

Chromosome rearrangement and genome complexity in *Hibiscus syriacus*

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Rose of Sharon (*Hibiscus syriacus*) is one of the most widespread garden shrubs globally and has a complex genome structure resulting from multiple rounds of polyploidization events during its diversification and evolution. Here, we report two reference genomes for *H. syriacus* varieties, Baekdansim and Gangneung, with assembly sizes of 1.94 Gbp and 1.99 Gbp, respectively. Synteny-based analysis revealed consistent chromosome pairing patterns across both varieties, including six sets of syntenic relationships among three chromosomes, two sets among four chromosomes, two sets among five chromosomes, and one set among six chromosomes. These findings indicate that extensive chromosomal rearrangements occurred during consecutive diploidization processes. The observed syntenic patterns provide strong support for the hypothesis that these varieties have undergone diploidization from a dodecaploid ancestor, with extensive unequal chromosome pairing and rearrangement playing a key role in their genomic evolution.

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