Reappearance of Salmonella serovar Choleraesuis var. Kunzendorf in Danish pig herds

Salmonella enterica serovar Choleraesuis is a porcine adapted serovar which may cause serious outbreaks in pigs. Here we describe outbreaks of salmonellosis due to S. Choleraesuis in four Danish pig farms in 2012–2013 by clinic, serology, and microbiology and compare the isolates to those of a previous outbreak in 1999–2000. The infection was in some herds associated with high mortality and a moderate to high sero-prevalence was found. In 2012–2013 the disease contributed to increased mortality but occurred concomitant with other disease problems in the herds, which likely delayed the diagnosis by up to several months. Nine isolates from the four farms in 2012–2013 and 14 isolates obtained from the outbreak in Denmark in 1999–2000 were subjected to typing using pulsed-field gel electrophoresis (PFGE). Seven isolates were selected for whole genome sequencing (WGS). The PFGE results of 23 isolates displayed five different profiles. The isolates from 2012 to 2013 revealed two distinct profiles, both different from the isolates recovered in 1999–2000. Two of the 2012–2013 farms shared PFGE profiles and had also transported pigs between them. The profile found in the two other 2012–2013 farms was indistinguishable but no epidemiological connection between these farms was found. Analysis of the number of single nucleotide polymorphisms (SNPs) from the WGS data indicated that the isolates from the farms in 2012–2013 were more closely related to each other than to isolates from the outbreak in 1999. It was therefore concluded that the infection was a new introduction and not a persistent infection since the outbreak in 1999. It may further be suggested that there were two or three independent rather than a single introduction. The re-introduction of S. Choleraesuis in Denmark emphasizes the importance of strict hygiene measures in the herds. Further investigations using WGS are now in progress on a larger collection of isolates to study clonality at European level and trace the origin of the infections.

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