

# Large-scale deep re-sequencing reveals cucumber's evolutionary enigma

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In a collaborative study published online today in *Nature Genetics*, researchers from the Genome Centre of Chinese Academy of Agricultural Sciences (CAAS), BGI, and other institutes present a cucumber genomic variation map that includes about 3.6 million variants revealed by deep resequencing of 115 cucumbers worldwide. This work provides new insights for understanding the genetic basis of domestication and diversity of this important crop, and provides guidance for breeders to harness genetic variation for crop improvement.

Cucumber is a major [vegetable](#) crop consumed worldwide as well as a model system for sex determination and plant vascular biology. In 2009, [cucumber](#) became the seventh plant to have its genome sequence published, following the well-studied model plant *Arabidopsis thaliana*, the poplar tree, grapevine, papaya, and the crops rice and sorghum. More

efforts have been put into cucumber genomics research since then.

As a part of these efforts, researchers from CAAS and BGI re-sequenced 115 cucumber lines sampled from 3,342 accessions worldwide, and also conducted de novo sequencing on a wild cucumber. In total, they detected more than 3.3 million SNPs, over 0.33 million small insertion and deletions (indels), and 594 presence-absence variations (PAVs), and then constructed a comprehensive variation map of cucumber.

Furthermore, researchers did a suite of model-based analyses of population structure and phylogenetic reconstruction. The results indicated that the three cultivated groups (Eurasian, East Asian, and Xishuangbanna) each are monophyletic and genetically quite homogeneous, but the Indian group shows clear evidence of substructure and genetic heterogeneity. Their further analysis also provide evidence on the ancestral status of the Indian group, which holds great potential for introducing new alleles into the cultivated gene pool.

To understand the population bottlenecks during [domestication](#), researchers made a comparison analysis between vegetable and grain food crops. The comparison result indicated that the three vegetable crops (cucumber, watermelon, and tomato) probably underwent narrower bottleneck events during domestication than the grain food crops (rice, maize, and soybean). In addition, they also identified 112 putative domestication sweeps in the cucumber genome. These findings provide additional impetus for the use of wild germplasm in future vegetable breeding.

Wild cucumber is an extremely bitter fruit. An essential step in the domestication of the wild cucumber into a eatable vegetable must have degenerated its bitter taste. Two genetic loci, Bi and Bt, are known to confer bitterness in cucumber. In this study, researchers found that the

Bt locus was delimited to a 442-kb region on chromosome 5 that harbors 67 predicted genes.

They further investigated the genomic basis of divergence among the cultivated populations for identifying genes controlling important traits. The most obvious trait is the orange endocarp, which distinguishes the Xishuangbanna group from the other groups. This trait is caused by the accumulation of large amounts of  $\beta$ -carotene that was reported to be controlled by a single recessive gene *ore*. In this study, researchers discovered a key natural variation in a  $\beta$ -carotene hydroxylase gene that could be used to breed cucumber with enhanced nutritional value.

Xin Liu, Project Manager from BGI, said "This study not only generates valuable genomic resource including additional wild reference genome, genome-wide variations for further studies and breeding applications on cucumber, but also gave us a better picture about how the cucumber genome evolved during domestication. It is also a good example for studies on vegetable or other economic crops. Large scale sequencing approach and genome wide analysis can be applied on different economic crops for better understanding their evolutionary process and specific traits, providing unique opportunities for further applications."

**More information:** A genomic variation map provides insights into the genetic basis of cucumber domestication and diversity, [DOI: 10.1038/ng.2801](https://doi.org/10.1038/ng.2801)

Provided by BGI Shenzhen

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