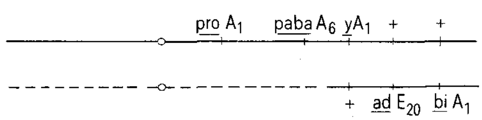
agar added. Strains of A. nidulans used, all derived from Glasgow stocks, were: Diploid biA1/MSE strain, obtained from a heterokaryon between strain biA1 which requires biotin and the Master Strain E (MSE) of McCully and Forbes[20], through the Roper's method[21], and Duplication strain A of Nga and Roper[3] (figure). Ethidium bromide (EB) Sigma was added to CM in different concentrations all of which did not reduce, or only slightly reduced, the growth of the used strains. Conidia were inoculated in the centre of 10 cm diameter petri dishes containing CM without and with EB added, and after 7–8 days incubation at 37 °C sectors were scored. Sectors from diploid strain were classified in 2 categories: macrosectors (with more than 20 conidiophores) and microsectors (with 20 or less conidiophores).

Results and discussion. Tables 1 and 2 give the number of sectors produced by duplication and diploid strains growing on medium with and without EB added. In both cases the number of sectors decreases in the presence of the drug which indicates a possible similarity between the mechanisms of sector production both in diploid and duplication strains. These results are in agreement with



Duplication strain A. Linkage groups I and II are shown by unbroken and broken lines respectively. Centromeres are designated by open circles ad E20, biA1, paba A6, pro A1 and yA1 are respectively genes for adenine biotin, p-aminobenzoic acid, proline requirements and yellow conidia.

those obtained after treatment of diploid and duplication strains with 2 fungicides[17] and with the results of diploids bearing duplications[23]. At least in the case of the fungicide, 1,4-oxathiin, whose mode of action is inhibition of respiration, it is known that it reduces, in low concentrations and in the same pattern as shown by EB, the number of sectors from both diploid and duplication strains[17]. It is then possible that EB, which also acts on mitochondrial DNA, reduces indirectly the number of sectors due to a lack of energy as a consequence of inhibition of respiration. It is however also possible that EB can affect directly the haploidization and/or mitotic crossing over, due to its action upon DNA[18] and on the repair mechanism[22]. Biochemical studies and also genetical studies, including the isolation of EB resistant mutants, could provide a better understanding of the action of the drug in relation to the number of sectors produced by both kinds of strains. In any case, it could be suggested that EB could be used to yield preservation in commercial fungal strains. Certain commercially useful strains may show an instability pattern due to low-yielding derivatives in the population of stored spores of the strain. Reduction of instability is in part achieved by environmental control or through a balanced lethal system[24], or even through point mutations[15]. EB could also be useful for this purpose when added to cultures of duplication or diploid strains.

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Sex chromosome polymorphism in Oryzomys longicaudatus philippii (Rodentia, Cricetidae)[1]

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Summary. Oryzomys longicaudatus philippii has a diploid number 2N = 56 (N.F. = 70). A polymorphism of X-chromosomes is described and a duplication as causal mechanism is postulated. The degree of chromosomal differences among the 4 karyological forms of O. longicaudatus and between those forms with O. l. philippii, enable us to postulate the level of full species for all of them.

Sex chromosome polymorphisms are not usual among rodents. They have been described in Peromyscus[3], Akodon[4,5], Mus[6,7], Spermophilus[8], Neotoma[9], Tatera[10], Zygodontomys[11,12], Bandicota[13] and Nesokia[14]. In the present paper, a polymorphism of sex chromosomes of Oryzomys longicaudatus philippii is described for the first time, and the karyotype and idiogram of the species has been constructed. On the other hand, the systematic significance of the chromosomal variants of O. longicaudatus is discussed.

