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Investigation of genetic and molecular bases of CABMV resistant/susceptible cowpea genotypes through molecular docking

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Abstract:
Cowpea (*Vigna unguiculata* L. Walp) is one of the most important and widely cultivated legumes in the world, particularly in Africa and Latin America, being one of the main sources of dietary protein and folic acid for millions of people. Currently, Brazil is the third largest producer in the world, behind Nigeria and Niger. The productivity of cowpea is reduced by the action of abiotic and biotic stresses, especially diseases, caused by viruses. Cowpea aphid born mosaic virus (CABMV) is a Potivirus that infects the crop, causing great damage. Potiviruses depend on host plant translation factors for survival, their genome-linked viral protein (VPg), as well HC-Pro (helper component-proteinase), need to interact with eukaryotic translation initiation protein eIF4E and / or eIFiso4E to replicate and infect systematically. Some studies have indicated that loss-of-function mutations in components of the translation complex, "eukaryotic translation initiation factor 4E," are associated with stable resistance (recessive resistance) to various Potiviruses. To our knowledge, no locus of resistance The objective of this work was to investigate the genetic and molecular basis of CABMV resistant / susceptible cowpea genotypes, aiming at the identification of the initiating factor of the eukaryotic 4E 'resistant' eukaryotic translation and To this end, the locus Vu.eIF4E (Vigun06g182700.1) and Vu.eIFiso4E (Vigun07g011000.1) were cloned and sequenced from three cowpea genotypes, namely: 'Susceptible' BR-14-mulatto and 'susceptible and interesting' Boca-Negra cultivar. A sequence analysis identified a few polymorphs (SNPs) that result in the substitution of amino acids in the Vu.eIF4E protein that may affect interactions with VPg and contribute to resistance / susceptibility. Some of the identified SNPs, such as G358C, A379C, A382C, C615G and T619C in the coding sequence results in a substitution of the amino acids (Pro> Arg), (Ala> Asp), (Ala> Glu), (Gly> Arg) and Ala> Val) in the Vu.eIF4E protein, respectively, and may corroborate for resistance to CABMV. Our hypothesis is that the Vu.eIF4E locus controls the monogenic recessive inheritance of CABMV resistance in cowpea, based on mutations that play an important role in the structural stability of the interaction of the Vu.eIF4E protein with the CABMV VPg. To test this hypothesis, we will investigate the interaction between Vu.eIF4E and Vu.eIFiso4E proteins with viral VPg and HC-Pro using the *in silico* molecular docking mechanism. Molecular docking analyzes will indicate which Vu.eIF4E and / or Vu.eIFiso4E interact with the VPg and / or HC-Pro of the CABMV. For further validation of the hypothesis, the two-hybrid yeast assay (Y2H) will be performed.