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Progress on the development of a genome sequence for red raspberry *Rubus idaeus*

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A draft pseudo chromosome assembly of the highly heterozygous diploid red raspberry variety 'Heritage' (*R. idaeus* subsp. *vulgatus* Arrhen. x *R. idaeus* subsp. *strigosus* Michx) is presented. Approximately 90x coverage of the genome (~6x in pairs with insert greater than 2 kb) was used to assemble the sequence into 11,502 scaffolds. Detailed internal analysis of the assembly reveals two highly divergent haplotypes, consistent with previous linkage studies in raspberry, which likely contribute to the relatively high number of scaffolds. A genetic map was created using Genotyping by Sequencing and approximately 3400 markers from the map were used to assign scaffolds to linkage groups. Large-scale agreement between the scaffolds and the genetic map is apparent and only 0.2 percent of the scaffolds are mapped to by markers from more than one linkage group. Despite the high density of the genetic map it allowed assignment of only 60% of bases to pseudomolecules due to the relatively high number of scaffolds produced by the assembly. Efforts are now underway to improve the pseudomolecule assembly by incorporating synteny with the *Fragaria vesca* genome and additional paired data to assign more scaffolds to linkage groups. Gene finding with GeneMark ES+ estimates a gene content of 36009, which is approximately 1,200 more than *F. vesca*. Gene-family analysis and comparison to strawberry continues.