different procedure has been estimated to be 60,000 (K. B. JACOBSON and P. PFUDERER, J. biol. Chem. *245*, 3938, 1970). 2. The locus of another glycolytic enzyme, hexokinase, has been mapped to 2–79 ± (D. J. FOX, K. MADHAVAN, and H. URSPRUNG, unpublished). Note the proximity of this locus to that of α-Amylase (Table I).

Zusammenfassung. Durch Verwendung elektrophoretischer Enzym-Mutanten ist es möglich, bei *Drosophila melanogaster* die chromosomale Position der entsprechenden Strukturgene zu bestimmen. Über 20 Gene sind auf diese Weise lokalisiert worden. Untersuchung der Gewebe- und Stadienspezifität dieser Enzyme, im Verband mit zytogenetischer Analyse der Riesenchromosomen, verspricht wertvolle Einblicke in das Problem der Genregulation. In den vorliegenden Tabellen sind die bereits erzielten Ergebnisse zusammengestellt.

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Karyotypes of Bats of the Subfamily Carolliinae (Mammalia; Phyllostomatidae) and Their Evolutionary Implications[1]

The North American leaf-nosed bats of the family Phyllostomatidae are a most complex group of animals. Some members are adapted to feeding on other vertebrates, insects, fruit, nectar, blood (Desmodontinae, see FORMAN et al.[2]), and we have observed *Carollia* feeding on tender stems of plants. Even though several extreme morphological modifications are found and form the basis for the several subfamilies, the phylogenetic affinities of most groups are not easily understood. Karyotypic characteristics were used by BAKER[3] to hypothesize phylogenetic affinities and to delineate several lines of evolution within the family. One line of evolution involved the Carolliinae and part of the Glossophaginae. At that time karyotypic data for the Carolliinae were based on two species of *Carollia*.

In this present communication we describe the chromosomes of another species of *Carollia* and two species of the other genus (*Rhinophylla*) of the Carolliinae.

Methods and Materials. Specimens were collected from natural populations with the aid of mistnets. Chromosomal preparations were made at nearby field stations. A 2 hour in vivo culture of bone marrow was followed by treatment with a 1% sodium citrate solution. Fixation was by methanol, acetic acid (3:1). Mitotic slides were blaze dried and stained with Giemsa's blood stain. Testicular meiotic preparations were by the aceto-orcein squash technique. Voucher specimens are deposited in the collection of mammals, Department of Biology, Texas Tech University. To measure the relative size of the *X* to the autosomes, microphotographs were made and the length of the chromosomes were measured with a pair of dial calipers.

The total length of the *X* chromosome was devided by the total length of the haploid autosomal complement. The *X* chromosome is easily determined in species of *Carollia* because of its secondary constriction[4,5]. The *X* of *Rhinophylla* cannot be positively determined by comparing the karyotypes of males and females, but the determination of the general size of the largest heteromorphic element in males is reasonably accurate. Fundamental number is considered to be the number of arms of the autosomal complement.

[1] We thank Dr. C. J. MARINKELLE and A. CADENA of the Universidad de Los Andes for assistance and facilities. PVT. GENARO LOPEZ assisted with the field work. Dr. R. STRANDTMANN translated the summary. Supported by National Science Foundation Grant No. GB-8120.

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Size of the *X* chromosome to the autosomal genome

Karyotype Catalogue Number and Species		Sex	Locality in Colombia	Size of *X* in relationship to haploid autosomal size expressed as a percentage			No. of cells measured
				Low	Mean	High	
Z75	*Carollia castanea*	♀	Villavicencio	15.64	16.44	17.10	6
Z137	*Carollia subrufa*	♀	Leticia	14.94	17.32	18.71	6
Z3	*Carollia perspicillata*	♀	Restrepo	16.17	17.70	18.31	8
Z146	*Carollia perspicillata*	♀	Leticia	15.44	16.51	19.61	5
Z62	*Carollia perspicillata*	♂	Leticia	16.82	18.25	19.92	8
Z124	*Rhinophylla fischerae*	♂	Leticia	6.04	6.94	8.31	7
Z125	*Rhinophylla pumilio*	♀	Leticia	5.36	6.34	7.86	8
Z192	*Rhinophylla pumilio*	♂	Leticia	5.02	5.39	5.65	4

See text for method of determination.

