Global transcriptome analysis of two peanut wild species (*Arachis stenosperma* and *A. duranensis*) under biotic and abiotic stress

Guimarães PM[1]*; Brasileiro ACM[1]; Morgante CV[1]; Roberts PA[3]; Pappas Jr GJ[1]; Silva Jr O[1]; Leal-Bertioli SCM[1], Martins A[2]; Moretzsohn M[1]; Bertioli D[2]

[1]EMBRAPA Recursos Genéticos e Biotecnologia Parque Estação Biológica, Brasilia, DF, Brazil;
[2]University of Brasilia, Brasilia, DF, Brazil
[3]University of California, Riverside, USA

**E-mail: messenbe@cenargen.embrapa.br*

Keywords: Arachis, functional genomics, nematode, hydric stress

Legumes are an important source of protein for humans and livestock. Cultivated peanut (*Arachis hypogaea*) is one of the most widely grown grain legumes in the world, thanks to its high protein and unsaturated oil contents. Worldwide, the major constraints to peanut production are drought, foliar fungi and nematodes. Wild *Arachis* species, which are exclusively South American in origin, have high genetic diversity and have been selected during evolution in a range of environments and biotic stresses, constituting a rich source of allele diversity. *Arachis stenosperma* harbors resistances to a number of pests, including *Meloidogyne* spp. and foliar fungi, whilst *Arachis duranensis* has shown high tolerance to hydric stress. A 454 "GS-FLX" transcriptome analysis from cDNA collections from multiple tissues and individuals generated a total of 7,814 unique sequences for *A. stenosperma* and 12,840 for *A. duranensis*, of which 29% had no match in the public database. This data was used to sample large numbers of expressed genes and also to detect simple sequence repeats (SSRs) and single nucleotide polymorphisms (SNPs), as these species are parentals for reference mapping populations. Additionally, a deep coverage of transcripts produced during the pathogenic interaction of *M. arenaria* and *A. stenosperma* was conducted using Illumina "Hi-Seq 2000", resulting in 115 million reads of which a significant number were found to be differentially expressed in each of the four time points of the interaction analyzed. This study should facilitate basic and applied research on the genetics and evolutionary studies of peanut, contribute to the development of molecular markers for other legumes and facilitate comparative genomics and the study of adaptive variation across the genus.