The animals were collected with Sherman live traps in the province of Valdivia, Chile, from July 1974 to October 1975. 11 males and 9 females were studied cytologically and classified in accordance to Osgood[15]. The skins and skulls were deposited in the Collection of Mammals at the Institute of Ecology and Evolution of the Universidad Austral of Chile (IEEUA). Mitotic plates were obtained by the standard air dried technique[16]. Chromosomes were classified according to Levan et al.[17]. A total of 140 good metaphases were photographed and 75 were selected for the construction of the idiogram. The length of each chromosome is given as a percentage of female haploid set. All the specimens studied have a diploid number 2N = 56 (N.F. = 70) with 21 pairs of acrocentric autosomes and 6 pairs of metacentrics (figure 1). Pair 1 is approximately one-third larger than the succeeding one. Metacentrics have values of arm ratio (r) which fluctuates between 1.45 and 1.61 (table 1, figure 2). The female karyotype exhibits a clear polymorphism in the length of the short arm of the X. 3 different forms in the analyzed females were found (figure 3a): one with 2 submetacentric X's (r = 1.87), 6 with one submetacentric and one subtelocentric X and 2 with both subtelocentric X's (r = 3.65). The differences between the values of the total length of the X's and their short arms are significant (table 2). The Y chromosome is subtelocentric. Both submetacentric and subtelocentric X's were found in males, one of which presented the former chromosomal morphology

