The peanut crop has a very narrow genetic basis, and a limited number of alleles for crop improvement. The wild species of peanut are genetically diverse, and have been selected under diverse evolutionary pressures for millions of years. Accessions of all the 80 described Arachis species are available at the Brazilian Peanut Germplasm Collection, maintained at Embrapa Genetic Resources and Biotechnology - CENARGEN (Brasília-DF, Brazil). We have studied wild species with two questions in mind: which species can effectively donate genes to cultivated peanut, and what useful characteristics can the wild species donate?

Wild diploid species have diverse physiological responses to drought stress that may be useful if introduced to the peanut crop. However, we have also shown that the genetics of these physiological responses is complex: the wild species' drought physiology can fundamentally change when they are incorporated into a tetraploid form.

Microscopic characterization of the resistance response of wild peanut species has shown that some species block attack by nematodes, late leaf spot and rust before penetration. These responses can be classified as immunity, and would be highly valuable if introduced to peanut varieties.

Whilst wild species are a source of useful traits for the peanut crop, they are diploid and produce sterile hybrids with cultivated peanut. Furthermore, they are not suitable for agriculture. We have worked to overcome infertility barriers, by the incorporation of wild diploid genomes into a tetraploid form that can be crossed with peanut, and producing cultivated peanut lines with small introgressed fragments of the wild genomes. This is being done using molecular breeding, where crosses and line selections are carried out using information from molecular markers in combination with phenotypic selection. So far, lines which are agronomically adapted and have improved disease resistance against foliar diseases, the most important yield constraints in Brazil have been produced.

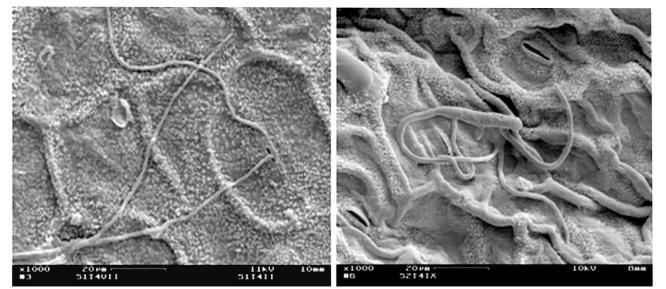


Fig. 4: Cercosporidium personatum hyphal penetration into stomatal openings 72 hours after inoculation observed only in A. hypogaea cv. IAC-Tatu (left) but not in A. stenosperma "V10309" (right).



Fig. 5: Wild genes confer improved disease resistance to cultivated peanut. Top left: an elite variety at end of season under heavy disease pressure. Bottom left: a sample of seeds from the same elite variety. Top right: a breeding line with wild genes introgressed derived from the same elite variety at end of season. Much improved disease resistance. Bottom right: a sample of seeds from the same line. The quantity of pods are approximately proportional to average vields in 2010/2011 trials, a season with heavy disease pressure

#### **5th International Conference of the Peanut Research Community**

After visiting all other continents, the 5th International Conference of the Peanut Research Community is being held in South America, the origin of cultivated peanut. The aim of this AAGB meeting is to bring together scientists involved in all aspects of peanut research and technology, both pure and applied. Whilst maintaining a broad focus, the meeting has a special emphasis on promoting exchange of ideas within, and at the interfaces of, modern genetics, genomics and biotechnoloav. http://www.cenargen.embrapa.br/aagb2011 Email: AAGB 2011@cenargen.embrapa.br



Brasília, DF - Brazil June 13<sup>th</sup> to 15<sup>th</sup>, 2011









# **The Peanut Genetics and Genomics Research Group**





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### The Peanut Genetics and Genomics Research Group

Peanut, or groundnut (Arachis hypogaea L.) is grown throughout the tropics and subtropics and is the fourth most important oilseed in the world. In Asia it provides almost as many calories as soya, in Africa the production exceeds that of all other legumes put together, and in the Americas it is an important crop for domestic consumption and exportation. Cultivated peanut and all its close wild relatives (species in the genus Arachis) evolved in South America.

The Peanut Genetics and Genomics Research Group is based in EMBRAPA, and the Federal and Catholic Universities of Brasília. Research is carried out in collaboration with partners in India, the Americas, Africa and Europe and aims to increase our knowledge of peanut's biology and to apply this knowledge to improve the quality, productivity, and sustainability of this crop.

