

Proteomic Variations in Commercially Important Penaeid (Brachyuran: Decapoda: Penaeidae) Shrimp by Using Isozyme (Amylase) as Biomarker Tool

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INTRODUCTION

The worldwide distribution of Penaeid shrimps is well known in tropical and subtropical waters. Shrimps are consumed globally and always remain a significant source of income and commercial importance (Vandeputte, and Haffray, 2014). In estuaries and coastal zones they constitute a significant portion of exploitable resources. Wild species show more genetic diversity as compared to farmed shrimps (Benzie, 2001). The SDS PAGE (soluble protein) and NATIVE PAGE can be used as a biochemical marker method for commercially significant shrimps for their genetic diversity of species samples so that they can be readily recognized.

OBJECTIVES

The aims of this research were to use proteomic analysis to identify differentially expressed proteins as biomarkers in Penaeid shrimps or to use western blot analysis to validate identified biomarker proteins associated with species recognition.

METHODS

The shrimp species were collected from various coastal areas through purchasing or random collection during 2018 and 2019. In the present study, the nine species of Penaeids were evaluated through Gel electrophoresis and generally soluble protein (SDS), Amylase (Native) and Commasie (Native) brilliant blue stain were used to compare the contiguous specie specific protein and as well as to clarify the variable expression of protein patterns. The differential expression of competitor proteins may be recognise by using western blot investigations. In an effort to create a link between variables and the expression of candidate biomarker proteins the POP-GENE software was used and standard statistical analysis was performed.

RESULTS

Analysis of genetic variations via SDS and NATIVE gel analysis showed reproducibly similar proteomic patterns for each group in most of the biomarkers but amylase showed significant difference among all. Genus *Fenneropenaeus* showed highest genetic diversity as compared to *Penaeus* > *Metapenaeus* > *Metapenaeopsis* > *Parapenaeus* > *Parapeneopsis*. Approximately 4 different expressions in each species were observed by staining the gel. Amylase expressed the different protein bands and identified by comparing them with rest of the biomarkers and SDS PAGE. Multiple bands were identified, of which five proteins bands were reported as being differentially expressed for amylase and these five bands have been chosen as candidate biomarker proteins for identification and relatedness. For further protein specification results, these proteins may be further checked by western blot analysis. Amy-1 has been confirmed to differentiate greatly among the candidate biomarker proteins in most organisms. Recognition of biochemical (protein) markers may enable

commercial recognition of shrimp species where morphological characteristics such as carapace and body colours are missing.

CONCLUSION

Using proteomic research, the differentially expressed five protein band in shrimp species were identified. Amylase was found to be the most specific biomarker method in the detection of shrimp species relative to the rest of the enzymes. The genetic diversity ratio was higher in the *Fenneropenaeus* and *Penaeus* genera. *Metapenaeus*, *Parapenaeopsis* and *Parapenaeus* had showed less gene pool diversions.

KEYWORDS

Isozymes, Penaeid shrimps, Pakistan, NATIVE PAGE, Amylase.

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