GENETIC VARIATION WITHIN AND AMONG POPULATIONS OF SPINY EELS IN THE WESTERN AND EASTERN REGIONS OF SABAH, MALAYSIA.

Chai Suan, Hor

Institute for Tropical Biology and Conservation, Universiti Malaysia Sabah, Jalan UMS,

88400 Kota Kinabalu, Sabah, Malaysia Email: suanhor@gmnail.com

ABSTRACT

The spiny eels *(Macrognathus* spp.*)* or locally known as “Tilan” or ”Salan” (Sabah) are from the family of Mastacembelidae, and commonly found in forest streams and rivers with sand, gravel or boulders in Southeast Asia. Faunal similarities among the countries of Southeast Asia suggests that many exchanges among the animal species occurred during the Pleistocene epoch where Peninsular Malaysia, islands of Sumatra, Java and Borneo were connected by the Sunda shelf when the sea level was about 120m below the present level. There is a lack of information on the drainage connection in Sabah (North Borneo) that resulted in species migration. This study attempts to determine if there are significant genetic differentiations among western and eastern populations of *Macrognathus* spp. in Sabah, since the eastern rivers are not known to have been connected to the Sunda shelf in the past. In this study, samples were collected based on different geographical locations i.e. Suwatan River and Membakut River in western Sabah and, Maliau Basin and Danum Valley in the east. A total of 139 samples of *Macrognathus* spp. have been collected from four study sites i.e. 37 samples from Membakut River, 22 samples from Suwatan River, 40 samples from Maliau Basin and 40 samples from Danum Valley. DNA has been isolated and quantified using standard extraction protocols. Enrichment of a spiny eel microsatellite library through the 5’ anchored PCR technique and subsequent cloning into pCR2.1 vector and transformation into TOPO Top10’ competent cells are in progress. Further laboratory steps i.e. alkaline lysis miniprep of plasmid, plasmid yield estimation and restriction digestion of plasmid DNA, DNA sequencing, primer design and screening for PCR amplification will be carried out. Also, DNA sequence analysis of the COI gene will be preformed to accurately barcode the *Macrognathus* species for DNA fingerprinting purposes.

Keywords: Macrognathus spp., genetic variation, DNA microsatellite