ISSN: 1391-8796 Abstracts of Presentations 1st Ruhuna International Science & Technology Conference University of Ruhuna, Matara, Sri Lanka January 22-23, 2014



Investigation of the possibility of utilizing two mitochondrial gene regions to differentiate two *Penaeus* species: A preliminary study

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Black tiger prawn *Penaeus monodon* and Green tiger prawn *P. semisucatus* show similar morphological characters up to some extent thus are difficult to differentiate them especially at their larval stages. This preliminary investigation focused on the possibility of utilizing genetic based approach to distinguish the above two *Penaeus* species. Two mitochondrion gene regions i.e. 12S rRNA and 16S rRNA, were partially amplified using universal primers and sequences were obtained for analysis. For 12S rRNA gene region, the percentage of base composition for *P. monodon* was A: 34.79%, C: 11.34%, G: 17.78%, T: 36.08% and for *P. semisulcatus* it was A: 36.36%, C: 13.51%, G: 17.40% and T: 32.73%. For 16S rRNA gene region the percentage of base composition for P. monodon was A: 34.43%, C: 12.70%, G: 18.85%, T: 34.02% and for *P. semisulcatus* it was A: 33.40%, C: 12.09%, G: 20.70% and T: 33.81%. Genetic distance (p distance) between P. monodon and P. semisulcatus was 18.4% and 8% for 12S rRNA and 16S rRNA gene regions respectively. The utility of restriction enzymes to discriminate these two Penaeus species was investigated and possibility of application of three restriction enzymes on this purpose was determined. P. monodon shows high growth rate compared to P. semisulcatus thus extensively used in aquaculture industry. Therefore, correct identification of two *Penaeus* species is important when selecting brood stocks and the larval stages from the wild catch for culturing purposes.

Keywords: 12S rRNA and 16S rRNA, mitochondrial genes, *Penaeus monodon*, *P. semisulcatus*

Acknowledgements: Funding is provided by NSF/RG/2010/BT/02

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