Virulence associated factors, antimicrobial resistance, and in silico serotyping of Streptococcus suis
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Background
Streptococcus suis is a common cause of disease in pigs with a significant economic impact on swine production, due to decreased performance and mortality as well as increasing antimicrobial resistance (AMR) associated with S. suis. Factors related to host, environment, and bacteria may play a role in the development of S. suis disease. Although several virulence-associated factors (VAF) including capsular polysaccharide (CPS), muramidase-released protein (MRP), extracellular protein factor (EPF), and suilysin (SLY) have been suggested to be involved in S. suis pathogenesis, the actual involvement of many VAFs in S. suis disease development remains controversial. Three key VAFs (EPF, SLY and MRP) have been characterized as important for virulence in serotype 2 isolates; however, virulent S. suis strains which do not produce or carry genes encoding these proteins are regularly reported in literature. The objective of this study was to describe the distribution of serotypes, VAF and AMR genes in S. suis isolates recovered from systemic (blood, meninges) and non-systemic (tonsil, rectum) sites of sick and healthy pigs using whole genome sequencing (WGS).

Materials and methods
In total, 273 S. suis isolates- recovered from 112 nursery pigs (47 isolates from systemic and 136 from non-systemic sites of 65 sick pigs; 90 isolates from non-systemic sites of 47 healthy pigs) on 17 Ontario farms between 2013 and 2018- were studied. The isolates were grouped into four different categories: Systemic-confirmed (SC), Non-systemic-confirmed (NSC), Non-systemic-probable (NSP) and Non-systemic-healthy (NSH). The SC (n=47) and NSC (n=65) isolates were recovered from systemic and non-systemic sites of 32 pigs, respectively, that were both symptomatic and confirmed to have S. suis recovered from at least one systemic site. The NSP (n=71) isolates were obtained from 33 non-systemic sites of symptomatic pigs, for which S. suis was not recovered from any systemic site. The NSH isolates (n=90) were recovered from 47 healthy pigs. All isolates were subjected to WGS and serotyped in silico using WGS data.

Results
Using in silico typing, 21 serotypes were identified with serotypes 9 (13.9%) and 2 (8.4%) as the most frequent serotypes, while 53 (19.4%) isolates remained untypeable. There were significant differences in the serotyping results by PCR and in silico serotyping (p < 0.001). Most of the PCR-untypable isolates were re-classified to serotype 9 (9%, 8/87,) and 21 (10%, 9/87). The relative frequency of VAF genes in isolates from systemic (p < 0.001) and non-systemic (p < 0.001) sites in sick pigs was higher compared to isolates from non-systemic sites in healthy pigs. Although many VAF genes were abundant in all isolates, three genes including dltA (p < 0.001), luxS (p = 0.01) and traA (p = 0.02) were more prevalent in isolates recovered from systemic sites compared to non-systemic sites of pigs. None of the serotype 2 isolates carried efp or sly genes. Furthermore, all the serotype 9 isolates except for one mrp+ isolate belonged to the mrp-sly-epf– genotype. Overall, 62% (168/273) of the total isolates, 58% (106/183) of SC, NSC and NSP isolates collectively, and 69% (62/90) of NSH isolates- belonged to the mrp-sly-epf – genotype. Among the isolates, 98% had at least one AMR gene and 79% had genes associated with at least four drug classes. The most frequently detected AMR genes were tetO conferring resistance to tetracycline, and ermB conferring resistance to macrolide, lincosamide and streptogramin (MLS).

Conclusion
In silico typing can improve the classification of S. suis. Further, VAFs were determined to be more prevalent in isolates recovered from pigs with clinical signs of S. suis infections. However, the wide distribution of VAFs genes in S. suis isolates in this study suggests that other host and environmental factors may contribute to S. suis disease development. In fact, the VAFs may not be the direct cause of S. suis disease but it is likely that their presence increases the likelihood of disease development under certain circumstances. The high frequency of AMR genes within the isolates poses problems not only within the swine industry but also in public health.

Source: