



Brazilian cowpea transcriptome project: over five million expressed sequence tags to understand salinity and virus resistance

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The Cowpea Genome Project in Brazil was able to generate one of the most extensive expression panels considering legume crops around the world. This crop is the most important protein source for Brazilian and African semi-arid regions. Biotic and abiotic stresses have been seriously affecting the productivity of this crop, despite of the existing phenotypic and genetic variability in Brazilian germplasm. Considering biotic stress main concerns regard virus disease that may affect up to 80% of the productivity during the wet season. Aiming to change this situation, the NordEST network (<http://www.vigna.ufpe.br/>) was established, including 12 Laboratories, to generate genomic data useful for cowpea breeding and biotechnology programs. Efforts include generation of over five million transcripts, including 12 EST libraries for biotic (severe mosaic virus) and abiotic (salinity) stresses; with nine SuperSAGE libraries for salinity and severe mosaic virus and two LongSAGE libraries for potyvirus. Two narrow crosses (400 inbred lines F7-F8) have been developed for mapping purposes, and

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markers (including gene markers, CAPs, dCAPs, DAF, SSR, AFLP, ISSR and RGAs) were developed in order to fine map regions responsible for both above mentioned virus resistance, as well as abiotic stresses and other features (including QTLs) as productivity under drought and salinity conditions, seed color and form as well as plant architecture. Physical chromosome maps are being developed, including microsatellites, rDNA and *Phaseolus vulgaris* BAC probes and shall also integrate marker bulks from important regions of the genetic map, allowing the rapid transference of data among both crops for breeding purposes. The generated data reveals that the main features that collaborate to abiotic and biotic resistance are active in the first hours after stress begin, bringing important clues for breeding purposes.

Key words: Cowpea, Transcriptome, Genetic and Physical Mapping, Virus Resistance.

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