BioNumerics®

RELEASE NOTE

# *KLEBSIELLA OXYTOCA*

## for whole genome sequence typing

*We are proud to present a schema for true whole genome multi-locus sequence typing (wgMLST) of Klebsiella oxytoca in BioNumerics. When used in combination with our Calculation Engine, typing K. oxytoca isolates up to strain level using whole genome sequencing is now easily accessible to everyone.*

### What is the schema exactly?

Based on the known diversity within the species *K. oxytoca*, a pan-genomic wgMLST schema was developed. This schema, with high discriminatory power, allows for the detection of subtype- or outbreak-specific markers, thus enabling more powerful classification and outbreak definition tools.

### Which loci are present?

Starting from the 84 annotated, publically available reference genomes, capturing the whole diversity of the species, our in-house developed schema creation procedure uses a sampling-based multi-reciprocal BLAST procedure to determine those sets of alleles that make up the stable loci in the genome. A per-locus allele assessment procedure then determines the central prototype allele, and thus the definition of the locus. For maximal consistency with classical multi-locus sequence typing initiatives the wgMLST schema consisting of 16,270 loci is then complemented with the 7 MLST loci[1].

### How will it help you?

By using BioNumerics and the integrated powerful calculation infrastructure, analyzing whole genome sequencing data for *K. oxytoca* has become a lot more straightforward. Our cloud based Calculation Engine offers a high-throughput environment for all your sample processing needs. Its quality-controlled de novo assembly possibilities allow you to easily assemble whole genome sequencing data without the need of local computing power. The two allele detection procedures (assembly-based and assembly free) allow you to perform fast and reliable allele calling for e.g. cluster detection which can be combined with whole genome SNP analysis to obtain the utmost resolution within your sample comparisons.

**The BioNumerics wgMLST schema for *K. oxytoca* has been tested, validated and approved by our microbiologists.**

**Great care has been taken to create an analysis procedure that minimizes sample artifacts, while maintaining an enormous discriminatory power that supersedes the core genome schema.**

**With turnaround times of less than 30 minutes per sample and the ability to process multiple samples simultaneously, the power of high-performance computing will be brought to your desktop with a few clicks.**

### Interested?

Request a calculation engine project today to get started:


**References:**

(1) Herzog KA, Schneditz G, Leitner E, Feierl G, Hoffmann KM et al. 2015. Genotypes of Klebsiella oxytoca isolates from patients with nosocomial pneumonia are distinct from those of isolates from patients with antibiotic-associated hemorrhagic colitis. J Clin Microbiol. 52(5):1607-1616.


APPLIED MATHS

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