

## 中国学者破解兰花进化的百年谜团

### Chinese scholars have solved the hundreds years mystery of orchid evolution

兰花的起源、进化和多样性的形成，被达尔文称为“令人讨厌之谜”。100 多年来，全世界无数科学家不断致力于解开这一谜团，均未取得突破性进展。



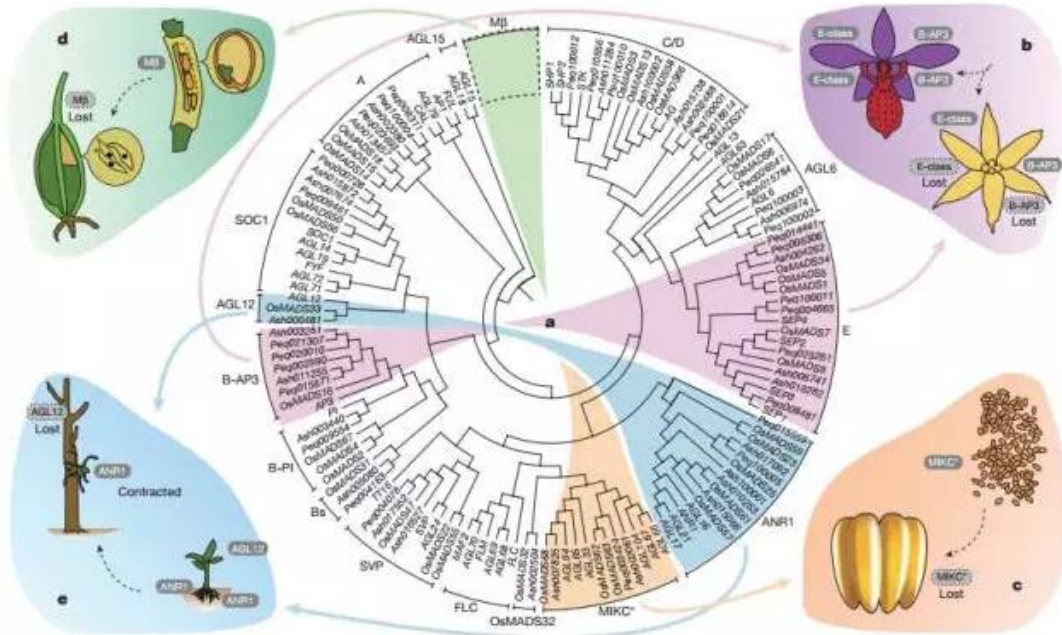
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【Nature 系列】9 月 21 日，国家兰科中心刘仲健教授领衔的国际研究团队以深圳拟兰（*Apostasia shenzhenica*）为主要研究对象，并结合其它兰科和非兰科植物的转录组及基因功能分析，揭示了兰花的起源及其花部器官发育、生长习性以及多样性形成的分子机制和演化路径，相关研究发表在国际顶级学术期刊《自然》杂志上。

研究团队通过对深圳拟兰进行全基因组测序，以及对小兰屿蝴蝶兰（*Phalaenopsis equestris*）、铁皮石斛（*Dendrobium catenatum*）进行全基因组重测序，发现所有现存兰花的祖先曾在第三次生物大灭绝事件（6600 万年前）之前发生了一次全基因组复制事件，开启了现生兰花的起源。

通过对深圳拟兰与其它兰花以及被子植物的基因组比较，研究者发现兰花有 474 个特有基因家族，从中可窥视兰花新的基因家族及其扩张和收缩的进化历史，以及揭示了其唇瓣、合蕊柱、花粉块、无胚乳种子的发育、地生与附生习性进化的分子机制。

不仅首次完整重建了兰花进化的基因工具包和演化的路线图，还揭示了兰花花部器官发育的分子机制，更正了人们对兰花进化的传统认知，填补了植物学研究的多个空白，同时也为兰花保护提供重要的理论依据和指导。



兰科植物形态进化与花器官发育调控基因 (MADS-box) 有关, 图片来自 Zhang GQ et al. 2017. nature



**The *Apostasia* genome and the evolution of orchids**  
**深圳拟兰基因组和兰花的进化**

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 2017年9月21日  
 doi:10.1038/nature23897

Constituting approximately 10% of flowering plant species, orchids (Orchidaceae) display unique flower morphologies, possess an extraordinary diversity in lifestyle, and have successfully colonized almost every habitat on Earth. Here we report the draft genome sequence of *Apostasia shenzhenica*, a representative of one of two genera that form a sister lineage to the rest of the Orchidaceae, providing a reference for inferring the genome content and structure of the most recent common ancestor of all extant orchids and improving our understanding of their origins and evolution. In addition, we present transcriptome data for representatives of Vanilloideae, Cyripedioideae and Orchidoideae, and novel third-generation genome data for two species of Epidendroideae, covering all five orchid subfamilies. *A. shenzhenica* shows clear evidence of a whole-genome duplication, which is shared by all orchids and occurred shortly before their divergence. Comparisons between *A. shenzhenica* and other orchids and angiosperms also permitted the reconstruction of an ancestral orchid gene toolkit. We identify new gene families, gene family expansions and contractions, and changes within MADS-box gene classes, which control a diverse suite of developmental processes, during orchid evolution. This study sheds new light on the genetic mechanisms underpinning key orchid innovations, including the development of the labellum and gynostemium, pollinia, and seeds without endosperm, as well as the evolution of epiphytism; reveals relationships between the Orchidaceae subfamilies; and helps

clarify the evolutionary history of orchids within the angiosperms.