



Thesis Abstract

Biometric, genetic and molecular evaluations targeting conservation and improvement of *Passiflora* spp

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Brazil is considered to be the main center for genetic diversity of species of *Passiflora* and is the largest producer and consumer of “yellow” passion fruit (*Passiflora edulis* Sims f. *flavicarpa* O. Deg) in the world. Due to anthropic activity in native areas of wild specimens and because the average yield for the passion fruit crop is well below its productive potential, there is a need for genetic research aimed at the conservation and improvement of these species of *Passiflora*. The low production of Brazilian passion fruit is explained in part by the imbalance of orchards and by the occurrence of diseases, especially passion fruit woodiness, caused by Cowpea aphid-borne mosaic virus (CABMV). This study is described in six chapters. Chapter 1 describes the research about the influence of seven chosen measures of distance and 14 similarity coefficients on results obtained from multivariate analysis of nine fruit physical-chemical descriptors from 14 “yellow” passion fruit plants and of 16 RAPD primers in 20 plants. The influence of the distance measures, of the similarity coefficients and of the grouping analysis methods was demonstrated in studies of genetic variability of *Passiflora*. In Chapter 2, using the unweighted pair-group method with arithmetic mean (UPGMA) and Mahalanobis' generalized distance, previously evaluated in the first chapter, the intra- and interspecific genetic dissimilarity was determined regarding nine fruit physical-chemical descriptors among 14 and eight genotypes of “yellow” passion fruit and “sleep” passion fruit, respectively. Descriptors contribute mostly to genetic divergence, and the crosses preferred for the development of physico-chemical attributes of fruit were identified. In Chapter 3, using UPGMA clustering and the Dice coefficient evaluated in the first chapter, intraspecific genetic distances were determined in four species of *Passiflora*, based on RAPD primers. Distance values were estimated and the narrowing of the genetic base for breeding and wild species is discussed. Chapter 4 compares the efficiency of four phytopathometric variables in evaluations of passion fruit plants vs CABMV pathosystem. It was shown that the phytopathometric variable index of infection intensity (III) and global leaf disease index (GLDI) have

advantages in relation to grading scale, and are equally effective in the early identification of passion fruit genotypes more resistant to CABMV and of more severe viral isolates, useful in breeding programs. In Chapter 5, GLDI, evaluated in the fourth chapter, and variables linked to the productivity of the genotypes were used to determine the gradient for resistance of 87 genotypes of “yellow” passion fruit to isolate CABMV UESB-01. Significant associations between the extent of leaf symptoms and the morpho-agronomic characteristics related to productivity were detected ($5.17\% \leq R^2 \leq 11\%$; $0.002 \leq P \leq 0.028$), as it was possible to select genotypes contrasting in CABMV resistance. In Chapter 6, 32 microsatellite primers (SSR) available in the literature were used to evaluate the cross-amplification of these primers in 18 *Passiflora* spp. Cross-amplification was observed for all species, confirming the possibility of using this strategy of amplification.

Key words: CABMV; Germplasm characterization; Genetic diversity; Genetic breeding; Passion fruit; Resistance