

The *Orychophragmus violaceus* genome

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Orychophragmus violaceus, a plant of the genus *Orychophragmus* in Brassicaceae, gets its name 'Er-yue-lan' as its flowering starts in February of the lunar calendar. The seeds of *O. violaceus* have high oil content and rich unsaturated fatty acids. Meanwhile, *O. violaceus* can also be eaten as a leafy vegetable, 'Zhuge' in China. Therefore, *O. violaceus* has high ornamental value, edible value, and economic value (Fig. 1). With the development of genome sequencing technology and bioinformatics, it is possible to explore the genes involved in these traits at the genome level. Recently, two reports have obtained a high-quality *O. violaceus* genome at the chromosome level using second- and third-generation sequencing technology, and explored its evolution and genes related to important agronomic traits.



Fig. 1 The photograph of *Orychophragmus violaceus* plant with blooming flowers. Credit: Veer Photo.

One report was originated from the Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, and relevant cooperative institutions (DOI: [10.1016/j.xplc.2022.100431](https://doi.org/10.1016/j.xplc.2022.100431)). In the study, Nanopore and Hi-C sequencing were used to obtain a high-quality genome of *O. violaceus* containing 12 chromosomes, with a genome size of 1.34 Gb and Scaffold N50 of 100.34 Mb. A total of 55,389 protein-coding genes were detected, and 98% of 1,614 BUSCO genes were identified in the *O. violaceus* genome.

Studies have shown that the large-scale expansion of repetitive sequences is the reason why the *O. violaceus* genome is larger than other diploid genomes of Brassicaceae. It was found that *O. violaceus* experienced a specific genomic tetraploid event, and its karyotype is tPCK, which is the same as that of *Brassica* vegetable crops such as Chinese cabbage. The study reconstructed two sets of ancestral genomes of *O. violaceus*,

named Ov1 and Ov2. It was found that the gene density of Ov1 was higher than that of Ov2, and more genes were a higher expression in Ov1 than Ov2. These results indicate that subgenome dominance exists in *O. violaceus*, and its ancient polyploidy belongs to the allotetraploid. The genome tetraploidy of *O. violaceus* occurred about 8.57 million years ago, which is similar to the ancient hexaploidy of common genomes of *Brassica* species. However, the ancient tetraploid event of *O. violaceus* is independent of the ancient hexaploid event of *Brassica*, which indicates that *O. violaceus* is not the tetraploid ancestor of Brassicaceae crops.

Through genomics and transcriptomics analysis of *O. violaceus*, it was found that *DGAT1*, *FAD2*, and *FAD6*, the key genes for oil biosynthesis, simultaneously expanded and retained more gene copies through ancient tetraploid and tandem repeat, and the copy number expansion of these genes played an important role in the formation of high yield oil of *O. violaceus*.

Another report came from the College of Plant Science and Technology, Huazhong Agricultural University, and relevant cooperative institutions (DOI: [10.1016/j.xplc.2022.100432](https://doi.org/10.1016/j.xplc.2022.100432)). Pacbio and Hi-C sequencing techniques were used in the study to obtain a high-quality genome at the chromosome level of *O. violaceus*, with a size of 1.25 Gb. A total of 61,097 protein-coding genes were identified, and 97.8% of the BUSCO genes were identified in the genome of *O. violaceus*.

O. violaceus is a diploid undergoing an extra whole-genome duplication (WGD) after the Brassicaceae specific α -WGD event. Karyotype analysis showed that most chromosomes were broken and rearranged relative to tPCK karyotype of the ancestor species. According to karyotype comparison with the genome of *Isatis indigotica*, the evolutionary process of the *O. violaceus* genome is different from that of related species of *Brassica*.

Through transcriptomic analysis of *O. violaceus* seeds at different development stages, it was found that there were no new genes different from those in *Brassica napus* from the functional annotation of genes expressed at the peak of dihydroxy fatty acid synthesis, including *FAD2*, *FAE1*, and other genes known to participate in the synthesis of special fatty acids. Furthermore, *OvDGAT* genes (*OvDGAT1-1*, *OvDGAT1-2*) were identified as candidate genes related to the synthesis of dihydroxy fatty acids in *O. violaceus*. The study provides an important reference for the future industrial utilization of special fatty acids through genetic engineering transformation and the use of the *O. violaceus* gene as a genetic resource.

In summary, the two studies mentioned above have assembled a high-quality genome of *O. violaceus*, enriching our understanding of the evolutionary process of ancient polyploidy of Brassicaceae. It provides abundant data resources for compa-

rative genomics and functional genomics research of *O. violaceus* and other Brassicaceae crops.

Conflict of interest

Xiaoming Song is an Editorial Board member of the journal *Vegetable Research*. He was blinded from reviewing or making decisions on the manuscript. The article was subject to the journal's standard procedures, with peer-review handled independently of this Editorial Board member and his research group.

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