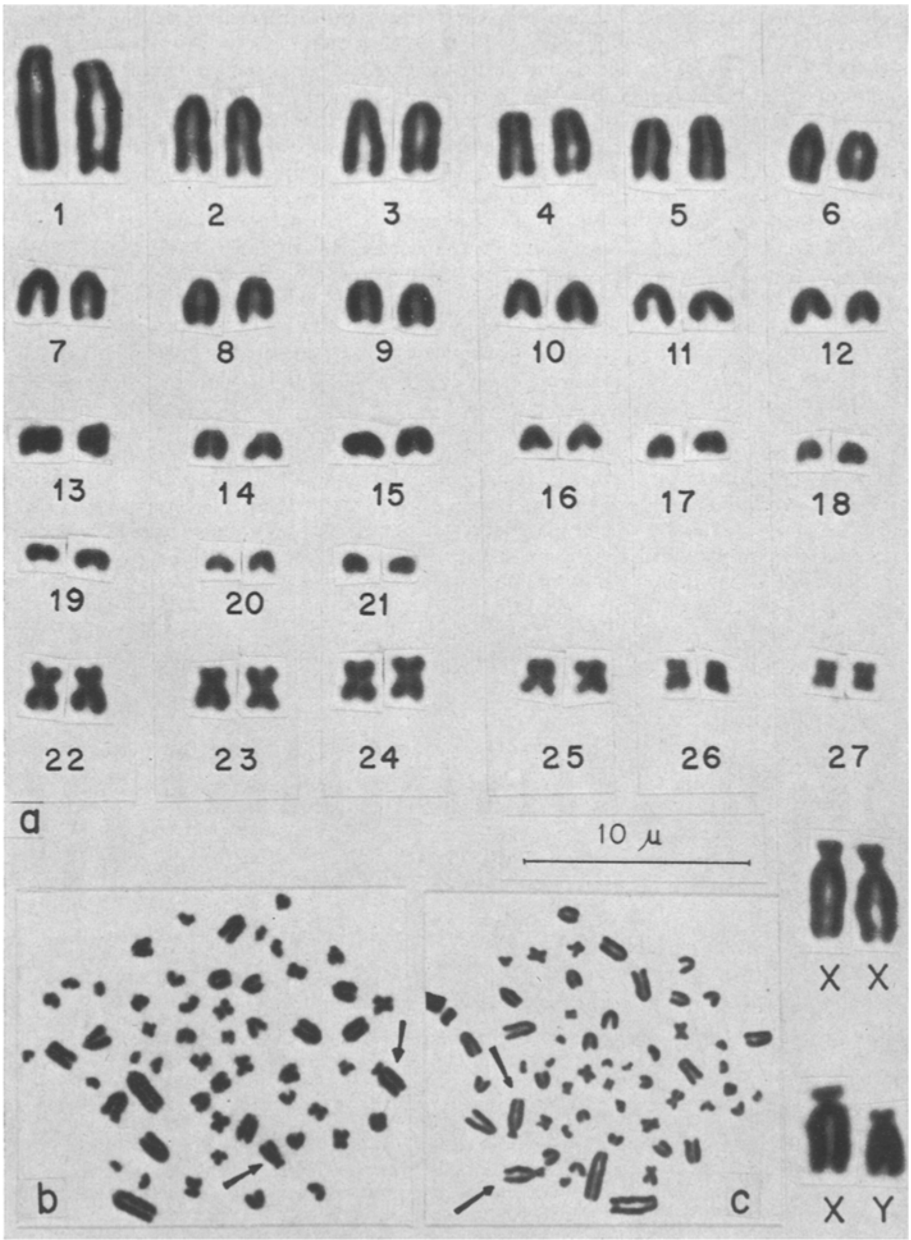

Fig. 1. *a* Karyotype of O. longicaudatus philippii; *b* mitotic plate of a male; *c* mitotic plate of a female.

Table 1. Measures of chromosomes of Oryzomys longicaudatus philippii (TL, total length LA, long arm; SA, short arm)

Chromosome No.	$\bar{X}$	S.D.	$\bar{X}$	S.D.	$\bar{X}$	S.D.	r	Chromosome No.	$\bar{X}$	S.D.	$\bar{X}$	S.D.	$\bar{X}$	S.D.	r
1	9.57	0.51	–	–	–	–	–	16	2.18	0.14	–	–	–	–	–
2	6.27	0.40	–	–	–	–	–	17	2.04	0.23	–	–	–	–	–
3	5.89	0.26	–	–	–	–	–	18	1.89	0.16	–	–	–	–	–
4	5.42	0.25	–	–	–	–	–	19	1.75	0.15	–	–	–	–	–
5	5.07	0.20	–	–	–	–	–	20	1.65	0.11	–	–	–	–	–
6	4.38	0.17	–	–	–	–	–	21	1.49	0.12	–	–	–	–	–
7	3.89	0.16	–	–	–	–	–	22	3.77	0.35	2.26	0.21	1.51	0.17	1.54
8	3.63	0.14	–	–	–	–	–	23	3.43	0.18	2.05	0.14	1.38	0.10	1.51
9	3.47	0.10	–	–	–	–	–	24	3.22	0.17	1.91	0.10	1.31	0.10	1.45
10	3.32	0.14	–	–	–	–	–	25	2.97	0.23	1.74	0.15	1.23	0.16	1.49
11	3.04	0.16	–	–	–	–	–	26	2.44	0.19	1.52	0.15	0.92	0.12	1.61
12	2.79	0.15	–	–	–	–	–	27	2.13	0.20	1.32	0.13	0.81	0.12	1.56
13	2.62	0.14	–	–	–	–	–	X_{sm}	8.39	0.91	5.43	0.56	2.96	0.45	1.87
14	2.49	0.14	–	–	–	–	–	X_{st}	7.49	0.54	5.77	0.36	1.72	0.36	3.65
15	2.44	0.23	–	–	–	–	–	Y	5.35	0.50	4.15	0.50	1.20	0.39	3.71

and 10 the latter (figure 3b). The presence of 28 bivalents normally paired, included the sex bivalent (which pairs end-to-end) has been detected.

Taking into account that the most frequent formulae are xx and xY (X being the one bearing duplication), the simplest explanation for this polymorphism is by means of a duplication in the short arm of the X. According to this interpretation, XX females and XY males would be negatively selected with respect to xx and xY. Therefore, 50% of males and 25% of females would be normal, thus giving an inbalance in the population sex ratio. In counting the 94 animals, 61 were found to be males and 33 females. These figures (which correspond to a 2:1 sex ratio), if interpreted as representatives of population, would suggest the selective value of the above-mentioned genotypes. On the other hand, duplicated homozygous animals have been found, but these individuals would be less viables or would be less fertile than normal ones.

