

What: Follow-up communication concerning recent case series of high mortality in US assembly yards caused by *Streptococcus equi* subsp *zoepidemicus*.

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Subject: Genetic analysis of *Streptococcus equi* subsp *zoepidemicus* from US cases and archives

Streptococcus equi subsp. *zoepidemicus* (*S. zoepidemicus*) was isolated from two recent cases of high sow and feeder pig mortality (~ 30 – 50% mortality in affected groups) in US assembly yards (Oct 2019).

This organism is a sporadic cause of disease in multiple animal species, but has rarely been associated with disease outbreaks in US swine.

Previous communique: <https://www.swinehealth.org/wp-content/uploads/2019/10/Streptococcus-equi-ssp-zoepidemicus-as-cause-of-high-mortality-of-swine-in-assembly-yards-10-8-2019.pdf>

Previously genetic analyses of *S. zoepidemicus* suggests there are at least seven variants (types). Most isolates are from equine, occasionally canine, and are sporadically isolated from many other animal species and humans.

Phylogenetic analyses based on *szP* single gene sequence and maximum common genome sequences are used to differentiate strains of *S. zoepidemicus*. Gene *szP* sequences from over 70 isolates and genome sequences of more than 30 strains worldwide, including sequences from the two recent cases of high mortality in the US assembly yards, were compared (summarized in Figure 1). In both phylogenetic analyses, the recent US strains are strikingly similar to the ATCC strain isolated from swine outbreak(s) of high mortality in China in the mid-1970s that reportedly involved the loss of more than 300,000 pigs^(1, 2). The swine isolates from the recent cases of high mortality in US assembly yards are tightly clustered within type 6 based on the *szP* sequence clustering, and are more distantly related to other isolates in this cluster and the other six Types based on maximum common genome sequences.

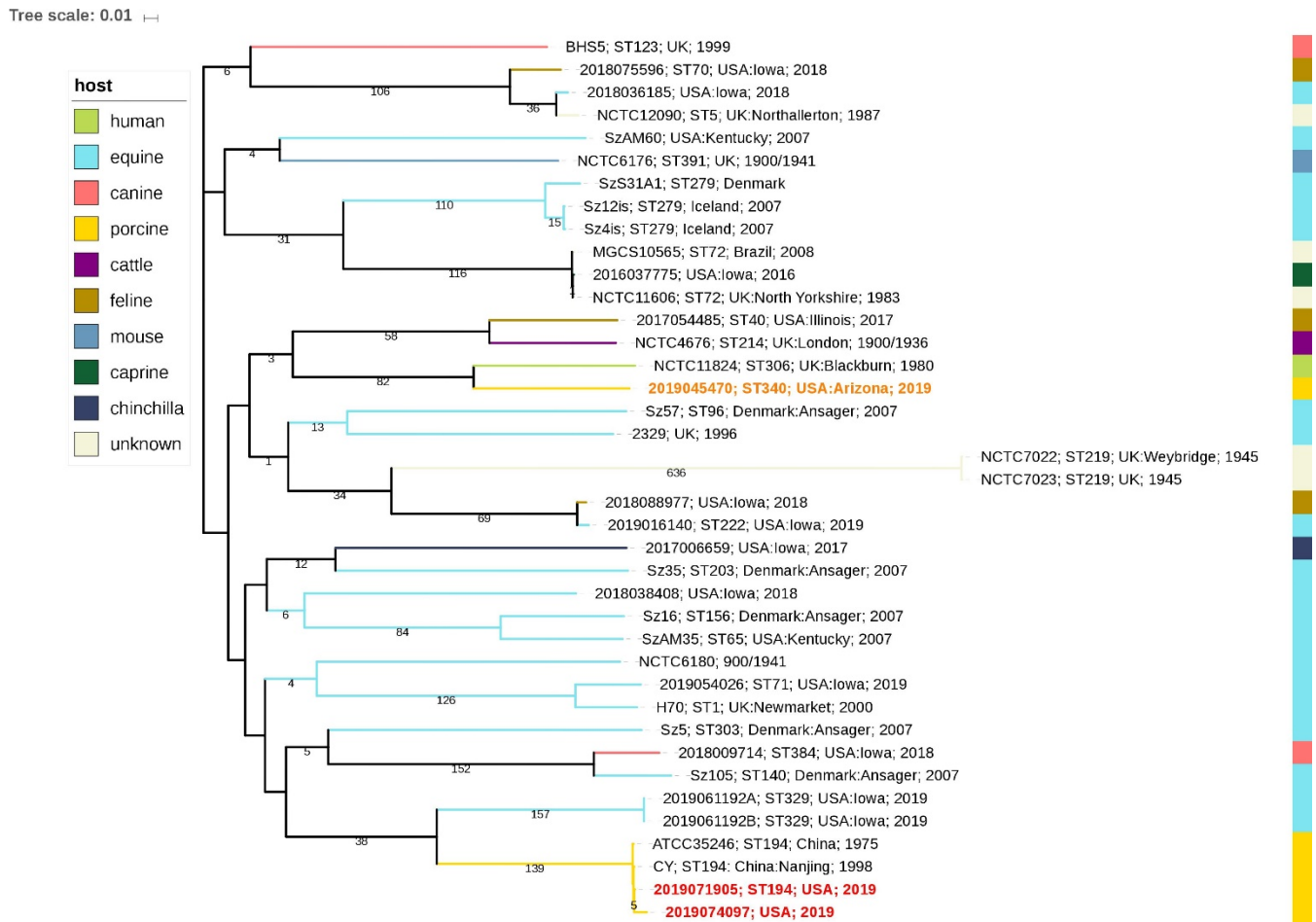
In short, these further characterization results suggest these recent case series for US assembly yards were related and caused by the same variant of *S. zoepidemicus*. Previous isolations of *S. zoepidemicus* from clinical ill pigs have been rather limited in the US (e.g., only 6 isolations from cases over past 10 years at ISU VDL). Thus, there is minimal information concerning the novelty of this particular variant of *S. zoepidemicus*, as compared to past findings in US swine.

An observation of elevated swine mortalities in western Canadian assembly yards due to *S. zoepidemicus* was reported in the second quarter of 2019. (Canadian West Swine Health Intelligence Network). More recently, M Costa reported an incident of elevated mortality and abortions caused by *S. zoepidemicus* in four related commercial sow farms located in Manitoba, Canada in April 2019⁽³⁾. The *S. zoepidemicus* isolate from the case series involving the four commercial sow farms in Manitoba was also reported to be genetically similar to the aforementioned ATCC strain of *S. zoepidemicus* associated with the high swine mortality event in Sichuan province in China in the 1970's⁽³⁾.

Awareness should reinforce biosecurity efforts, particularly related to transport and collection points.

Further study is needed to better understand the relevance and prevalence of *S. zoepidemicus* in North American swine.

Figure 1: Phylogenetic tree of 38 *S. zooepidemicus* strains based on maximum common genome sequence



*The isolates from the two recent cases of high mortality in US assembly yards strains are marked in red, and all isolates are identified by country of origin and year isolated.

Reference

1. Feng ZG, Hu JS: Outbreak of swine streptococcosis in Sichan province and identification of pathogen. Anim Husbandry Vet Med Lett. 1977, 2: 7-12
2. Liu PH, Shen FS, Wang YK, Zhang SH: Identification of swine Streptococcus isolates in Shanghai. Chin J Vet Med. 2001, 21: 42-46
3. Costa M O., Lage B.: *Streptococcus equi* subsps. *zooepidemicus* associated with sudden death of swine in North America. bioRxiv. October, 2019. <http://dx.doi.org/10.1101/812636>