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Brief Communication

Genomes of single- and double-petal jasmines (*Jasminum sambac*) provide insights into their divergence time and structural variations

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Jasmine *Jasminum sambac* (L.) Aiton belongs to the genus *Jasminum* of the Oleaceae family. It is commercially cultivated worldwide for its sweetly fragrant flowers, and it is widely used in the fields of food, medicine and industry. Jasmine flowers are used to extract essential oils on a commercial scale and make jasmine tea, a well-known Chinese tea produced from tea leaves and fresh jasmine flowers. Despite the high economic and ornamental value of jasmines, the genetic and breeding research lags behind other flowers and tea plants (Wang *et al*., 2021).

Jasmine flowers present single-(SP), double-(DP) and multi-petal (MP) phenotypes, which are related to their flower yield, stress resistance and aroma. Notably, SP flower shows a fresh and elegant aroma, but its cultivation area is small because of its weak resistance and low yield. At present, the DP jasmine plant has become the leading commercial germplasm because of its high-yield flowers and strong resistance.

Here, the genome sizes of SP and DP jasmines were estimated by flow cytometry to be 547 and 580 Mb, respectively (Table S1). Karyotype analysis in root tip and leaf cells revealed that DP jasmine cell has a diploid genome with 13 pairs of chromosomes, whereas SP jasmine root and leaf tissues contain a chimeric composition of diploid and triploid cells with 13 chromosomes each (Figure 1a–c). This unstable karyotype may be an important factor in the worse resistance and fertility of SP jasmine in the current cultivation compared with DP jasmines. These results were further confirmed by Smudgeplot based on high-fidelity (HiFi) reads data (Figure S1).

We generated 15.35 Gb of HiFi PacBio subreads for SP jasmine and 12.11 Gb for DP jasmine on the PacBio Sequel II platform with an estimated coverage depth of at least 30-folds for each genome (Table S2, Material S1). The initial de novo assemblies using hifiasm yielded contig-level sequences of 653.28 and 535.89 Mb for SP and DP genomes, respectively (Table S3). To generate non-redundant genome sequences, the haplotigs and contig overlaps in the initial assemblies were removed by purge_dups program based on PacBio read depth and a K-mer counting strategy, which resulted in two purged assemblies of 502.27 and 486.97 Mb with improved contig N50 values of 7.34 and 11.82 Mb for SP and DP jasmine genomes, respectively (Figure 1d and e and Tables S3–S5), and observed that most redundant sequences have been removed by purge-dups (Figure S2). These two genomes were further anchored into 13 super-scaffolds representing all chromosomes by incorporating PacBio HiFi subreads and physical mapping data from Hi-C (Figure S3 and Tables S6 and S7) using the ALLHIC pipeline. The final assemblies contain 44 contigs (>2 kb) for SP jasmine genome and 210 contigs (>2 kb) for DP jasmine genome. Genome assembly quality was also assessed based on long-terminal repeat (LTR) retrotransposons and LTR Assembly Index (LAI). LAI scores for SP and DP jasmine genomes were estimated to be ~28.16 and ~24.35, respectively (Figure 1e), which are much higher than that of the recently published MP jasmine genome using nanopore data (Xu *et al*., 2021). This finding indicates the better continuity and completeness of our jasmine monoploid genomes, which recovered more repetitive sequences. In addition, compared with the recently published MP jasmine genome, our two newly assembled jasmine genomes showed improvements in gene completeness according to BUSCO assessment results (Table S8). Genome annotation predicted 24 002 and 23 574 protein-coding genes with 96.6% BUSCO completeness in the two jasmine genomes, respectively (Figure 1e). Moreover, 307.62 and 298.26 Mb repetitive sequences (TE) were annotated in SP and DP Jasmine genomes, respectively, and both sequences accounted for 61.25% of the genome size (Table S9).

