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)

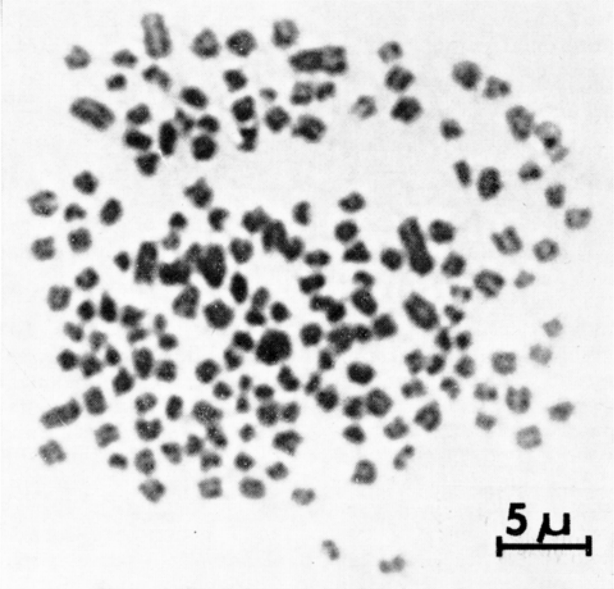
In spite of the considerable phylogenetic interest of lampreys to vertebrate evolutionists, cytotaxonomists did not begin to actively study their chromosomes until about 1960. The papers on lamprey chromosomes were summarized by ROBINSON and POTTER[1], except for two recent reports[2,3]. Of the 8 species 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.

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

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tilis (L.) from Russia[4,5]. However, counts of 120 and 156 were later reported for the same species from Holland and Italy respectively[6,7]. Wide variation in chromosome number was also reported for *Entosphenus reissneri*, with counts of 94–96[8] and 165–174[9]. These discrepancies either represent true geographic variation in chromosome number or errors on part of the investigators. The possibility that these variations result from polyploidy was discussed by POTTER and ROTHWELL[3]. Aside from these two problems, the numbers of chromosomes in lampreys are beginning to show definite trends. The following species are allied by sharing high chromosome numbers: *Lampetra zanandreai*, $2n = 142$[7]; *L. planeri*, $2n = 146$[7]; *L. aepyptera*, $2n = 164$[2]; *P. marinus*, $2n = 168$[3]; and now *I. gagei*, $2n = 164$. Two species of lampreys from Australia, *Mordacia praecox* Potter[1] and *M. mordax* (Richardson)[10], have low diploid counts of 76.

Thus, Northern Hemisphere lampreys tend to have very high diploid chromosome numbers (142–168) and no, or very few, metacentric-submetacentric chromosomes; conversely, Southern Hemisphere lampreys have relatively low numbers (76) and many metacentric-submetacentric chromosomes. In addition, the chromosomes of the Southern Hemisphere lampreys[1,10] are roughly twice the size of the Northern Hemisphere species[2,3]. It was suggested that the high chromosome numbers of Northern Hemisphere lampreys were derived by polyploidization[2,3,11]. If this is the case, an ancestral Northern Hemisphere lamprey with a polyploid number of 140 to 170 acrocentric-telocentric chromosomes, may have invaded the Southern Hemisphere, subsequently undergoing karyotypic evolution involving centromeric fusion. This would have produced a karyotype of metacentric-submetacentric chromosomes, longer-sized chromosomes, and a low diploid number similar to that found in today's Southern Hemisphere lampreys.

The specimens used in this study were preserved and deposited in the University of Alabama Ichthyological Collection, catalogue Nos. 3370–3375.

Résumé. L'étude des chromosomes somatiques d'une lamproie de l'Amérique du Nord, *Ichthyomyzon gagei* Hubbs and Trautman montre que l'equipement chromosomique diploide est composé de 164 chromosomes, qui sont acrocentriques ou télocentriques et très petits (moins de 3,5 µm). Il n'y a pas de différences entre le karyotype de *I. gagei* et celui de *Lampetra aepyptera* (Abbott). Les rapports de *I. gagei* avec les autres lamproies et l'évolution du caryotype sont examinés.

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Some Observations on the Cytology of Induced Interchanges in *Sorghum*

The occurrence of plants with chromosomal interchanges in grain sorghums ($2n = 20$) have been reported among the progenies of haploids[1–3]. These studies were limited to observations on post-pachytene stages of meiosis. In the grain *Sorghum* variety I.S. 84, the pachytene stage of meiosis was found favourable for detailed study, which prompted the present study of induced interchanges. Dry seeds of this variety were irradiated with γ-rays at 10, 20, 30, 40 and 50 Kr at B.A.R.C., Bombay, and were sown directly in field plots. All the plants that survived and reached maturity were examined cytologically for chromosomal aberrations, employing standard acetocarmine technique.

Figure A depicts the pachytene stage in the untreated material. The 10 differentiated pachytene bivalents can be traced, end to end, and basically they conform to the pattern observed originally in *S. subglabrescens*[4] and in other grain sorghums[5]. The ten chromosome types were given reference numbers 1–10 in the order of decreasing length. Most of the chromosome types can be recognized on the basis of total length, arm ratio, degree of heterochromatinization and the presence of conspicuous chromomeres on specific loci. The longest chromosome is the nucleolar chromosome (No. 1). Chromosome 2 has submedian centromere. Chromosome 6 has a subterminal and 7 a submedian centromere. All the remaining chromosomes (3, 4, 5, 8, 9 and 10) have approximately median centromeres.

Cytological screening of about 500 treated plants led to the isolation of 2 plants, each with a single reciprocal translocation and another heterozygous for 2 translocations. In each of these plants no fewer than 10 pachytene and 100 metaphase I cells were studied. In the plant with single interchange (No. 1–10–5) observations on analyzable pachytene cells revealed 'cross-shaped' configurations involving chromosomes 6 and 7. Appreciable variability in the position of the cross was observed in different pairing associations. However, the points of breakage were determined to lie in the heterochromatic regions of short and long arms of the chromosomes 6 and 7. Consequently, 1 of the 4 paired arms of the interchange complex at pachytene was observed to be very much shorter, thereby limiting the frequency of chiasma formation in it. As expected, the formation of chain of 4 at metaphase I was observed in 63% of the cells examined. A ring of 4 was realized in 8% of the cells at this stage and the rest forming only bivalents.

In the second plant (No. 1–11–3) the nucleolar chromosome was observed to form a pairing association with chromosome 10 of the complement. Judging from pachytene configurations it can be ascertained, that the translocation break points lie approximately in the middle of the long arm euchromatic regions of both the chromosomes. Analysis at metaphase I revealed, 39% of the cells with a ring of 4 and 21% with a chain of 4 chromosomes. The remaining 40% formed only bivalents.

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