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ANALYSIS OF GENETIC DISTANCE IN SPECIES OF ARACHIS (*Sect. Caulorrhizae*) THROUGH CROSSABILITY *Marilda Augusta Peres Oliveira*^{1,2} e *José F. M. Valls*^{2,3}. 1: UNESP/Botucatu-S.P., 2: CENARGEN/EMBRAPA - D.F., 3: Pesquisador CNPq.

Crossability of accessions of *A. pintoi* and *A. repens* is being analysed for establishment of the genetic distance between species *Sect. Caulorrhizae*. The four morphologically distinct accessions of *A. pintoi* and one of a *A. repens* in use present distinct reproductive behavior: GK 12787 and V13468 are prolific. GK 12787 derives from a single plant collected in Bahia, in 1954, always increased in isolation and may represent a single, completely homozygous genotype. V 13468, also autogamous, results from a self-pollinated individual plant of a variable population collected in Goiás. After a single generation in isolation, homozygosity is not necessarily high. V13167, V13338 and *A. repens* Nc 1579 are individual clones, vegetatively collected from nature and may show heterozygosity. The three accessions do not set seed in isolation, but produce them in field conditions in a genebank including many accessions of *Caulorrhizae* and without restriction to the activity of pollinators. This suggests the presence of self-incompatibility. The experimental design was partial diallel 5x4. Near 500 crosses were made producing 51 seeds, of which 25 developed normal plants. Parents accessions showed high pollen stainability and regular meiosis, with $2n=20$. Intra-specific crosses generated fertile F1 hybrids. Interspecific crosses produce infertile F1 hybrids, but selfed maternal types were also harvested from the pots. Autogamous development in this case, was confirmed by morphological and molecular markers. In spite of the lack of fruits production in the interspecifics F1s, all hybrids showed high pollen stainability. The results so far support the taxonomic distinction of *A. pintoi* and *A. repens*. Incompatibility barriers will be further explored by new reciprocal crosses, including in additional accessions. F2 seeds will be germinated for the study of segregation based on morphological and molecular markers (RAPD).

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ISOZYME CHARACTERIZATION AND DIVERSITY OF ETHNOVARIETIES OF CASSAVA (*Manihot esculenta* Crantz). *Maria Inez Fernandes Faraldo* e *Paulo Sodero Martins* - Depto. Genética - ESALQ/USP, Piracicaba-SP.

The main objective of this work was the characterization and quantification of isozyme variation of cassava germplasm (*Manihot esculenta* Crantz) from areas of traditional agriculture in the southern region of the State of S. Paulo. The ethnovarieties were analysed by starch gel electrophoresis (penetrose 30, 13%) using fresh young expanded leaves extracts. Twelve loci were detected and studied, nine of them polymorphic. These loci belong to five enzymes: malate dehydrogenase (MDH - E.C. 1.1.1.37), leucine aminopeptidase (LAP - E.C. 3.4.1.1.1), shikimate dehydrogenase (SKDH - E.C. 1.1.1.25), alfa-esterase (Alfa-EST - E.C. 3.1.1.1) and aspartate aminotransferase (AAT - E.C. 2.6.1.1). Peroxidase was discarded because showed no band polymorphism. The observed isozyme polymorphism is related to the geographical distribution, being the populations from the southern region of the State of S. Paulo more variable than the Ribeira Valley populations. Variability within and between populations and index of genetic similarity by the Simple Matching and Jaccard methods, were estimated. The traditional system of agriculture of caícaras and black communities maintain and amplify the level of intraspecific variability, through introgressive hybridization, gene flow, recombination, mutation and introduction of new varieties. The main conclusions are: 1-) estimate mean heterozygosity indicate high levels of genetic variation within cassava gardens ($H_o=0,242$), with mean, higher than those observed in the literature ($H_o=0,225$); 2-) results show higher degree of variability within gardens, being garden 1 (Pedrinhas-1) the most polymorphic (75,0% of variability); 3-) the intraspecific variability is related to the local social and cultural community structure and, 4-) the ethnovarieties were grouped in four phenetic groups.

