

PRESS RELEASE

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The first peanut genomes sequenced

The International Peanut Genome Initiative releases the first peanut genome sequences to the public.

Alexandria, VA – The International Peanut Genome Initiative (IPGI) — a multinational group of crop geneticists working in cooperation for several years — has successfully sequenced the genome of the peanut.

The new peanut genome sequence will be available to researchers and plant breeders across the globe to aid in the breeding of more productive, more resilient peanut varieties.

Peanut (*Arachis hypogaea*), also called groundnut, is an important crop both commercially and nutritionally. Globally, farmers tend about 24 million hectares of peanut each year, producing about 40 million metric tons. While the oil and protein rich legume is seen as a cash crop in the developed world, it remains an important sustenance crop in developing nations.

Scott Jackson, director of the University of Georgia (UGA) Institute of Plant Breeding, Genetics and Genomics at the College of Agricultural and Environmental Sciences, serves as chair of the International Peanut Genome Initiative.

“The peanut crop is important in the United States, but it’s very important for developing nations as well,” Jackson said. “In many areas, it is a primary calorie source for families and a cash crop for farmers.” According to plant geneticist

Rajeev Varshney of India, “Improving peanut varieties to be more drought, insect and disease resistant, using the genome sequence, can help farmers in developed nations produce more peanuts with fewer pesticides and other chemicals and help farmers in developing nations feed their families and build more-secure livelihoods”

The effort to sequence the genome of the peanut has been underway for several years. According to plant geneticist, Peggy Ozias-Akins, UGA-Tifton, GA, while peanuts have been successfully bred for intensive cultivation, relatively little was known about the legume’s genetic structure because of its complexity.

Plant geneticists David and Soraya Bertioli of Brazil expressed their enthusiasm for the new possibilities offered by the genome sequence, “Until now, we’ve bred peanuts relatively blindly compared to other crops. These new advances are allowing us to understand breeding in ways that could only be dreamt of before.”

The peanut grown in fields today is the result of a natural cross between two wild species, *Arachis duranensis* and *Arachis ipaensis* that occurred in the north of Argentina between 4,000 and 6,000 years ago. Because its ancestors were two different species, today’s peanut is a tetraploid, meaning the species carries two separate genomes which are designated A and B sub-genomes.

To map the peanut’s genome structure, IPGI researchers sequenced the two ancestral parents, because together they represent the cultivated peanut. The sequences provide researchers access to 96 percent of all peanut genes in their genomic context, providing the molecular map needed to more quickly breed drought-resistant, disease-resistant, lower-input and higher-yielding varieties.

The two ancestor wild species were collected from nature decades ago. One of the ancestral species, *A. duranensis*, is widespread but the other, *A. ipaensis*, has only ever been collected from one location, and indeed may now be extinct in the wild. When grappling with the thorny problem of how to understand peanut’s complex genome, it was clear that the genomes of the two ancestor species would provide excellent models for the genome of the cultivated peanut: *A. duranensis* serving as a model for the A sub-genome of the cultivated peanut and *A. ipaensis* serving as a model for the B sub-genome. Fortunately because of the long-sighted efforts of germplasm collection and conservation, both species were available for study and use by the IPGI.

Knowing the genome sequences of the two parent species will allow researchers to recognize the cultivated peanut's genomic structure by differentiating between the two subgenomes present in this crop. Being able to see the two separate structural elements will also aid future gene marker development — the determination of links between a gene's presence and a physical characteristic of the plant. Understanding the structure of the peanut's genome will lay the groundwork for new varieties with traits like added disease resistance and drought tolerance.

University of California, Davis genome researchers Lutz Froenicke and Richard Michelmore are optimistic that these genome sequences will serve as a guide for the assembly of the cultivated peanut genome that will help to decipher genomic changes that led to peanut domestication, which was marked by increases in seed size and plant growth habit. The genome sequence assemblies and additional information are available at <http://peanutbase.org/files/genomes/>.

The International Peanut Genome Initiative brings together scientists from the United States, China, Brazil, India and Israel to delineate peanut genome sequences, characterize the genetic and phenotypic variation in cultivated and wild peanuts and develop genomic tools for peanut breeding. The initial sequencing was carried out by the BGI, Shenzhen, China. Assembly was done at BGI, USDA-ARS, Ames, IA, and UC Davis, Davis, CA. The project was made possible by funding provided by the peanut industry through the Peanut Foundation, by MARS Inc., and three Chinese Academies (Henan Academy of Agricultural Sciences, Chinese Academy of Agricultural Sciences, Shandong Academy of Sciences). A complete list of the institutions involved with the project and the other funding sources is available at www.peanutbioscience.com.

About the peanut

In the U.S. peanuts are a major row crop throughout the South and Southeast. While they are an economic driver for the U.S. economy, the legume is also crucial to the diets and livelihood of millions of small farmers in Asia and Africa, many of whom are women. Apart from being a rich source of oil (44–55 percent), protein (20–50 percent) and carbohydrates (10–20 percent), peanut seeds are an important nutritional source for niacin, folate, calcium, phosphorus, magnesium, zinc, iron, riboflavin, thiamine and vitamin E.