTL for plant height and days to heading. The identified association between markers and tolerance should be useful to pyramid favorable alleles for BYD tolerance into single oat lines.

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