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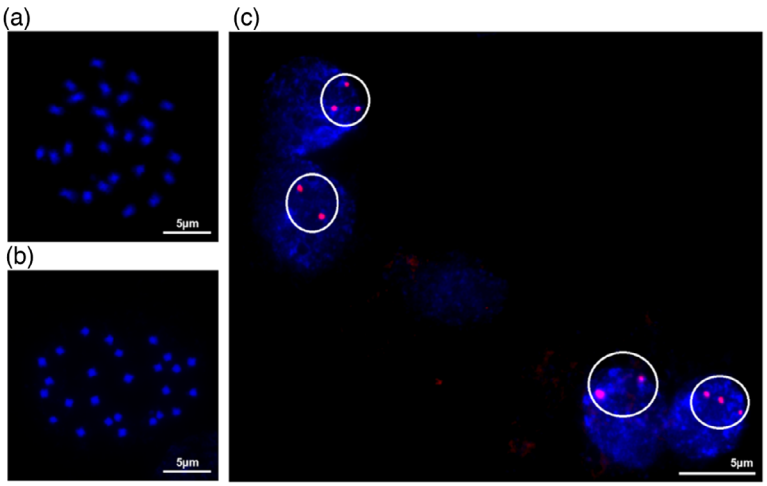
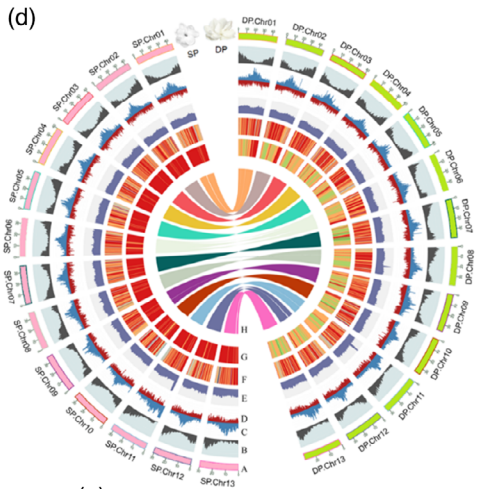
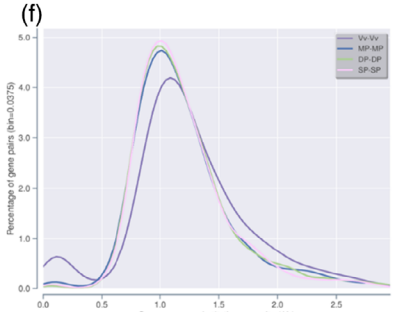
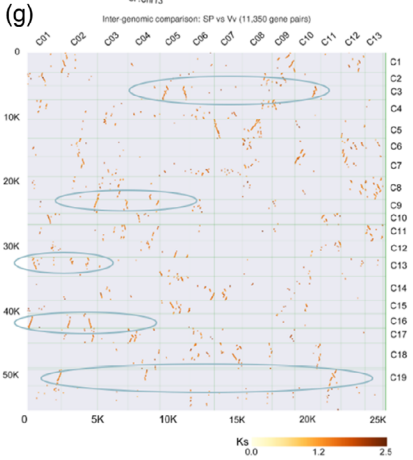


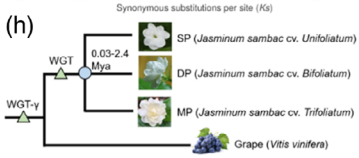


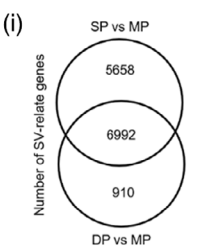
(e)

