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Published in:
Annual Report on Zoonoses in Denmark 2013

Publication date:
2014

Document Version
Publisher's PDF, also known as Version of record

Molecular serotyping of *Salmonella* isolates

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Serotyping is the standard method for subtyping *Salmonella* and information about serotypes is pivotal for understanding the epidemiology of *Salmonella*. Serotyping is done by slide agglutination using specific antisera that detects differences on cell surface structures: Somatic (O) lipopolysaccharides and flagellar antigens (H). Some *Salmonella* strains, particularly from non-human sources, autoagglutinate (exhibit a rough phenotype) when typed by traditional slide agglutination. This feature is associated with the loss of the outer membrane, which changes the hydrophobicity of the bacteria. Therefore serotyping by agglutination cannot be performed on such isolates and this causes data gaps, when subtyping data is needed, e.g. for *Salmonella* source attribution. To overcome this obstacle, serotypes can instead be determined on DNA level, i.e. by determining the presence of genes encoding the O and H antigens using molecular serotyping.

During 2012 a molecular DNA based serotyping method was implemented at the National Food Institute, Technical University of Denmark, and during 2013 this method was used as a supplement to the traditional serotyping based on agglutination. The DNA based molecular method detects genes mediating the corresponding O and H antigens and thus it is based on the White-Kauffmann-Le Minor scheme. The assay is a multiplex bead-based suspension array based on the Luminex xTAG technology and detects the major O groups and H antigens [1, 2]. It can directly identify the most important serovars of *Salmonella*, but in some cases there is a need to supplement the DNA based data with additional slide agglutination tests. DNA based molecular serotypning has proved to be a valuable tool in the routine typing of *Salmonella*, and further the method enables serotyping of rough isolates.

The possibility to serotype rough isolates was utilized in a study of rough *Salmonella* isolates from pig carcasses obtained in the national surveillance program for fresh meat. A total of 211 rough strains isolated during the period 2005-2012 were analyzed using molecular serotypning. The typing enabled serovar identification of 168 of the strains (80%). The identified serotypes were Typhimurium (n=92; 44% of the 211 strains), Derby (n=40; 19%), 4,[5],12:i:- (n=22; 10%), Infantis (n=8; 4%) and others (n=6; 3%). Serotyping results for strains isolated during the same years from pig carcasses, where traditional serotyping was possible (smooth strains) (n=1,233) showed a similar serovar pattern, where Typhimurium (n=547; 44%), Derby (n=399; 32%) and 4,[5],12:i:- (n=72; 6%) also were the most commonly identified serotypes. Studies are in progress to serotype the remaining 43 rough strains that could not be typed in the first approach, using other DNA based techniques to further assess the difference in results between molecular and traditional serotyping. In conclusion, our preliminary data suggests that molecular serotyping of rough *Salmonella* strains mirror the serotypes obtained using traditional serotyping for smooth strains.

References

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