Allozyme variation in a freshwater mussel population (*Coelatura kunenensis* Mousson, 1887) from Southern Africa

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Abstract

Gene products of 35 protein coding loci in *Coelatura kunenensis* (Mollusca-Lamellibranchiata) were examined by horizontal starch gel electrophoresis. Electrophoretic analysis of enzymatic proteins revealed genetic variation at 12 (34.3%) of the loci studied. Values of 28.57 (0.95 criterion), 1.43 (±0.12) and 0.075 (±0.025) were obtained for the percentage of polymorphic loci, the mean number of alleles per locus and average heterozygosity respectively. Genetic variation compares favourably with values obtained for other species in general, but it is less than previous estimates based on fewer loci for intertidal mollusc and freshwater bivalve species.

Introduction

Coelatura is the valid name for the genus of unionid bivalves previously amended to *Caelatura* (Rosenberg et al., 1990), and although many Southern African species of the family Unionidae have been described, only four are recognised (Appleton, 1979). These are *Unio caffer, C. framesi, C. kunenensis* and *C. mossambicensis. C. kunenensis* is a western species confined to the Kunene, Okavango and Upper Zambezi River systems, and found in lentic and often seasonally inundated areas. Appleton (1979) was able to identify functional females (with marsupia and embryos), suggesting a dioecious mode of reproduction.

Despite the above-mentioned reports, no information is available on genetic variation or other aspects regarding the biology of this species. Mussels are, however, suitable for monitoring heavy metal pollution (Balogh, 1988; Pynnoenen, 1990), trace element pollution (Baudo and Galanti, 1988), the effect of pH on electrolyte balance in hemolymph in hard and soft water (Pynnoenen, 1991), tolerance against insecticides (Varanka, 1987), the relationship between fluctuations in environmental factors and meat to shell ratio (Blay, 1990), and DNA-adduct measurements as biomarkers in the assessment of both the biologically relevant exposure to carcinogens and the pathological consequences of such exposure (Kurelec et al., 1989).

Some freshwater mussel species are threatened with extinction due to indiscriminate use of insecticides, pollution and/or deterioration in the quality of mussel habitats by eutrophication through agricultural runoff (Hochwald and Bauer, 1988). Mussels are known for their nutritional value and the feasibility of application of protein enrichment by electropolarity treatment in mussel culture had a positive effect on protein content (Mani et al., 1988). Not only are mussels an excellent source of protein for human consumption and suitable as indicator species for pollution monitoring, but other species also rely on freshwater mussels to survive. For example, Nystroem and Pehrsson (1988) found that small individuals may be selected against since mussel-feeding diving ducks prefer them to larger mussels. The European bitterling, *Rhodeus amarus,* also practices rather unusual methods of spawning by using the favourable conditions in the gills of living freshwater mussels for the embryonic development of its fry (Heschl, 1989). This dependency of some species on mussels may also explain why a single emphemeropteran nymph and small leeches were found in the pallial cavities of 16.3% of the *C. kunenensis* (Appleton, 1979). In addition, the dissection of catfish showed the presence of freshwater mussels in their alimentary tracts (personal observations). As a result of the above-mentioned findings and applications for freshwater bivalves, there is great potential for their artificial culture. Mussel culture would also be beneficial for conservation stocking purposes. Successful rearing of juvenile parasitic freshwater mussels (Unionidae) is possible (Hudson and Isom, 1984) and *in vitro* culture and rearing of mussels involve only nominal cost (Isom, 1987).

The success of conservation efforts can be enhanced by knowing the genetic structure of the species in question and since the artificial culture of freshwater mussels is possible, the apparent importance of such fundamental and applied data (e.g. to be used in genetic selection programmes) has become evident. This study therefore aims to provide information on the allozyme diversity of wild *C. kunenensis.* Variability in nuclear DNA, as studied with allozyme electrophoresis, was chosen as a suitable biochemical technique based on recommendations by Grant and Leslie (1993). These authors suggested that it be used in preference to the analysis of uniparentally inherited organellar DNA (such as mitochondrial DNA) because species from Southern Africa showed little or no variation when the latter method was used compared to high levels of variability with allozyme electrophoresis.

Material and methods

Fifty *C. kunenensis* were obtained from the Upper Zambezi River system near KatimaMulilo,Namibia(24°25'S, 17°29'E). Samples were stored in liquid nitrogen and transported to the laboratory. Total body extracts were prepared and analysed by starch gel electrophoresis (12% gels), using the electrophoretic procedures, buffers, method of interpretation of gel banding patterns and locus nomenclature referred to by Van der Bank et al. (1992). Loci were numbered beginning at the anodal end of the gel, and cathodally migrating allozymes were designated by a minus sign. Statistical analysis of allozyme data was done using **BIOSYS-1** (Swofford and Selander, 1981).

It is important to note that distilled water or buffer solutions should not be added to samples prior to homogenation since

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