

Figure 2. Absence of crosslinked complex in psoralen-treated individual preparations of 16S and 23S RNAs under reconstitution condition and a mixture of the two under nonconstitution condition. 300 μ g of 16S RNA (A) and 570 μ g of 23S RNA (B) were treated under reconstitution condition (as described in the legend to figure 1 curve B) with trimethylpsoralen (150 and 285 μ g respectively). A mixture of the two (C) in 0.5 ml containing 100 mM NaCl, 10 mM Tris HCl, pH 7.4 and 1 mM EDTA was separately treated with 435 μ g of psoralen. All the three samples were subjected to sucrose density gradient centrifugation as described in the legend to figure 1.

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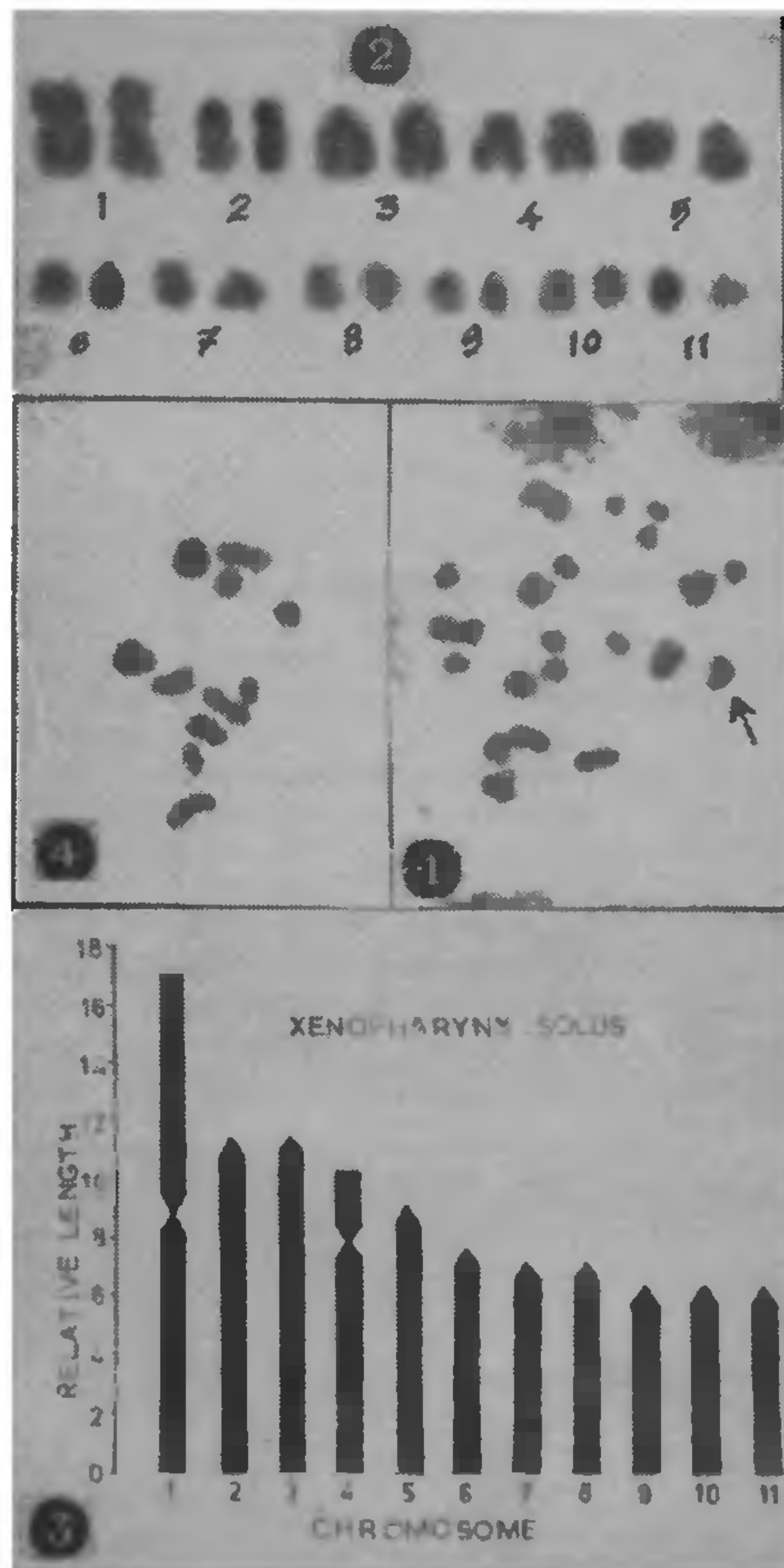
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KARYOLOGICAL STUDY IN THE DIGENETIC TREMATODE *XENOPHARYNX SOLUS*

