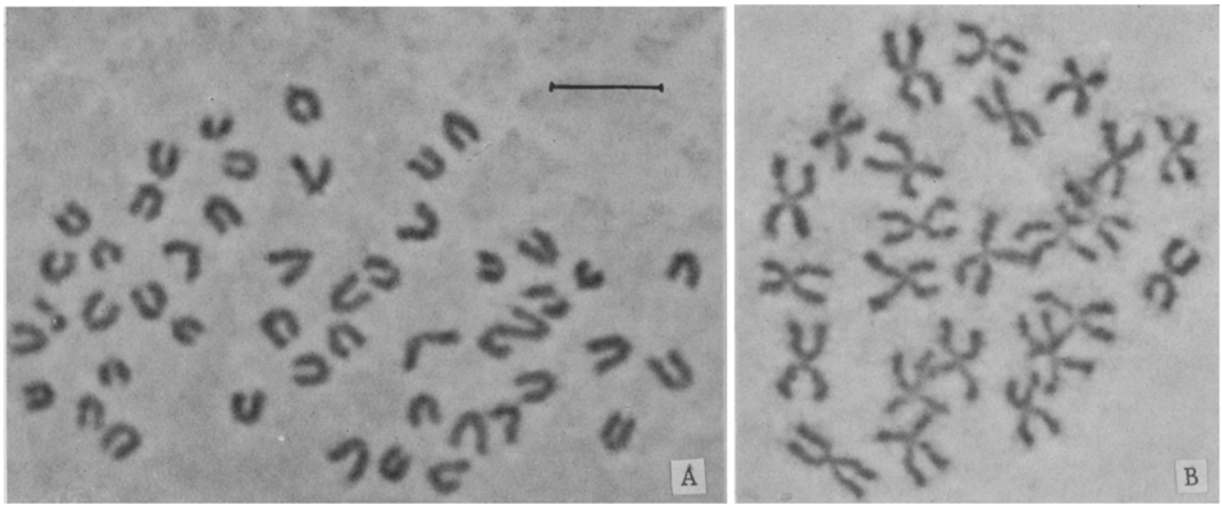

Fig. 4. Somatic chromosomes at metaphase of 2 goodeid fishes: A) *Hubbsina turneri* $2n$=48, and B) *Characodon lateralis* $2n$=24.

have XY chromosomes though they are similar and undetectable by present techniques.

Among the karyotypes of goodeid fishes, *Hubbsina turneri* de Buen has the simplest pattern, with 48 acrocentric chromosomes in both sexes (Figure 4a). The species with the most derived karyotype is *Characodon lateralis* Günther, which has 24 large metacentrics (Figure 4b) plausibly formed by Robertsonian fusions. Other goodeid species have karyotypes comprising various patterns and diploid numbers that are often reduced by centric fusions.

The ancestral karyotype of the species reported here probably had 48 chromosomes, as in the majority of species in the Goodeidae (26 among 38 examined). The diploid number was subsequently reduced by successive Robertsonian fusions, as in some other goodeids. But the involvement of the Y chromosome in the fusion with an autosome produced the multiple sex chromosome system so far unique in this family, and only the second known example among fishes.

The 2 species, 1 in the family Cyprinodontidae and 1 in the Goodeidae, which were found to possess multiple sex chromosomes have several features in common: 1. both species have a very limited distribution and are localized as small populations; 2. both are small and exhibit distinct sexual dimorphism; 3. both species belong to the suborder Cyprinodontoidea; 4. both families representing these 2 fishes have species in which the karyotypes include large metacentrics derived by Robertsonian fusions; 5. both live in Mexico; and 6. both species possess unique morphological characters among the species in their respective families (to be described elsewhere).

The specimens used in this study are preserved in the collections of the Museum of Zoology, University of Michigan[6].

Zusammenfassung. Bei einer bisher nicht beschriebenen mexikanischen Fischart werden 41 Autosomen beim Männchen und 42 beim Weibchen gefunden. Die Befunde sprechen für ein System multipler Sexualchromosomen dieser Fische.

T. Uyeno[7] and R. R. Miller

Museum of Zoology, The University of Michigan, Ann Arbor (Michigan 48104, USA),
16 August 1971.

[6] This research was supported by the U.S. National Science Foundation grant No. GB 14871 to R. R. Miller, and No. GB 8212 to the Museum of Zoology (N. G. Hairston), The University of Michigan.
[7] Present address: Nippon Luther Shingaku Daigaku, 3-10-20 Osawa, Mitaka, Tokyo (Japan).

