growth rate since 1978. The founder population is 34 (11 are still alive), and all except three have contributed descendants. The Studbook concludes that the population is still too small for an adequate breeding program. Some founders are over represented, but the coordination recommend that none should have their breeding curbed, although emphasis will be given to encouraging breeding in the under represented lines. The studbook keepers would be most grateful for information on any research projects on captive or wild populations of this species.

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## A Study on the Behavior of Adolescent Female Muriquis

Research is being carried out on the migration of adolescent female muriquis, *Brachyteles arachnoides*, at the Caratinga Biological Station, Minas Gerais. In muriqui groups the proportion of adult females remains nearly constant as a result of the migration of the adolescents, an important feature of the sociodemography of this species (Strier, 1991). The study aims to clarify why females emigrate, and the social mechanisms involved. Data have been collected to answer these, and other related questions, using the observation technique of "focal-animal" (10 minute observation periods), possible due to the tameness of the group under study (see Strier, 1992). Data was collected over 12 months, from August 1994 to July 1995, and has resulted in 1555 focal animal samples. Dr Karen Strier of the Anthropology Department, University of Wisconsin, Madison, USA, and Sandra Hartz, Federal University of Rio Grande do Sul, Porto Alegre, Brazil, are supervising the research, which is supported by a U. S. National Science Foundation Grant (BNS958298), the Liz Clayborne and Art Ortenberg Foundation, the Chicago Zoological Society, and the Lincoln Park Zoo, Chicago.

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## Variability in Constitutive Heterochromatin in South American Primates

In March 1995, Júlio César Pieczarka defended his thesis on the nature and variability of constitutive heterochromatin in South American primates. The thesis formed part of the requirements for a doctoral degree in Genetics and Molecular Biology at the Federal University of Rio Grande do Sul, Porto Alegre, Brazil. His supervisor was Dr. Margarete Suñe Mattevi, and the study was supported by the Universidade Federal do Pará (UFPA), the Universidade Federal do Rio Grande do Norte (UFRGS), the Fundação de Amparo à Pesquisa do Rio Grande do Sul (FAPERGS), the Financiadora de Estudos e Projetos (FINEP), the Brazil Science Council (CNPq), the Brazilian Higher Education Authority (CAPES), and Eletronorte (Centrais Eléctricas do Norte SA). The following is a summary of the thesis.

The aim of the work was to assess the distribution and variability of constitutive heterochromatin in 10 platyrrhine primate species, and examine the digestion mechanism of DNA by *in situ* restriction enzymes, in a broad study of the reaction of heterochromatin to these enzymes. The following callitrichids were studied: *Cebuella pygmaea*, *Callithrix geoffroyi*, *C. argentata*, *C. humeralifera*, *C. emiliae*, *Saguinus fuscicollis fuscicollis*, *S. mystax*, and *Leontopithecus rosalia*. These species show constitutive heterochromatin with very different patterns of distribution, despite the similarity of their karyotypes in terms of chromosome number and morphology. Two cebid species were studied: *Aotus* and *Ateles paniscus paniscus*, both of which have considerable quantities of heterochromatin. The determination of correct chromosomal pairs in each karyotype was made by sequenced G/C-banding. The constitutive heterochromatin was analyzed by determining the *in situ* digestion pattern using seven restriction enzymes (*Hinf*I, *Mbo*I, *Alu*I, *Rsa*I, *Dde*I, *Hae*III and *Msp*I), sequenced RE/C-banding, and fluorochrome banding (Chromomicyn $A^3$ and DAPI). This study permitted the following conclusions:

Concerning constitutive heterochromatin in the callitrichids:

a) There are at least four distinct types of constitutive heterochromatin in *Callithrix geoffroyi*; three in *C. argentata*, *C. humeralifera*, and *C. emiliae*; four in *Cebuella pygmaea*; five in *Saguinus f. fuscicollis*; three in *S. mystax*; three in *Leontopithecus rosalia*; and three in *Ateles paniscus* and *Aotus*.

b) The comparative study of bands in the callitrichid genera shows that their size and position remain unaltered during the evolution of the groups, but not their composition.

c) Chromosomes with rearrangements that some taxa have different heterochromatic compositions in their alternative forms.

d) The composition of distal heterochromatin in callitrichids suggests a unique origin. It is possible that this constitutive heterochromatin was originally accumulated in the distal band of the short arm of chromosome 6.

