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Molecular typing and epidemiology of *Salmonella* ser. Typhimurium phage type DT41 in Danish poultry production in 2013.

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Worldwide, *Salmonella* causes many food borne outbreaks every year as it is easily spread to humans via the food production chain. *Salmonella enterica* serovar Typhimurium phage type DT41 has previously been isolated from broiler breeder flocks in Denmark where older poultry in particular was infected. However, in the final quarter of 2013 an increase in *S*. Typhimurium DT41 was observed in Danish poultry production. Some flocks were from farms that had previously been infected with DT41. However, some flock farms have not been registered with earlier occurrences of DT41 as far as records go back (2005). To further study the epidemiology and identify possible sources of the outbreak, forty-one isolates from both egg producers (n=8), broilers and broiler breeder flocks (n=29), but also a feed pellet sample (n=1), hatches (n=1) and fresh meat (n=2) were characterized further by phage typing and multi locus variable number of tandem repeat analysis (MLVA).

Thirty-eight isolates were found to belong to phage type 41 and for three isolates the phage type could not be determined (RDNC) but was epidemiologically linked. Based on the MLVA type the isolates were split into 8 types. When a maximum divergence at one locus was permitted these could be gathered into four groups. One group of MLVA types was identified in the production chain from broiler breeder to broilers and fresh meat. Another group represented consumer eggs and broilers, and based on epidemiological data it could be concluded that spreading between flocks had occurred. Thus, the outbreak was complex with no unambiguous pattern.

The source of the newly introductions remain unclear. However, further studies are in progress using whole genome sequencing and pulsed-field gel electrophoresis to investigate this in more detail. Furthermore, *in vivo* and *in vitro* stability of the outbreak isolates will be evaluated.