ABSTRCT

In many countries, including Sri Lanka, freshwater prawn industry is mainly based on *Macrobrachium rosenbergii* which is called as giant freshwater prawn. However, now there is a growing interest in many Asian countries to use *Macrobrachium malcolmsonii* as a potential candidate in aquaculture programs due to its high growth rate. In Sri Lanka, *M. malcolmsonii* has been reported mainly from the estuaries of eastern part of the country. Although, the adults of two species show a few morphological differences, the appearance of young individuals of both species are identical. Therefore, in many occasions identification and separation of the above two species is difficult. The aim of this study was to distinguish *M. rosenbergii* and *M. malcolmsonii* using morphological and molecular data. Twenty one *M. rosenbergii* individuals from *Nilwala* River estuary and twenty six *M. malcolmsonii* individuals from *Gal Oya* estuary were used in morphometric analysis. After data were subjected to normality test, nine characteristics were used in Decriminant Function Analysis. Among them seven characteristics were derived as contributors that help in delineating two species which need to be confirmed using the results of heritability tests. To determine the utility of Single Stranded Conformation Polymorphism (SSCP) method in distinguishing *M. rosenbergii* and *M. malcolmsonii*, partially amplified mitochondrial 16S rRNA gene regions for both species were sequenced. The derived sequence lengths of both DNA fragments were approximately 430 bp to 440 bp and the estimated nucleotide difference between sequences of two species was approximately 19 bp. Then, SSCP technique was carried out using the same PCR product. However, the SSCP technique failed to differentiate DNA fragments derived from 16S rRNA gene region for two freshwater prawn species *M. rosenbergii* and *M. malcolmsonii*. This may be due to the formation of more stable and similar secondary structures for this gene region. Further studies are suggested to conduct SSCP method using more variable gene regions.