To surmise a deletion requires a more speculative interpretation, since, generally, the loss of chromosomal chromatin provokes a deleterious effect. Therefore, we would have to assume that such an effect is not present in homozygous animals; furthermore, we would be compelled to accept the selective advantage of these animals in regard to the normal ones.

Polymorphism due to a deletion of sex chromosomes has been described in A. azarae[5], and a dosage compensation mechanism (that would keep the population sex ratio unchanged) has been proposed. This mechanism cannot be extended to O. l. philippii situation because of the change in the population sex ratio.

The genus Oryzomys is highly multiform (2N = 52–80, N.F. = 54–112)[18]. Subgenus Oligoryzomys, to which O. longicaudatus belongs, is characterized by the presence of one or more great acrocentric or subtelocentrics, the remaining of the set being mostly acrocentric[18]. Our species agree with subgenus chromosomal characterization, but do not present large biarmed elements. 4 karyological variants have been reported for O. longicaudatus, every one of which may well represent a distinct species in Gardner's opinion[18]. We agree with this hypothesis and furthermore postulate the level of full species for O. l. philippii. It may also be inferred that O. longicaudatus is a complexive taxon in which everyone of the karyological variants is a valid species, because of chromosomal rearrangements may act as cytological barriers.

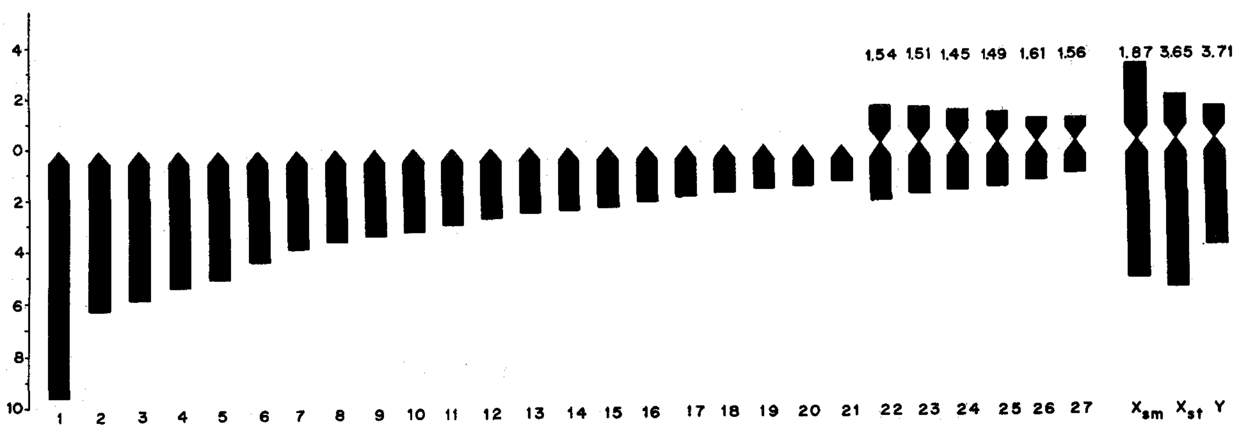

Fig. 2. Idiogram of Oryzomys longicaudatus philippii.

Table 2. Values of t and p testing the statistical significance of mean values of total length and short arm of the X chromosomes of Oryzomys longicaudatus philippii

Length	t	p
Total	2.4182	< 0.025
Long arm	1.4144	< 0.10 to > 0.05
Short arm	5.5419	< 0.0005

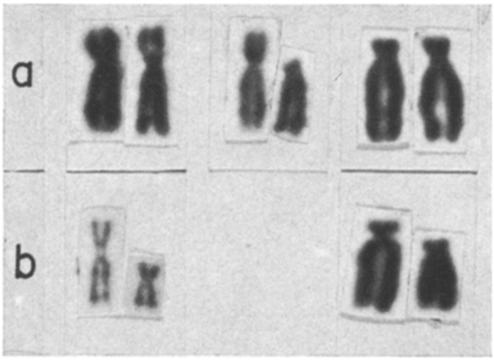

Fig. 3. Different forms of sex chromosomes of O. l. philippii. *a* In females; *b* in males.

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