

## 22) PRELIMINARY GENETIC LINKAGE MAP OF COWPEA (*Vigna unguiculata*)

Amorim, L.L.B.<sup>1</sup>; Onofre, A.V.C.<sup>1</sup>; Carvalho, R.<sup>2</sup>; Moretzsohn, M.C.<sup>3</sup>; Ferreira Neto, J.R.C.<sup>1</sup>; Silva, R.L.O.<sup>1</sup>; Correia, C.N.<sup>1</sup>; Silva, M.D.<sup>1</sup>; Sittolin, I.M.<sup>4</sup>; Rocha, M.M.<sup>4</sup>; Andrade, G.P.<sup>5</sup>; Pio-Ribeiro, G.<sup>5</sup>; Kido, E.A.<sup>1</sup>; Benko-Iseppon, A.M.<sup>1</sup>

<sup>1</sup>UFPE/Genética, Recife, Brazil; <sup>3</sup>Embrapa Cenargen, Brasília, Brazil; <sup>4</sup>Embrapa Meio-Norte, Teresina, Brazil; <sup>2,5</sup>UFRPE/Biologia e Agronomia, Recife, Brazil.

### ABSTRACT

There are still few genomic tools available for cowpea, despite of its importance as a crop in Latin America. A partial molecular linkage map of the cowpea diploid genome is presented including the segregation of cowpea severe mosaic virus (CPSMV) resistance region. The present map is based on 19 SSR, 59 AFLP, 6 DAF and 27 ISSR markers segregating in a F<sub>6</sub> population including 97 individuals. Map analyses were carried out using JoinMap (version 3.0) with a minimum LOD score of 3 and the Kosambi function. 119 loci were detected, 82 of which were placed on 13 linkage groups, covering 1,094 cM, with an average distance of 13.3 cM. Yet, this map did not cover the entire genome; there are two more linkage groups than the haploid chromosome number of 11. The phenotypic evaluation of the CPSMV revealed a quantitative pattern, with a single associated marker (ISSR-878) at a distance of 28.7 cM, still too far to allow marker assisted selection. Therefore, the generated cross and the map described here represent the first step towards a collaborative project that includes the development of an integrated saturated map including genomic SSR and EST-derived SSR, RGAP, RGAs, SCAR and CAPS, among other molecular markers, and also additional phenotypic traits including QTLs, as well as fine mapping of virus resistance. Financial Support: CAPES, FACEPE, CNPq, RENORBIO/FINEP/BNB.