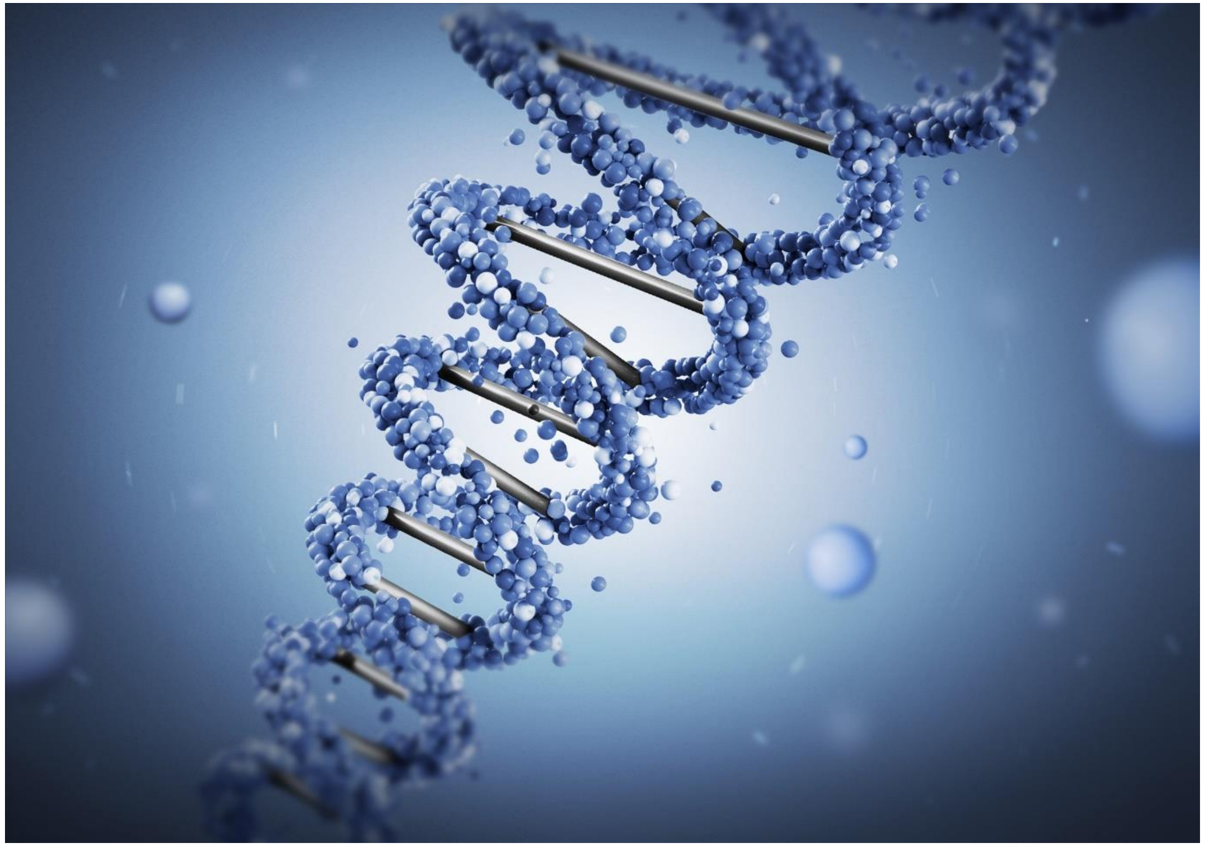
Transcriptome Analysis of Wild Relatives of Peanut under Drought and Fungal Infection



