Peanut genome sequenced, one of the most cultivated commercial species in the world

The study on 'Arachis hypogaea', was published in 'Nature Genetics' and proves that one of the populations that gave rise to it is from Argentina

A group of scientists sequenced the genome of *Arachis hypogaea*, one of the most cultivated peanut species in the world. The study, which was attended by CONICET researchers working at the Institute of Botany of the Northeast (IBONE, CONICET-UNNE) and was published yesterday in the journal 'Nature Genetics', demonstrates that this popular legume emerged from the hybridization of two populations originating in South America and one of them is from Argentina.

The work involved researchers from the United States, Argentina, China, India, Japan and France; and used various sequencing technologies to obtain complete genome information, with unprecedented quality. In addition, the process allowed to reveal the genetic mechanisms that have made the peanut so diverse and can present different characteristics in the growth habits of the plants, the color of the flowers, the size and shape of the seeds.

This study will become the frame of reference for future research on the biology of the species. “Genome sequencing allows us to investigate the genetic architecture of peanuts. We have the catalog of genes in their chromosomal context, which has enormous potential for the development of genetic improvement projects that allow, for example, to obtain varieties tolerant to different diseases, to drought or with a better proportion of fatty acids”, highlights one of the authors of the work, the principal investigator of CONICET at IBONE and the Faculty of Exact, Natural and Surveying Sciences (FACENA) of the Universidad Nacional del Nordeste (UNNE), Guillermo Seijo.

The sequencing of multiple ancient races and wild materials made it possible to identify that the maternal parental of the peanut is originally from the NOA region, more precisely from the province of Salta. “The results determined that it originated in a unique hybridization and chromosomal duplication event that dates back to about 10,000 years, generating a wild allotetraploid similar to the current Arachis monticola that is located in the provinces of Jujuy and Salta, which was later domesticated and it gave rise to Arachis hypogaea”, explains another of the authors of the paper, the assistant researcher of CONICET at IBONE, Sebastián Samoluk.

For this work, two studies carried out by IBONE researchers in 2004 and 2012. were taken as a reference. In the first, wild species that acted as peanut progenitors were established: Arachis ipaensis and Arachis duranensis. In the second, the most similar populations were proposed that would have intervened in the origin of the crop.

The sequencing of the genomes of the two wild species considered parental - also published in Nature Genetics in 2016 - proved that the subgenome “B” comes from the paternal donor Arachis ipaensis, corresponding to a small relictual population in southern Bolivia, which would have been transported from the north of that country by the ancient settlers, during prehistory. However, that investigation had failed to determine which one would have acted as the maternal donor of the "A" subgenome.

This new study on the genome of cultivated peanuts and their comparison revealed that the population of Arachis duranensis living in the Salta town of Río Seco is, among the modern representatives of the species, the one that is most likely to have acted as a donor of the subgenome "TO". Read more..