New Evidence of a 38-Chromosomes Karyotype in South American Populations of the Roof Rat, *Rattus Rattus* L. (Rodentia, Muridae)

In previous issues of this periodical, the occurrence of new cases of chromosome multiformity[1] in the species *Rattus rattus* has been described[2,3]. The known 'normal' karyotype of this wide-spread and highly polytypic Eurasiatic species was reported by several authors[4–6] to be composed of 42 chromosomes, among which no pair of large metacentrics is present. This karyotype was studied from strains probably derived from Japanese and European populations. More recently, it was confirmed in wild *Rattus rattus* from Japan, Formosa, Thailand, Philipines, Java and Celebes[7], as well as from India[8].

Disagreements with these results were reported earlier for strains from North America[9,10] of the same species, which showed 40 chromosomes, and later by the occurrence of monomorphic populations with 38 chromosomes comprizing 2 large metacentrics in populations from Argentina and Brasil[2,11] and in island and inland populations from Tuscany, Italy[3]. Similar monomorphic $2n = 38$ forms

have recently been found in wild populations from Australia, New Zealand and New Guinea, probably introduced by man[12]. Moreover, 1 population with chromosome polymorphism comprising individuals with 42 and 38 chromosomes was reported for Japan[13], whereas another polymorphic system comprizing individuals with 38, 42 and 54 chromosomes has recently been described in 1 population from near El Cairo, Egypt[14]. Other populations of *Rattus rattus* from Japan and Thailand[55] and from Malaysia[16,17] are known to show other kinds of polymorphism.

Rattus rattus is, therefore, highly variable in chromosome number and structure, showing both geographic (and subspecific ?) multiformity and polymorphism[1] in karyotypes. In order to test the extent of these variations, we studied new samples from South America, coming from such distant localities as Caripe, Venezuela (in the State of Monagas), and Mehuin, Chile (in the Province of Valdivia). 1 male and 1 female individual were available from Caripe, and the corresponding specimens are now catalogued in the Institute of Tropical Zoology, Central University of Venezuela. 3 males and 3 females from Mehuin were studied, from speciemes now in the Institute of Zoology, Austral University of Chile (Valdivia), the above-mentioned Venezuelan Institute, and the Museum of Natural History, University of Kansas. Chromosome spreads were obtained by the known colchicine-hypotonic pretreatment technique, using both bone-marrow and spleen. Karyotypes were constructed from the Mehuin specimens, but the sample from Venezuela proved to be quite consistent with them, both in chromosome number and structure.

All the specimens studied proved to have a karyotype of $2n = 38$ chromosomes, identical with those described by BIANCHI et al.[2] for Argentinian and Brazilian populations, as demonstrated in the Figure. As regards the Tuscanian populations, our results are in close agreement, with only a slight exception. CAPANNA et al.[3] described in them the 18th pair as being metacentric, instead of submetacentric as shown by BIANCHI et al.[2] and in our results. The Egyptian variant of 38 chromosomes described by BADR and BADR[14] would correspond, in this respect, strictly to the Tuscanian form. However, karyometric comparative testings would have to be performed in order to substantiate this difference. Another feature which must be pointed out in our karyotype is that this pair of autosomes is slightly heteromorphic in all the individuals studied, one of the chromosomes showing the centromere more terminal in position than the other. This heteromorphism is also seen in the figures published by BIANCHI et al.[2].

Though more information on further populations from South America is obviously required, these results suggest that South American populations of *Rattus rattus* are monomorphic for the $2n = 38$ chromosome variant of the species. *Rattus rattus* is a weed species in South America, introduced by man during repeated travels from the Old World, into different harbours throughout the Continent. From those introductory points, the colonizers invaded the surroundings, creating wild populations. In view of the occurrence of only 38 chromosome forms in different and quite distant points, it seems safe to conclude that the South American populations came from monomorphic Mediterranean populations, as those described by CAPANNA et al.[3] for Tuscany.

We suggest that this invasion might have occurred repeatedly at various points of the South American coast on the arriving ships. Likewise, we also suppose that through those repeated introductions, some 42-chromosomes stocks from elsewhere might also have been introduced. The descendants of these latter probable invasions either have not yet been discovered, or were unsuccessful as colonizers due to some inferior fitness of the 42-chromosomes form as compared with the already established 38-chromosomes form. The occurrence of monomorphic populations with 38 chromosomes in Australia, New Zealand and New Guinea could also be explained by the same argument.

