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Genomic insights into the origin, domestication, and diversification of *Brassica juncea*

***Lei Kang*[1]**

Lunwen Qian
Hao Chen
Liu Yang
Zhongsong Liu

[1] Hunan Agricultural University, Changsha, China

Background:

Brassica juncea (L.) Czern. et Coss is a diverse and important agricultural species. It is grown worldwide for a condiment, an oilseed and a vegetable. Four subspecies have been proposed based on crop use and morphology: *juncea* (seed mustard), *integrifolia* (leaf mustard), *napiformis* (root mustard) and *tumida* (stem mustard).

Objective:

Despite early domestication around 3000 BC, the evolutionary history of this ancient allotetraploid species remains uncertain. To obtain a comprehensive overview of the origin, domestication, and diversification of *B. juncea*, we performed this project.

Methods:

We first de novo assembled a high-quality genome sequence of the yellow-seeded *B. juncea* var. Sichuan Yellow (SY) using PacBio long reads combined with BioNano optical and Hi-C chromatin interaction maps. We then re-sequenced 480 *B. juncea* accessions from all over the world, combine with the chloroplast and mitochondrial genomes to perform population genomic analyses. Furthermore, we carried out scans for selective sweeps as well as genome-wide association studies (GWAS) for flowering time and seed weight, and identified candidate genes for morphological diversification in diverse *B. juncea* subspecies.

Results:

The final SY assembly captured 933.5Mb of genome sequence, with 867.3Mb (~92.9%) anchored into chromosomes. A total of 92,878 gene models were predicted, and 95.5% were functionally annotated in public databases. Nuclear and organelle phylogenies of 480 accessions worldwide supported that *B. juncea* is most likely a single origin in West Asia, 8,000–14,000 years ago, via natural interspecific hybridization. Subsequently, new crop types evolved through spontaneous gene mutations and introgressions along three independent routes of eastward expansion. Selective sweeps, genome-wide trait associations and tissue-specific RNA-sequencing analysis shed light on the domestication history of flowering time and seed weight, and on human selection for morphological diversification in this versatile species.

Conclusions:

Our results not only elucidate the complex evolutionary and domestication history of *B. juncea*, but also pave the way for future research and breeding of this morphologically diverse condiment, oilseed, leaf, stem, and root vegetable species.