



基于月季泛基因组解析月季种质多样性与结构变异及其育种应用

Abdelhafid Bendahmane

Université Paris-Saclay, CNRS, INRAE, Université d' Evry,
Institute of Plant Sciences Paris-Saclay (IPS2), 91405, Orsay, France

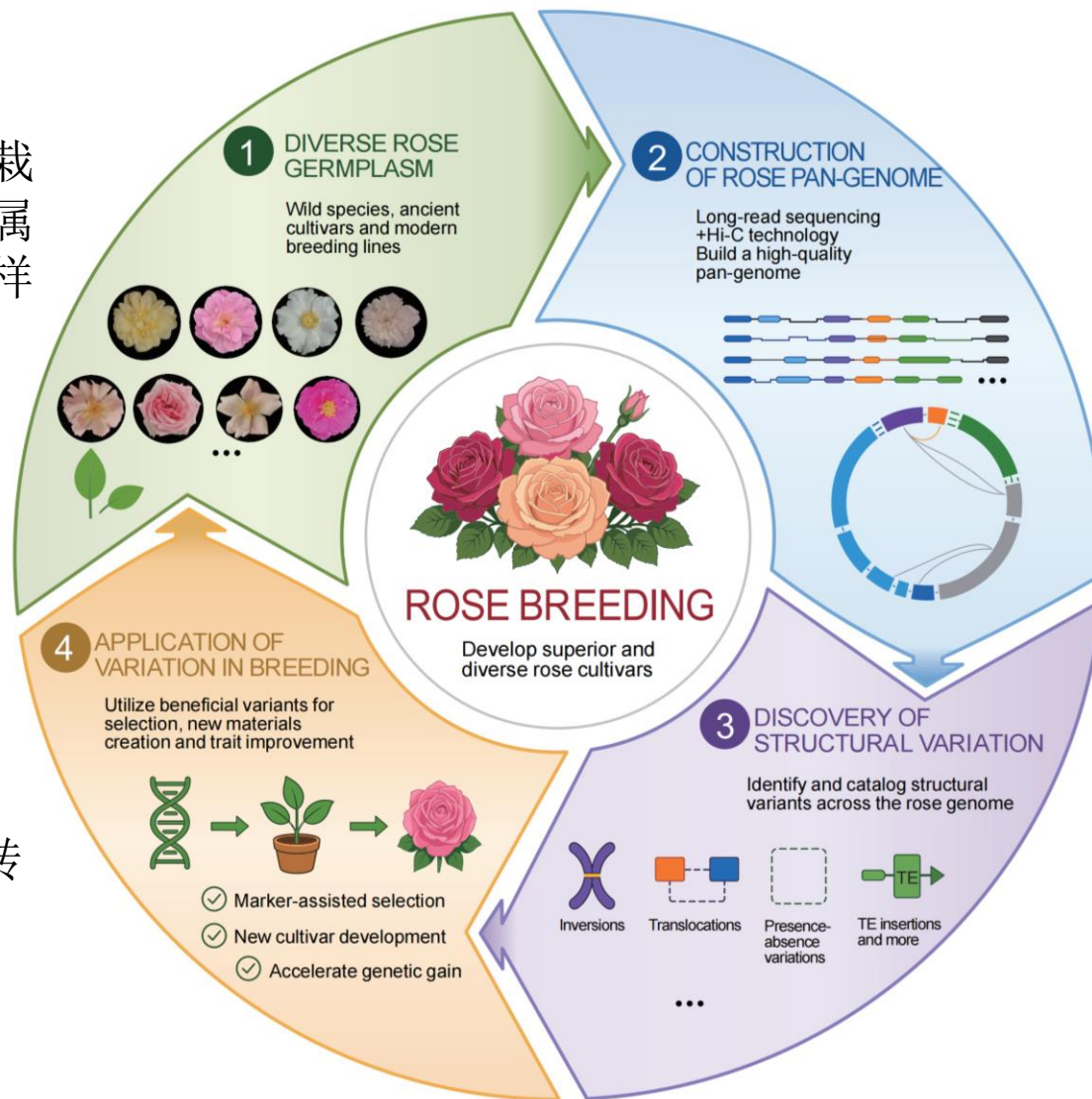


Abdelhafid Bendahmane. 2026. A pan-genome framework for exploiting germplasm diversity and structural variation in rose breeding. *iMetaOmics* 3: e70125. <https://doi.org/10.1002/imo2.70125>

