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* geneindicating 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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Staphylococcus 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.

SF OR 19

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 10^5 cfu g^{-1} was inoculated on to sardine (*Sardinella longiceps*) and packed

in polyester-polyethylene laminated pouches. The packs were divided into 7 lots. One lot was used as control air pack and for other 6 lots, different combinations of CO_2 and O_2 (100:0; 80:20; 60:40; 40:60; 20:80; 0:100) were flushed before sealing the pouches. All the packs were stored on ice (0-2^{0}C) and the survival of *Y enterocolitica*, total aerobic plate counts and biochemical quality was monitored at regular intervals. Total volatile base nitrogen content increased with the storage period, which correlated well with the total aerobic plate counts. The gas combination of 80:20 (CO_2:O_2) exhibited better inhibitory effect for *Y. enterocolitica* compared to other gas compositions. The use of MAP with combination of 80:20 (CO_2:O_2) can be used for extending the shelf life of perishable food commodities like fishes significantly which helps in expanding the marketing of fishes to distant locations with maximum control with respect to major food borne pathogens.

SF OR 20

Development of DIG labeled probes for detection of *Salmonella*

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The genus *Salmonella* has zero tolerance in food and the presence of this pathogen is a serious concern world over. A DIG-labeled probe was developed to enumerate the pathogenic, food borne *Salmonella* by targeting *hns* and *invA* genes. The presence of hns and *invA* genes in all the isolates included in the study were confirmed by performing polymerase chain reaction (PCR) followed by agarose gel electrophoresis to confirm *Salmonella* by observing the specific band. From the same isolates, DNA were isolated, amplification and purification were performed which were then subjected to quantification of labeling efficiency, DNA spotting, hybridization and immunological detection. Dot blot hybridization revealed that all the PCR products obtained with *hns* and *invA* primers hybridized with the probe confirming the specificity of this primer to detect *Salmonella* by evident positive color reaction. DIG labeled *hns* and *invA* probes that were developed in this study showed similar efficacy in detecting Salmonellaas thePCR. The present investigation revealed that both *hns* and *invA* probes developed were simple, reliable and specific for enumerating *Salmonella* with the minimum probe volume that in turn assures its efficient application in detecting/enumerating *Salmonella*. This method subverts the necessity to perform agarose gel electrophoresis followed by gel documentation and can be performed on the PCR product directly. It can also lend itself to using the probes to perform colony hybridization on agar plates with suspected *Salmonella*.

SF OR 21

Effect of liquid smoke and chitosan treatment on inhibition of *Listeria monocytogenes* in fishmodel system

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