Microsatellite variation in the african catfish *Chrysichthys nigrodigitatus* (LACEPEDE, 1803) (Siluroidei, Claroteidae)

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Variation at three microsatellite loci was examined in four natural populations of the West african catfish *C. nigrodigitatus*: Senegal (n=46), Selingue Dam, Niger (n=54), Ebrie lagoon, Ivory Coast (n=32) and Volta Lake (n=28). One farmed population, Sial (Société ivoirienne d'aquaculture lagunaire) in Ebrie Lagoon, created with 700 founders and farmed for five generations, was also examined (n=85). Summary statistics are given in Table 1.

The number of alleles was high in all three loci (29 to 30) and the number of the average number of alleles per population varied from 22.0 to 6.67. Heterozygosities were also high, but interestingly the higher mean heterozygosity was exhibited by the locus with the smaller number of alleles. Smaller heterozygosities were observed in Selingue dam and Sial farm, whereas the three natural populations had higher and comparable heterozygosities. Between 17% to 60% of alleles were « private », that is they were observed only in one population. The number of private alleles across loci varied among populations from 16 to zero. The farmed population had no private allele, an observation consistent with the history of the population. The Dam population has also a small number of private alleles, but the low number of Volta is unexpected. On the basis of neutrality and random mating, one can compare effective population sizes. The five populations appear to fall into three categories in this respect: Niger Dam and Sial Farm are the smaller, followed by Volta, followed by Senegal and Ebrie. It is interesting to note that the levels of polymorphism in the natural populations of species living in rivers can be as high as marine species, suggesting that these populations have a long history and have mantained large sizes.

	Microsatellite Locus			Population				
	Cn1	Cn2	Cn3	Niger	Senegal	Ebrie	Volta	Sial
N	231	251	254	-	-	-	-	-
Na	-	-	-	54	46	32	28	85
A	38	30	29	-	-	-	-	-
Aa	-	-	-	12.7	20.3	22.0	14.0	6.67
np	13	18	5	4	13	16	3	0
Ha	0.88	0.68	0.92	0.74	0.89	0.89	0.85	0.76
FIS	-0.008	0.097	0.050	0.057	0.162	0.058	0.016	-0.062
Ne,i	-	-	-	1400	4000	4000	2800	1600
Ne,s	-	-	-	3500	20500	20500	10800	4100

Table 1
Summary statistics of microsatellite variation at three loci in five populations of the West African catfish *Chrysichthys nigrodigitatus*. Note: N =Total number of animals scored, Na = number of animals scored averaged over loci, A= total number of alleles observed, Aa= number of alleles observed averaged over loci, np= number of private alleles, Ha = average heterozygosity over populations (first set of columns) or over loci (second set of columns), Nei = effective population size (averaged over loci) under the step-wise mutation model. In both estimates of Ne, mutation rate was assumed to be $u = 5 \times 10^{-5}$.

Note that the farmed population suffered an important reduction of polymorphism within five generations, relatively to the levels of the population of origin, despite an aquaculture practice aiming at keeping high levels of polymorphism. A dam effect can be also seen, but a sample from the Niger river should be analyzed to test for levels of polymorphism outside the Selingue Dam.

Most populations are in Hardy-Weinberg equilibrium. An exception is the sample from Senegal river, at Dagana, where a trend for excess of homozygotes is present in all loci, with significant values for two out of three loci. Given the high levels of polymorphism, inbreeding seems not a probable cause of this excess. One possibility is that the excess is artifactual (*e.g.* variation in the efficiency of PCR). Another possibility is a temporal or ethological Walund effect, whereupon non-random mating is a consequence of differences in the time or behavior of spawning. If this type of breeding structure is shown to be true, it will be of basic importance for management decisions and conservation policy for this species.

A highly significant heterogeneity was observed in all pair-wise comparaisons of samples for all three loci. It is of interest that this holds even for the farmed population relatively to the population of its origin. Random drift can be highly effective in causing allele frequency changes even when the founder population is large (700 animals) and the time since establishement of the farm is small (five generations). Large differences between wild populations, on the other hand, imply a long history of effective, if mot absolute, isolation.

Based on these three loci a factorial analysis of correspondence provides a relatively good assignment of individuals to populations. For the most polymorphic samples (Ebrie lagoon and Senegal river) there is considerable overlap. In a pilot experiment involving a small number of animals scored for five instead of three loci, the assignment was infallible. Thus, a relative small increase in the number of microsatellite loci (provided they are as polymorphic as the three reported here) and estimates of frequencies based on larger sample sizes will suffice for the assignment of individuals to their population of origin.

These results show that microsatellite is the tool of choice for population monitoring, preservation of genetic diversity and breeding programs in aquaculture. The same individuals used in a study of allozyme and morphological variation (ADEPO-GOURENE *et al.*, 1997). Allozymes showed a relatively high variability in populations from the middle of the geographic distribution of the species (Ivory Coast), relatively to almost complete monomorphism in the Northern (Senegal) and Southern (Congo) extremes. This may mean that the species has originated in the middle of the distribution and extended its presence in both directions, North and South. The present study shows that microsatellites are as variable in Senegal as in Ivory Coast (Ebrie Lagoon). The difference between allozymes and microsatellites is most likely due to the difference in mutation rate, which is much higher in microsatellites. This means that microsatellites have much « shorter memory » of the evolutionary history of the population and can be used most profitably to read the recent history of the species.

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References

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