Chromosome rearrangement and genome complexity in hexaploid *Hibiscus syriacus*: Insights from pseudochromosome assembly and comparative analysis

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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. We constructed two reference genome assemblies for hexaploid *H. syriacus* accessions (Gangneung and Baekdansim) with long read sequencing and Hi-C scaffolding, resulting in 1.87 Gbp and 1.82 Gbp size of the assembly. Both varieties had 12 typical groups of chromosomes shown in hexaploid genome containing three syntenic chromosomes and two extraordinary groups with four and two syntenic chromosomes. Comparison of genome structures suggested that extensive chromosomal rearrangements occurred in during consecutive diploidization processes. Further analysis also indicated that chromosome size and repeat contents were remarkably different in two syntenic chromosomes, Chr9 in Baekdansim and Chr 36 in Gangneung. A substantial expansion in Chr9 of Baekdansim was observed, primarily influenced by a repeat burst after variety divergence event. Population analysis using 116 re-sequencing datasets of worldwide collection of *H. syriacus* indicated the high genomic complexity of *H. syriacus*. Further evolution of *H. syriacus* will be presented in the poster.

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