BIOMÉRIEUX

wgMLST SCHEMA

BIONUMERICS®
MICROBIAL DATA ANALYSIS SOFTWARE

Bacillus subtilis

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 *BACILLUS SUBTILIS* wgMLST SCHEMA?

Bacillus subtilis is a ubiquitous bacterium commonly found in soil and the gastrointestinal tract of ruminants and humans. It is considered the best studied Gram-positive bacterium and a model organism to study bacterial chromosome replication and cell differentiation. Moreover, it is widely used in the biotechnology industry for the production of secreted enzymes.
A wgMLST schema can be used to type and identify strains with interesting traits.

Bacillus subtilis subschemes
7,746 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!

1. Make sure you have a BIONUMERICS license

2. Request a Calculation Engine project

3. Learn from our wgMLST tutorial movies