Results. A brief description of the chromosomes of the species studied is as follows: *Carollia castanea* H. Allen (Figure 1). $2N = 21\,♂♂, 20\,♀♀$; $FN = 36$.

The karyotype of this species is like that reported for *Carollia subrufa* and *C. perspicillata*[3]. The autosomes consist of a very large pair of submetacentric elements, 2 large pairs of subtelocentric elements and 6 pairs of smaller biarmed elements. The X is a subtelocentric element with a distinct secondary constriction on the longer arm. The larger Y is a medium sized acrocentric and the smaller Y is dot sized. In 6 spreads the size of the X chromosome to the haploid autosomal complement varies from 15.64 to 17.10 with a mean value of 16.44 (Table). Similar values were found for *C. perspicillata* and *C. subrufa* (see Table). Meiotic studies on 4 male *C. perspicillata* revealed a meiotic pattern identical to that described by Hsu et al.[4,5] for that species.

Rhinophylla fischerae Carter (Figure 2). $2N = 34$, $FN = 56$. The autosomes consist of 10 pairs of metacentric or submetacentric elements, 2 pairs of subtelocentric elements, 3 pairs of acrocentric elements, plus a very small pair of chromosomes. The X is a medium sized submetacentric, and the Y is a small acrocentric. In 7 spreads the size of the X chromosome to the haploid autosomal complement was from 6.04 to 8.31 with a mean value of 6.94.

Rhinophylla pumilio Peters (Figure 3). $2N = 36$, $FN = 62$. The autosomes consist of 14 pairs of metacentric or submetacentric elements plus 2 pairs of medium sized and one pair of small acrocentrics. The X is a medium sized metacentric, and the Y is a small acrocentric. In 12 spreads from 2 animals the size of the X chromosome to the haploid autosomal complement was 5.02–7.86 with a mean 6.02.

Discussion. The chromosomal characteristics of the hypothesized line of evolution (Baker's Group B)[3] involving *Carollia* (Subfamily, Carolliinae) and *Choeroniscus* and *Choeronycteris* (Subfamily, Glossophaginae) were a low diploid number (16–21), a low fundamental number (24–36), and an XX/XY_1Y_2 sex determining system. The chromosomes of *Carollia castanea* agree with these values, but the chromosomes of *Rhinophylla fischerae* and *R. pumilio* have none of these characteristics. Karyological differences between the 2 genera are further demonstrated by the length of the X chromosome to the total length of the haploid autosomal genome (Table). The values for *Rhinophylla* are near those reported for most mammalian species studied, whereas the values for *Carollia* are approximately three time that value. In light of the lack of variation reported by Ohno[6], these different values appear to be quite significant.

In fact the chromosomes of *Rhinophylla* are much more like those of members of two other lines of evolution (Groups C and F) hypothesized by Baker[3] than they are like Group B. This presents a situation similar to that found in the subfamily Glossophaginae where two karyotypically distinct groups are present.

Interpretation of these data is difficult. The two logical choices are: 1. Even though the two genera (*Carollia* and *Rhinophylla*) are closely related (at the subfamily level) in the evolution of these genera there have been so many changes in the chromosomes that all cytological similarities have been lost; and 2. The cytological differences show true relationships of the respective genera (*Carollia* to the *Choeroniscus* group, and *Rhinophylla* to the Phyllostomatine or Stenodermine group). The second alternative would mean that the two genera should not be placed in the same subfamily.

Several authors have suggested that successful chromosomal changes are unlikely because of the selection pressure of mitosis and meiosis. Such information favors the second interpretation of the chromosomal divergence in the Carollinae. Conversely, the subfamily taxon within the Phyllostomatidae is probably quite old which would allow considerable time for the establishment of such cytogenetic divergence.

