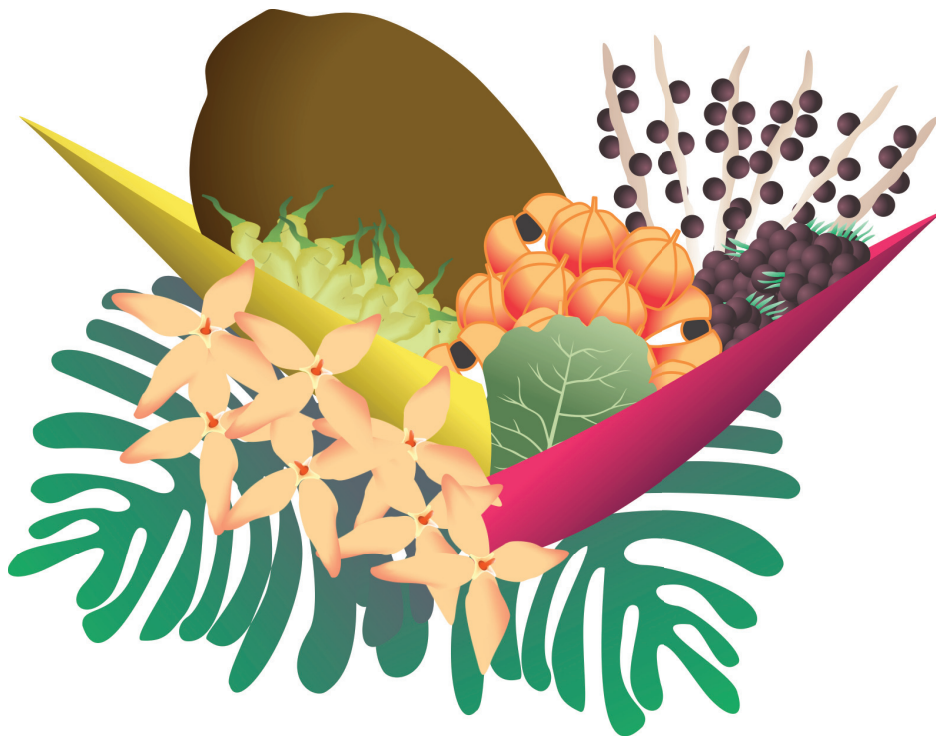


Anais da LXI (61ª) Reunião Anual  
da Sociedade InterAmericana  
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Annals of LXI (61<sup>a</sup>) Annual Meeting  
of the InterAmerican Society  
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Anales de la LXI (61<sup>st</sup>) Reunión Anual  
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## FR035: GENETIC DIVERSITY AMONG CITRUS GENOTYPES USING MORPHOLOGICAL TRAITS

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The assessment of genetic diversity among the accessions from germoplasm bank (GB) give us information about potential parents to be used in breeding programs. Knowing the genetic variability through divergence studies is essential in the process of identifying new sources of interest gene. Therefore, the aim of this study was to identify the genetic diversity using phenotypic data from 10 accessions of GM. The genotypes were oranges (SCS454 Catarina, Champanha, SCS457 Souza), tangerines (Clemenules, Okitsu, Mexerica Rio, Oota Ponkan, Tankan EEI, Ponkan) and hybrid (Fallglo). The fruit farm was planted in 2010 in Biguaçu SC/Brazil. Plants with five years old and grafted on Swingle are in spacing of 4 x 6 meters. Fruits of three plants were evaluated for morphological traits: mass, juice volume, width, length, shell thickness and number of seeds. The experimental design was delineation randomized with three repetitions, where each repetition was composed of five fruit. The mean euclidean was estimated and generated the UPGMA clustering, using the Genes software. The distances ranged from 0.12 up 0.89 between genotypes Oota Ponkan/Ponkan and Bahia Souza/Mexerica Rio, respectively. Using global criterion for cutting the dendrogram, it was observed significant difference at 85% of the distance value. This led to the formation of three groups among the genotypes. Groups I, II and III were formed respectively by: Mexerica Rio, SCS454 Catarina, Oota Ponkan, Ponkan, Okitsu and Tankan; Clemenules and Champanha; and Bahia Souza and Fallglo. We conclude that there is variability among the three orange genotypes and that tangerine Clemenules differs from the others for the characteristics evaluated.

**Keywords:** *Citrus* spp.; mean euclidean; UPGMA.

**Financial Support:** Fapesc; Finep.

## FR063: GENETIC DIVERSITY OF *Conotrachelus humeropictus* Fielder (COLEOPTERA: CURCULIONIDAE) DETECTED BY ISSR MARKERS

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The fruit borer (*Conotrachelus humeropictus* Fielder) is a native pest that affects cocoa (*Theobroma cacao* L.) and cupuassu (*Theobroma grandiflorum* Will. Ex Spreng. (Schum.) plantations in Amazon region. Studies have focused on biology and authors believed that there to be two distinct species that corresponded a host tree cocoa and cupuassu. None previous work has studied molecular markers for fruit borer population genetic analysis. In this study, it was examined genetic diversity between 96 insects sampled from two host tree from two geographic locations using ISSR markers. The samples included 76 adults captured in cocoa tree field CEPLAC Experimental Station in Rondonia State and 20 adults emerged from larvae collected from infested fruit cupuassu in Embrapa Western Amazon Experimental Station, in Amazonas State. Total genomic DNA was extracted, quantified and diluted according of molecular routine protocol. Nine primers ISSR produced two hundred forty-five highly reproducible polymorphic bands with an average of 27.2 markers per primer; among these. The UPGMA dendrogram showing the genetic relationship among the 96 insects was generated based on the Dice similarity coefficient. The genetic similarity values ranged from 0.35 to 0.79, suggesting that ISSR markers detected a very high level of polymorphism in *C. humeropictus*. Two distinct groups were inferred of the cluster analyses, in which insects from Rondonia were separated of the insects from Amazonas state. In conclusion, the results indicated that the groups corresponded more with the geographic structure than insect hosts.

**Keywords:** variability; fruit pests; *Theobroma*.

**Financial Support:** Embrapa and Fapeam.