摘要

1) 广泛收集野生种、古老栽培品种及现代月季等蔷薇亚属代表性种质，确保了遗传多样性。

4) 推动月季育种从传统表型选择向基因组辅助精准育种转型。



2) 构建了高质量的单倍型解析的月季泛基因组，为后续变异解析提供了参考基因组资源。

3) 构建月季泛变异图谱，系统解析结构变异及其与重要观赏性状形成的遗传关联。

泛基因组资源为月季分子设计育种提供了可直接靶向的遗传变异基础，加速从传统选育向精准育种转型。

亮点

(A) Diverse germplasm resources

Wild species



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

Ancient&early cultivars



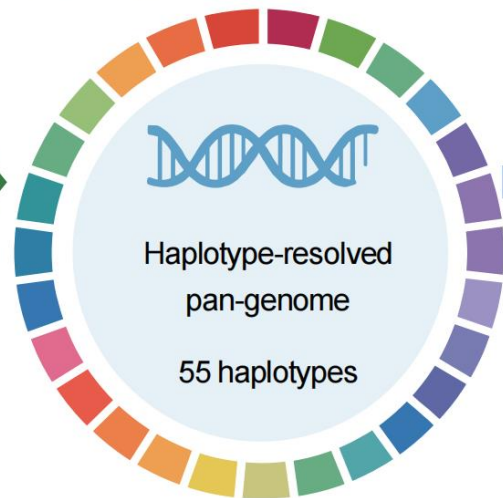
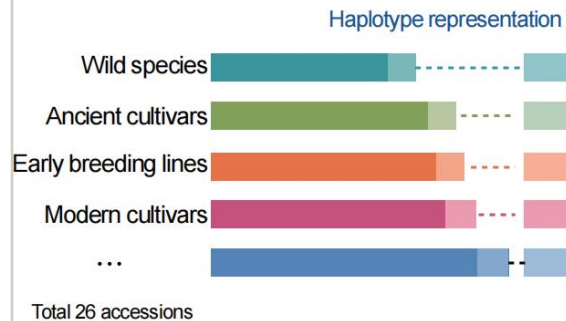
'Old Blush' 'Mutabilis' 'Yu Ling Long'

Modern cultivars & breeding lines



'La France' 'Pink Noisette'

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



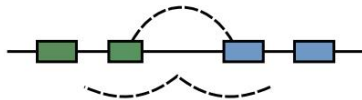
- >1.7 million presence-absence variations (PAVs)
- >1,500 inversions
- >61,000 translocations

(C) Structural variation landscape

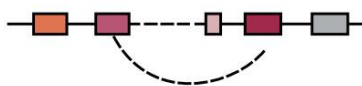
Presence-absence variations (PAVs)



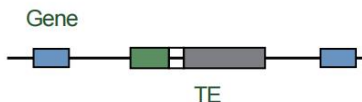
Inversions



Translocations



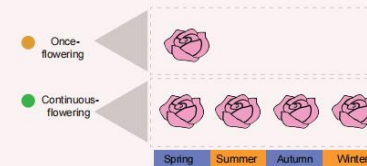
TE-associated variations (~70%)



(D) Links to key ornamental traits

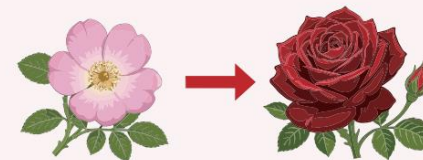
Continuous flowering

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'*)

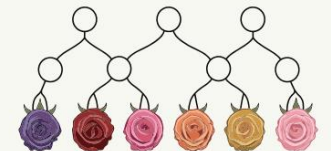


(E) Implications for breeding

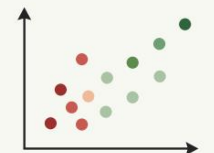
Identification of trait-associated SVs



Discovery of lineage- specific alleles



Genomics-assisted selection



Molecular design & gene editing





总结

- ❑ Zhang 等人（2026）构建覆盖26份月季种质资源的高质量单倍型解析泛基因组；
- ❑ 揭示广泛存在的结构变异和种间渐渗，完善月季基因组演化框架；
- ❑ 阐明 *RcKSN*、*AP2L* 和 *CCD4* 等关键基因相关结构变异驱动连续开花、重瓣和花瓣颜色等重要观赏性状的形成；
- ❑ 提出月季泛基因组驱动分子育种框架，为月季分子设计育种提供新的理论依据和基因组资源。

Abdelhafid Bendahmane. 2026. A pan-genome framework for exploiting germplasm diversity and structural variation in rose breeding. *iMetaOmics* 3: e70125. <https://doi.org/10.1002/imo2.70125>

iMeta(宏): 生物和医学顶级成果发表平台

iMeta WILEY



iMeta(宏)期刊由宏科学创办，对标**Cell**的生物/医学综合期刊，**SCIE**、**PubMed**收录，影响因子(IF)44.4，位列全球第47，中国第4，**分区表生物学1区Top**，外审平均21天，投稿至发表中位数87天(比同水平期刊快3倍)，欢迎高影响力的研究、方法和综述投稿，CNS外审稿件可带意见和回复转投。

iMetaOmics (宏组学)，定位IF>15对标**NC/SA**的生物/医学综合期刊，已被**ESCI**、**PubMed**等收录。

iMetaMed (宏医学)定位IF>15的医学综合期刊，欢迎投稿！



主页: <http://www.imeta.science>

出版社: <https://wileyonlinelibrary.com/journal/imeta>

iMeta: <https://wiley.atyponrex.com/journal/IMT2>

投稿: iMetaOmics: <https://wiley.atyponrex.com/journal/IMO2>

iMetaMed: <https://wiley.atyponrex.com/journal/IMM3>



office@imeta.science

imetaomics@imeta.science



宣传片



iMeta



更新日期
2026/6/17