A high number of chromosomes in the hillstream cyprinid, *Tor putitora* (Pisces)

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Summary. The karyotype of a cyprinid fish occurring in India, *Tor putitora*, is described. The diploid complement comprises 100 chromosomes. The modal number in this family being 2n = 50, *T. putitora* appears to be another case of tetraploidy.

Of some 130 species from 54 genera of cyprinid fishes so far cytologically studied[2-6], a high diploid number of 100 ± 4 chromosomes has been reported only in 2 genera, *Cyprinus* and *Carassius*. The present paper reports the occurrence of a similarly high number in yet another species and genus of cyprinids, *Tor putitora*.

Materials and methods. 10 adult specimens, 4 males and 6 females, were captured from the Yamuna river near Kulhal (U.P., India). The colchicinized specimens were subjected to the citrate flame-drying technique described elsewhere[7] for the preparation of slides for cytological observations. Morphology of chromosomes has been described following Levan et al.[8]. In the karyotypes (figures 2 and 3) the biarmed (meta-, submeta- or subtelo-centric) and the rod-shaped (acrocentric) chromosomes have been arranged separately in descending order of lengths.

Results. The kidney metaphase complements in both male and female had 100 chromosomes in the majority of cells examined (figure 1) although the numbers varied between 96 and 104 in some others (table). Karyotypes of both males and females consisted of 50 pairs of homomorphic chromosomes comprising 5 pairs of metacentric (Nos. 1, 5, 7, 11 and 18), 12 pairs of submetacentric (Nos. 2, 4, 5, 9, 10, 12, 14–16 and 20–22), 7 pairs of subtelocentric (Nos. 3, 8, 13, 17, 19, 23 and 24) and 26 pairs of acrocentric (Nos. 25–50) chromosomes. No sex element could be recognized among the complement. The chromosomes Nos. 7, 8 and 21 had their centromeric indices in the borderline of 2 morphological entities. The chromosomes from the longest to the shortest one measured between 2.7 μm and 1.0 μm in

Frequency distribution of chromosome numbers in different somatic spreads of both sexes of *Tor putitora*

Sex	Number of chromosomes								
	96	97	98	99	100	101	102	103	104
Male	3	1	4	3	14	3	2	–	1
Female	2	–	3	1	13	2	3	–	1
Total	5	1	7	4	27	5	5	–	2

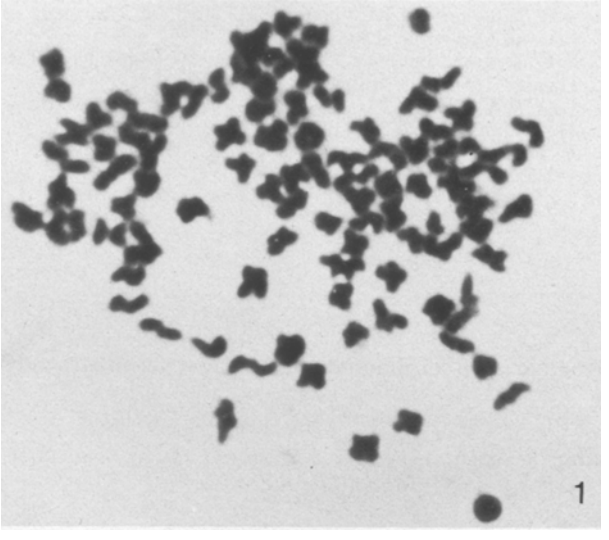

Fig. 1. Photomicrograph of a female somatic metaphase complement of *Tor putitora*. 3 of the chromosomes, lying at some distance, are not shown.

