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The Use of Pyrosequencing to Analyze Microbial Populations in Poultry Management to Minimize Downstream Food Contamination [Abstract]

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The Use of Pyrosequencing to Analyze Microbial Populations in Poultry Management to Minimize Downstream Food Contamination [Abstract]

The use of antibiotics in animals grown for human consumption has been banned in many parts of the world and is becoming less favorable in the US. With less or no antibiotics fed, the risk of microbial contamination of food is higher when processed. In the current study, the objective was to identify and compare the effect of both ceca and litter microbial communities present before and after treatment. The treatments consisted of 1) challenging newborn chicks at 3 days and then again at 38 days with either *Salmonella enteritidis* or *Campylobacter jejuni* or no bacteria in the presence of or without probiotics added to the feed and 2) windrow composting or no composting of litter as part of poultry house management. Aseptically ceca and litter samples were collected and stored at 4°C until processed. Bacterial genomic DNA was isolated from both sets of samples using either the Promega SV Wizard Genomic DNA Purification kit (Ceca) or Zymo-spin soil microbe DNA midiprep kit (litter). The DNA from each sample was then amplified using 16s universal forward and reverse primers containing the specific Roche defined library-L specific sequences as well as Multiplex Identifiers (MID) to allow for automated software identification of the samples after pooling, multiplexing and sequencing. We report the bioinformatic pipeline and the microbial distributions at the genus and species level for each treatment. Pyrosequencing can be used to obtain valid comparisons between effects of various treatments on pathogenic versus beneficial bacteria in growth and management of animals used for human consumption.