

## Development of a web tool for Escherichia coli subtyping based on fimH alleles - DTU Orbit (09/11/2017)

### Development of a web tool for Escherichia coli subtyping based on fimH alleles: Running title: Development of E. coli fimH sub-typing web-tool

The aim of this study was to construct a valid publicly available method for in silico fimH sub-typing of Escherichia coli particularly suitable for differentiation of fine-resolution subgroups within clonal groups defined by standard multi-locus sequence typing (MLST). FimTyper was constructed as a FASTA database containing all currently known fimH alleles. The software source code is publicly available on <https://bitbucket.org/genomicepidemiology/fimtyper>, the database freely available at [https://bitbucket.org/genomicepidemiology/fimtyper\\_db](https://bitbucket.org/genomicepidemiology/fimtyper_db), and a service implementing the software available at <https://cge.cbs.dtu.dk/services/FimTyper>. FimTyper was validated on three datasets; (i) containing Sanger sequences of fimH alleles of 42 E. coli isolates generated prior to the current study, (ii) whole-genome sequence data of 243 third-generation cephalosporins-resistant E. coli isolates, and (iii) a randomly chosen subset of 40 E. coli isolates from dataset (ii), which were subjected to conventional fimH sub-typing. The combination of the three datasets enabled an evaluation and comparison of FimTyper on both Sanger sequences and WGS data. FimTyper correctly predicted all 40 fimH sub-types from the Sanger sequences from dataset (i), and successfully analyzed all 243 drafted genomes from dataset (ii). FimTyper sub-typing of the Sanger sequences and WGS data from dataset (iii) were in complete agreement. Additionally, fimH sub-typing was evaluated on a phylogenetic network of 122 ST131 E. coli isolates. There were perfect concordance between the typology and fimH-based sub-clones within ST131 with accurate identification of the pandemic multidrug resistant clonal subgroup ST131-H30. FimTyper provides a standardized tool, as a rapid alternative to conventional fimH sub-typing, highly suitable for surveillance and outbreak detection.

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