with mCCDA (1/37, 2.7%; P < 0.0001). However, there was no statistical difference between enrichment of samples for either 24 h or 48 h. The majority of strains isolated were identified as C. jejuni, while C. coli was found only in 2 samples. Moreover, all contaminant strains analyzed were recovered from cultures plated onto mCCDA and were phenotypically characterized as Proteus mirabilis. This study suggests that enrichment in Bolton broth for 24 h following plating onto PA not only allows shorter and reliable isolation of thermophilic Campylobacter from chicken, but also avoids P. mirabilis spreading. Yet, further studies are still needed to validate this culture-based protocol.

Key Words: Campylobacter jejuni, Proteus mirabilis, selective culturing, food safety

494P Cheap extraction of bioactive compounds of berry pomace and their mode of action against Campylobacter jejuni. S. Salaheen*, C. Nguyen, D. Hewes, and D. Biswas, University of Maryland, College Park, MD.

Berries are rich in several phytochemicals such as phenolic acids, proanthocyanidins, anthocyanins and other flavonoids and these compounds exhibit a wide range of biological effects including antioxidant, antimicrobial, anti-inflammatory and vasodilator. This study was designed to develop economically feasible bioactive extracts from the extremely cheap byproducts of blackberry and blueberry known as pomace and evaluate their effective roles in reduction of Campylobacter jejuni colonization in poultry gut. Different ratios of ethanol and water were used as solvents for phenolic extraction from berry pomaces. The extracts were then used to test their roles in inhibition and host cell-C. jejuni interactions using cell culture model. Our results indicated that 0.6 mg GAE/mL of blackberry or blueberry pomace extracts reduced the growth of C. jejuni significantly (P < 0.05) at 24 h. These bioactive extracts also altered the physicochemical properties of C. jejuni such as cell surface hydrophobicity and autoaggregation of this bacterial pathogen. Swimming and swarming motility were reduced by 85 to 90% and 30 to 40% due to exposure to blackberry and blueberry pomace extracts, respectively. qRT-PCR data suggested that blackberry pomace extract induced the expression of C. jejuni virulence gene flaA (flagellar filament-A) by 3- to 5-fold. Moreover, attachment of C. jejuni to chicken fibroblast cells (DF1) was reduced by ~30–40% in the presence of berry pomace extracts. These findings suggest that bioactive extracts of both blackberry and blueberry pomaces might be effective feed additive or water supplement in reducing C. jejuni shedding and its cross-contamination into poultry and poultry products.

Key Words: pomace, Campylobacter jejuni, phytochemical

495P Evaluation of methods and plating media for detection of Campylobacter in ceca from 66 different broiler flocks across 11 months. M. E. Berrang, N. A. Cox, R. J. Meinersmann, B. B. Oakley, and D. E. Cosby*, USDA-ARS Russell Research Center, Athens, GA.

Due to high numbers of other bacteria, detecting Campylobacter in cecal contents can be challenging. On each of 66 sample days from April 2013 through February 2014, a single cecum was collected from a commercial broiler evisceration line. Cecal contents were expressed, diluted, blended and plated on each of 3 different media: Campy-cefex agar (CCA), Campy-Line agar (CLA) and RF Campylobacter jejuni/C. coli chromogenic agar (RFCA). Each plating medium was inoculated using 2 methods: directly onto agar or through a 0.45 μm nitrocellulose filter laid on the agar surface and removed once all liquid had passed through. Because of a high number of non-Campylobacter background colonies on media without filters, counting Campylobacter colonies was not always possible. Therefore plates were scored categorically by a single observer where 0 indicated no colonies and 1, 2 and 3 were assigned for low to high numbers of Campylobacter; a second score was assigned in the same way for numbers of non-Campylobacter colonies. Campylobacter was detected in 32 of 66 flocks (48.5%). Campylobacter was detected in each month and on all media. CCA plates had more non-Campylobacter background growth than the other plates (mean count score of 2.86), making observation of characteristic colonies difficult. RFCA and CLA both had lower average count scores for number of background colonies (1.86 and 2.00 respectively). RFCA scored highest on detection of Campylobacter colonies with a mean count score of 1.14 compared with 0.43 for both CCA and CLA. Filter use was completely effective for control of non-Campylobacter background colonies. Zero non-Campylobacter colonies were detected from any filtered sample regardless of medium. Likewise, plating medium did not affect detection of Campylobacter colonies from filtered samples; the mean Campylobacter colony count score from each medium was 1.00. In general, RFCA performed better than CCA and CLA for detection of Campylobacter from cecal samples. However, the filter method was the most effective means tested for control of non-Campylobacter background colonies regardless of medium used.

Key Words: Campylobacter, broiler ceca, plating media, detection method

496P Diversity of Campylobacter jejuni strains from broiler chicken farms in Brazil. C. S. L. Vaz*[1], D. Voss-Rech[1], J. S. Pozza[2], and G. L. Mattos[1], [1]Embrapa-Brazilian Agricultural Research Corporation, Concordia, SC, Brazil, Concordia, SC, Brazil, [2]Universidade do Contestado, Concordia, SC, Brazil.

Broilers are a potential reservoir for Campylobacter jejuni strains, which are responsible for the majority of human campylobacteriosis cases. Currently there are no fully effective strategies to prevent broilers of C. jejuni colonization. However, subtyping of strains might offer further insight in Campylobacter epidemiology at farm level. This study aimed to evaluate the genotypic patterns of C. jejuni isolated from broiler flocks. A total of 178 strains obtained from 2010 to 2011 were analyzed. Strains were isolated from cloacal swabs, feces, drag swabs, litter, darkling beetles (Alphitobius diaperinus) and drinking water taken from 23 broiler flocks in 4 Brazilian broiler producing companies. Whole DNA from C. jejuni strains was digested by SmaI followed by pulsed-field gel electrophoresis analysis (PFGE). Similarity of PFGE profiles was calculated by the Dice coefficient and a dendrogram was generated by cluster analysis using the unweighted pair group method with arithmetic averages. C. jejuni ssp. jejuni ATCC 33560 and Arcobacter skirrowii ATCC 51132 strains were used as controls. In total, 33 PFGE profiles could be distinguished within the C. jejuni isolates analyzed. Distinct patterns were found in the control strains. Furthermore, only one PFGE profile was shared by strains from 2 broiler companies, whereas the remaining genotypes comprised profiles unique to each given broiler producing company. Interestingly, the majority of strains isolated from Alphitobius diaperinus showed 100% similarity to the strains isolated from broilers in the flock, which may indicate a particular significance of darkling beetles as vectors and reservoir of C. jejuni in broiler houses. Although broiler flocks were colonized by a variety of C. jejuni strains, the predominance of unique genotypes in each studied broiler producing company suggests that particular sources might be involved on the transmission of C. jejuni in broiler farms.

Key Words: Campylobacter, PFGE, food safety, Alphitobius diaperinus