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The prevalence of bacterial contamination and microbial diversity using 16S rRNA gene sequencing, of commercial eggs from retail market in Scotland

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In this study, the aim was to describe bacterial diversity of table eggs using both culture and molecular approach. Total viable counts (TVCs) were obtained from shell and content of 88 commercial eggs in Scotland. Eggs from 3 different sources were sampled including organic farm (22 eggs), free range (33 eggs), and caged system (33 eggs). Free range eggs had higher TVCs isolated from eggshell, a mean of 5.5 logs CFU/eggshell, and 5.2 log (caged eggs) CFU/eggshell. Egg content ranged from 3 log (organic egg) to 2.4 log (caged egg) cfu/ml. ANOVA test showed no significant difference between the two variables TVCs and housing system for both eggshell, and content respectively ($p < 0.14$, 0.59). 59 bacterial isolates were genotyped by 16S rRNA sequencing. The results obtained indicate large number of eggs inspected was contaminated with *Staphylococcus* bacteria. Among the bacterial strains isolated (59 in total), *Staphylococcus equorum* was the most occurring strain (32%), followed by *Micrococcus luteus* (17%), and rest of the sequences were less than (10%). No evidence was found for presence of *Salmonella*, *Escherichia coli*, *Campylobacter*, *Listeria monocytogenes*, or *Clostridium perfringens*. The proportion of Gram-positive bacteria was significantly higher than Gram-negative bacteria ($p < 0.05$). It can be concluded that table eggs sold in Edinburgh's groceries were of good quality for human consumption.

Biography

Mohammed Alawi is a PhD student in Heriot-Watt University in School of Life Science Department of Microbiology.

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