

## Microbial Diversity and Succession Associated with Processing Waters at Different Broiler Processing Stages in an Abattoir

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### Abstract

**Introduction:** The high organic content of associated process water provides an alternative for low-cost and non-invasive sample collection. The diversity of bacteria in processing water indicates potential contamination along the slaughter process. This study investigates the association of microbial genetic diversity from the processing environment with the microbial genetic diversity of chicken meat.

**Methodology:** Water samples from scalders, defeathering, evisceration, carcass-washer, chillers, and post-chill carcass rinsate were collected from a largescale abattoir. Carcass rinsate and associated process water samples were serially diluted and incubated with growth media for *Campylobacter* spp. and *Escherichia coli*. DNA was also extracted from the water samples, and Illumina MiSeq was used to analyse the microbial communities.

**Results and Discussion:** The highest counts of *E. coli* and *Campylobacter* spp. were from water samples in the carcass washers and evisceration drains, while the lowest was on the post-chill carcass rinsate. The richness and evenness of bacteria communities increased from scalding through defeathering and evisceration to chilling, which revealed (i) potential contamination from feathers and gastro-intestinal content; (ii) cross-contamination within batches, and (iii) persistence of bacteria during carcass washing and chilling. Cluster analysis revealed that the abundance of bacteria in the defeathering tub is the best indicator of chicken carcass contamination. This indicates limited efficacy once the feather follicles have been contaminated after plucking.

**Conclusion:** The study concluded that the genetic diversity in processing water is effective in source-tracking contamination and can be used as an indicator to determine the final products' microbial quality and to estimate the safety and quality of chicken meat.

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