# 典型案例

## 桃多组学数据信息化平台

**案例单位** ---------- 郑州果树研究所

**访问网址** ---------- http://www.nhgrc.cn

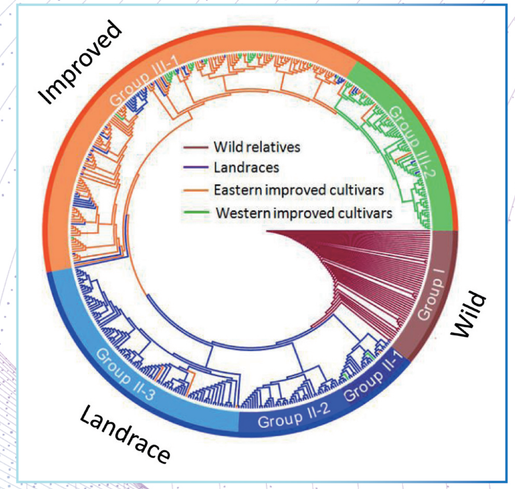
**主要功能** ---------- 桃起源于中国，遗传多样性丰富。平台依托丰富多样的桃种质资源，整合桃核心种质的表型组、基因组、转录组和代谢组信息，构建桃多组学数据库，提供桃主要农艺性状的分子标记和关键候选基因信息。

**技术亮点** ---------- 利用多组学数据库开发了大量的分子标记，有助于提升我国桃分子育种水平。在提供数据查询的基础上，具有全基因组关联分析功能。平台集成桃多组学数据，应用范围更广。

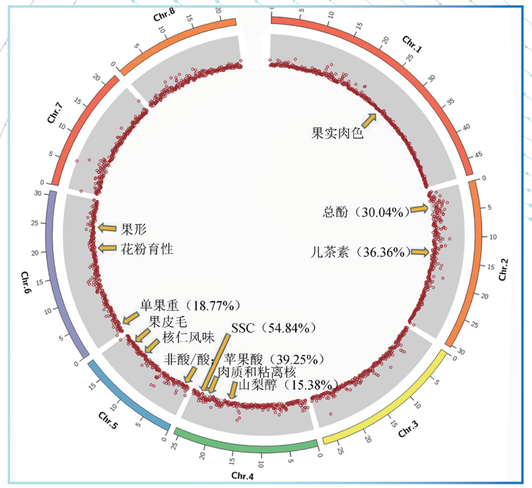
**服务对象** ---------- 桃科研人员、育种家

**服务成效** ---------- 利用桃多组学数据库，解析桃的起源与进化，表型数据在国家园艺种质资源信息网公开，基因组和转录组数据可在 NCBI 等网站公开查询。同时，系统分析了桃栽培类群的进化关系、群体结构和多样性水平，发现不同区域桃品种群分化明显，遗传多样性指数递减。精准定位了与桃果实品质相关的 8 个质量性状位点和 122 个数量性状位点，将 6 个质量性状标记的平均准确率由 69% 提高到 94.1%，发掘出功能基因 10 个，开发了包含 14 个果实重要性状的分子标记育种芯片。该成果有助于为桃远缘杂交提供理论支撑，为解析多年生果树的驯化与分化机制奠定基础。

在 *Nature Communications* 和 *Genome Biology* 等




桃的起源与进化路线解析




开发分子标记在染色体上的位置

中国农业科学院
科学技术成果奖
证 书

为表彰中国农业科学院科学技术成果奖获得者，特颁发此证书。

成果名称：桃分子标记育种技术体系的构建与应用
奖励类别：青年科技创新奖
获 奖 者：中国农业科学院郑州果树研究所

二〇一八年八月二十七日

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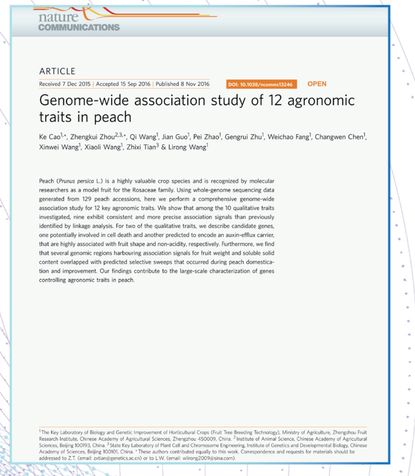
成果获得 2018 年度中国农业科学院科技成果奖



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Genome-wide association study of 12 agronomic traits in peach

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Peach (*Prunus persica* L.) is a highly valuable crop species and is recognized by molecular researchers as a model fruit for the Rosaceae family. Using whole-genome sequencing data generated from 129 peach accessions, here we perform a comprehensive genome-wide association study for 12 key agronomic traits. We show that among the 10 qualitative traits investigated, nine exhibit consistent and more precise association signals than previously identified by linkage analysis. For two of the qualitative traits, we describe candidate genes, one potentially involved in cell death and another predicted to encode an auxin-efflux carrier, that are highly associated with fruit shape and non-acidity, respectively. Furthermore, we find that several genomic regions harbouring association signals for fruit weight and soluble solid content overlapped with predicted selective sweeps that occurred during peach domestication and improvement. Our findings contribute to the large-scale characterization of genes controlling agronomic traits in peach.

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