Comparing the performance of each enzyme in the digestion of the heterochromatin in callitrichids;

a) The *Alu*I enzyme showed more intensive digestion than the others in the study of the centromeric heterochromatins in biarmed chromosomes.

b) None of the restriction enzymes used in this study showed significant digestion of the centromeric heterochromatins of acrocentrics.

c) The enzyme *RSa*I digested the distal constitutive heterochromatin found in all four callitrichid genera, showing a common origin for the heterochromatin.

d) The differential sensitivity to the other enzymes of the distal heterochromatin of the various taxa indicated that homogeneity is not complete in callitrichids.

The heterochromatin observed in some of the cebid taxa (*Ateles p. paniscus* and *Aotus* studied here, as well as *Saimiri*, *Cebus*, *Alouatta*, and *Chiropotes*) is equilocally distributed as it is in the callitrichids.

Analyzing the heterochromatin of Platyrrhini in a phylogenetic perspective, it was found that sensitivity to *Alu*I is a characteristic common to the constitutive heterochromatin of all. The callitrichids are still sensitive to *Rsa*I, whereas the cebids are sensitive to *Hinf*I and resistant to *Rsa*I. Amongst the callitrichids, *Saguinus* shares with the cebids the largest amount of the various types of constitutive heterochromatin.

The following was observed comparing the banding patterns, obtained with restriction enzymes, to C-banding produced by Barium hydroxide:

a) Variation in both the size of the band and its position.

b) There are bands observed only with AluI, with no correspondence in C-banding: cryptic bands.

c) There are C-bands with no correspondence to traditional heterochromatin regions.

Relating the structure of a given heterochromatin and its localization in the karyotype:

a) In most species the heterochromatic bands can be separated into four types, each with distinct characteristics: centromeric bands in biarmed chromosomes; centromeric bands in acrocentric bands; distal bands; and interstitial bands.

b) The centromeric bands of biarmed chromosomes are distinguishable from the centromeric bands of acrocentrics with regard to their composition. The former show heterogeneity, and the latter homogeneity.

c) As a rule, the distal bands are homogeneous, or at least show a clear common origin, whereas the interstitial bands are heterogeneous.

d) The degree of homogeneity of some bands must be produced by concerted evolution.

e) The destination of a specific constitutive heterochromatin will be defined by its localization in the karyotype. There are different chromosomal domains where the heterochromatins remain isolated from each other.

By comparing the date obtained in this study to the current hypothesis on equilocality, it is possible to conclude that the existence of nearly identical karyotypes with radically different distributions of heterochromatin eliminates some models that attempt to explain these distributions on the basis of interphase chromosomal configuration or on the types of rearrangements that would have occurred in the chromosomal evolution of the taxa.

Regarding the banding mechanisms by restriction enzymes:

a) *In situ* differential digestion of a given chromosome segment by a restriction enzyme is due to the distribution of cutting sites and to molecular interactions between DNA and the chromosomal components.

b) The use of sequenced C-banding made it possible to distinguish situations where a region was effectively digested by the enzyme from those where it merely produced a negative G-banding pattern.

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## Chromosomal Relations and Phylogenetic and Phenetic Analyses in the Callitrichidae

In March 1995, Cleusa Yoshiko Nagamachi defended her thesis on chromosomal relations and the phylogeny of the Family Callitrichidae. It formed part of the requirements for a doctoral degree in Genetics and Molecular Biology at the Federal University of Rio Grande do Sul, Porto Alegre, Brazil. The study was supervised by Dr. Margarete Suñe Mattevi, and supported by the Universidade Federal do Pará (UFPA), the Universidade Federal do Rio Grande do Norte (UFRGS), the Fundação de Amparo à Pesquisa do Rio Grande do Sul (FAPERGS), the Financiadora de Estudos e Projetos (FINEP), the Brazil Science Council (CNPq), the Brazilian Higher Education Authority (CAPES), and Eletronorte (Centrais Eléctricas do Norte SA). The following is a summary of the thesis.

