CONCLUSIONS

On the basis of present investigations on Tfs of *Channa punctatus* Bl., the following inferences can be made:

1) Extensive genetic polymorphism is displayed by Tf of *C. punctatus* which is applicable in identifying and typing its populations to monitor their dynamics.

2) The abundance of a homozygous phenotype, as reported for Tf BB of this fish, is an exception to the general observation made so far that heterozygote excess is because homozygotes are less viable in comparison with heterozygotes.

3) A similarity in iron binding rates displayed by BB and excess heterozygote BC suggests a role for the second functional site of Tfs, i.e. the cell receptor binding site in determining the viability of these phenotypes.

4) Polymorphism displayed by *C. punctatus* Tfs is under the control of a single locus, variants of which encode isoforms in the combinations typical of one or the other phenotype.

5) Inspite of recent origin of *C. punctatus*, its Tfs locus has undergone extensive mutations giving rise to atleast three different co-dominant alleles and their random combinations. Though *C. punctatus* is a highly specialized fish, its Tfs are structurally and functionally similar to those of other vertebrates. All Tfs studied so far invariably possess the same iron binding capacity indicates that the number of binding sites per molecule and most probably the structure of the relevant sites have been substantially conserved during evolution.
6) MC'F data suggests some agreement between classical morphometric data and evolutionary relatedness of immunological determinants of species other than that shown by Tfs of *C. gachua* and *C. striatus*. As originally proposed by Chandy (1955), *C. gachua* might have been the most generalized form, but immunologically its Tfs are more close to those of *C. striatus* indicating that during evolution similar changes were incorporated in their antigenic determinents. Divergence of *C. punctatus*, was ahead of these two i.e. *C. gachua* and *C. striatus*. 