CONCLUSIONS
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On the basis of the findings presented and discussed in this work dealing with cDNA cloning, phenotyping and biochemical characterization of transferrin isoforms of Channa gachua (including the comparison with other three species), the following conclusions may be made:

(1). Efforts to clone cDNA of a Tf isoform were partially successful. The cloned sequence, however, shows homology to conserved region of N as well as C domains of accessed sequences of four teleosts of different classes and origin (namely: Oncorhynchus mykiss, Oryzias latipes, Paralichthys olivaceus and Salmo trutta).

(2). Partial clone is, in any case, informative. A comparison of the portion of the accessed sequences of four teleosts, with the homologies of different degrees in N and C domains, reveals differences in AT:GC contents, occurrence of 30 Asn residues in a single stretch and specific positioning of Cys residues.

(3). Phenotyping of Tf variants by PAGE showed the presence of one banded and two banded homozygotes AA and BB only. Out of them, fast migrating BB is the most abundant one.
(4). Phenotype BB has been reported for the first time. It is obviously in lesser frequency than AA/BB phenotype. No heterozygote has been discovered so far.

(5). Protein bands initially identified in PAGE as those of Tf, could unambiguously be identified by incubating with FENTA, following which excepting Tfs all other protein bands take up CBB stain. This protocol should help to confirm the identity of Tf bands in gel replicas stained with CBB. For this purpose, superimposed or duplicate gels can be conveniently run under identical conditions.

(6). Biochemically, highly purified TfB isoform of *C. gachua* has all the attributes of a typical transferrin molecule: it is a glycoprotein of *M*ₐ = 72 kD with sialic acid as the constituent of carbohydrate moiety, typically binds 2 atoms of iron per molecule and diferric protein releases iron along a semi-biphaseic course as the pH values decline.

(7). One Tf isoform each purified from three other species of genus *Channa*: *C. punctatus*, *C. striatus* and *C. marulius* show close
resemblance in most of the above attributes (e.g. $M_r$, presence of sialic acid, pI values and conversion to diferric iron and its pH dependent release).

(8). Some interspecies differences, however, do exist. For instance: (i), Tfs of *C. gachua* and *C. punctatus* retain immunological cross-reactivity even after electrophoresis in SDS-PA gels, whereas Tfs of *C. marulius* and *C. striatus* do not; (ii), above noted distinction between Tfs of channid species into two subgroups is apparent from their IEF values; and, (iii) also from their iron binding capacities and pH dependence of iron release.

(9). The occurrence of a minimum number of Tf loci (two only) in *C. gachua*, in spite of being polyploid, has to have evolutionary implications.

(10). The results, thus, establish that though Tfs of *C. gachua* as well as three other species of genus *Channa* are similar to other teleost Tfs in several respects, they do posses a few specific characteristic of their own. The specific biochemical and immunological characteristics may be correlated with the differences between the primary functions of iron binding.
capacities and release. High iron binding capacities may have a
direct bearing upon the better chances of post-hatching survival
that may, in turn, determine the genetic composition that is
observed in a surviving population and discerned by Tf
polymorphism.