

Global research team decodes genome sequence of 90 chickpea lines

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In a scientific breakthrough that promises improved grain yields and quality, greater drought tolerance and disease resistance, and enhanced genetic diversity, a global research team has completed high-quality sequencing of not one but ninety genomes of chickpea.

[Nature Biotechnology](#) featured the reference genome of the CDC Frontier chickpea variety and genome sequence of 90 cultivated and wild genotypes from 10 different countries, as an online publication on 27 January 2013. The paper provides a map of the structure and functions of the genes that define the chickpea plant. It also reveals clues on how the sequence can be useful to crop improvement for sustainable and resilient food production toward improved livelihoods of smallholder farmers particularly in marginal environments of Asia and sub-Saharan Africa.

The research milestone was the result of years of genome analysis by the International Chickpea Genome Sequencing Consortium (ICGSC) led by the International [Crops Research](#) Institute for the Semi-Arid Tropics (ICRISAT) headquartered in Hyderabad, Andhra Pradesh India, involving 49 scientists from 23 organizations in 10 countries. ICRISAT is a member of the CGIAR Consortium.

The [global research](#) partnership succeeded in identifying an estimated 28,269 genes of chickpea after sequencing CDC Frontier, a kabuli (large-seeded) chickpea variety. Re-sequencing of additional 90 genotypes provided millions of [genetic markers](#) and low diversity genome regions

that may be used in the development of superior varieties with enhanced [drought tolerance](#) and [disease resistance](#). This will help chickpea farmers become more resilient to emerging challenges brought about by the threat of climate change. The genome map can also be used to harness genetic diversity by broadening the genetic base of cultivated chickpea genepool.

Chickpea is the second largest cultivated grain food legume in the world, grown in about 11.5 million hectares mostly by resource poor farmers in the semi-arid tropics. The highly nutritious, drought-tolerant chickpea contributes to income generation and improved livelihoods of smallholder farmers in African countries like Ethiopia, Tanzania and Kenya, and is crucial to the food security in India (being the largest producer, consumer and importer of the crop). Chickpea is also an important component of the pulse industry in Australia, Canada and USA.

"ICRISAT and its partners have once again demonstrated the power of productive partnerships by achieving this breakthrough in legume genomics," says Dr William Dar, Director General, ICRISAT. "Under the CGIAR Research Program (CRP) on Grain Legumes led by ICRISAT along with other CGIAR Consortium members and program as well as national partners, genome sequencing will play a crucial role in speeding up the development of improved varieties for smallholder farmer crops such as chickpea."

"In the face of the growing global hunger and poverty amid the threat of [climate change](#), the chickpea genome sequence will facilitate the development of superior varieties that will generate more income and help extricate vulnerable dryland communities out of poverty and hunger for good, particularly those in the drylands of Asia and sub-Africa for whom ICRISAT and our partners are working," Dr Dar adds.

"Genetic diversity, an important prerequisite for [crop improvement](#), is very limited and has been a serious constraint for chickpea improvement. This study will provide not only access to 'good genes' to speed up breeding, but also to genomic regions that will bring [genetic diversity](#) back from landraces or wild species to breeding lines," explains Dr Rajeev Varshney, coordinator of ICGSC and Director – Center of Excellence in Genomics, ICRISAT.

"At the moment, it takes 4-8 years to breed a new chickpea variety. This genome sequence could reduce to half the time to breed for a new variety with market-preferred traits." he adds.

According to Professor Jun Wang, Director of BGI, "The collaboration between BGI and ICRISAT has yielded significant achievements in orphan crops research, like the pigeonpea genome before and now, the chickpea genome. I believe that our partnership will revolutionize research on orphan crops, which are key staple crops in many low-income countries and are extremely important to smallholder farmers worldwide. The [chickpea](#) genome sequencing project was undertaken by the ICGSC led by ICRISAT, the University of California-Davis (USA) and BGI-Shenzhen (China) with key involvement of national partners in India, USA, Canada, Spain, Australia, Germany and Czech Republic.

Provided by BGI Shenzhen

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