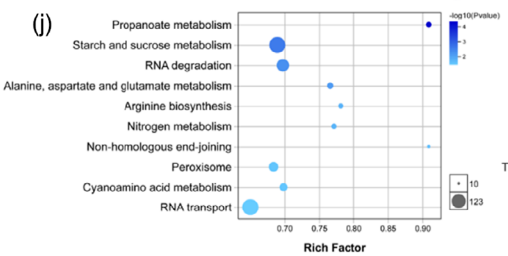
	Published MP (Xu et al., 2021)	SP	DP
Contig assembly size (Mb)	507.10	502.27	486.97
Contig N50 (Mb)	17.60	7.34	11.82
Chromosome-level assembly size (Mb)	505.50	499.00	482.51
Anchor rate (%)	99.68	99.35	99.07
No. of genes	22,137	24,002	23,574
Complete BUSCO ratio (%)	96.04	96.60	96.60
LAI	17.00	28.16	24.35
Quality value (QV)	40.00	56.96	59.08
Average gene length (bp)	4,226	4,036	4,050
Average CDS length(bp)	1,241	1,307	1,308
Average exon length(bp)	274	296	304
Average exon number per gene	6.4	5.7	5.8
Average intron length (bp)	474	516	513

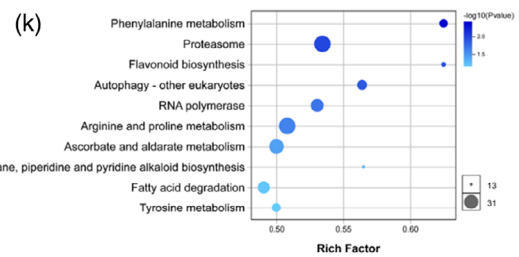


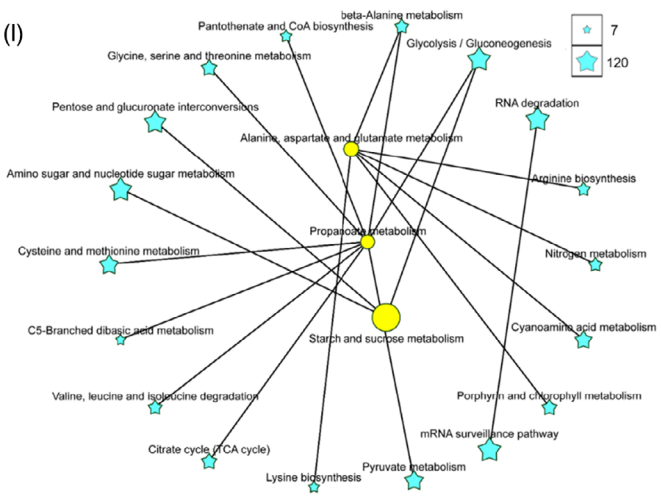












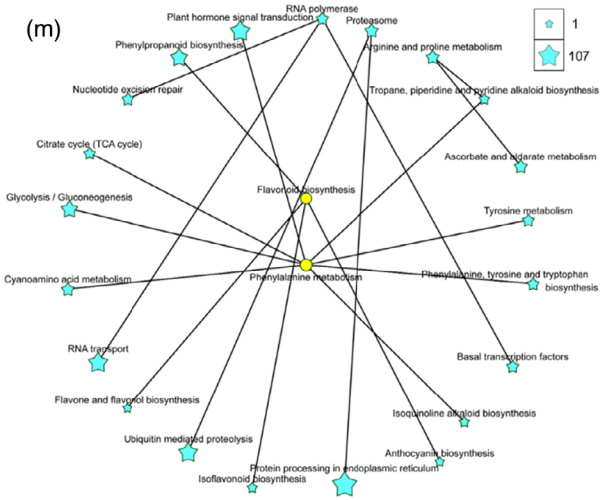


Figure 1 (a) Many SP cells have a diploid genome with 13 pairs of chromosomes. (b) All DP cells present a diploid genome with 13 pairs of chromosomes. (c) SP Jasmine presents a chimeric composition of diploid and triploid cells. (d) Genomic features of the SP and DP jasmine genomes along 13 pseudochromosomes. A: chromosomes, B: gene density, C: LTR Gypsy, D: LTR Copia, E: TEs, F: InDels, G: SNPs, H: synteny between two genomes. (e) Assembly and annotation statistics. (f) Homology dot plot between SP jasmine and grape chromosomes. (g) *Ks* distribution of gene pairs in grape and the three types of jasmine. (h) Schematic diagram of the WGT and divergence time of the three types of jasmine. (i) Venn diagram of SV-related genes. (j) Top 10 KEGG pathways of SV-related genes between SP and MP jasmine. (k) Top 10 KEGG pathways of SV-related genes between DP and MP jasmine. (l) Network of the KEGG pathways of SV-related genes between SP and MP jasmine. (m) Network of the KEGG pathways of SV-related genes between DP and MP jasmine.

The genomic collinearity between grape and the three jasmine types were analysed. We observed that the *Ks* peaks of SP and DP jasmines were on the left side of the grape peak (Figure 1f), and the syntenic blocks between grape and SP or DP jasmine showed a 1 : 3 syntenic relationship (Figures 1g and S4). This result suggests that SP and DP jasmines experienced an additional WGT event after the WGT-γ, which is consistent with MP jasmine (Xu *et al*., 2021). In addition, we found that most of the homologous gene pairs were caused by the subsequent WGT event (*Ks*: 1.1–1.3, Figures 1g and S4), and the homologous gene pairs affected by the WGT-γ event were lost and scattered in the genome. We further calculated the divergence time among the three types of jasmines. The base substitution rate of jasmine was calculated as $r = 1 \times 10^{-8}$–1.3×10^{-8} with reference to the