with the enzyme. The 3β-HSDH (Fig. 1) was moderate and the 17β-HSDH was in traces while the G-6-PDH (Fig. 2) activity was intense.

It is now well established that 3β-HSDH enzyme plays a key role in the early biosynthesis of all the biologically active steroid hormones, while 17β-HSDH has a role mainly in the biosynthesis of sex steroids[5]. The presence of these two enzymes in the Leydig and Sertoli cells of the hawk suggests their ability to synthesize sex steroid hormones as reported earlier for some domestic birds[1-3,7-11]. Further, the presence of an intense G-6-PDH activity in the same sites as that of 3β-HSDH and 17β-HSDH provides an additional indirect evidence for their steroidogenic potential in the testis of hawk since, G-6-PDH is known to generate NADPH needed for hydroxylations during steroidogenesis[12]. It is suggested that in the testis of hawk Leydig cells form the principal site and Sertoli cells may form additional site of steroid hormone synthesis. The fact that the above enzyme activities occurred at the regeneration phase of the testis suggests albeit indirectly that testicular steroids may be involved in the spermatogenetic processes of the hawk.

April 20, 1981.

1. Lofts, B., *Gen. Comp. Endocrinol. Suppl.*, 1972, 3, 636.
2. —, and Murton, R. K., "Reproduction in birds," In *Avian Biology*, Eds. D. S. Farner and J. R. King, Academic Press, New York, 1973, 3, 1.
3. Guraya, S. S., *Int. Rev. Cytol.*, 1976, 47, 99.
4. Salim Ali, *The Book of Indian Birds*, Bombay Natural History Society, Bombay, 1961.
5. Baillie, A. H., Ferguson, M. M. and Hart, D. Mck., *Developments in Steroid Histochemistry*, Academic Press, New York, 1966.
6. Saidapur, S. K. and Nadkarni, V. B., *Indian J. Exp. Biol.*, 1972, 10, 425.
7. Woods, J. E. and Domm, L. V., *Gen. Comp. Endocrinol.*, 1966, 7, 559.
8. Garnier, D. H., Tixier Vidal, A., Gourdji, D. and Picart, R., *Z. Zellforsch. Mikrosk. Anat.*, 1973, 144, 369.
9. Tingari, M. D., *Histochemical J.*, 1973, 5, 57.
10. Bhujle, B. V. and Nadkarni, V. B., *Pavo*, 1976, 14, 61.
11. —, — and Appaswamy Rao, M., *Gen. Comp. Endocrinol.*, 1979, 38, 153.
12. Samuel, L. T. and Eik-Nes, K. P., "Metabolism of Steroid hormones," In *Metabolic Pathways*, Ed. Greenberg, D. M., 1968, 2, 169.

THE KARYOTYPE OF *TRICHOGASTER FASCIATUS* (OSPHRANEMIDAE, PISCES)

N. K. Tripathy and C. C. Das
Post Graduate Department of Zoology
Berhampur University, Berhampur 760 007
India

Recent improvements in cytological techniques have generated fresh interest among fish cytologists, to study the karyotypes of this group. The present communication, which deals with the chromosomes of a freshwater fish—*Trichogaster fasciatus*, collected from the local ponds, is the outcome of our investigation undertaken to resolve, as far as possible, the discrepancies in the previous reports[1-3].

The somatic metaphases were obtained from the gill epithelium and the meiotic chromosomes from the testes of mature male individuals by the colchicine-Gimsa-air-drying technique. The morphometric analysis is based on the technique of Levan *et al.*[4],

The $2n$, as determined from 10 male and 11 female specimens, was 46. The $2n$ was confirmed by our observations of 23 bivalents in the meiotic metaphases obtained from the testes of the males (Fig. 1). The karyotype was differentiable into 9 pairs of metacentrics, 6 pairs of submetacentrics and 8 pairs of telocentrics (Fig. 2). Thus the fundamental arm number (NF) was 76 and the relative lenghts of the chromosomes ranged between 2·82% and 5·67% in a

