Molecular Characterization of *Vibrio* Species in Coastal Shrimp Farms

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Abstract

Sustainable shrimp aquaculture demands geographically tailored strategies to manage microbial risks and enhance animal health. This study focuses on the spatial distribution and preliminary characterization of *Vibrio* species from major shrimp farms in the districts of Tamil Nadu, including Pudukottai and Ramanathapuram. The study also examines the influence of the key environmental parameters on *Vibrio* abundance in different shrimp farms. The study employed the Modified Moore Swab (MMS) technique to sample water from eight distinct shrimp farm sites across the two districts. Around 29 *Vibrio* isolates were obtained using selective enrichment and plating methods, indicating a high prevalence of the genus in the regional aquaculture environment. The prevalence of these isolates was mapped and correlated with the key environmental parameters (salinity, temperature, pH, and TDS) unique to the sampling locations. This environmental monitoring allows correlation of local ecological parameters with the observed strain prevalence and dominance. Genomic DNA was extracted from all isolates for Whole Genome Sequencing (WGS) and metagenomic analysis. These high-resolution molecular approaches will link the geographical origin and environmental conditions to the isolates' genetic makeup, allowing for the characterization of virulence determinants, antimicrobial resistance (AMR) profiles, and genes responsible for probiotic traits. Future genomic analysis, informed by these environmental data, will guide

the identification and selection of robust, native strains to enhance regional biosecurity and address the ecological determinants of *Vibrio* prevalence.

Keywords: *Vibrio* species, Shrimp aquaculture, Whole genome sequencing, Antimicrobial resistance