

Workshop on Biotic and Abiotic Stress Tolerance in Plants: the Challenge for the 21st Century

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Brazil. Seventeen F_{4:5} and seven F_{5:6} lineages were used as treatment together with controls 'Grand Rapids'(resistant) and 'Regina 71'(susceptible) apart from the Santa Clara tomato cultivar. The sowing was done over expanded polystyrene trays with the substrate infested by *M. incognita* race 1 eggs in the proportion of 20 eggs cm⁻³ of substrat. The trays were maintained in a greenhouse about 45 days after infestation, each plant was evaluated individually for the following characteristics: visual level of root-knots, number of root-knots and number of eggs. Every lineages was compared to the 'Regina 71' and 'Grand Rapids' for each characteristic, using Dunnett (5%) test, obtaining the significance in relation to each control, classification each lineage as resistant homozigote, susceptible homozigote or segregated. The results obtained showed that five lineages F_{4:5} (AFX-020C-06-13-02, AFX-020C-06-20-03, AFX-020C-06-20-02, AFX-020C-06-20-04) and one lineage F_{5:6} (AFX-018D-02-23-15-01) were considered resistant homozigote for the evaluated characteristics, and maybe being used as new sources of resistance to *M. incognita* race 1 in lettuce breeding program.

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S04P04

Molecular diversity of monouredinial *Phakopsora pachyrhizi* isolates collected in Brazil.

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Brazil is the second largest producer of soybean and although it has a great potential to increase production, abiotic and biotic factors have limited the obtention of higher yield in soybean. Among these factors highlight the disease Asian soybean rust caused by the obligate *biotrophic fungus* *Phakopsora pachyrhizi*. The variability of *P. pachyrhizi* isolates has often resulted in the development of virulent strains following the release of rust resistant cultivars. Thus, there is a need to study the geographic distribution of genetic variability of *P. pachyrhizi* isolates aim to develop lines with broad-based resistance. The analysis of the molecular diversity were based in DNA sequences of Internal Transcribed Spacer 1 (ITS1) of 24 single urediniospore isolates of *P. pachyrhizi* derived from infected soybean leaves collected from five different states in Brazil. Additionally a total of 209 sequences ITS1, including sequences deposited in databases, were used to generate a phylogenetic tree to investigate the origins of Brazilian isolates. The geographic distribution revealed that each state harbors a mixture of isolates of *P. pachyrhizi*. The phylogenetic tree revealed six *P. pachyrhizi* groups (I-VI): groups I, III and V formed by a mixed of global isolates; group IV, including exclusively North American and African isolates; group VI containing isolates from North American and China; and group II, except for one Indian and one Paraguay isolates, was formed of exclusively by North American and Brazilian isolates. These findings suggest that *P. pachyrhizi* found in Brazil should be originated from multiple and independent dispersal events.

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S04P05

Development of EST derived-SSRs of *Theobroma grandiflorum* for molecular breeding

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Simple sequence repeats (SSRs) markers are widely used in breeding programs, and SSRs associated to expressed sequence tags (ESTs) could be quite efficient in the selection of genotypes of interest. The breeding program of cupuassu (*Theobroma grandiflorum*) lacks molecular tools to assist the selection of genotypes with desirable characteristics, such as disease resistance, fruit quality or productivity. The objective of this study was to identify SSRs in cupuassu ESTs, and to design and validate primers for molecular marker development. First, 441 ESTs containing 498 EST-SSRs were