

ABSTRACT

In this dissertation the microbiology of shrimp processing in Sri Lanka was compared with poultry processing in the United Kingdom. Shrimp processing is a non-automated worker-oriented activity with a low throughput, while poultry processing is highly automated with a very high throughput rate.

The coliform counts of poultry were high (10^5 /g) as was the incidence of *Escherichia coli* in this product. The samples taken at all stages from after bleeding to after evisceration showed that coliform log counts decreased progressively from 6.8 to 5.3 which suggested an improvement in microbiological quality due to processing. Farm shrimp had very low coliform counts generally below 10^2 /g but they carried high numbers of *Vibrio*, usually in the product at harvest. The farm shrimp were also found to carry *Salmonella* in a few samples both raw and processed.

The isolates of *E.coli*, *Salmonella* and *Staphylococcus aureus* were characterised in order to differentiate them and allow points of cross-contamination to be detected in hazard analysis. *E.coli* counts were rarely detected in samples at the harvest but occasionally recovered from raw as well as cooked product in different stages of peeling at 3-10/g. Two samples of headless shell-on frozen shrimp, three samples of shrimp at the harvest and four samples at the receiving point of the factory also showed *Salmonella*. *S.aureus* was only isolated from all but one sample of cooked shrimp.

In general, isolates were identified and then compared by four techniques: (1) plasmid profiling (2) ribotyping (3) biochemical characteristics using API profiling (4) antibiotic resistance.

The high plasmid carriage rate of 152 (93%) isolates of *E.coli* allowed plasmid profiling to be used in recognising the sites of cross-contamination of poultry processing. The appearance of four new strains after scalding proved this to be the most important site of cross-contamination, with plucking of lesser importance in this regard. No new strains were detected after evisceration suggesting that it did not cause any cross-contamination during this study. One multiple plasmid-bearing strain was shown to be dominant at all stages of processing, since it represented at least 40% of isolates at each stage of processing.