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GENETIC DIFFERENTIATION AMONG SIBLING SPECIES A, B, C, AND D OF ANOPHELES QUADRIMACULATUS (DIPTERA:CULICIDAE) Sudhir K. Narang and Jack A. Seawright, U.S. Department of Agriculture Gainesville, Florida, U.S.A.

Electrophoretic, molecular and cytogenetic methods were used for the identification of 4 sympatric sibling species (A, B, C, and D) of the A. quadrimaculatus complex from the southeastern U.S. Species-specific diagnostic allozymes were identified in a sample of each population by electrophoresing individual gravid females and chromosomal identification of their progeny. A dichotomous allozyme taxonomic key was developed from single- and two-loci diagnostics (Ayala and Powell, Proc. Nat. Acad. Sci. U.S.A. 69: 1094-1096. 1972). In addition, total DNA of individual adults of each sibling species was probed to determine species-specific restriction fragment length polymorphism of mitochondrial DNA.

The diagnostic loci between species were A:B-- Idh-1 & Idh-2, Had-1, Est-4, Est-5, 6Pgd-1 & Ao; A:C-- Idh-1 & Idh-2, Had-1, Had-3, four esterase loci, Got-2, Pep-2, Pgi, 6Pgd, & Xdh; A:D-- Idh-1 & Idh-2, Got-1, Got-2, Pep-2, Pep-4, Est-2 & Me; B:C-- Idh-1 & Idh-2, Had-1, Had-3, Got-2, Pep-2, Pgi, 6Pgd-1 & four esterases; B:D-- Idh-1 & Idh-2, Got-1, Got-2, Pep-2, Pep-4 Est-2 & Me; C:D-- Idh-1, Idh-2, Got-1, Had-1, Had-3, Pgi, Me & Pep-4. Genetic relationships among sibling species will be presented.

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GENETIC DIFFERENTIATION BETWEEN 21 AMERINDIAN POPULATIONS OF COLOMBIA. Alvaro Espinel and Helena Groot de R., Laboratorio de Genética Humana, Biología, Universidad de los Andes, A.A. 4976, Bogotá, Colombia.

The geographic location and the linguistic diversity found in Colombia, make an excellent opportunity to study the genetic and demographic differentiation of southamerican ethnias. In this report are presented the comparisons done between the information of genetic polymorphisms collected by our team for seven populations, four populations reported by Kirk et al. (1974) and ten eastern populations inhabitants of the limits with Venezuela, analyzed by Layrisse and Wilbert (1966). Only ten red cell antigens were studied in common for those populations (ABO, Rh (CDE), P, Le, MNSs, Fy and K). The allelic frequencies were used for the analysis of genetic divergence, employing an adaptation for microcomputers of Biosys-1 (Swofford and Selander, 1981).

The locus that contributes more to the divergence of the populations was Lewis (Fdt = .455 average other loci = .172). The cluster analysis reflects a clear divergence between the savannah groups (Piaroa, Guahibo and Cuiva) and the people of the mountain (Yupa and Bari). A noteworthy difference between the same populations studied 20 years ago by Layrisse and our recent data suggest a strong rate of admixture performed during this period of time.

33.21.57

FREQUENCY OF SOME GENETIC POLYMORPHISMS IN AMERINDIAN POPULATIONS OF COLOMBIA. Helena Groot de R., Alvaro Espinel, Fabiola Valenzuela and Diana Sicard. Laboratorio de Genética Humana, Biología, Universidad de los Andes, A.A. 4976, Bogotá-Colombia.

A General research dealing with demographic and genetic aspects of the Amerindian groups of Colombia was carried out during the last three years; some of the results are reported here. Blood samples were obtained from volunteers of the following groups: 5 Arawak inhabitants of the Savannah; 3 Tukano, 1 Puinave from the Amazon region and 2 Macro-Chibcha from the West Andean region. The red cells were tested with 28 antisera, electrophoretic analyses were done for six proteins, also GMs of the IgG were determined.

The Paez group showed an increase of heterozygosity of some loci tipically monomorphic in Amerindian people, (ABO, RhD, K, Tf). In general all the red cell antigens showed a significant heterogeneity between the populations studied, they do not follow the typical pattern for Amerindians. Tf, C3 and PGM were poorly polymorphic as compared to the results obtained for Hp, EsD and AP, were a great heterozigosity was observed. The degree of aculturization seems to show a proportional increase of alien genes with the subsequent loss of gene pools and perhaps the loss of adaptations to their specific environment.

33.21.58

GENETIC VARIABILITY OF SIX POPULATIONS OF Setaria viridis COLONISING DIFFERENT OPEN HABITATS. Bouchra Rherissi, Irène Till-Bottraud, Jean Pernès, Laboratoire de Génétique et Physiologie du Développement des Plantes, C.N.R.S., F- 91198 Gif-Sur-Yvette, France.

The genetic diversity was studied on six populations of Setaria viridis (wild ancestor of Foxtail millet, Setaria italica) from South-East France using enzyme polymorphism and morphological variability. Setaria viridis colonises different open habitats (garden, vineyard and road side).

Very low levels of polymorphism were detected. The population from St Rémy de Provence is the only one with 4 polymorphic loci out of 11 loci studied, the other populations have only 2 polymorphic loci. Signifcant morphological variability between the six populations was observed for eight charactes only out 20 studied (strong heritability). Here again the population from St Rémy de Provence is the most polymorphic. The level of variability seems to depend on the level of habitat heterogeneity. The characters that are variable in this wild species are relevant to domestication.

33.21.59

GENETIC STRUCTURE OF SOUTHWESTERN NIGERIAN POPULATIONS. Omo S. A. Aromose, Dept. of Biological Sciences, University of Benin, Benin City, Nigeria.

The genetic structure of the populations of southwestern Nigeria presently known as Bendel State is still obscure. This area is situated $5^{o}.00 - 7^{o}.35$ north of the equator in the tropical belt of coastal west Africa. It is uniquely ideal for the study of genetic diversity due to its complex ethnic composition of tribes and the social stratifications based on language and religion.

In this report a summary of the evolutionary relationships between some major groupings in this area based on genetic, anthropometric and linguistic data is presented.

33.21.60

CHROMOSOMAL POLYMORPHISM IN MICRASPIS CARDONI (COCCINELLIDAE : COLEOPTERA). Om P. Mittal, Tajinder K. Gill and Punam Daid, Dept. of Zoology, Panjab University, Chandigarh-160014, India.

The present karyological observations for Micraspis cardoni have been carried out on its spermatogonial metaphase, metaphase-I, and metaphase-II plates carrying different chromosome numbers in different individuals. The different individuals show 2n=20, 22, 24, 26 or 28 chromosomes in addition to 1 to 3 supernumeraries. However, the normal diploid number has been confirmed as 20 with 9 pairs of autosomes and a pair of sex-chromosomes. In one of the individuals a sex trivalent could also be observed distinctly. These chromosomal numerical variations have been examined in individuals collected from the same population showing no morphological difference in their general appearance.