

wgMLST  
SCHEMA

# BIONUMERIC<sup>®</sup>

MICROBIAL DATA ANALYSIS SOFTWARE

*Staphylococcus epidermidis*

## 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 EPIDERMIDIS* wgMLST SCHEMA?

*Staphylococcus epidermidis* is part of the normal human skin flora and is usually not pathogenic, although patients with compromised immune systems are at risk of developing infections. *S. epidermidis* is known to form biofilms that grow on plastic surfaces and is thus of particular concern for people with catheters or other surgical implants. Being part of the normal skin flora, *S. epidermidis* is also a frequent contaminant of samples for diagnostic use. A wgMLST schema can help in identifying the sources of contamination or a hospital outbreak.

*S. epidermidis* subschemes

4,870 wgMLST loci + 7 MLST loci

## HOW WILL IT HELP YOU?



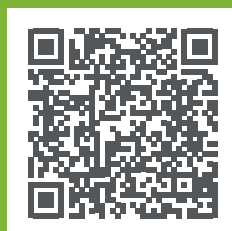
Turnaround  
time < 30 min



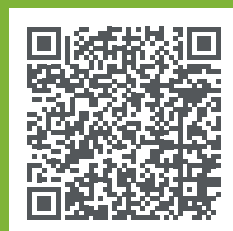
Simultaneous  
sample processing  
possible

- ✓ 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

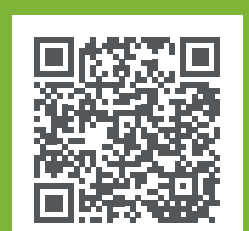
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