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THERE is no general agreement on the generic and

specific characters of most digenetic trematodes and the morphology of adult forms is often used to draw boundaries between genera and species. A survey of literature reveals that thousands of species are described, redescribed and/or synonymized¹. Comparative cytology may through new light on their cytotaxonomy². Fourteen species of the family Plagi-orchidae are known for their cytology. Their diploid chromosome number³ ranges from 12 to 22. The



Figures 1-4. Haematoxylin squashes of cleaving eggs from uterine coils and testes of *Xenopharynx solus*. 1. Metaphase with 22 chromosomes. Arrow shows an overlap of two chromosomes (\times ca. 1400). 2. Karyotype (\times ca. 2200). 3. Idiogram of *X. solus*. 4. Metaphase I exhibiting eleven bivalents (\times ca. 1600).

TABLE I
Quantitative characteristics of metaphase chromosomes of *X. solus*

Chromosome pair number	Length of chromosome (in microns)			Relative length $\bar{X} \pm SE$	Arm ratio $\bar{X} \pm SE$	Centromeric Index $\bar{X} \pm SE$	Chromosome classification
	Short arm	Long arm	Total length				
1	2.1	2.2	4.3	17.0 ± 0.5	1.4 ± 0.2	48.8 ± 0.6	IM
2	—	—	2.9	11.5 ± 0.4	—	—	T
3	—	—	2.9	11.5 ± 0.5	—	—	T
4	0.6	2.0	2.6	10.3 ± 0.6	3.3 ± 0.3	23.1 ± 0.5	S
5	—	—	2.3	9.1 ± 0.4	—	—	T
6	—	—	1.9	7.5 ± 0.5	—	—	T
7	—	—	1.8	7.1 ± 0.5	—	—	T
8	—	—	1.8	7.1 ± 0.7	—	—	T
9	—	—	1.6	6.3 ± 0.5	—	—	T
10	—	—	1.6	6.3 ± 0.4	—	—	T
11	—	—	1.6	6.3 ± 0.4	—	—	T

IM, Isobrachial metacentric; T, Telocentric; S, Subtelocentric.

chromosome cytology of *Xenopharynx solus* is reported here.

The adult parasites were collected from the gall bladders of the water snake *Tropidonotis piscator*. Mitotic stages were recorded from cleavage divisions of eggs and meiotic stages from testes by the technique described elsewhere⁴. A determination of relative lengths of chromosomes, centromere index and arm ratios are based on the standard procedures^{5,6}. The chromosome was classified using the nomenclature of Levan *et al*⁵ and White⁷.

The diploid chromosome number is 22 studied from cleavage divisions (figure 1). They can be classified into two categories.

Group I: Four pairs of chromosomes with total lengths varying between 4.3 and 2.6 μ are found in this group. Whereas the first pair is isobrachial and metacentric, the fourth is subtelocentric and the second and third pairs are telocentric.

Group II: Chromosomes pairs 5–11 with total lengths ranging from 2.3 to 1.6 μ are exclusively telocentric. The ratio between the shortest and longest chromosome is 1:2.7. The karyotype (figure 2) and idiogram (figure 3) constructed from the data (table I) confirm the chromosome number as 22. This is corroborated by the presence of 11 bivalents in metaphase I (figure 4). The quantitative data on chromosomes are furnished in table I.

Till recently 11 members of the family Plagiiorchiidae had been studied for their chromosome numbers. Chromosome counts of three more species namely, *Astiotrema reniferum* ($2n = 18$), *Tremiorchis ranarum* ($2n = 18$) and *X. solus* ($2n = 22$) now investigated have been added to this list. *X. solus* has the unique distinction of possessing nine pairs of telocentric chromosomes. This could be used to distinguish *X. solus* from other members of the family.

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