



Peanut Pan-Genome Study Uncovers Gene Behind 20% Yield Boost in Dense Planting

Researchers in China have built the most complete genetic map of cultivated peanut to date, and used it to identify a previously hidden gene that shrinks plant height by roughly half while lifting yields by about 20% under dense planting. The findings, published in Nature Genetics on September 15, 2026, could speed the breeding of peanut varieties suited to mechanical harvesting and smallholder farms alike.

The study was led by Shubo Wan of the Institute of Crop Germplasm Resources at the Shandong Academy of Agricultural Sciences, working with Rajeev Varshney, director of the Centre for Crop and Food Innovation at Murdoch University in Australia, and researchers from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), the Chinese Academy of Agricultural Sciences, and several other Chinese provincial academies. The team published its results on September 15, 2026, in Nature Genetics, under the title “Pan-genome-based resequencing of 2,320 accessions reveals structural variations and accelerates breeding advances in cultivated peanut.”

Most crop genome studies rely on a single reference genome, a kind of master blueprint that researchers compare all other varieties against. That approach misses variation that does not exist in the reference plant. To get around this limitation, the team built what is called a pan-genome: a composite genetic map assembled from 14 separate, high-quality peanut genome sequences that together represent all six botanical varieties of cultivated peanut (*Arachis hypogaea*). Ten of those genome assemblies were newly generated for this study, with four drawn from previously published work.

With that broader map in hand, the researchers then resequenced, or read the DNA of, 2,320 peanut accessions collected from 87 countries and regions. This sample covered the large majority of core germplasm, the diverse seed and plant material kept in gene banks, held by both ICRISAT and the United States Department of Agriculture. Comparing all of that genetic data against the pan-genome let the team catalog structural variations, meaning larger-scale differences in DNA such as insertions, deletions, and rearranged segments, that a single reference genome would not have caught.

Among the traits the team focused on was plant architecture, particularly how tall a peanut plant grows and where its flowers and pods form. Using the pan-genome, they traced a chromosomal segment carrying a gene that had gone undetected in earlier peanut genome studies. This gene reduces both plant height and internode length, the space between joints on the stem, producing a compact, dwarf plant type.

The researchers used this discovery to help develop a new dwarf line, named LuAi-1, that stands about 50% shorter than its parent variety while yielding around 20% more when planted at higher density. Shorter, more compact plants can be spaced closer together without excessive shading or lodging, where plants fall over, which is what allows the yield gain per unit of land. Varshney said the research shows it is possible not just to develop dwarf peanut varieties, but to substantially raise yield alongside plant height reduction.

Beyond the dwarfing gene, the pan-genome and resequencing dataset also flagged variants linked to flowering time, giving breeders additional targets for adapting peanut varieties to different growing seasons and latitudes. The team has deposited the genome assemblies and variant data in public repositories, including NCBI and China’s National Genomics Data Center, along with analysis code on GitHub, so other breeding programs can use the resource directly rather than starting from scratch.

Why it matters for breeders and mechanized harvesting

Plant architecture is a practical bottleneck in peanut production. Taller, sprawling plants are harder to harvest mechanically and tend to compete more with each other for light and nutrients when sown densely. A validated dwarf gene that breeders can select for directly, rather than relying on slower trial-and-error crossing, shortens the path to varieties that suit both combine harvesters in large operations and tighter planting patterns on smaller plots. Because the pan-genome also captures diversity from wild and landrace peanut material that conventional breeding programs rarely use, it gives plant breeders a wider pool of genetic options for traits beyond height, including disease resistance and drought tolerance, in future work.

Source: <https://www.global-agriculture.com/ag-tech-research-news/peanut-pan-genome-study-uncovers-gene-behind-20-yield-boost-in-dense-planting/>