It is to be pointed out, however, that the chromosomes of this greatly polytypic species are far from being known in all their geographic forms. It would not be surprizing if further research could demonstrate a more widespread occurrence of populations with 38 chromosomes, which could be potentially responsible for the invasion of different colonizing areas. *Rattus rattus* is mainly an Indo-Malayan species[18], the status of the subspecies of which, and their evolutionary characteristics, are still obscure. The occurrence of 38-chromosome forms, both as monomorphic populations or as part of a polymorphic system in the peripheral areas of distribution and in colonizing populations, would suggest, moreover, some kind of selective advantage of this variant outside the geographic center of distribution of the species.

As regards the mechanism of transformation of original $2n = 42$ stocks into the $2n = 38$ forms, the suggestion of various authors[3,13,14,17] of Robertsonian rearrangements by centric fusion seems to the present authors to be a cogent explanation[19].

[1] In the cytogenetic literature related to Mammals, multiformity is often confused with polymorphism. Multiformity is the occurrence of different chromosome complements found within the members of a given taxon (P. V. TOBIAS, S. Afric. J. Sci. *50*, 134 (1953); O. A. REIG and P. KIBLISKY, Chromosoma *28*, 211 (1969)). Chromosomal polymorphism, in accordance with the established use in the modern literature on the theory of evolution, is the occurrence, within a given population, of more than one type of chromosome set, differing in number, in structure or in both.

[2] O. N. BIANCHI, J. PAULETE-VANRELL and L. A. DE VIDAL RIOJA, Experientia *25*, 1111 (1969).

[3] E. CAPANNA, M. V. CIVITELLI and R. NEZER, Experientia *26*, 422 (1970).

[4] K. OGUMA. J. Fac. Sci. Hokkaido Univ. *4*, 35 (1935).

[5] S. MAKINO, J. Fac. Sci. Hokkaido Univ. *9*, 19 (1943).

[6] R. MATTHEY, Arch. Julius Klaus-Stift. *31*, 294 (1956).

[7] H. YOSIDA, H. TSUCHIYA, H. T. IMAI and T. UDAGAWA, A. Rep. natn. Inst. Genetics Japan *19* (1968); *9* (1969).

[8] G. P. SHARMA, O. P. MITTAL and T. K. SANDHY, Mamm. Chrom. Newsletter *12*, 32 (1971).

[9] G. PINCUS, J. Morph. *44*, 515 (1927).

[10] J. C. CROSS, J. Morph. *52*, 373 (1931).

[11] J. PAULETE-VANRELL, Mamm. Chrom. Newsletter *11*, 99 (1970).

[12] T. H. YOSHIDA, K. TSUCHIYA, H. IMAI and K. MORIWAKY, Jap. J. Genet. *44*, 89 (1969).

[13] T. H. YOSHIDA, A. NAKAMURA and T. FUKAYA, Chromosoma *16*, 70 (1965).

[14] F. M. BADR and R. S. BADR, Chromosoma *30*, 465 (1970).

[15] A. GROPP, J. MARSHALL, G. FLATZ, M. OLBRICH, K. MANYANONDHA and A. SANTADUSIT, Z. Säugetierkunde *35*, 363 (1970).

[16] H. S. YONG and S. S. DHALIWAL, Mamm. Chrom. Newsletter *11*, 30 (1970).

[17] H. S. YONG, Experientia *27*, 467 (1971).

[18] J. R. ELLERMAN, *The Families and Genera of Living Rodents* (British Museum, London 1941), vol. 2.

[19] We thank the Multinational Programme in Genetics of the Organization of American States for making possible the work of the senior author in Chile. The work was also partially financed by Grant No. 2/1971, Comisión de Investigación Científica, Facultad de Odontología, Universidad de Chile, and Grant No. 37/70/D, Comisión Chilena de Energía Nuclear.