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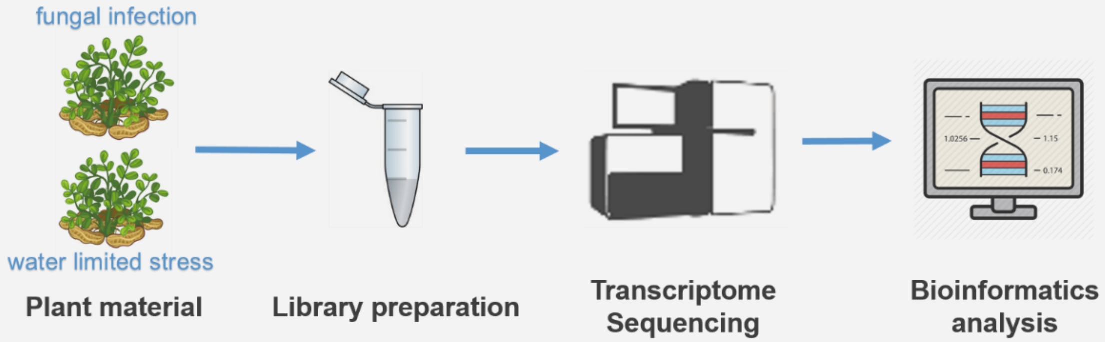
The major constraints to cultivated peanut (*Arachis hypogaea*) are drought and fungal diseases. Two Wild *Arachis* species with high genetic diversity have been selected during evolution in a range of environments and biotic stresses. *A. stenosperma* harbors resistances to a number of pests and fungal diseases, while *A. duranensis* has shown improved tolerance to drought. Transcriptome sequencing enables the gene expression profiling of the two wild relatives of peanut under drought and fungal infection.

Features

- Quantitative measurements of RNA molecules at a single base-pair resolution
- Analysis of the set of all molecules such as mRNA and noncoding RNAs
- A comparable or lower price than many other methods

Applications

- Discovery of novel transcripts, splice variants, and gene fusions
- Elucidate genes involved in responses to certain biological processes
- Can be applied to any species, no matter whether a reference genome is available



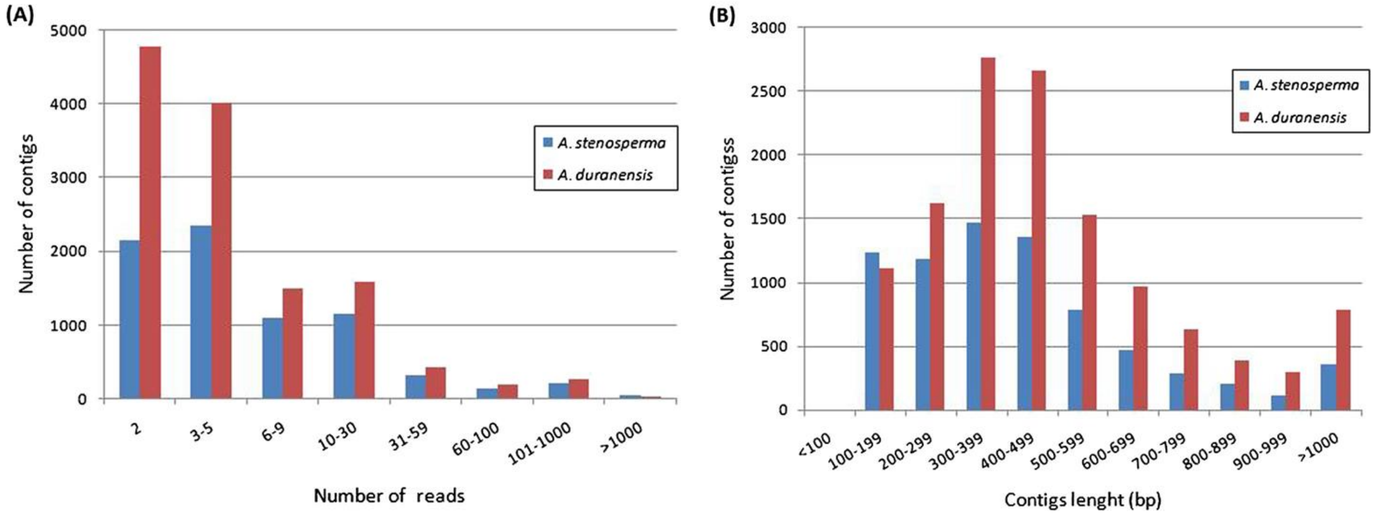
fungal infection
water limited stress
Plant material → Library preparation → Transcriptome Sequencing → Bioinformatics analysis

