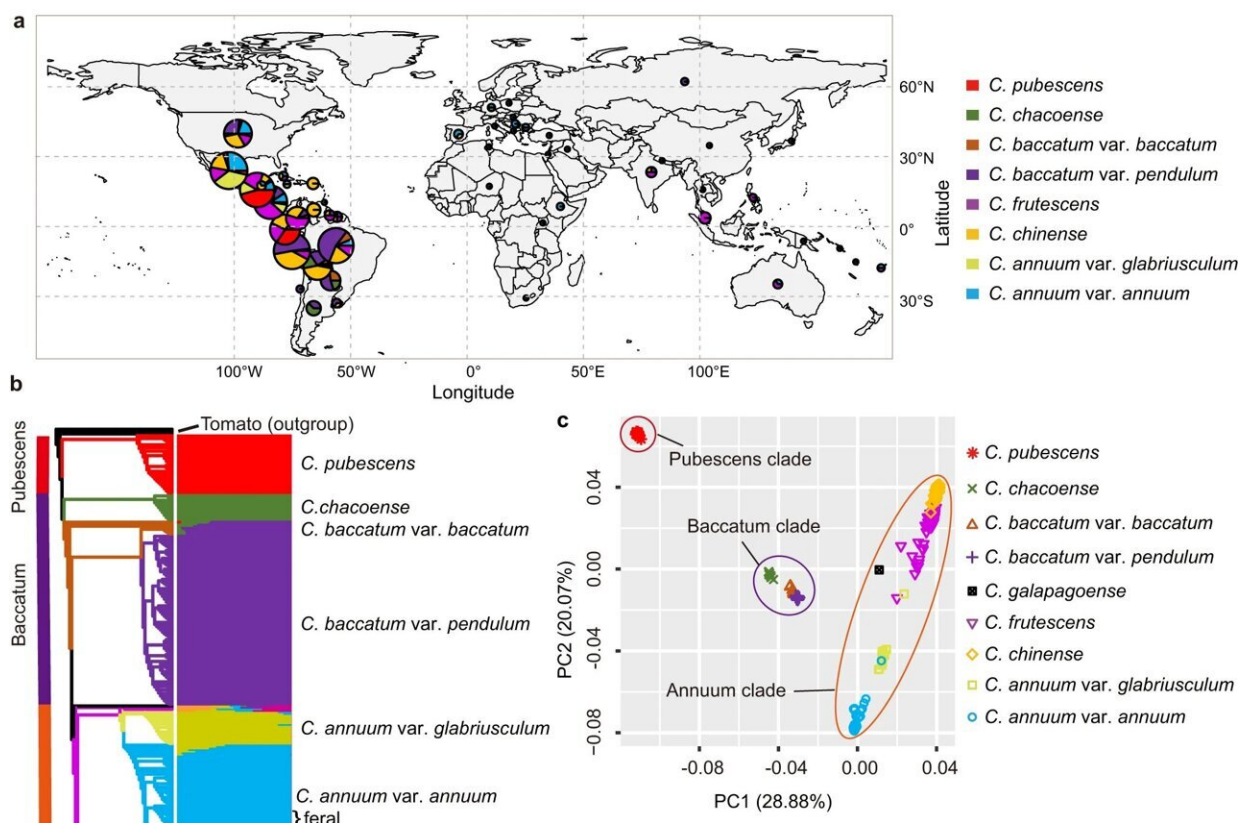


# Unlocking the genetic code of peppers: New study reveals insights into domestication and diversity

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Phylogeny and population structure of *Capsicum* accessions. **a** Geographical distribution of the core pepper accessions (after taxonomy correction). The size of the pie corresponds to the total number of accessions from the selected geographical region. For *C. galapagoense*, only one accession with unknown geographic information was available and is not presented on the map. **b** Maximum likelihood phylogenetic tree and population structure of the core

pepper accessions. **c, d** Principal component (PC) analysis, PC1 versus PC2 (**c**) and PC2 versus PC3 (**d**), of the core pepper accessions. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-41251-4

Peppers are a versatile, flavorful, and widely popular crop, used not only as a healthy food source but also for their medicinal properties.

In a pioneering study recently published in [Nature Communications](#), an international team of researchers, including scientists from the Boyce Thompson Institute, has sequenced the genomes of key cultivated and wild pepper species, offering unprecedented insights into pepper evolution, domestication, and [genetic diversity](#).

"Our analyses have allowed us to identify genes associated with critical traits, including fruit shape, flavor, and stress responses. This opens up a world of possibilities for agricultural advancements and the development of more resilient, flavorful varieties," said Professor Zhangjun Fei, one of the study's lead authors.

The *Capsicum* genus, commonly called pepper or paprika, belongs to the nightshade family and includes about 35 species. The researchers discovered that the two main domesticated species have been selectively bred in different ways, affecting traits like fruit size, shape, and spiciness. They also found that some species have borrowed genetic traits from others, which could help them better resist pests and [environmental stress](#).

"Our findings suggest that the pepper's domestication is more complex than previously thought," said Fei. "The unique genomic regions we've identified could be significant in developing pepper varieties tailored for specific environmental conditions and those with enhanced fruit

quality."

The researchers began by assembling high-quality genomes for three pepper species using advanced sequencing technologies. They constructed a comprehensive graph pan-genome using these genomes as a basis. The team then resequenced the genomes of 500 pepper varieties, covering all five domesticated species and their wild relatives. Using these extensive data, they created a detailed variation map to analyze the genetic differences between these [species](#).

"Our study provides valuable genomic resources that deepen our understanding of pepper genetics, facilitating future functional studies and greatly enhancing breeding efforts," concluded Fei.

The resulting [pepper genome sequence and variants database](#) can be searched, viewed, and analyzed and is maintained by the Fei Lab.

**More information:** Feng Liu et al, Genomes of cultivated and wild *Capsicum* species provide insights into pepper domestication and population differentiation, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-41251-4](#)

Provided by Boyce Thompson Institute

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