Molecular epidemiology of multidrug resistant bacteria

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Project description and research aims:

- Study the molecular epidemiology of carbapenemase-producing Enterobacteriaceae (CPE) in Finland.
- Study the epidemiology of livestock-associated MRSA in Finland.
- Apply whole genome sequencing as a molecular tool in outbreak investigations: different species need separate protocols and cut-offs, and at least the 7-8 most common outbreak species should be covered.
- Develop sophisticated pipelines to detect and analyze resistance and virulence markers from whole genome sequences of multidrug resistant pathogens.
- Develop tools for combining molecular and epidemiological data; constructing species-specific databases containing all sequenced strains, to enable the detection of hidden outbreaks.
- Develop a system for compiling the information produced by whole genome sequencing.

Publications:

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