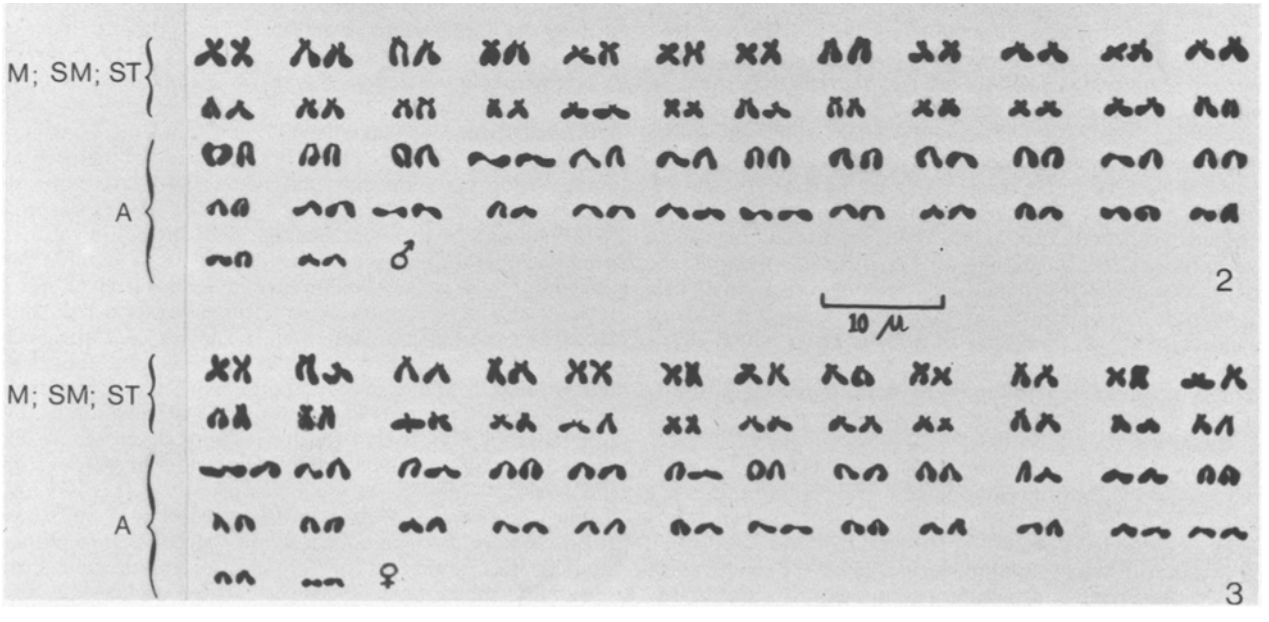

Fig. 2. Karyotype prepared from camera lucida drawings of a metaphase plate of male *Tor putitora*. Fig. 3. Karyotype prepared from a female metaphase. M, SM, ST: metacentric, acrocentric and subtelocentric chromosomes; A: acrocentric chromosomes.

males and between 2.6 µm and 0.8 µm in females. Unfortunately, our preparations from testis material did not yield meiotic stages suitable for analysis, so that we were unable to ascertain the haploid number of elements, or to study meiotic behaviour of chromosomes in this species.

Discussion. So far as the present author is aware, the karyomorphology of *T. putitora* had not been studied earlier. As stated before, only 2 genera, *Carassius* and *Cyprinus*, are known to comprise species characterized by high diploid numbers of 100 ± 4 chromosomes[2-6]. Ohno et al.[9] also studied the DNA content of *Carassius auratus* and *Cyprinus carpio* and obtained DNA values 50–52% that of placental mammals, as compared to 20–22% that of placental mammals in 2 other species of cyprinids with 50 chromosomes, the suggested modal number in this family[5,6]. Therefore, Ohno et al.[9] suggested that diploid-tetraploid relationships exist in this family. Polyploid origin was also suspected in some catostomid fishes on the same basis[10]. Correspondingly, a tetraploid origin may be suggested for *Tor putitora*. This hypothesis should be tested first by measurements of DNA content; the study of meiosis may give additional information. However, artificial crosses between closely related species might be especially informative, considering that allopolyploidy is now known to be a factor of evolution among lower vertebrates.

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Dynamics of phosphoglucomutase heat sensitivity polymorphism in Culicidae

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Summary. In 6 species of mosquitoes of the genera *Aedes* and *Culiseta* (Culicidae, Diptera) the frequency of phosphoglucomutase (PGM) heat sensitivity alleles is inversely correlated with the temperature of the environment where larvae develop. These data suggest that different selective values are associated with the PGM thermoresistant and thermosensitive genotypes in the different habitats.

The question as to whether protein polymorphisms are as a rule adaptive or neutral is still unsolved[2]. This is essentially due to the fact that most of the genetic variations at present identified are of the electrophoretic type, that is variations which can reasonably be held to be selectively neutral. In principle, a direct approach which measures variations in fitness of the most common genotypes for a reasonably large number of genes would be most suited to this problem. However, as the sensitivity of direct methods is so poor that only the most conspicuous effects are detected, it is necessary to use an indirect approach, that is to look for the magnified consequences of any weak selective forces operating. To this end a promising strategy could be to search for a specific genetic effect which could confer on a population exposed for a long period of time to an ecological factor a better adaption to that factor itself. In this case the results are self-explanatory if they confirm the expectations.

We have chosen temperature as a stringent ecological factor and alleles with different degrees of sensitivity to heat denaturation as the genetic characteristic on which temperature could have acted.

If we admit that temperature can influence the inactivation rate of an enzyme and therefore ultimately its activity, it is reasonable to expect that there exists a positive correlation between heat stability of allelic enzymes and the activity associated with them. In that it is likely that the enzymatic activity has on average a selective value, it is to be expected that the selective value of alleles with different heat stability is related to the thermal conditions of their areas of distribution.

Different species of Culicidae (Diptera) and the phosphoglucomutase *(Pgm)* locus have been chosen for the present study. Culicidae offer excellent material for our purpose because they are represented by a series of species adapted to developing in different ecological niches within rather broad temperature ranges[3]. The *Pgm* locus is suitable for this purpose because the Mendelian inheritance of heat-sensitivity and electrophoretic variants observed at this locus has been demonstrated in 1 species of Culicidae[4]. Formal genetics data have been obtained for the *Pgm* electrophoretic alleles in several other species of Culicidae[5]. In this paper we report that in 6 species of mosquitoes the frequency of *Pgm* thermosensitive alleles decreases as the temperature of the environment where the larvae develop increases.

Table 1 reports the information most relevant to our study for the 6 natural populations of the species of mosquitoes studied. Determination of the electrophoretic and heat sensitivity phenotypes was performed following the method described by Trippa et al.[6] for single homogenates of *Drosophila melanogaster*. Figure 1 shows the comparison