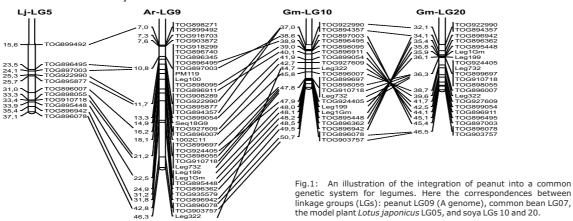
## Genetics

Successful crop varieties combine together distinct desirable characteristics, yield, disease resistance, nutritional qualities etc. The inheritance of these characters is usually complex, and genetic analysis is needed to understand it. Cultivated peanut has very low genetic diversity, and in contrast to most wild peanut species, is tetraploid with an AABB-type genome. Historically this combination of tetraploidy and low genetic diversity hampered the development of modern genetics for peanut.

In order to provide a structured basis for genetics, three immortalized mapping populations were developed. One population represents the diploid AA genome, one the BB and one the tetraploid AABB. All three populations include the genetic diversity from wild species and together allow the genetic mapping of almost any gene. In addition, the tetraploid population includes complete wild and cultivated peanut genomes and thus allows the exploration of the key genetic changes that occurred during the domestication of peanut.

The construction of genetic maps requires markers, and over more than a decade this group has developed thousands of genetic markers. In addition, analysis of different marker types has identified those that are most informative and useful for breeders and researchers.

The genetic maps produced have served as a reference for alignment of maps created by other research groups and breeders, in India, the USA, Japan and Africa. In addition the maps have allowed, for the first time, the cross-referencing of peanut genetic maps with those of other legumes, such as bean and soya.



#### Genomics

Genomics allows us to understand the biology of crop plants at the most basic level and in a detail that was unimaginable only a few years ago.

In order to dissect the tetraploid genome of cultivated peanut, Bacterial Artificial Chromosome (BAC) Libraries were constructed for the most probable diploid ancestors of cultivated peanut. Each library, which consists of tens of thousands of bacterial colonies ordered in arrays, represents one of the components (A or B) of the peanut genome in fragments that are amenable to study.

These BAC libraries have allowed the sequencing of corresponding regions of the A and B genomes and the dating of the evolutionary divergence of the ancestral species of cultivated peanut at some 3 to 4 million years ago. Some of the major evolutionary processes that occurred during this 3-4 million years of divergence have also been defined. Whilst most genes were highly conserved, the transposon content ("Junk DNA") of the genomes underwent major changes. In addition, we have discovered evidence of a large-scale structure in the peanut genome of conserved and variable domains. The variable domains are rich in transposons and genes that control disease resistance.

Although they only make a small fraction of the genome, genes are the fundamental determinants of traits. We have worked to characterize genes that determine selected characteristics of agronomic importance. DNA sequencing, transcript profiling and genetic mapping has revealed genes and genomic regions that are involved in peanut's responses to attack from foliar leaf diseases and nematodes and to drought. Grain guality is also a top priority in peanut production, and the properties of peanut oil are a key component of this. To aid the incorporation of the high oleic trait into Brazilian adapted cultivars we are using molecular markers. In addition, we have discovered new genes involved in oil and resveratrol synthesis, sequenced and genetically mapped them.

New technologies allow the generation of sequence data on a much larger scale than before. We have used this to build a wild Arachis transcriptome database (http://lbi.cenargen.embrapa.br/arachis/node/1). These new generation technologies will also be key in sequencing the entire peanut genome. The peanut genome is particularly challenging because of its size (about the same as the human genome) and because it consists of two highly similar components (A and B). The genetic mapping populations and the genomic tools described here are an integral part of the genome sequencing project and should aid in obtaining a high quality and complete sequence.

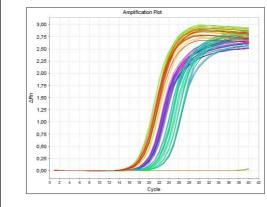
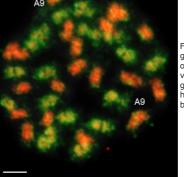


Fig 2: Real-time RT-PCR amplification plots of nematode-responsive genes from th resistance wild specie A. stenosperma showing increase SYBR® Gree fluorescence ( $\Delta Rn$ ) with PCR cycle number.



ig 3: The A and B nome components tetraploid peanut sualized by whole enome *in-situ* bridization. Scale

