GENOTYPIC CHARACTERIZATION OF A MONOPHASIC VARIANT OF SALMONELLA ENTERICA SEROTYPE TYPHIMURIUM IN SWINE IN USA MIDWEST

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Abstract

Background

Non-typhoidal Salmonella enterica are a major human foodborne pathogens worldwide (Kirk et al., 2015). Salmonella enterica is divided into six subspecies and approximately 2,500 serotypes according to the Kauffmann-White scheme (Brenner et al., 2000). Serotype 4,5,12:i:-, a monophasic variant of S. Typhimurium lacking the 2nd phase flagellar antigen. Salmonella 4,5,12:i:- has emerged globally in both humans and animals (Echeita et al., 2001; Switt et al., 2009; Centers for Disease Control and Prevention (CDC), 2013) and pork products and pigs are implicated as important sources of human infections (Mossong et al., 2007; Hauser et al., 2010).

Distinct clades of S. 4,5,12:i:- of apparently separate S. Typhimurium ancestry were previously characterized in Europe and USA, (Soyer et al., 2009). The existence of distinct clades was supported by different phenotypic antimicrobial resistance patterns: USA isolates were generally susceptible to antimicrobials while European isolates demonstrated multidrug resistance to tetracycline, ampicillin, sulphonamides and streptomycin (Mossong et al., 2007; Switt et al., 2009; Hauser et al., 2010).

Numerous European S. 4,5,12:i:- strains have been genotypically characterized, but to date the genotypic characteristics and ancestry of USA strains is not well documented. Whole genome sequencing (WGS) was used to characterize and compare S. 4,5,12:i:- collected from swine in the USA Midwest with S. Typhimurium from this region and with S. 4,5,12:i:- isolates from other locations in the USA and Europe.

Methods

Maximum likelihood phylogenetic trees were constructed using the WGS reads of S. 4,5,12:i:- collected from swine in the Midwest with S. Typhimurium collected from livestock in the Midwest and with S. 4,5,12:i:- collected from different sources (i.e. human, animal and environment) in Europe and USA. The presence of resistance genes was determined using multiple BLAST searches.

Results

In the first part of the analysis, we found that the S. 4,5,12:i:- collected from swine in the Midwest were located in a distinct clade from the majority of the S. Typhimurium collected from livestock in the Midwest. In the second part of the analysis, we found
that S. 4,5,12:i:- isolates from Europe and USA were located in two main clades, regardless of their origin. In addition, the majority of the isolates collected during 2014-2016 (84%), including all swine samples, belonged to an “emerging” clade. Most (80%) of the isolates in this clade demonstrated multidrug resistance including resistance to tetracycline, ampicillin, sulphonamides and streptomycin.

Conclusions

This study results suggest that the S. 4,5,12:i:- found in swine in the USA Midwest did not originate from livestock S. Typhimurium isolates in the USA Midwest. This local clade belongs to a globally multidrug resistance clade. The occurrence of multidrug resistance to multiple antimicrobial classes in these isolates is of concern.

References


