

TLI Development of Cross-species Resources for Comparative Genomics in Tropical Crop Legumes

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Background

This project aims to define the ancestral genetic framework of chickpea, cowpea, common bean, and groundnut. If breeders and biotechnologists know how chromosome segments in one species relate to corresponding chromosome segments in other related species, then they will gain insight into the molecular basis of agronomic traits between crop species, and between crops and well-characterised genomes of reference legumes.

During the past year, we have focused on a set of 1440 low-copy genes for allele re-sequencing, leading to the description of thousand of single nucleotide polymorphisms (SNP).

Our current efforts focus on (1) collecting DNA and/or seed from project partners for genetic mapping experiments, (2) continued allele re-sequencing for additional genotypes nominated for common bean and groundnut, and (3) curation of SNP calls.

Although not part of the original project, we also hope to incorporate candidate genes for disease resistance into our SNP data set to develop markers that can be directly applied by breeding programmes in sub-Saharan Africa.

Activities

- Last year, we developed bioinformatics tools to identify, compare, and then prioritise a set of low-copy genes present in the public genome sequences of three reference legumes (*Medicago truncatula*, *Lotus japonicus*, and soybean). From a set of 11,250 sequence alignments, we focused on a subset of 1545 genes that were highly conserved and contained features (eg, introns) desirable for discovering genetic variation. We designed and tested 5760 oligonucleotide primers in appropriate pairwise combinations, using DNA from chickpea, common bean, cowpea, and groundnut.
- Based on success in PCR amplification, we obtained a set of about 1440 genes for allele re-sequencing in each targeted legume species. Each of these gene markers has corresponding genome locations in one or more of the reference legume genomes.
- To date, we have conducted allele re-sequencing for all genes in two parents of each of common bean and chickpea, and four parents of cowpea. For groundnut, 10 diploid mapping

parent accessions were first surveyed, and *A. duranensis* 2 and 25 were selected as suitably polymorphic for full analysis. As of the writing of this abstract, we have validated 11,545 single nucleotide polymorphisms in these four species, representing an average of 376 orthologous genes in each species.

- Within the next 9 months, we will continue allele re-sequencing in additional target genotypes, and we will work to complete the design of an oligonucleotide pooled all (OPA) platform for genotype analysis, using the Illumina® GoldenGate assay.