Specimens Examined: *Carollia castanea*, Colombia: Meta: Villavicencio ($2\,♀♀$); Amazonas: Leticia ($2\,♂♂$);

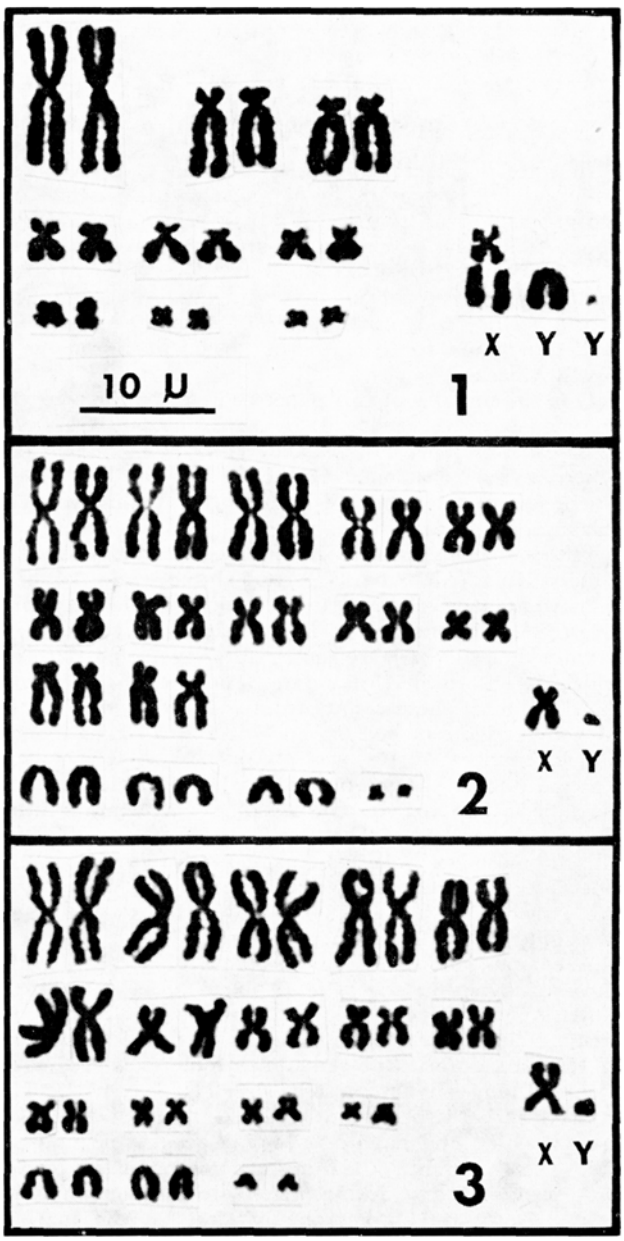

Fig. 1. Representative karyotype of a male *Carollia castanea* collected from Leticia, Colombia.

Fig. 2. Representative karyotype of a male *Rhinophylla fischerae* collected from Leticia, Colombia.

Fig. 3. Representative karyotype of a male *Rhinophylla pumilio* collected from Leticia, Colombia.

[6] S. Ohno, in *Sex Chromosomes and Sex-linked Genes* (Springer-Verlag, New York 1967), vol. 1, p. 192.

Carollia perspicillata, Colombia: Meta: Restrepo (1 ♂ and 1 ♀); Amazonas: Leticia (2 ♀♀); Amazonas: Monkey Island (1 ♂); *Carollia subrufa*, Colombia: Meta: Villavicencio (1 ♂); Amazonas: Leticia (1 ♀); *Rhinophylla fischerae*, Colombia: Amazonas: Leticia (1 ♂); *Rhinophylla pumilio*, Colombia: Amazonas: Leticia (3 ♀♀ and 3 ♂♂).

Zusammenfassung. Es werden die Kennzeichen der Chromosomen von *Rhinophylla fischeri*, *R. pumilio* und *Carollia castanea* beschrieben. Für die Gattung *Carollia* ist bei niedriger Diploidzahl (21 ♂♂, 20 ♀♀) eine niedrige «nombre fondamental» (34–36) charakteristisch. Für die Gattung *Rhinophylla* wird eine grössere Diploidzahl (34–36) und eine grössere «nombre fondamental» (56–62) gefunden.

