

Mapping of the waxy bloom gene in ‘Black Jewel’ in a parental linkage map of ‘Black Jewel’ × ‘Glen Ample’ (*Rubus*) interspecific population

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Red raspberry, *Rubus idaeus* L., is an economically important temperate crop. Today's consumer prefer fruit produced without the use of chemical plant protection, which makes growing raspberries challenging. Breeding new cultivars with genetic resistance against pests and diseases could solve this issue. Mapping resistance genes is a good way to design markers and thus ease the otherwise lengthy breeding process.

Black raspberry (*Rubus occidentalis* L.), although of less economic importance, is closely related to the red raspberry. Their close relation makes their genetic information easily useable for both species. The current amount of genetic data available on both species eases the mapping of breeding relevant traits.

One such trait, controlled by gene B, is the amount and form of visible epicuticular wax on canes, called waxy bloom. This trait has been shown to influence resistance / susceptibility to several cane diseases in raspberry, but has not been fully studied in conjunction with other morphological traits. Gene H, which controls cane pubescence, was previously reported to be likely closely associated with gene B.

In this study, we used an interspecific population of *R. occidentalis* and *R. idaeus* segregating for waxy bloom to identify the de novo SNPs through tunable genotyping-by-sequencing. The linkage maps created for both species were then used to map the identified SNPs to the seven chromosomes of *Rubus*.

This study delivers new information on the location of gene B, which we mapped to chromosome 2 of *R. occidentalis*. The genetic map we created consists of 443 markers spanning 479.76 cM. Another important finding of this study is the poor transferability of *R. idaeus* SSRs to *R. occidentalis* and discrepancies in their locations on chromosomes compared to previous studies.