This study comprised the first broad inter- and intrageneric cytogenetic (G, C, G/C and NOR banding) and cytotaxonomic study of the family Callitrichidae, including representatives of all four genera: *Cebuella pygmaea*; *Callithrix argentata* group (*C. argentata*, *C. emiliae*, *C. chrysoleuca*, *C. humeralifera*, and *C. mauesi*); *Callithrix jacchus* group (*C. aurita*, *C. geoffroyi*, *C. jacchus*, *C. kuhli*, and *C. penicillata*); *Leontopithecus* (*L. chrysomelas*, *L. rosalia*); and *Saguinus* (*S. midas midas*, *S. m. niger*). The aim was to characterize each species, group, and genus in terms of their chromosomes, as well as to determine the types of chromosomal rearrangements that have occurred in the karyotypic differentiation of the members of the family. The results were converted to numeric data and submitted to phenetic and cladistic analyses to determine phylogenetic relationships and clusters among the callitrichids. The phenetic analysis was performed using the NTSYS-pc program (UPGMA method) and the cladistic analysis with the NTSYS-pc (NJ method) and PAUP programs. *Cebus apella* was used as an outgroup in the cladistic analysis. The results obtained allow for the following conclusions.

1) Callitrichids share nearly all the euchromatic chromosome segments.

2) Considering only the euchromatic portion, within species groups and genera were all found to be homosequential, with no chromosome rearrangement differentiating their karyotypes.

3) Chromosomal rearrangements were found which differentiated groups and genera, with five distinct karyotypes as follows: a) a reciprocal translocation differentiates *Cebuella* (2n = 44) from the *Callithrix argentata* group (2n = 44); b) a centric fusion/fission rearrangement and a paracentric inversion differentiate both *Cebuella* and the *C. argentata* group from the *Callithrix jacchus* group (2n = 46): c) a reciprocal translocation and a paracentric inversion differentiate *Leontopithecus* (2n = 46) and *Saguinus* (2n = 46) from the *C. jacchus* group; and d) *Saguinus* diverges from all others by a paracentric inversion and pericentric inversions in at least three pairs of acrocentric autosomes.

4) The variations in the content of chromosomal material are due to differences in the amount of noncentromeric constitutive heterochromatin, the distribution patterns of which are characteristic in each group or genus. This suggests that the accumulation mechanisms of these constitutive heterochromatins might have occurred after the differentiation of the distinct group comprising the callitrichids.

5) The phenetic and cladistic analyses separate the genus *Cebus* from the callitrichids, which form a clade. In the callitrichids, the results show that the marmosets (*Cebuella* and *Callithrix*) form a subclade: *Cebuella* and the *C. argentata* group being more closely related to each other than to the *C. jacchus* group. *Leontopithecus* and *Saguinus* are also very closely related, indicating that, if not derived from each other, they share a close common ancestor. *Leontopithecus* are karyotypically closer to the marmosets (*C. jacchus* group) than is *Saguinus*.

6) On the basis of information obtained from chromosomes, and taking into account the evolutionary pathways, it was possible to suggest the karyotype of an ancestor, as well as proposals for the origin, differentiation and dispersion of the callitrichids. If evolution occurred in the direction of a body size increase (primitive hypothesis), the ancestral form would have a karyotype similar to those of marmosets. If, on the other hand, evolution was in the direction of a body size decrease (phyletic dwarfism), the karyotype of the ancestor would be similar to those of tamarins. Both are chromosomally plausible. However, when taking into account the current distributions of the callitrichids, the proposal involving phyletic dwarf-