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.

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?

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HOW WILL IT HELP YOU?

- 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!

1. Make sure you have a BIONUMERICS license
2. Request a Calculation Engine project
3. Learn from our wgMLST tutorial movies