

AMPLIFICATION AND SEQUENCING OF MITOCHONDRIAL CONTROL REGION IN CULTURED LITOPENAEUS VANNAMEI

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The marine aquaculture industry in northeastern Brazil has seen a significant growth in recent years. At this moment, the white shrimp *Litopenaeus vannamei* is by far the most important among the cultured species. *L. vannamei* has a wide distribution range, from northern of Mexico to northern of Peru. Mitochondrial DNA has been widely used in genetic variability studies of marine organisms, including crustaceans. Mitochondrial markers are known to be excellent tools for population genetic analyses. Due to its high polymorphism, the control region might be useful as a genetic marker for monitoring genetic diversity in aquaculture stocks. In this study, mitochondrial DNA control region from *L. vannamei* sampled from Brazilian breeding stocks, was amplified and sequenced to estimate the intraspecific variability and its potentiality for use in support of aquaculture. Primers were designed to amplify the whole 1000 bp of the control region. Successful amplification was obtained for all ten samples tested. PCR products were directly cycle-sequenced and the resulting products read on an ABI 3100 automated sequencer. *L. vannamei* mtDNA control region seems to present enough polymorphism to be used for studying genetic variability among cultured broodstocks. The primers designed for this study may also be useful in studies of native shrimp populations.

Supported by: FUNCAP, FINEP

Key words: Control Region, *L. vannamei*, Amplification, Sequence

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