

wgMLST SCHEMA

BIONUMERIC[®]

MICROBIAL DATA ANALYSIS SOFTWARE

Staphylococcus pseudintermedius

WHAT IS wgMLST AND WHY DO YOU NEED A SCHEMA FOR IT?

Whole genome MLST (wgMLST) is an extension of the more traditional MLST, allowing a much higher typing resolution. It offers a fast and cost-effective way to analyze bacterial genomes. A schema is essential for the wgMLST technique to work as it defines the loci to which allele numbers are assigned. It represents the basis for a stable nomenclature that you can use to communicate about outbreaks, epidemics, evolution, etc...

WHY DID WE DEVELOP A *STAPHYLOCOCCUS PSEUDINTERMEDIUS* wgMLST SCHEMA?

Staphylococcus pseudintermedius is primarily an opportunistic pathogen most prevalent on the skin and in mucosa of dogs and cats causing skin and ear infections. However, recently more and more cases of transmission to humans are reported, in whom it may also cause more serious infection of lung and heart tissue. A wgMLST schema can help identifying transmission routes and typing of the zoonotic strains.

S. pseudintermedius subschemes

4,424 wgMLST loci + 7 MLST loci

HOW WILL IT HELP YOU?



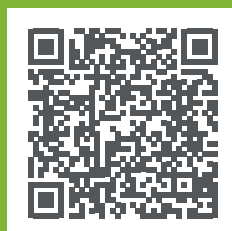
Turnaround
time < 30 min



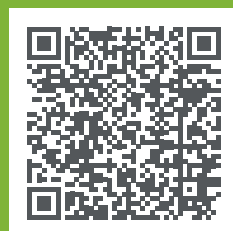
Simultaneous
sample processing
possible

- ✓ Defines a **robust set of loci**, validated and approved by our microbiologists
- ✓ Contains **minimal sample artifacts**, while keeping great discriminatory power
- ✓ Represents the known **diversity** of the species
- ✓ Allows **detection of markers** specific to a certain strain, enabling powerful classification and outbreak identification

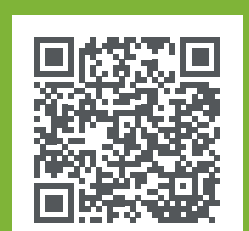
TRY IT ON YOUR OWN DATA TODAY!



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