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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

Cluster III
Mid- and South Jutland

Cluster I
highly distant, may be ancestral Danish strains

Cluster II
mostly North, heavily enriched by plasmids

Plasmid sharing highlights non-visible contacts between genomically different or trade-isolated herds

Location of herds by cluster and plasmid profile (colours)

Trade network centered around markets

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