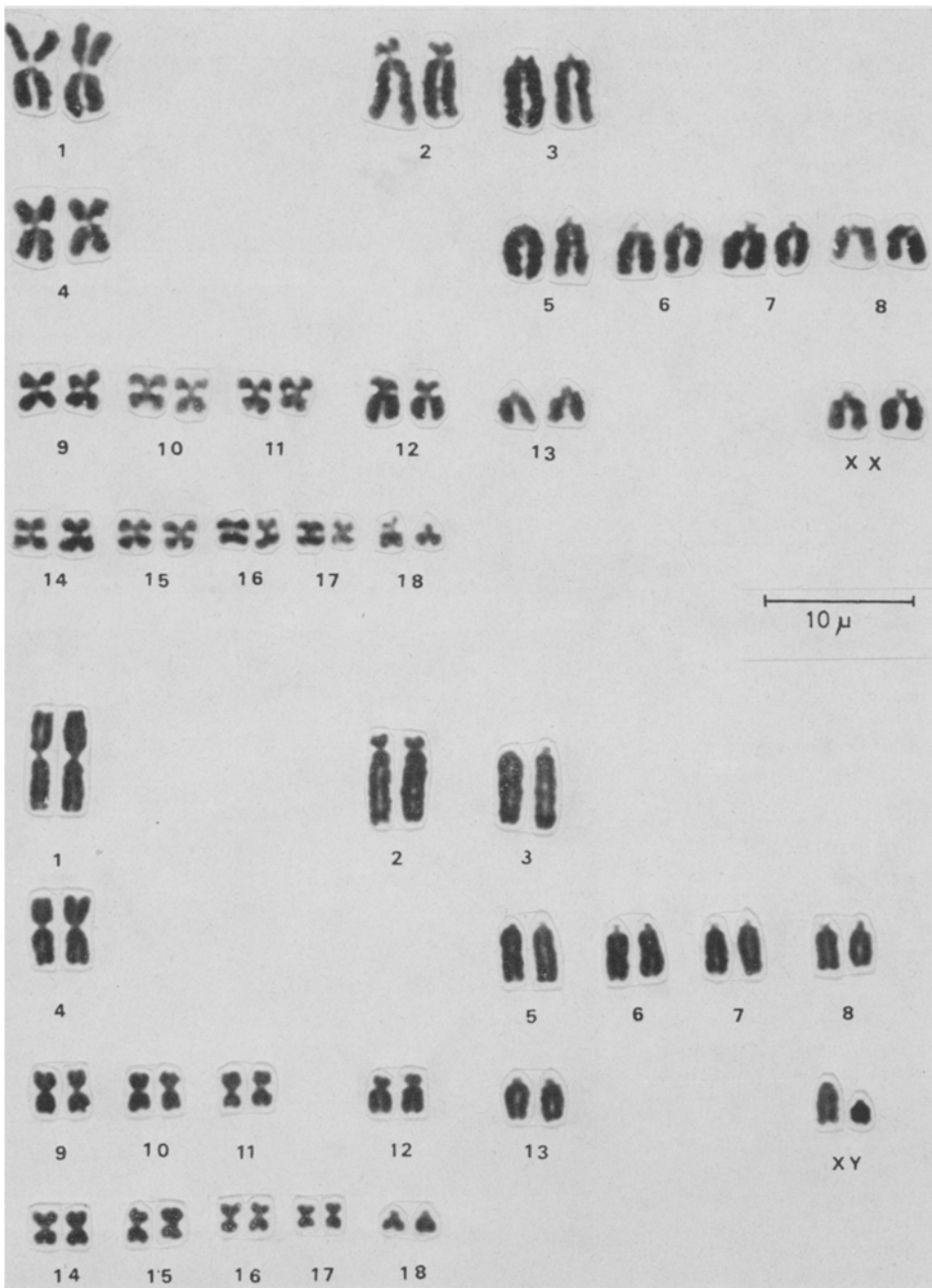

Fig. 1. Karyotypes of *Rattus rattus* L. from Mehuin (Valdivia, Chile). Upper: female; lower: male. Bone-marrow. Giemsa stain.

Resumen. En dos poblaciones de *Rattus rattus*, una de Mehuin (Valdivia, Chile) y otra de Capripe (Monagas, Venezuela), se encontró un cariotipo de $2n = 38$ cromosomas en todos los individuos estudiados. Este cariotipo corresponde al que presentan en forma monomórfica otras poblaciones de la rata negra de América del Sur y de Italia, y difiere del cariotipo normal de la especie, que es de 42 cromosomas. Se postula que las distintas poblaciones sudamericans de *Rattus rattus* deben haber invadido el Continente, acompañando al hombre, en distintas irrupciones, a partir de una forma de 38 cromosomas de origen mediterráneo.

O.A. Reig[20, 21], J.V. Pincheira[20], A.O. Spotorno[20], and P. Waller[22].

Laboratorio de Citogenética,
Departamento de Genética,
Facultad de Medicina,
Universidad de Chile,
Zañartu 1042, Santiago de Chile (Chile),
3 August 1971.

[20] Department of Genetics, University of Chile, Santiago.
[21] Present address: Department of Zoology, University College London, Gower Street, London WC1 (England).
[22] Department of Genetics, University of Adelaide, Adelaide (South Australia).