images and FT-IR spectra. A batch adsorption study was carried out at different adsorbent dosage, contact time and initial concentration. Fluoride concentration was determined using Ion chromatography. Maximum fluoride removal efficiency of 85.37% from water was obtained using a combination of 2.5% chitosan coated activated carbon and 1% alumina.While a maximum fluoride removal efficiency of 66.88% was obtained using a combination of 2.5% chitosan coated cuttle bone carbon and 1% alumina. Both the combinations effected optimal fluoride removal efficiency of 94.58 and 75.63 % respectively at a contact time of 120 minutes. Combination of CCBC and alumina was found to be more effective with higher fluoride removal efficiency at higher initial concentration of fluoride when compared to combination of CCAC and alumina.

SF OR 15

Effect of organic acid on survival of *Staphyococcus aureus* and enterotoxin production in fish during drying

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This study was aimed to investigate the effect of organic acid against *S.aureus* and enterotoxin production in fish during drying. Shark (*Carcharhinus falciformis*) procured from the local fish market was deskinned, cut into small pieces and then decontaminated with 5ppm chlorine. Shark meat pieces were inoculated with three different levels of *S.aureus*: a low level of 3log cfu/g, a medium level of 5log cfu/g and a high level of 7log cfu/g. The meat was then washed with four different concentrations (1, 3, 5 and 7%) of propionic acids separately and dried in an electric drier for 24hr. Moisture and water activity of fresh meat was 75.9% and 0.98, which decreased to 10.6% and 0.63 during drying. In 3log cfu/g inoculated samples there was about 1.52, 2.63, 2.73 and 3.31 log reduction in *S.aureus* for 1, 3, 5 and 7% treated samples at the end of drying. Enterotoxin was not detected in any of the samples including the control samples after drying. In 5logcfu/g inoculated samples, there was remarkable reduction in the *S. aureus* count for 5% and 7% treated samples (3.3 and 4.38 log cfu/g) compared with other treated samples. Enterotoxin was not detected in 5 and 7% treated samples. In 7log cfu/g inoculated samples there was about 0.67, 1.89, 4.16 and 4.43 log reduction in *S. aureus* count for 1, 3, 5 and 7% treated samples at the end of drying. Enterotoxin was detected in all the treated samples except in 7% propionic acid. Therefore 7% was found effective for samples contaminated with 7 log cfu/g. It was concluded that propionic acid was highly effective in decontaminating meat surfaces and are shown to be safe, simple, efficient, and cheap which can be highly recommended for commercial applications for decontaminating of fish during drying.

SF OR 16

Progression of microbes associated with quality and safety of chill stored *Caranx melampygus*

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Fish, which is a good source of low calorie, high protein food with a range of health

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* $7\log_{10}\text{cfug}^{-1}$ 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 $\log_{10}$ cfu g^{-1} to 7.5 $\log_{10}$ cfu g^{-1}, 2.5 $\log_{10}$ cfu g^{-1} to 7.3 $\log_{10}$ cfu g^{-1}, 2 $\log_{10}$ cfu g^{-1} to 7.6 $\log_{10}$ cfug^{-1}, 2.5 $\log_{10}$ cfug^{-1} to 4.7 $\log_{10}$ cfu g^{-1}, 3.8 $\log_{10}$ cfu g^{-1} to 4.9 $\log_{10}$ cfu g^{-1}, 2 $\log_{10}$ cfu g^{-1} to 3.6 $\log_{10}$ 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.

SF OR 17

Genetic relationship of pathogenic V*ibrio 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