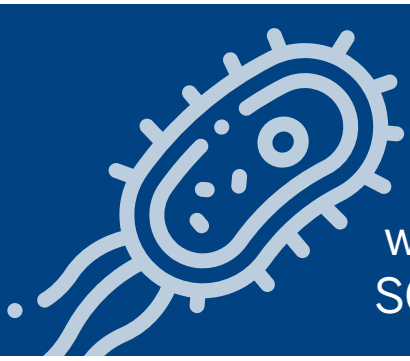
BIOMÉRIEUX



wgMLST SCHEMA

BIONUMERICS®

MICROBIAL DATA ANALYSIS SOFTWARE

Micrococcus spp.

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 *MICROCOCCUS* spp. wgMLST SCHEMA?

Micrococcus spp. is an ubiquitous bacterium that is commonly isolated from human skin, animal and dairy products, and grows well in environments with little water or high salt concentrations. Although it is not considered pathogenic for healthy people, it plays an important role in biotechnology. High-resolution typing can enhance the identification of beneficial strains for a certain application as each strain may have other traits over other strains. In the food industry, certain strains, which can be identified by wgMLST, play an important role in spoilage, especially for milk.

Micrococcus spp. subschemes

8,207 wgMLST 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 genus, including *M. aloeverae, M. luteus*, *M. lylae* and *M. terreus*
- ✓ Allows **detection of markers** specific to a certain strain, enabling powerful classification

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