Outbreak of Salmonella enterica serovar Typhimurium phage type DT41 in Danish poultry production - DTU Orbit (28/09/2019)

Salmonella enterica subspecies enterica serovar Typhimurium (S. Typhimurium) is one of the most prevalent serovars in Europe - where both poultry and poultry related products are common sources of human salmonellosis. Due to efficient control programs, the prevalence of S. Typhimurium in Danish poultry production is very low. Despite this, during the past decades there has been a reoccurring problem with infections with S. Typhimurium phage type DT41 in the Danish poultry production without identifying a clear source. In the end of 2013 and beginning of 2014 an increased isolation of S. Typhimurium DT41 was noted mainly in this production, but also in other samples. To investigate this is in more detail, 47 isolates from egg layers (n = 5, 1 flock), broilers (n = 33, 13 flocks), broiler breeding flocks and hatches (n = 5; 2 flocks and 1 environmental hatchery sample), feed (n = 1), poultry slaughter house (n = 3, environmental sample and meat) were typed with multi locus variable number of tandem repeat analysis (MLVA) and pulsed-field gel electrophoresis (PFGE) to investigate the epidemiology of the outbreak. Based on PFGE results isolates were divided into four groups (Simpson's index of diversity (DI) = 0.24 ± 0.15). Due to the low DI, PFGE was not sufficient to provide information to unravel the outbreak. Based on MLVA typing the DT41 - (42/47 isolates) and the RDNC isolates (5/47) were split into nine groups (DI = 0.65 ± 0.14). When a maximum divergence at one locus was permitted these could be gathered into four groups. Using this criterion, combined with epidemiological information, a spread of one type from broiler breeders to broilers and further to the poultry slaughter house was plausible. In conclusion, although it could be concluded that a spread within the broiler production pyramid had taken place the source of the sudden increase of S. Typhimurium DT41 remains unclear. To investigate this in more detail, further studies using whole genome sequencing to obtain a higher discriminatory strength and including isolates from a longer period of time and from various sources are in progress.

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