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## Characterisation of *S. equi* strains by whole genome sequencing isolated from 2016 to 2019 in France

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## 19 | Argentinian *Streptococcus equi* subsp. *equi* isolates clustered in the same group according to cgMLST

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**Background:** Strangles is a worldwide infectious disease that affects the upper respiratory tract of horses and is caused by *Streptococcus equi* subsp. *equi* (*S. equi*). Recently, a high number of *S. equi* isolates obtained from 19 countries were analysed using the Pathogenwatch core genome Multilocus Sequence Typing (cgMLST) web bioresource. All of the isolates recovered from Argentina (n=15) belonged to the same cluster and were closely related to a limited number of isolates from the United Kingdom and the United Arab Emirates.

**Objective:** To study genome diversity among Argentinian *S. equi* isolates and define their epidemiological relationships.

**Study design:** Epidemiological investigation using genomic analysis.

**Methods:** Genomic DNA from 44 isolates of *S. equi* were sequenced on a NextSeq 500 sequencer system (Illumina) and analysed within Pathogenwatch alongside the 15 previously described Argentinian *S. equi* genomes and the genome of strain 4047, which was included as a reference. The dendrogram was reconstructed from pairwise cgMLST scores using the APE package.

**Results:** Argentinian genomes were closely related and differentiated into three clusters. The *S. equi* 4047 genome was an outlier. Most of the isolates recovered from the same outbreak were closely related with some exceptions: UBA21Gd (*seM*-131) and UBA22Gd (*seM*-132) strains isolated from Daireaux in 2012 and UBA27Gd (*seM*-135) and UBA28Gd (*seM*-135) strains isolated from Trenque Lauquen in 2012. All of the isolates obtained from carriers during 2013 clustered in the same group. The strain UBA8Md that was isolated from a guttural pouch empyema belonged to a different cluster.

**Main limitations:** Further outbreak investigation and genome sequencing will strengthen the dataset.

**Conclusions:** Although *S. equi* isolates are closely related, the high resolution provided by cgMLST enabled their differentiation and the identification of genetically related strains affecting horses in Argentina.

**Ethical animal research:** Research ethics committee oversight not currently required by this journal: the study was performed on material collected previously during clinical procedures.

**Informed consent:** Not stated.

**Competing interests:** A.S. Waller is employed by Intervacc AB.

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## 20 | Characterisation of *S. equi* strains by whole genome sequencing isolated from 2016 to 2019 in France

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**Background:** The prevalence of strangles, one of the most frequently diagnosed infectious diseases of horses worldwide, remains underestimated in France, despite causing economic losses to the equine industry. *Streptococcus equi* subsp. *equi* (*S. equi*) is the causative agent and its persistence in guttural pouches of sub-clinical carriers plays an important role in the spread of the disease.

**Objectives:** The aim of this study was to use whole genome sequencing to understand the genetic relationships of *S. equi* isolates recovered in France from 2016 to 2019 and compare them with international data.

**Study design:** Longitudinal field study.

**Methods:** The French Network for epidemio-surveillance of equine diseases (RESPE), collected 55 isolates from 23 horses implicated in 13 different outbreaks. DNAs from 18 of these strains were extracted, purified and whole genome sequenced according to Illumina recommendations. Genomes were analysed using Pathogenwatch and visualised in Microreact.

**Results:** All isolates were classified as ST-179, recognised as “classic” *S. equi*. Genomes clustered into BAPS2 (Bayesian Analysis of Population Structure) but fell into two groups. Sequences in the first group, from different outbreaks (two in 2016 and one in 2017), differed from only some SNPs across the core genome and their closest relatives were previously recovered from horses in the United Arab Emirates. The second group were most closely related to other strains from France, Belgium, Spain, Sweden and the United Kingdom.

**Main limitations:** Not all available isolates have been sequenced to date and the history of the horses from which these isolates were derived requires further investigation.

**Conclusions:** Genomic analyses are undergoing to understand the differences between isolates from horses with acute strangles and sub-clinical carriers, by highlighting differences in genes involved in virulence, resistance, persistence or evasion of the immune system.

**Ethical animal research:** Research ethics committee oversight not required: retrospective analysis of clinical data.

**Informed consent:** Owners gave consent for their animals' inclusion

**Competing interests:** None declared.

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