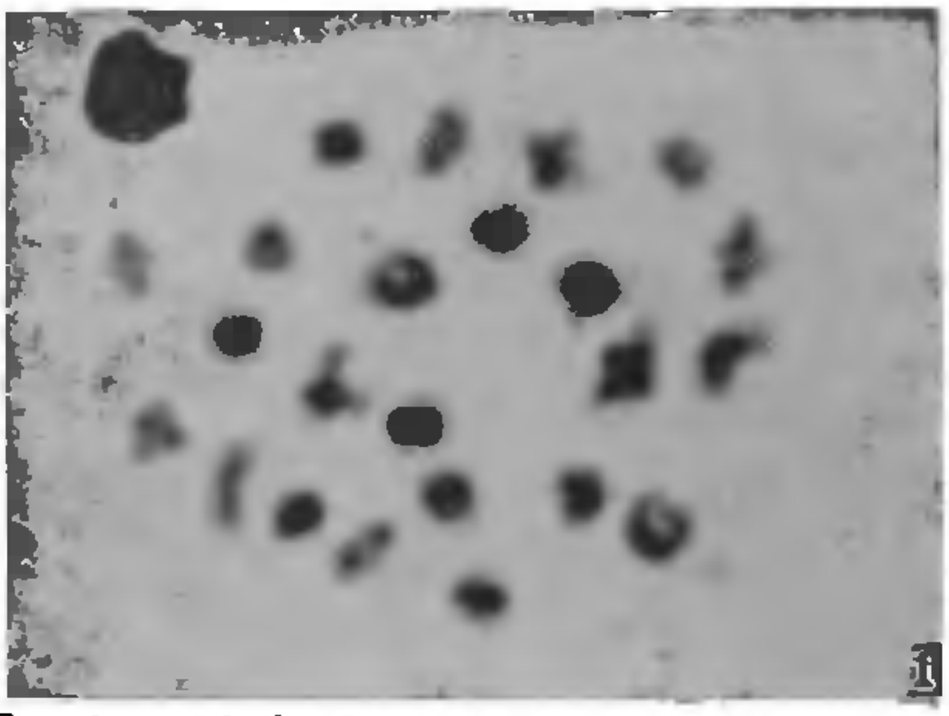

Fig. 1. Meiotic Bivalents of *T. fasciatus*, × 1500.

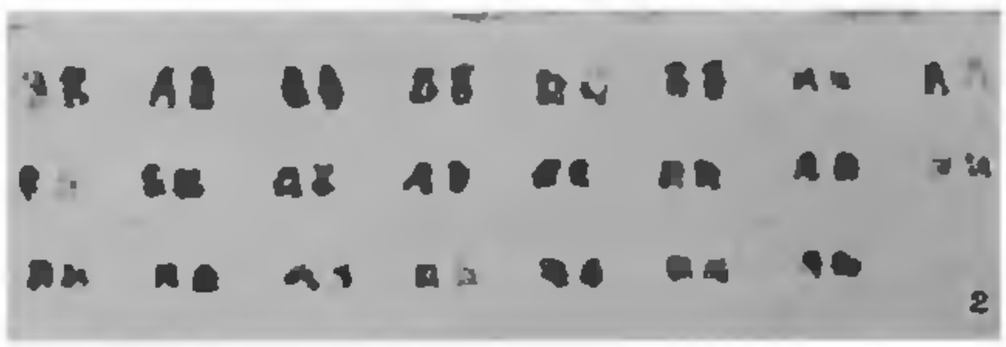

Fig. 2. Karyotype of *T. fasciatus*, × 1500.

total haploid genome length of 38·93 micra. Hence our data on the NF match those of Manna and Prasad[3] and deviate from those of Kaur and Srivastava[1] and Nayyar[2]. A genome length of 38·17 micra in the speciments studied by Manna and Prasad approximates that of the individuals studied by us, but the chromosome number in our specimens (*i.e.*, $2n = 46$) falls short by two from the diploid number reported by Manna and Prasad.

Since $2n = 46$ can be derived with ease from $2n = 48$ by way of fusion of two pairs of telocentrics, these two forms, differing in their diploid number, can be races of the same species, or, what is more credible, the form studied by us may be a subspecies of the form studied by Manna and Prasad. On the contrary, these two forms could as well be two different species or might be representing an instance of chromosome number polymorphism by the same species. That is, the simple fusion of two pairs of chromosomes of one form has brought down the chromosome number in the other. A similar mechanism of fusion/fission has also been advocated for the variation of $2n$ from 32 to 48 in several species of the genus *Fundulus*[5].