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ELECTROPHORETIC PROFILES OF GLYCOPROTEINS FROM *PHASEOLUS VULGARIS*. *Christiane Luiza Belele*, *Marcelo Prudêncio Giovanini* and *Luiz Ricardo Goulart*. Laboratório de Genética Molecular, Universidade Federal de Uberlândia, Campus Umuarama, Bloco 2E - Sala 24, 38.400-902, Uberlândia, MG.

All available morphological and molecular data suggest that cultivated common bean (*Phaseolus vulgaris*) has multiple domestication centers: Middle American and Andean. Each of these centers holds 6 gene pools; 1 to 6 for Middle American and 7 to 12 for Andean. The electrophoretic pattern of the major seed glycoprotein (phaseolin), has been used in biochemical analysis as a molecular marker to facilitate characterization and separation of common bean cultivars. Fourty cultivars of *Phaseolus vulgaris* had their glycoproteins extracted from the seeds according to ROMERO et al. (1995) and separated by molecular weight using 8 and 10% SDS-PAGE (LAEMMLI, 1970). The phaseolin profile of the Middle American group did not present clear differentiation among cultivars in their gene pools. The Brasil 2 and Apetito Blanco cultivars, gene pools 1 and 6, respectively, did not match with the previous description (SINGH et al., 1991). An intermediate pattern, between Middle American and Andean, could be observed for the Apetito Blanco cultivar. In the Andean group, gene pools 10 and 12, represented respectively by Barbunya and Mortino cultivars, showed different patterns between themselves and in comparison to the other gene pools that had a type T phaseolin. The cv. Barbunya had a protein pattern similar to the S phaseolin of the Middle American group. Such similarity can be explained by the introduction of cultivars from the Middle American Center to the Andean Center. Two other glycoproteins identified by Schiff staining, were also analysed. In the Middle American, most cultivars presented proteins with an estimated molecular mass of 70 and 56 kDa, while the Andean group presented bands with 71 and 58 kDa. An exception was observed for cv. Small White of the Middle American group that had an intermediate size between Andean and its own group.

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VARIABILITY ON THE ROTENONE LEVELS IN SPECIES OF *Derris* spp. (FABACEAE) COLLECTED FROM DIFFERENT REGIONS OF AMAZONIA. *José Paulo Chaves da Costa*¹, *Muracy Bélo*¹ e *Sérgio Melo Alves*².

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The species of genus *Derris*, are leguminous plants known by the general name of "timbó" whose roots, besides fixing nitrogen, are carrier of a source of insecticide, which acts also on fish, whose essential substance is the rotenone. The roots are utilized for the capture of fish, by the amerindians and ictiologists, as well as on the control of domestic animals insects and ectoparasites. This work had the purpose to verify the variability on the rotenone level on germoplasms of "timbó" species, collect in the different regions of Amazonia, localized at the provable "forest refuges" that occurred at the pleistocene. The rotenone was extracted of roots powder of *D. nicou*, *D. urucu* and *Derris* sp. and analysed with the liquid chromatography with colun PEGASIL-ODS, with UV-VIS detector (wavelength at 280 nm). The results have shown that for *D. nicou* a 4.26% mean of rotenone, for *D. urucu* a 3.76% value and for *Derris* sp. of 0.18%. The variance analysis carried out in order to verify differences on the rotenone levels among the species, have shown significative values ($F= 4,95$; $P< 0,05$). Through the Tukey test there has been no significative differences between *D. nicou* and *D. urucu* levels. Such species showed to possess higher rotenone content and differed significantly from *Derris* sp. For the effect among plants inside of each region or "refuge" there has been significative differences for *D. nicou* ($F= 161,97$; $P< 0,001$) and *D. urucu* ($F=16,44$; $P<0,001$) and for *Derris* sp. ($F= 10,88$) there has been no significative difference. Plants with the major rotenone levels were in the region where there should exist the "East Peruvian refuge" for *D. nicou* as well as for *D. urucu*.

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