Chickpea genome clues to more robust crops

Multinational research reveals pathways to boosting the world’s second largest legume crop. Biplab Das reports.

An international research team has identified genes responsible for heat and drought tolerance in chickpeas. This finding may be useful for developing more robust, high-yielding varieties of the important food crop.

In a paper published in *Nature Genetics*, the team reports to have detected other genes that provided key insights into the crop’s genetic diversity, domestication, post-domestication divergence and agronomic traits such as yield and disease resistance. They have also traced back the crop’s origins to the Fertile Crescent, and its subsequent spread across the Asia and Africa.

The research involved scientists from 21 institutions, who mapped the genomes of 429 lines of cultivated and wild chickpeas from 45 countries. Chickpea, formally known as *Cicer arietinum*, is the second largest cultivated legume in the world. It is an important source of protein, and also contains beta-carotene, a precursor of vitamin A and minerals including phosphorus, calcium, magnesium, iron and zinc.

Drought and heat have been shown to reduce the crop’s yield by more than 70%. Being winter-savvy, its productivity may decrease further if temperatures rise due to global warming. The researchers say that identifying genes for drought and heat tolerance is a step towards making climate-ready crops that can help avert such yield loss.

While scanning the genomes, the scientists identified genes related to stress response, DNA repair, protein kinase activity, seed development, germination and flower development. They discovered several unique genes, including a disease-resistant gene.

“We identified several candidate genes for 13 agronomic traits,” says lead author Rajeev Varshney, from the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in Hyderabad, India.

“For example, we identified three key genes which could help the crop tolerate temperatures up to 38 degrees Celsius, enhancing its productivity.” During the domestication, ancient farmers preferentially selected genes for traits such as yield and disease resistance. Genes influencing traits not selected disappeared from the genomes of cultivated lines.

Varshney and his colleagues painstakingly tracked down the missing genes. To assess the losses, they divided the crop into different groups, depending on their seed types. These included common commercial lines known as Desi and Kabuli, as well as other cultivated and wild lines.

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