

Peanut Genome Initiative Research Progress Chart (updated 26 August 2011)

Priority	2007	2008	2009	2010	2011	2012
Molecular Markers	Library of 10,000 expressed peanut genes	Gene chip with 8400 genes markers; 5500 gene markers for A genome genetic map	6000 new DNA markers positioned on genetic map	Customized microarrays with genes for disease resistance & peg development	Customized microarrays for food safety,	Adoption of marker assisted selection of traits in all breeding programs
Key Traits	Conventional breeding & inheritance studies	Developed germplasm with PAC and RKN resistance	Early maturing, high O/L varieties for improved flavor characteristics in yield tests	Varieties with stacked traits (PAC, RKN, O/L) in yield test	Agronomic varieties with improved water use efficiency	
Genomic Maps	Useful mapping populations for QTL discovery	Discovery of QTL for Key Traits	First SSR-based genetic map of the peanut genome	SNP-based genetic reference map of the peanut genome	Genetic maps of A, B, AB genomes with sufficient DNA markers for anchoring sequences and QTL discovery	16 CAP populations for mapping high-oleic CBR, TSWV, Early & Late leaf spots, white mold & Sclerotinia blight genes
Germplasm Collection	Flavor & quality analysis of UPPT entries	Initial evaluation of oil; tocopherol, folate, amino acid in core collection	Entry of seed composition descriptors in the USDA GRIN database	Ensure seed viability in germplasm collection	Phenotypic analysis of germplasm collection	High throughput capacity for association of genotypes with disease resistance traits
GM Methods	Gene gun used to transform plants with the desired foreign DNA sequences	Breakthrough protocol for efficient transformation frequency	Ability to create stable transformations and reduce time to regenerate fertile GM plants	Ability to transform any peanut genotype	Methods that target specific genes or regions of chromosomes	Ability to insert stacked genes for multiple traits
Biotech Peanut	Transform peanut with resistance to Sclerotinia blight (OK)	Transform peanuts with resistance to Sclerotinia (VA), Stem Rot	Transform peanuts with elevated folate	Transform peanuts with modified protein composition (reduced allergenic potential)	Transformed peanuts with drought tolerance	Yield assessment of current GM peanuts
Regulatory Approval	Initiated regulatory approval process for GM Sclerotinia resistance	Demonstrated little problem with pollen transfer between field grown peanuts	Operative agreements for freedom to operate with GM technology	Regulatory approval for field testing of transgenic material	Methods to control volunteer GM peanuts in commercial production systems	Deregulation of GM peanuts
Gene Discovery	Ability to create gene markers in chemically mutated peanuts	Discovered 3 DNA markers for ara-h2 (allergen protein genes)	Characterize the alleles for the high O/L trait	Discovery of TSWV resistance genes & appropriate gene markers	Amphidiploids to facilitate transfer of genes from wild to cultivated peanut	Routine use of bridge species for development of interspecific hybrids
Gene Characterization	Biotechniques to silence genes in peanut	Silenced the expression of a major allergen, ara-h2	Eliminate genes for specific peanut proteins, oil and fatty acids	Ability to identify mechanism for genetic resistance to PAC	Ability to identify mechanism for genetic resistance for TSWV & leaf spot resistance	Ability to identify mechanism for genetic resistance for drought tolerance
Animal Test Model	Inbred pigs (F2) selected for hypersensitivity to peanut, monoclonal antibodies against swine IgE	Inbred pigs (F3) selected for hypersensitivity to peanut, monoclonal antibodies against swine IgE	Inbred pigs (F4) selected for hypersensitivity to peanut, ELISA assay for swine IgE	Inbred pigs (F5) selected for hypersensitivity to peanut, histology, immunology	Distribute uniform pig lines on a fee basis for clinical, animal & plant research on food allergy	
Peanut Information System	Alignment with the National Legume Information System	Transcript assembly & EST database for advanced DNA marker discovery	Interactive access to portions (gene clusters) in the peanut genome sequence	State of art interactive genomic database for peanut	Advanced software for comparing genome sequences among species	Access to all sequenced plant genomes through LIS affiliation in the Virtual Plant Information System
Genome Sequencing	Estimated A genome size at 1.7Gb with many repeting sequences; BAC libraries for A, B, AB genomes; Diploid & Tetraploid cDNA libarres with 1.1 and 1.4 million bp; 4000DNA markers anchored to BAC sequences; Peanut Genome Index with 35,000 contiguous EST sequences			Established Peanut Genome Consortium for peanut genome mapping	Genomics planning workshop in Brazil; Launched Peant Genome Sequencing Project	Implementation of genome sequencing and reassembly, diploid and tetraploid species