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21) GENETIC DIVERSITY AMONG COWPEA CULTIVARS AS REVEALED BY ISSR AND DAF MARKERS.

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ABSTRACT:

Adequate parental choice is among the breeder's most important decisions. This work aimed to evaluate the genetic diversity in cowpea (*Vigna unguiculata*) accessions with contrasting features considering drought and biotic stress by ISSR (Inter Simple Sequence Repeat) and DAF (DNA Amplification Fingerprinting) markers. Forty-six primers were employed for the characterization of Patativa, BRS-Pajeu, BRS Xique-Xique, Santo Inácio, Pingo-de-Ouro, CNCx-689-128G, MNC99-510F-16-1 and BRS-Paraguaçu cultivars. The 16 ISSR primers and 30 DAF generated 108 polymorphic bands. A matrix of pairwise genetic distances generated was subjected to neighbor-joining analysis using MEGA version 4.0. Results revealed that the closest samples to each other were BRS-Xique-Xique and BRS-Paraguaçu (p-distance=0.015), while the most distant were CNCx-689-128G and Pingo-de-Ouro (p-distance=0.093). The distinct genetic separation among cowpea cultivars found in this study supports previous phenotypic variation and performance under biotic and abiotic stresses. Cowpea BRS-Patativa (tolerance to Cowpea severe mosaic virus; sensitive to bruchid) can be crossed with BRS-Pajeu (susceptible to CPSMV; resistant against bruchid) to develop a linkage map. Construction of a detailed genetic map will allow precise and vast amount of useful information for cowpea breeders interested in the identification, and manipulation of traits to their maximum advantage. Financial Support: CNPq, CAPES.