

## ESCHERICHIA COLI FUNCTIONAL GENOTYPING

### Conventional vs whole genome methods: the advantages

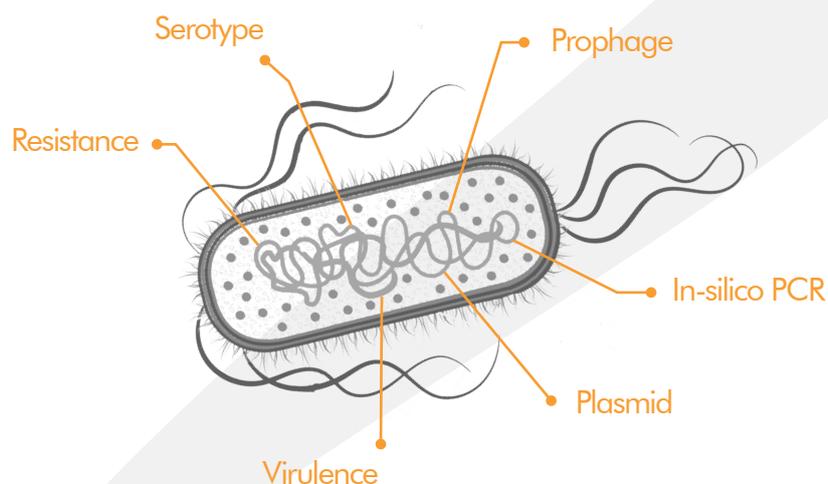
Foodborne bacteria such as enterohemorrhagic *E. coli* pose a major threat to public health. To detect outbreaks in an early stage and prevent widespread infections, being able to accurately identify and characterize these bacteria in a rapid manner is of key importance. Conventional methods for serotyping, virulence profiling, and antimicrobial susceptibility testing are time-consuming and often require complex workflows. Alternatively, whole genome sequence data provides highly detailed genotypic information and has the potential to replace some of these conventional methods.

### *E. coli* genotyping in BioNumerics

Various *E. coli* genotyping tools have been bundled in one single BioNumerics application, making it a very user-friendly and easy-to-use typing tool. Screening for all or a subset of traits can be launched with one single click and the genotyping analysis results are summarized in an easy accessible and customizable report. The typing results are stored in the BioNumerics database and can be analyzed in combination with other data sets at any time.

### Impressive list of genotyping tools

The *E. coli* genotyping application contains public databases for serotype, virulence and resistance prediction, as well as plasmid and prophage detection. The reference databases are based on the data sets available from Center for Genomic Epidemiology, DTU, combined with private knowledge. An in-silico PCR tool is also implemented, making it possible to detect e.g. Shiga toxin gene subtypes and virulence genes, mimicking the wet lab PCR.



## YOUR ADVANTAGES



WHY USE **BioNumerics**  
FOR YOUR *E. COLI* TYPING?

- ✓ Impressive list of genotyping tools
- ✓ Fast BLAST screening
- ✓ Rich database environment
- ✓ Detailed reporting

## Fast BLAST screening

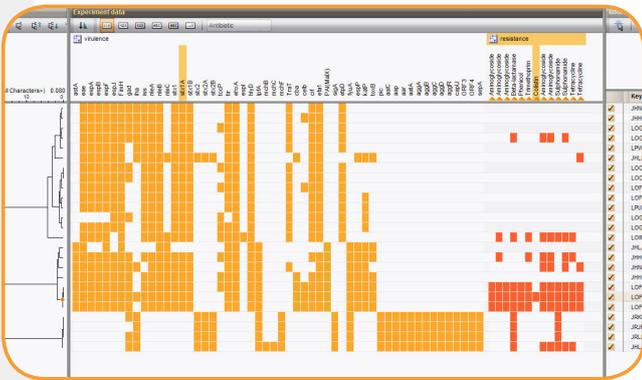


The various *E. coli* genotyping tools start from the assembled sequences stored in the BioNumerics database, and use a BLAST-based approach to detect and identify the genes of interest. A minimum sequence identity and minimum length coverage needs to be specified to detect the best matching target sequence in the genome.

## Rich database environment



The typing results are recorded as information fields and/or character data in the BioNumerics database and can be clustered and analyzed together with other data sets leading to a more efficient interpretation of the data.



## Detailed reporting



The genotyping results are combined with strain information and presented clearly in a customizable report. A summary of predicted serotype, virulence and resistance prediction, as well as plasmid and prophage detection is displayed.

Hyperlinks are present linking to the detailed BLAST results of the predicted traits. Detailed BLAST results include locus identifiers, BLAST similarity scores, and descriptive information on the detected genes.

**Details**  
**O-type**  
 Predicted: O88 (discrimination: 99.04%)

Locus	Serotype	Identity (%)	Length (%)	Start	End	Ref. length	Accession
wzx	O88	99.52	100.00	3449006	3450463	1458	AB812037
wzy	O88	99.76	100.00	3446799	3448073	1275	AB812037

**H-type**  
 Predicted: H19 (discrimination: 85.24%)

Locus	Serotype	Identity (%)	Length (%)	Start	End	Ref. length	Accession
fliC	H19	99.95	99.95	3966921	3968752	1833	AY337479

**Resistance**  
 No matches found.

**Virulence**

Locus	Identity (%)	Length (%)	Start	End	Ref. length	Accession	Notes
fliA	94.87	100.00	4494005	4494550	546	L43373	Subunit A of F17 fimbriae
fliG	99.42	100.00	4489630	4490661	1032	CP001162	Adhesin subunit of F17 fimbriae
FimH	97.45	100.00	3270713	3271615	903	AJ225176	
hly	98.93	100.00	3811999	3812836	842	U07174	
hly	98.98	100.00	4800835	4801228	394	CP001509	Increased virulence

### NOTE:

The *E. coli* functional genotyping plugin is a free online add-on. The minimum configuration for installation of the plugin includes the "Character Data", "Sequence Data" and "Genome Analysis Tools" modules. Please contact us for more information.



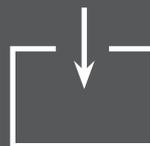
## CONVINCED? INTRIGUED? TRY IT FOR YOURSELF!

[www.bionumerics.com](http://www.bionumerics.com)

Scan the QR codes to access each step



1. Make sure you have a **BioNumerics** license (also see note above).



2. Download the free plugin directly from the software. No admin rights needed!



3. Watch tutorial movies or download sample data for use in **BioNumerics**.

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