previous method (Badouin *et al*., 2017). Finally, the divergence time between SP and DP, DP and MP and SP and MP jasmines were determined to be 0.03–2.4 Mya (*Ks* = 0.0006–0.049383), 0.035–5.76 Mya (*Ks* = 0.0007–0.115248), 0.015–5.28 Mya (*Ks* = 0.0003–0.105704), respectively, by calculating the *Ks* value. The divergence time of the three jasmines were very close; however, the divergence time between SP and DP jasmines may be more representative because of the large difference between the sequencing and assembly of MP jasmine with SP or DP jasmine (Figure 1h).

We identified 52 547 (134.99 Mb) and 26 773 (76.25 Mb) SVs, representing 26.88% and 15.66% of the genome, by comparing the raw HiFi reads of SP and DP jasmine with the MP jasmine genome, respectively (Tables S10 and S11). The SV-related genes of SP vs. MP were much more than those of DP vs. MP (Figure 1i). KEGG analysis showed that the SV-related genes of SP vs. MP were mainly involved in the energy metabolism regulation network with propanoate metabolism, starch and sucrose metabolism, and alanine, aspartate and glutamate metabolism pathways as the core (Figure 1j and l), which may be related to the weak environmental adaptability of SP jasmine. The SV-related genes of DP vs. MP were mainly involved in the secondary metabolism regulation network with phenylalanine metabolism and flavonoid biosynthesis pathways as the core (Figure 1k and m), which may contribute to the rich aroma of DP jasmine as a suitable raw material for jasmine tea.

In summary, these results greatly deepen our understanding of the evolution and differentiation of jasmine species and provide resources for the research on functional genomics of jasmines.

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Conflict of interest

The authors declare no conflict of interest.

Authors' contributions

N.Y., X.Z., S.J., and P.W. conceived and designed the research. P.W., H.L., W.Y., and Y.H. collected the samples. P.W., J.F., J.Y., M.J., Y.H., Q.C., H.L., W.Y., M.G., Y.Z., Z.L. and G.C. performed the genome assembly and data analysis. P.W. and J.F. wrote the manuscript. N.Y., X.Z., S.J., J.Y., and P.W. revised the manuscript.

Data availability statement

All data are publicly available in the BIG Data Center (https://bigd.big.ac.cn/) under project number PRJCA006739.

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Supporting information

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Figure S1-S4 Supplementary Figures.
Table S1-S11 Supplementary Datasets.
Materials and methods S1 Supplementary materials and methods.

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