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Development of a Simple Sequence Repeat (SSR) Genetic Map in Ornamental Viburnum

The goal of this project was to augment a new genetic map of *Viburnum* with simple sequence repeat (SSR) and sequence-tagged site (STS) markers, which in addition to improving the resolution of the map, will provide landmarks that are transferable among populations. A segregating population resulting from a cross between *V. carlesii* and *V. lantana* was screened with 49 pairs of SSR primers developed from *V. lantana* and 31 pairs of STS primers developed from genes in *Medicago truncatula* and *Pisum sativum*. Ten of the SSR and five of the STS primer pairs produced polymorphic bands. Each polymorphic band was scored as present or absent for each individual within the population, and these markers were added to the existing genetic map using Quickmap software. This improved *Viburnum* map provides a foundation for increasing breeding efficiency through marker-assisted selection, and may also offer useful tools for future comparative genomic and QTL studies, and serve as a genetic model for the family *Caprifoliaceae*.