ACRONYM: SpARK

Title: The rates and routes of transmission of multidrug resistant Klebsiella clones and genes into the clinic from environmental sources

Keywords: Multidrug resistant Klebsiella pneumoniae; environmental reservoirs; transmission; gene content diversity; whole genome sequencing; mathematical modelling; nosocomial infection

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Abstract:

Klebsiella pneumoniae (Kp) is a leading cause of multidrug resistant hospital-acquired infections globally, and is responsible for an increasing public health burden in the community. In order to control the spread of Kp through targeted surveillance and intervention policies it is necessary to identify the sources of emergent community and health-care associated infection from the interlinked and varied niches encompassing “the environment”.

To address this, we will sample from multiple clinical, community, agricultural, veterinary and environmental settings in and around a single town, Pavia, in Northern Italy, and supplement these data with matched samples from France and elsewhere. We will use whole genome sequencing of community (mixed-colony) samples to assay accessory gene abundance and distribution.

This contrasts with the more common approach based on phylogenetic analysis of single colonies, which would be of limited utility over broad environmental scales due to the complexity of transmission chains, environmental dormancy, and high rates of recombination. In contrast, our gene-centric approach provides a much more efficient means to understand ecological adaptation, the distribution of resistance and virulence genes, and to identify key environmental reservoirs from which clinical clones emerge.

A key deliverable of this project will be the establishment of a pan-genome database (‘pangenomium’) that will integrate with both existing Kp genome community resources established by project partners (BIGSdb-kp, and wgsa.net).