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Molecular typing and epidemiology of *Salmonella* serovar Typhimurium phage type 41 (DT41) in Danish poultry production in 2013/2014

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**Aim**
- To study the epidemiology and identify possible sources of an outbreak of *Salmonella enterica* serovar Typhimurium phage type DT41 in Danish poultry in 2013-2014
- Evaluate different typing methods in outbreak detection

**Introduction**

Surveillance of *Salmonella* in the poultry industry is essential to increase food safety. Previously, *Salmonella* Typhimurium DT41 has been isolated from broiler breeder flocks in Denmark, particularly in older poultry flocks [1]. In the final quarter of 2013 an increase in DT41 cases was observed in the Danish poultry production [2]. At some of these farms DT41 had previously been found, but for others no records of such has been identified during the past ten years.

**Results**

**Phage typing:**
- 42 isolates were DT41 (Figure 1)
- 5 isolates reacted but did not confirm with any phagetype pattern (RDNC). Epidemiological link with DT41 isolates

**PFGE typing:**
- Four different profiles (Figure 1).
- DI was 0.24

**MLVA typing:**
- Nine profiles
  - If a maximum divergence at one locus was permitted, isolates could be divided into four groups (Figure 1, marked in grey)
  - DI was 0.65

**Discussion**

Based on these results along with epidemiological data it could be concluded that spreading between flocks had occurred, making the outbreak very complex with no distinct pattern. One MLVA profile was identified through the whole production pyramid – from broiler breeder flocks to broilers and in meat sample at slaughter house. If isolates only were phage – and PFGE typed it would appear as though the feed isolate was closely related to the other isolates. However, when taking the MLVA profile into account, there was a difference of three loci to the closest relation. The source of the introductions of DT41 remains unclear. However, further studies are in progress using whole genome sequencing to increase the discriminatory strength, hopefully enabling clarification of the epidemiology.

**Conclusion**

- *Salmonella* serovar Typhimurium DT41 was spread through the production pyramide, but also new introductions had occurred
- Use of more discriminatory typing methods is needed to enable identification of the source

**Materials and Methods**

- Forty-seven Danish *Salmonella* Typhimurium isolates from 2013 and 2014
  - Egg layers (n=5), broilers and broiler breeding flocks (n=37), feed (n=1), hatches (n=1), slaughter house (n=1), meat at slaughter house (n=2)

**References**

2. Anon 2014 Annual Report on Zoonoses in Denmark 2013, National Food Institute, Technical University of Denmark
3. Anderson 1977 J Hyg. (Lond) 78: 297-300