ABSTRACTS – 2008 88 annual Meeting of the American Society of Ichthyologists & Herpetologist July 23-28, 2008, Montreal, Quebec, Canada COMPLIED BY M.A. DONNELLY

Shape Variation between Contemporary and Archived Cichlids from Lake Nabugabo, Uganda: Evidence for Rapid Morphological Change

Igor Mitrofanov, Lauren Chapman

McGill University, Montreal, Canada

The explosive speciation of haplochromine cichlid fishes in Lake Victoria is unrivaled among vertebrates; however, $\approx 40\%$ of its endemic fishes disappeared between 1980 and 1986 associated with various anthropogenic perturbations, including introduction of the predatory Nile perch. Similar faunal collapse occurred in other nearby lakes that experienced Nile perch introduction, including Lake Nabugabo, a historic backwater of Lake Victoria. However, some native species persisted in the face of Nile perch predation by exploiting habitat refugia and/or via behavioural mechanisms; and, over the past decade, resurgence of some species has been reported. Resurging species may differ in phenotype from their pre-Nile perch conspecifics due to a variety of mechanisms including selection pressures associated with habitat refugia, predator pressure, and/or hybridization. As part of a larger collaborative study on rapid morphological change in cichlids of the Lake Victoria basin, we looked for evidence of phenotypic change in haplochromine cichlids of Lake Nabugabo that have shown signs of recovery. We compared collections of three species sampled in the early 1960's and archived at the British Museum of Natural History [Astatotilapia velifer (Trewavas, 1933), Haplochromis annectidens Trewavas 1933, Paralabidochromis beadlei (Trewavas, 1933)] with the same species sampled in 2005. Body shape was quantified using geometric morphometrics (whereby each fish was characterized using a set of landmarks); MANCOVA indicated significant differences between archived and contemporary in multivariate body shape traits. Shape variation reflected a smaller body depth, shorter head length, and forward displacement of the paired fins in recent collections. Such convergent change in the three species may indicate the need for increased maneuverability in structurally complex refugia (swamps) or in the face of predator attack.

0167 Poster Session I, Friday July 25, 2008

Higher-level Relationships of the Cypriniformes (Actinopterygii: Ostariophysi) Inferred from 238 Whole Mitochondrial Genome Sequences

<u>Masaki Miya¹</u>, Tetsuya Sado¹, Kenji Saitoh², Michael H. Doosey⁷, Henry L. Bart, Jr.⁷, Ignacio Doadrio⁸, Yazdan Keivany⁴, Jiwan Shrestha⁵, Vachira Lheknim⁹, Rafael Zardoya⁸, Mutsumi Nishida⁶, Richard L. Mayden³

¹Natural History Museum and Institute, Chiba, Chiba, Japan, ²Tohoku National Fisheries Research Institute, Miyagi, Japan, ³Saint Louis University, St. Louis, MO, United States, ⁴Isfahan University of Technology, Isfahan, Iran, Islamic Republic of, ⁵Nepal Academy of Science and Technology, Kathmandu, Nepal, ⁶Ocean Research Institute, University of Tokyo, Tokyo, Japan, ⁷Tulane University, New Orleans, LA, United States, ⁸Museo Nacional de Ciencias Naturales, Madrid, Spain, ⁹Prince of Songkhla University, Songkhla, Thailand

Fishes of the order Cypriniformes are almost completely restricted to freshwaters and number over 3400 species placed in six families, each with poorly-defined subfamilies and/or tribes. In the previous mitogenomic study based on 59 whole

mitogenome sequences (Saitoh et al. 2006), we confirmed monophyly of the Cypriniformes and found four major clades comprising Cyprinidae, Catostomidae, Gyrinocheilidae, and Balitoridae + Cobitidae (Psilorhynchidae not available), with the latter two loach families reciprocally paraphyletic. Interrelationships of these major clades, however, were ambiguous despite the longer nucleotide sequences used in the analyses. Also unavailability of several unusual taxa (e.g., Psilorhynchus, *Ellopostoma, Paedocypris*) prevented us from drawing explicit conclusions. The present study represents the second step towards resolution of the higher-level relationships of the world's largest freshwater-fish clade based on more extensive taxon sampling from 230 cypriniforms (including 4 species of Psilorhynchus, 1 species of Ellopostoma and 2 species of *Paedocypris*). Unambiguously aligned, concatenated mitogenome sequences from 13 protein coding genes (11,328 bp) were divided into three partitions (1st, 2nd, and 3rd codon positions) and preliminary phylogenetic analyses based on partitioned maximum likelihood method using RAxML 7.0 were conducted. The resultant phylogenies are largely congruent with the previous findings in Saitoh et al. (2006), although the addition of 177 species provides a much more detailed picture of cypriniform relationships. As for the unusual taxa, *Psilorhynchus* is the sister group of the subfamily Cyprininae (sensu lato); *Ellopostoma* is closely related to the subfamily Balitorinae (not Nemacheilinae as previously thought); and *Paedocypris* occupied a position sister to all the remaining members of the family Cyprinidae (not a rasborin as previously demonstrated). We identify a number of long branches in the resultant tree that we hope to bisect by adding species to our data matrices in the hope of obtaining an even clearer picture of cypriniform relationships.

0599 Poster Session II, Saturday July 26, 2008

Diet of Tiger Salamanders in North Dakota, With Implications for Flow of Heavy Metals through Wetland Food Webs

Heather Modrow

Minot State University, Minot, ND, United States

I used a series of larval and transformed A. mavortium from a population in northwest North Dakota and inspected gut contents in order to test the hypotheses that age, size, sex, maturation status, and life history stage influence food preferences. All sampled animals (n = 49) were collected from Swalls Lake, Ward Co. Stomachs were extracted, weighed, and prey content was keyed out to order. Number of each type of prey were counted. I used SVL, headwidth, sex, reproductive status (juvenile or sexually mature), and developmental stage (larval or transformed) as in a series of exploratory regression analyses (for SVL and headwidth) or ANOVAs (for sex, reproductive status, and development stage) in order to determine if any factor was associated with significant differences in prey type and abundance. Headwidth correlated significantly with prey variation and abundance. This means that salamanders with larger heads eat larger prey and more of them. The other significant factor was developmental status: larval salamanders (both paedomorphs and juvenile larvae) at different prey than transformed salamanders. Interestingly, all the prey in the guts of transformed salamanders were aquatic prey. This contrasts with the classic notion that transformed amphibians return to ponds only to breed. Supplemented with the observation that many of these transformed salamanders were juveniles, this suggests that salamanders return to pond for significant growth opportunities in addition to any reproductive potential.