



Comparative cytogenetic mapping of rRNA genes among naked catfishes: implications for genomic evolution in the Bagridae family

W. Supiwong^{1,3}, T. Liehr¹, M.B. Cioffi², A. Chaveerach^{3,5}, N. Kosyakova¹, X. Fan¹, T. Tanee^{4,5} and A. Tanomtong³

¹Jena University Hospital, Friedrich Schiller University, Institute of Human Genetics, Jena, Germany

²Departamento de Genética e Evolução, Universidade Federal de São Carlos, São Carlos, SP, Brasil

³Department of Biology, Faculty of Science, Khon Kaen University, Muangkhonkaen District, Khon Kaen, Thailand

⁴Faculty of Environment and Resource Studies, Mahasarakham University, Kantarawichai District, Mahasarakham, Thailand

⁵Genetics and Environmental Toxicity Research Group, Khon Kaen University, Khon Kaen, Thailand

Corresponding author: A. Chaveerach
E-mail: raccha@kku.ac.th

Genet. Mol. Res. 13 (4): 9533-9542 (2014)

Received October 17, 2013

Accepted May 7, 2014

Published November 12, 2014

DOI <http://dx.doi.org/10.4238/2014.November.12.2>

ABSTRACT. In the present study, the karyotype and chromosomal characteristics of 9 species of the Bagridae fish family were investigated using conventional Giemsa staining as well as dual-color fluorescence *in situ* hybridization to detect the 18S and 5S rDNA sites. In addition to describing the karyotype of several Bagridae catfishes, we established molecular cytogenetic techniques to study this group. The 9 species contained a diploid chromosomal number, varying from 50 (*Pseudomystus siamensis*) to 62 (*Hemibagrus wyckii*), while none contained heteromorphic sex chromosomes. 18S rDNA sites were detected in only 1 chromosomal pair among all species evaluated. However, 3 different patterns were observed for the distribution of the 5S rDNA: 2 sites were found in the genus *Mystus* and in *P. siamensis*,

multiple sites were observed in the genus *Hemibagrus*, and a syntenic condition for the 18S and 5S rDNA sites was identified in *H. wyckii*. The extensive variation in the number and chromosomal position of rDNA clusters observed among these Bagridae species may be related to the intense evolutionary dynamics of rDNA-repeated units, which generates divergent chromosomal distribution patterns even among closely related species. In summary, the distribution of repetitive DNA sequences provided novel, useful information regarding the evolutionary relationships between Bagridae fishes.

Key words: Fluorescence *in situ* hybridization; Freshwater fishes; Karyotype evolution; Molecular cytogenetics; Ribosomal DNA