

Genetic clusters and circulation of *Salmonella* Dublin in Jutland



Leonardo V. de Knegt¹, Egle Kudirkienė¹, Gitte Sørensen², Liza R. Nielsen¹, John E. Olsen¹

¹ Department of Veterinary and Animal Sciences, University of Copenhagen, Denmark, leonardo@sund.ku.dk

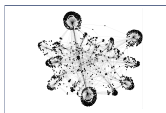
² National Food Institute, Technical University of Denmark / Statens Serum Institut, Denmark

BACKGROUND

2002: Danish *S. Dublin* surveillance program
2007: National eradication programme initiated
2010: Enforced trade restrictions in legislation
2013: Mandatory control and strict trade restrictions

CHALLENGE

Continued circulation of *S. Dublin*, but cattle movements too intricate to detect clear circulation patterns based on existing data. Many herds interconnected by 1st or 2nd or higher degree contacts



OBJECTIVE

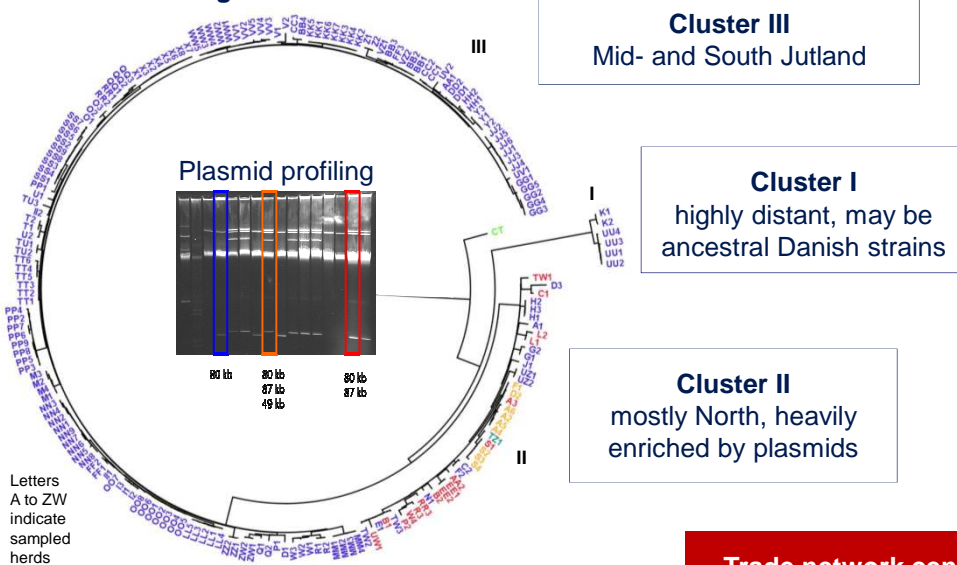
To use whole genome sequencing (WGS) to improve the understanding of strain circulation between herds

METHODS

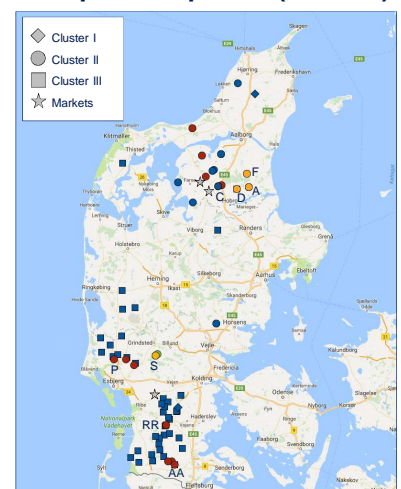
- *S. Dublin*: 197 isolates from 58 herds 1996 to 2016
- Sequencing: MiSeq 250 bp pair-end
- Assembly/Annotation: SPADes 3.9.1./Prokka 1.0
- Population structure analysis: CSI Phylogeny
- Genome content analysis: Roary/Scoary
- Movement of cattle between herds since 1994: from Danish Cattle Database

RESULTS

Core genome clusters



Location of herds by cluster and plasmid profile (colours)



Example of movement network

