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Specific Genomic Regions in Common Bean Condition Resistance to Multiple Pathogens

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To determine when a paper is to be presented, check the session number in the Program Schedule or the Conference at a Glance charts. The Author presenting the paper is indicated by an asterisk.

140

Specific Genomic Regions in Common Bean Condition Resistance to Multiple Pathogens

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A genetic linkage map of 170 RAPD markers mapped across 79 recombinant inbred lines (Dorado and XAN-176) reveal genomic regions that condition multiple disease resistance to fungal (Ashy Stem Blight—*Macrophomina phaseolina*), viral (bean golden mosaic virus—BGMV), and bacterial (common bacterial blight—*Xanthomonas campestris* pv. *phaseoli*) pathogens of common bean (*Phaseolus vulgaris*). A genomic site on linkage group US-1 had a major effect, explaining 18%, 34%, and 40% of the variation in phenotypic reaction to ashy stem blight, BGMV, and common bacterial blight disease, respectively. Adjacent to this region was a QTL conditioning 23% of the variation in reaction to another fungal pathogen, web blight (*Thanatephorus cucumeris*). A second genomic site on linkage group US-1 had minor affect on multiple resistance expression to the same fungal (15%), viral (15%), and bacterial (10%) pathogens. It is unknown whether these specific genomic regions represent a series of linked QTL affecting resistance to each disease separately or an individual locus with pleiotropic effect against all three pathogens.