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Somatic Chromosomes of the Lamprey, *Ichthyomyzon gagei* (Agnatha: Petromyzonidae)

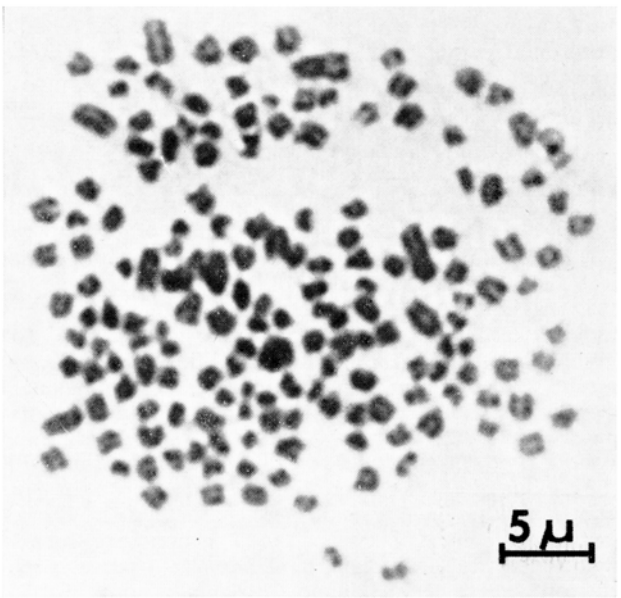
In spite of the considerable phylogenetic interest of lampreys to vertebrate evolutionists, cytotaxonomists did not begin to actively study their chromosomes until about 1960. The papers on lamprey chromosomes were summarized by ROBINSON and POTTER[1], except for two recent reports[2,3]. Of the 8 species studied, 4 are Old World forms[4–9], 2 Australian[1,10], 1 North American[2], and 1 common to the Atlantic coasts of Europe and North America[3].

It is the purpose of this paper to describe the somatic chromosomes of a second North American lamprey, *Ichthyomyzon gagei* Hubbs and Trautman. The genus *Ichthyomyzon* is endemic to the freshwaters of eastern North America and has not been represented in previous chromosome studies.

Fifteen specimens of *I. gagei* were collected from the Cahaba River (Alabama, USA) and chromosome preparations were made following the technique of HOWELL and DENTON[2]. Although over 100 metaphase figures were examined, only 22 were suitable for counting, one of which is shown in the Figure. The Table shows the distribution of these counts from 7 different specimens. Although counts ranged from 158 to 169, a strong modal diploid number of 164 was obtained. The low counts may be due to chromosome loss while the high counts may be attributed to chromosome fragmentation or chromatid separation. The position of the centromere in all chromosomes was subterminal to terminal. Considerable variation was found in chromosome size with the larger ones being 3.8 μm while the smaller ones were only 0.6 μm in length.

A comparison of the chromosomes of *I. gagei* with those of *Lampetra aepyptera* (Abbott)[2], the only other North American lamprey studied chromosomally, reveals striking similarities: both have modal diploid numbers of 164, subterminal to terminal centromeres, and almost identical ranges in chromosome size. This is of particular interest as both species are endemic to North America, non-parasitic, and have overlapping geographic ranges. With such a number of features in common, it is possible that *Lampetra* and *Ichthyomyzon* are of monophyletic origin. Both are chromosomally close to the marine lamprey, *Petromyzon marinus* L.[3], which has a modal diploid number of 168 and similar chromosome sizes. However, the centromeres in some of the longer chromosomes of *P. marinus* are median to submedian in position[3].

Apparently, the earliest diploid chromosome number reported for a lamprey was that of 60 for *Lampetra fluvia-*



Metaphase chromosome spread from gill epithelium of *Ichthyomyzon gagei*, $2n = 164$.

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Distribution of counts for the diploid chromosome number of *Ichthyomyzon gagei*

Diploid Nos.	158	159	160	161	162	163	164	165	166	167	168	169
No. of counts	1	1			2	3	9	2	2		1	1