Assay Overview

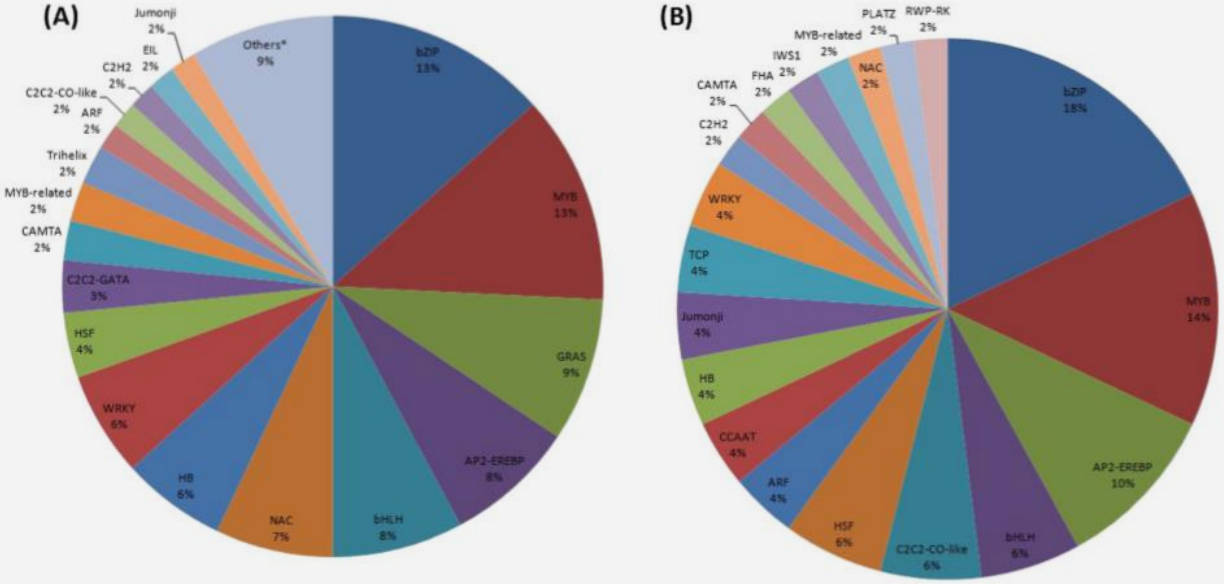
Fungi bioassays were performed on *A. stenosperma* and gradual water limited stress experiments were performed on *A. duranensis*. Total RNA was isolated from the plant materials, and used for transcriptome sequencing on Roche 454 GS-FLX System after poly-A removal. Raw 454 data were preprocessed for transcript clustering and functional annotation.

A total of 740,000 raw reads covering 211 Mb were generated in a single Roche 454 run on the four libraries constructed from the two *Arachis* species under biotic or abiotic stress and respective controls. After data pre-processing, a total of 7,723 contigs was produced for *A. stenosperma* and 12,792 for *A.duranensis*, with each contig being built from a relatively high number of reads (on average, 33 for *A. stenosperma* and 19 for *A. duranensis*).

Data Overview



Data Overview



*Others (≤ 1%): Alfin-like; BBR/BPC; CCAAT; G2-like; GeBP; IWS1; MADS; RWP-RK; TCP; TUB and zf-HD.

All transcription factors (TFs) in *A. duranensis* were assigned to 25 families that play important roles in eliciting stress responses like bZIP (13%), MYB (13%), NAC (7%), bHLH and AP2-EREB (8%) and WRK (6%). In *A. stenosperma*, a slightly different distribution of the TFs in 20 families was observed with bZIP (18%), MYB (14%), AP2-EREB (10%), bHLH (6%) and WRK (4%).

Reference:

Guimarães PM, *et al*. Global transcriptome analysis of two wild relatives of peanut under drought and fungi infection. *BMC genomics*, 2012, 13(1): 387.