



A pan-genome framework for exploiting germplasm diversity and structural variation in rose breeding

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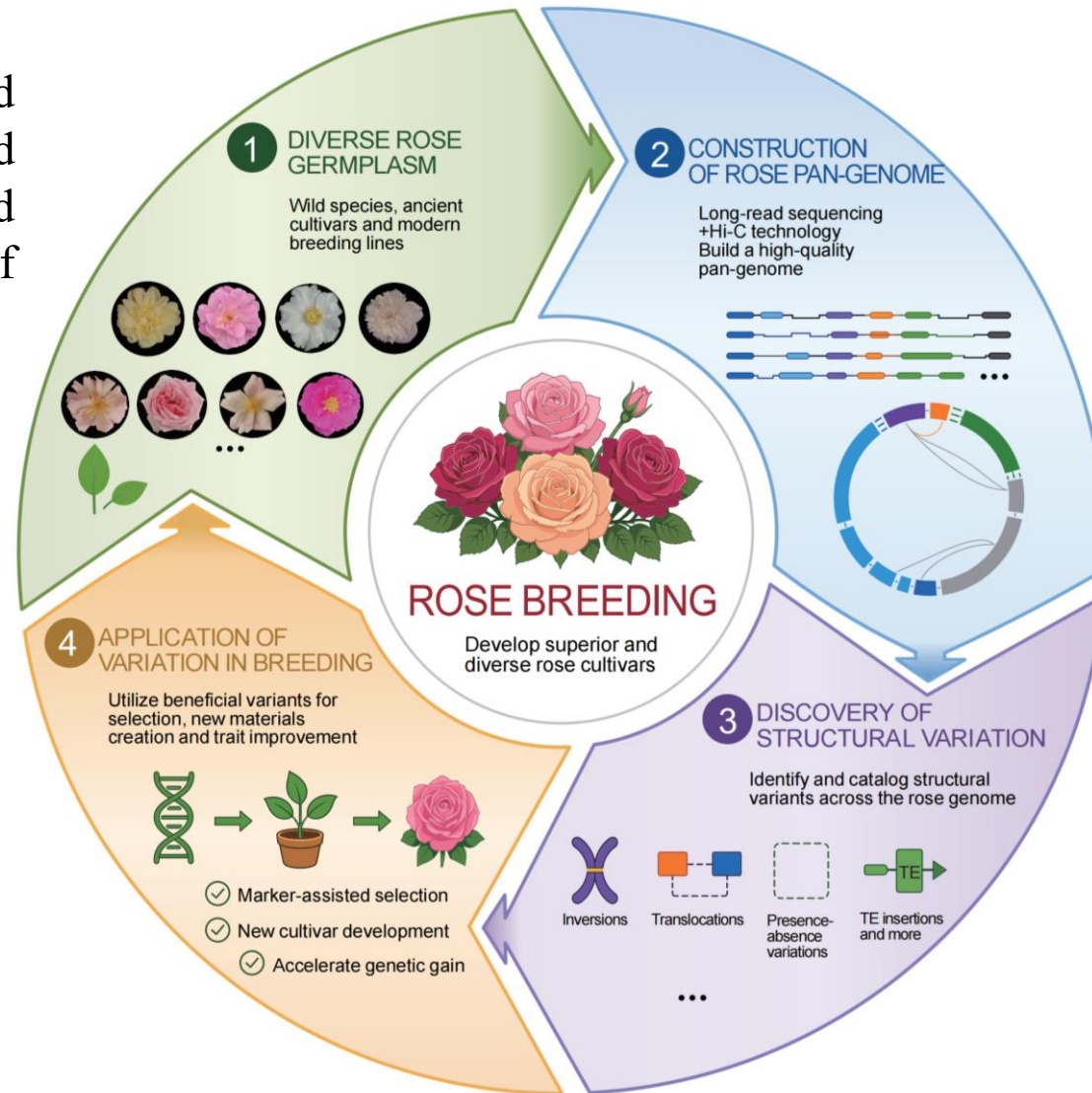


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Graphical Abstract

1) A wide collection of wild species, ancient cultivars, and modern breeding lines ensured the representativeness of genetic diversity.



2) A high-quality rose pan-genome was constructed, providing precise reference genomic resources for subsequent variation analysis.

4) This advances rose breeding from conventional phenotype-driven selection toward genomics-assisted precision breeding.

3) A pan-variation map of rose was constructed to systematically unravel the genetic associations underlying structural variations and their contributions to major ornamental traits.