In the evolution of karyotypes among fishes, several arguments have been made in favour of fusion/fission as the underlying mechanism(s)[6–8]. According to Chen[5] and Liepmann and Hubbs[9], fusion always leads to a decrease in the chromosome number and, therefore, the teleosts, as they progress phylogenetically more often come to show a decrease than an increase in their chromosome number. Judged by these postulates, the form studied by us, although has nearly the same genome length as the form studied by Manna and Prasad, could yet be evolutionarily a more recent one.

December 9, 1980.

1. Kaur, D. and Srivastava, M. D. L., *Caryologia*, 1965, **18**, 181.
2. Nayyar, R. P., *Genetica*, 1966, **37**, 89.
3. Manna, G. K. and Prasad, R., *Nucleus*, 1977, **20**, 264.
4. Levan, A., Fredga, K. and Sandberg, A. A., *Hereditas*, 1964, **52**, 201.
5. Chen, T. R., Comparative karyology of selected deep-sea and shallow water teleost fishes, *Ph.D. Thesis*, Yale University, 1967.
6. Nogusa, S., *Mem. Hyogo, Univ. Agric.*, 1960, **3**, 1.
7. Booke, H. E., *J. Fish Res. Bd. Can.*, 1975, **32**, 295.
8. Gold, G. R., Avise, J. C. and Gall, G. A. I., *Cytologia*, 1977, **42**, 377.
9. Liepmann, M. and Hubbs, C., *Texas Rep. Biol. Med.*, 1969, **27**, 427.

LOG-NORMAL DISTRIBUTION OF PARASITIZATION INDEX AND GASTRO-PARASITIC INDEX IN THE FISH-CESTODE RELATIONSHIPS OF HILL-STREAM FISHES

R. S. Chauhan and Sandeep K. Malhotra

Parasitological Laboratory
Department of Zoology, University of Garhwal
Pauri Campus, Pauri (Garhwal) 246 001, India

Logarithmic models relating to the cestode infection and body weight ratios of fish hosts and their cestode parasites have been proposed. The objective of the present investigation is to provide comprehensive information on the distribution patterns of cestode infected fish hosts in hill-streams at variable altitudes in Garhwal Himalayas. The precise role of fluctuations in the extremes of different environmental factors on species abundance of infected hosts is discussed. The data from a survey of 2224 fishes of 22 species in the Himalayan riverine ecosystem, *viz.*, 14, 1, 2, 1, 2, and 2 fishes of family Cyprinidae, Bagridae, Sisoridae, Saccobranchidae, Ophiocephalidae and Mastacembelidae respectively (see Malhotra[1]) have been used. A highly significant correlation ($P > 0{\cdot}01$) was obtained between Parasitization Index (P.I.) (Malhotra, Chauhan and Capoor[2]) and Gastro-Parasitic Index (G.P.I.) (Malhotra, Chauhan and Capoor[3]) for *Barilius bola* Ham. (Cyprinidae) and (*Mastacembelus armatus* Lac. (Mastacembelidae). The correlation was poor ($P > 0{\cdot}50$) for *Labeo dero* Ham. (Cyprinidae) and *Schizothorax plagiostomus* Heck. (Cyprinidae). Figs. 1*a*–1*c* and Figs. 2*a*–2*c* indicate log-normal distribution of the infected fish species in relation to P.I. and G.P.I. respectively at different altitudes (*viz.*, 395 mASL and 650 mASL) except for certain sample fluctuations in Figs. 1*b* and 1*c* for P.I. and Fig. 2*a* for G.P.I.

The log-normal distributions of infected fish species abundances (Figs. 1*a*–1*c* and Figs. Figs. 2*a*–2*c*) further confirm the views of Feller[4] that such distributions are typically the probable outcome of superimposing a number of random processes on each other so that they undergo "random walks". A general explanation in the present investigation lies perhaps in the unpredictability of the environment because to living things the environment fluctuates in ways that are hostile, both in time and space. Some species, the opportunists, meet the fluctuations in time merely by fluctuating their own abundances in a specified area during different times of the year. By the "random walk" process their relative abundances become log-normal. Other species can endure fluctua-