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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 breeding 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 pyramid, but also new introductions had occurred
- Use of more discriminatory typing methods is needed to enable identification of the source

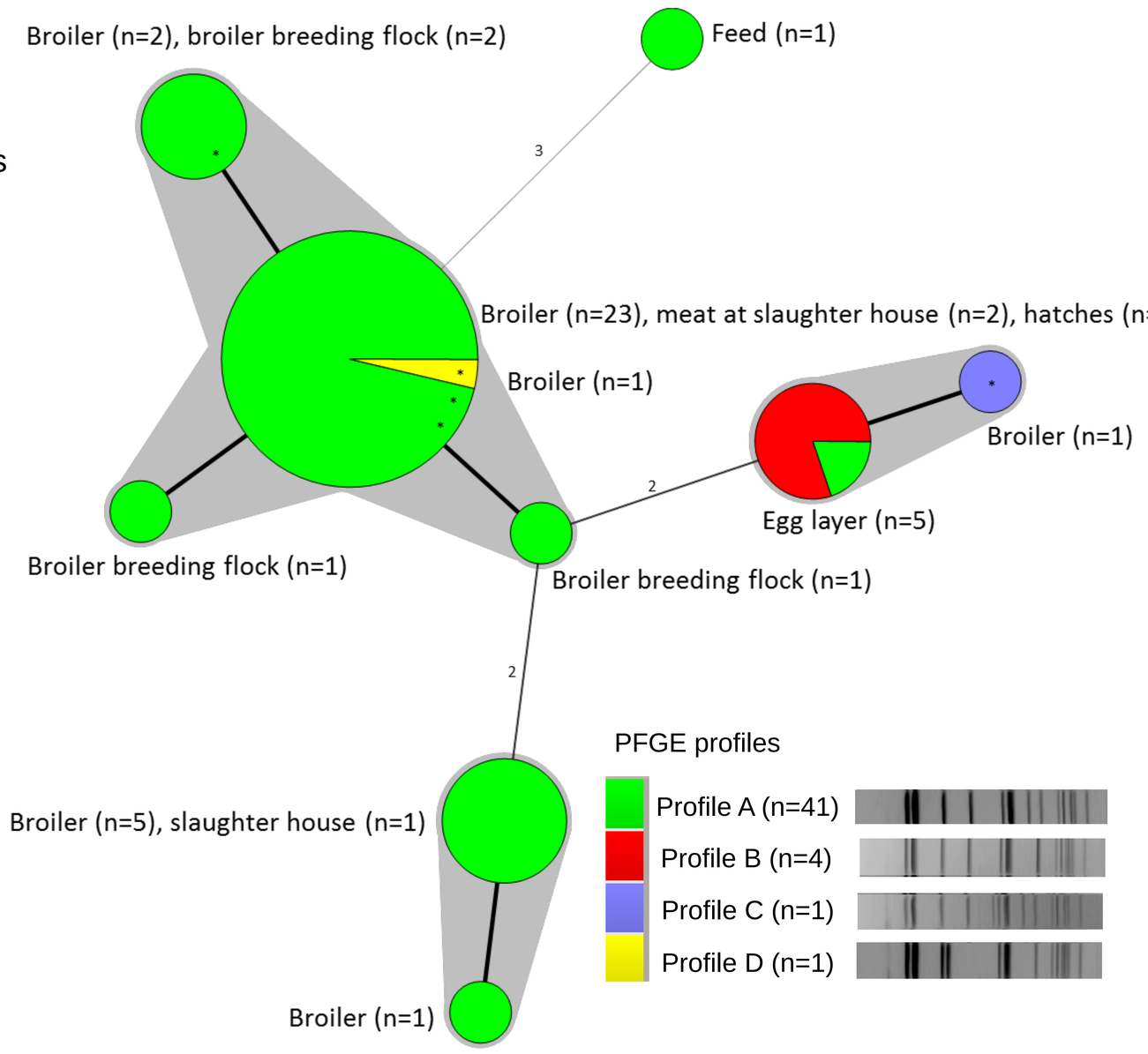

Figure 1:
DT41 isolates divided by MLVA profile, and colored based on PFGE profile. Stars indicate RDNC isolates. Partitioning is based on a maximum divergence of one locus with MLVA (Marked in grey). The sample source for each group is shown next to each circle.

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)
- Phage typing [3], pulsed-field gel electrophoresis (PFGE) [4], multi locus variable number of tandem repeat analysis (MLVA) [5].
- Data analysed and minimum spanning tree construction in Bionumerics v. 7.1 (Applied Maths)
- Discriminatory strength was evaluated by calculating Simpson's index of diversity (DI) [6]

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