These findings provide a genomic framework for understanding rose ornamental trait diversification and facilitate molecular breeding of roses.

Highlights

(A) Diverse germplasm resources

Wild species



R. banksiae *R. bracteata* *R. anemoniflora*

Ancient&early cultivars



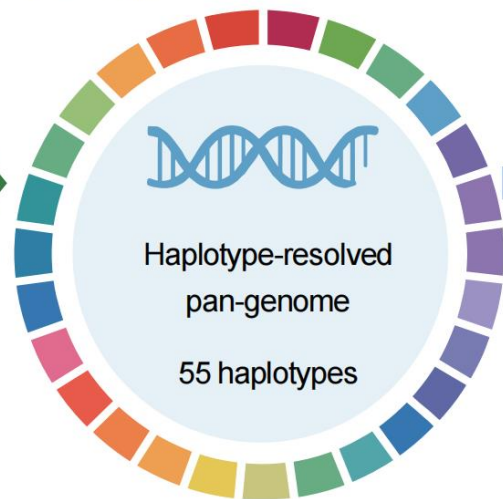
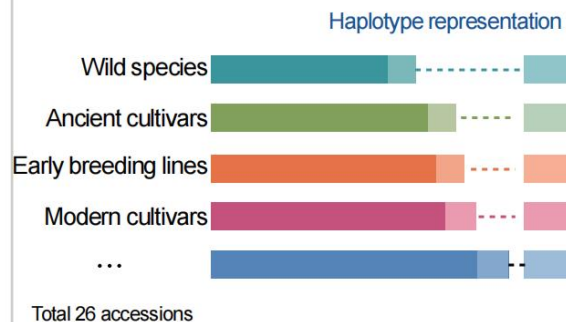
'Old Blush' 'Mutabilis' 'Yu Ling Long'

Modern cultivars & breeding lines



'La France' 'Pink Noisette'

(B) Pan-genome construction (26 accessions , 55 haplotypes)



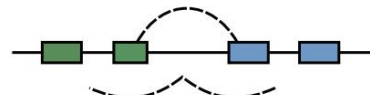
- >1.7 million presence-absence variations (PAVs)
- >1,500 inversions
- >61,000 translocations

(C) Structural variation landscape

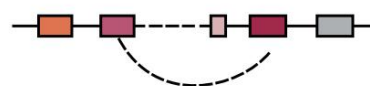
Presence-absence variations (PAVs)



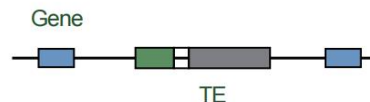
Inversions



Translocations



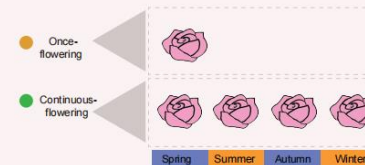
TE-associated variations (~70%)



(D) Links to key ornamental traits

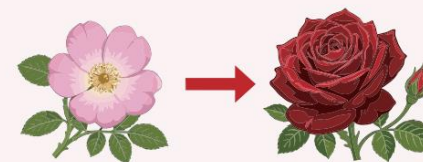
Continuous flowering

Chr3 inversion → loss of RcKSN (Chinenses-specific)



Double-flower formation

Structural variation at *AP2L* locus (TE insertion, regulatory changes, etc.)



Petal colour transition

Delayed expression of *CCD4* ('Mutabilis')

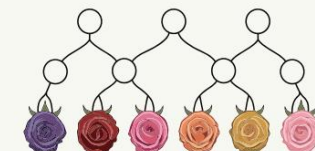


(E) Implications for breeding

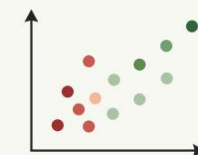
Identification of trait-associated SVs



Discovery of lineage-specific alleles



Genomics-assisted selection



Molecular design & gene editing





Summary

- ❑ Zhang et al. (2026) constructed a high-quality haplotype-resolved pan-genome covering 26 rose germplasm accessions;
- ❑ revealed widespread structural variations and interspecific introgressions, refining the framework of rose genome evolution;
- ❑ demonstrated that structural variations at key loci, including *RcKSN*, *AP2L*, and *CCD4*, underpin the development of major ornamental traits such as continuous flowering, double-flower formation, and petal color transition;
- ❑ established a pan-genome-enabled molecular breeding framework that offers a foundational genomic resource and theoretical basis for precision design breeding in rose.

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