

## Genetic secrets of peanut varieties unveiled

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By **Susheela Srinivas**

**Bengaluru:** Peanuts address nutritional demands in underdeveloped countries as they are a rich source of proteins and fatty acids. In a significant development, an international team of researchers led by plant geneticists at the Hyderabad-based International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) has decoded the complete set of chromosomes of two widely cultivated peanut varieties belonging to the subspecies *hypogaea* and *fastigiata*.

Genetic decoding — known as the reference genome sequence— helps in understanding cell-level mechanisms which make one variety score better than the other. For peanuts, the deciding factors are high oil and protein content, disease and heat resistance and high yield.

The gene sequencing is a complex and exhaustive process running in too many years. The process involves several stages: high-quality DNA is isolated from the target plant and cut into bits. It is then placed in a sequencing machine. With the help of special tools and bioinformatics programs, gene sequencing is synthesized.

Peanuts, with their farming history of more than 6000 years have complex genomes. In this study, the scientists found that its sequence was comparable in size to that of the human genome which had a little over 3 billion DNA base pairs with 83709 genes that control its traits. During this process, the team discovered that the peanut variety was a tetraploid — which means that the cultivated groundnut genome is home to two different sub-species genomes. They also found that the exchange of genomes was occurring with one dominating the other.



*Team of researchers at ICRISAT*

“The tetraploid nature is the result of natural hybridisation (crossing) of two wild species called *Arachis duranesnis* and *Arachis ipaensis*. The cultivated peanut genome is home to both the genomes of the sub-species. By living and coordinating together, this dual diploid genome decides the quality of crops we see in the fields,” explained Dr Rajeev Varshney, Research Program Director at ICRISAT.

Genome referencing provides researchers access to all the peanut genes, which, in turn, will boost gene discovery and marker development studies. “It will accelerate development of superior peanut varieties with high pod and oil yield, greater resistance to diseases, nutrition-rich, aflatoxin-free, and improved oil quality seeds,” added Dr Manish Pandey, senior scientist at ICRISAT.

This study will help expand genetic base for sustainable and resilient groundnut production to face the challenges brought about by climate changes.

The study involved scientists from research institutes in China, Taiwan, Australia, USA, Argentina, Brazil, Japan, France and Korea, besides India. The research was published in two papers in the journal [Nature Genetics](#). The Indian team included Manish K Pandey, Rajeev K

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**Varshney, Vanika Garg, Amir W Khan, Prasad Bajaj and Annapurna Chitikineni (ICRISAT); Polavarapu Bilhan Kavikishor (Osmania University) and Senjuti Sinharoy (National Institute of Plant Genome Research, New Delhi).**

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