Developing Genomic Resources in Black Raspberry

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Since the early 1900s, the black raspberry industry in the US has steadily declined due in large part to a lack of adapted and disease resistant cultivars. News regarding potential health benefits of black raspberries has revived interest in production and breeding new cultivars. We are developing the genomic infrastructure for black raspberry. Two mapping populations, ORUS 4305 and ORUS 4304, were propagated and planted in grower’s and research fields across five US production areas. Each segregates for a new source of resistance to the large raspberry aphid, an important vector to the black raspberry necrosis virus. This virus is a leading cause for the short life of plantings. Polymorphism screening of over 200 *Rubus* microsatellite markers in parents of ORUS 4305 identified 42 polymorphic microsatellite that are being used to construct a linkage map. Six cDNA libraries generated from five tissue types of ‘Jewel’ produced 704 Gbp of sequences. Initial assembly of the genome from a highly homozygous accession yielded an assembly of 268 Mbp. The low percent of SNP bases (0.06%) confirmed low heterozygosity. The transcript sequences will be assembled next and used to develop gene models for genome assembly. These developing genomic resources will be instrumental in building the infrastructure needed for identification of candidate genes or markers responsible for many traits of interest for development of improved black raspberry cultivars.