

benefits, is highly perishable and spoil faster than other muscle foods. The wide variety of microorganisms harbouring raw fish is one of the reasons for its faster spoilage. In this aspect the advancement of microbial growth is a major factor determining the shelf life of a product. Present study aimed to evaluate the Progression of microbes associated with quality and safety on chilled storage of *Caranx melampygus*. Chilled storage is an effective way of fish preservation since spoilage can be delayed and quality can be maintained through proper icing. Microbiological progression on the advancement of chilled storage was carried out in three days interval. Quantitative analysis was carried out for the exploration of Mesophiles, Psychrotrophs, Fecal Streptococci, *Pseudomonas* spp, Enterobacteriaceae, *E. coli*, *S. aureus*, Hydrogen sulphide producers, Histamine forming bacteria and *Brochothrix thermosphacta*. While qualitative analysis was performed for *Salmonella*, *V. cholerae*, *V. parahaemolyticus* and *L. monocytogenes*. Mesophilic and psychrotrophic count crossed the limit of acceptability i.e $7 \log_{10} \text{cfu g}^{-1}$ on 15th day of storage. The mean log values of *Pseudomonas*, Hydrogen sulphide producers, *B. thermosphacta*, Histamine producing bacteria, Enterobacteriaceae and Fecal streptococci counts from initial to 15th day of storage ranged from $2.1 \log_{10} \text{cfu g}^{-1}$ to $7.5 \log_{10} \text{cfu g}^{-1}$, $2.5 \log_{10} \text{cfu g}^{-1}$ to $7.3 \log_{10} \text{cfu g}^{-1}$, $2 \log_{10} \text{cfu g}^{-1}$ to $7.6 \log_{10} \text{cfu g}^{-1}$, $2.5 \log_{10} \text{cfu g}^{-1}$ to $4.7 \log_{10} \text{cfu g}^{-1}$, $3.8 \log_{10} \text{cfu g}^{-1}$ to $4.9 \log_{10} \text{cfu g}^{-1}$, $2 \log_{10} \text{cfu g}^{-1}$ to $3.6 \log_{10} \text{cfu g}^{-1}$ respectively. Based on the microbiological parameters, *Caranx melampygus* under chilled storage in flake ice gave a shelf life of 12 days. *Salmonella*, *V. cholerae*, *V. parahaemolyticus*, *L. monocytogenes* and *S. aureus* were absent in the analysed samples.

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Genetic relationship of pathogenic *Vibrio parahaemolyticus* isolated from aquaculture farms and hatcheries

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Despite stringent preventive actions being taken by the industrialists *Vibrio* sp. remains to be a major concern during the export of shrimp as evidenced by the data given in RASFF portal of the EU, which notifies the border rejection of two consignments and notification issued for four others in last one year from August 2016 to August 2017. Among the six consignments that were positive for *Vibrio parahaemolyticus*, three were from India. The presence of *V. parahaemolyticus* in the consignments can be attributed to its innate prevalence in saline environments of tropical areas. A study was conducted on the prevalence of *V. parahaemolyticus* in samples collected from aquaculture farms and hatcheries of Kerala during the period from 2014 to 2016. 42 samples including water, mud and shrimp were collected from 12 farms and 3 hatcheries of which 93% were positive for *V. parahaemolyticus*. 33 pathogenic isolates of *V. parahaemolyticus*, determined by the presence of either thermostable direct haemolysin (*tdh*) gene, *tdh* related haemolysin (*trh*) gene or Kanagawa phenomenon was isolated from as many as 7 samples. The pathogenic isolates were further subjected to ERIC PCR to understand the genetic relatedness among the isolates. The analysis of ERIC PCR fingerprints revealed extensive diversity

among the isolates. At 40% similarity, six major clusters were identified in the dendrogram. The clustering of isolates from different farms located in the same geographical location with high similarity (>90%) represented the regional spread of these isolates. The isolates that were clustered together with the reference clinical isolate were positive for *tdh* gene indicating genetic relatedness between these isolates. The study can be further extended to determine the genetic relationship of *V. parahaemolyticus* from frozen and processed samples which will help in elucidating the possible source of contamination.

SF OR 18

Staphylococcal enterotoxin genes in MRSA from seafood and environment

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S *taphylococcus aureus* is a versatile pathogen having variety of virulence determinants, capable of causing wide range of infections. *S. aureus* possessing enterotoxins are generally regarded as food poisoning organisms. Very few reports are available in MRSA from seafood for the presence of staphylococcal enterotoxins or their genes (*se*'s). This study was undertaken to determine the prevalence of *se*'s in 65 MRSA's isolated from seafood and aquatic environment by employing either single or multiplex PCR targeting 18 *se*'s. The study revealed that 18.5% of MRSA did not harbour *se*'s. *seb* and *see* were not found in any of the isolates. *see*, the most frequent enterotoxin gene identified in *S. aureus* worldwide is the predominant enterotoxin

found in this study. A total of 26 (40%) out of 65 MRSA isolates carried multi-enterotoxin genes. Enterotoxin gene cluster (*egc*) was found in 17 out of 65 MRSA strains and they harboured at least 3 genes of the *egc* (*seg*, *sei*, *sem*, *sen*, and *seo*). The isolates which possessed > 5 *se*'s were found to harbour *sea*, *sei* and *seg* genes invariably. The order of dominance of the *se*'s in the MRSA isolates from seafood and fishery environment were *sea* (70%) > *sen* (60%) > *seo* (50%) > *sem* (50%) > *sei* (35%) > *seg* (30%) > *sec* (10%) > *seh* (10%) > *sel* (10%) > *ser* (10%) > *sed* (5%). The possession of multiple-enterotoxin genes in MRSA indicates the strong potential of these isolates to cause food borne illness and stringent hygienic measures should be incorporated in the whole seafood production chain to avoid the entry of these pathogens into the food chain.

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Effect of modified atmosphere packaging on the survival of *Yersinia enterocolitica* in Indian oil sardine

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Modified atmosphere packaging (MAP) is commonly used preservation method to extend the shelf life of fishes. Although MAP is widely used for fishes, the report on the optimum gas composition for *Yersinia enterocolitica* is very scant. Hence, the present work was undertaken to assess the survival of *Y. enterocolitica* exposed to different gas composition. For this, *Y. enterocolitica* at 10⁵ cfu g⁻¹ was inoculated on to sardine (*Sardinella longiceps*) and packed