

The opium poppy genome and morphinan production supports saltation mode of evolution

With the support mainly by the National Natural Science Foundation of China, an international research team co-led by Prof. Ye Kai (叶凯) at Xi'an Jiaotong University, reported the opium poppy genome and morphinan production, which was published in *Science* (2018, 362: 343—347).

The flowers of opium poppy are often referred to as “flowers of evil”, because although their flowers are attractive, their fruits, the source of opium, induce addiction. The morphine alkaloids extracted from opium poppy are powerful analgesics and the narcotic ingredients also have significant antitussive and anti-cancer effects.

Professor Ye's team utilized various state-of-art genome sequencing techniques, sophisticated mathematical models, comprehensive data mining and analysis methods, allowing them to successfully decipher the opium poppy genome and reveal its evolutionary history. This study has shown that the opium poppy genome had a whole genome-wide duplication event 7.8 million years ago, and segmental duplication events occurred at least 110 million years ago. In addition, this was a gene fusion event to drive metabolic synthesis away from noscapine but towards morphinan. The super gene cluster of 15 genes on chromosome 11 is responsible for the biosynthesis of cough-suppressing and anticancer noscapine as well as analgesic morphine alkaloids. This study illustrated a saltation mode of evolution, in which major genome structural rearrangements suddenly enable completely novel functional traits. Future exploration of this saltation mode of evolution might shed light on Cambrian explosion of species, which seems inconsistent with the typical gradual pace of evolutionary changes proposed by Charles Darwin.

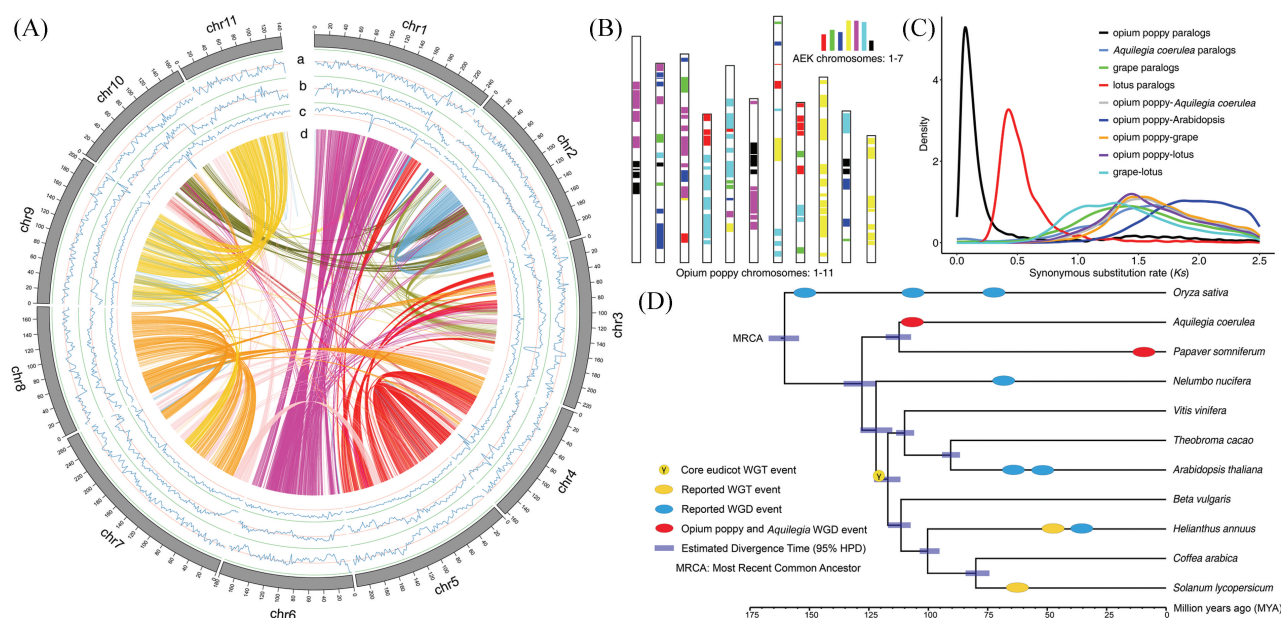


Figure Opium poppy genome characteristics and major evolutionary events.