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Paper Poster Session
Emergence and worldwide outbreaks of carbapenemase-producing bacteria

Correlating K. pneumoniae genomics with metadata. What makes an outbreak?

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Background: *Klebsiella pneumoniae* is an opportunistic pathogen of great importance, especially due to the high prevalence of multi-drug resistant strains. Among these are isolates that resist to carbapenems, mainly due to the presence of the plasmid-encoded gene bla_{KPC}. Carbapenem resistant *K. pneumoniae* infections have been reported mainly in hospital settings, affecting in particular immunocompromised patients, causing outbreaks with mortality rates up to 50%. Genomic studies are being performed, with the goal of shedding light on the genomic variability *of K. pneumoniae*, at the local, national and worldwide level. The *K. pneumoniae* species results to be divided in many genetically uniform clonal groups, which in some cases originated from big genomic recombination events. The clonal group 258 (CG258) has been shown to be the prevalent carrier of KPC resistance, thus resulting to be possibly the most important for global health. Indeed, causing thousands of nosocomial infections yearly worldwide.

Material/methods: During the first three months of 2015 a KPC *K. pneumoniae* outbreak occurred in the IRCCS S. Matteo Hospital of Pavia. The outbreak involved 47 patients, mainly hospitalized in the three Intensive Care Units. Isolates of *K. pneumoniae* were collected, DNA was extracted and subjected to whole genome sequencing using the Illumina MiSeq platform. Genomes were assembled using the software MIRA, and subjected to a SNP analysis pipeline developed in-house. Patients and whole-hospital microbiological metadata were also collected, with the goal to identify possible correlations between *K. pneumoniae* infections, specific genotypes, but also with presence/prevalence of other pathogens, patients characteristics and hospital procedures.

Results: Genomic analyses show that the outbreak was not due to a single *K. pneumoniae* clone, but comprised a significant genomic diversity. Specifically two clones were responsible for most cases, but other sporadic strains were detected. Indeed, the analyzed isolates result to belong to four different MLST profiles: ST258, ST512, ST101 and ST554. Despite such genomic variability, it is interesting to note that all the isolated CG258 *K. pneumoniae* strains belong to the previously identified four Italian clades. Analysis to examine the genomic differences between the isolates, and to determine whether correlations with metadata are present, are currently being performed.

Conclusions: Our hypothesis is that the emergence of *K. pneumoniae* outbreaks could be due not only to the presence of KPC strains but also to a set of other parameters. To test this

hypothesis we are analyzing this complex outbreak, as well as the metadata associated to patients and to the other pathogen species isolated between 2014 and 2015 in the hospital setting. The aim of this work is to look for patterns associated to *K. pneumoniae* outbreak emergence, and produce an outbreak risk index for hospitals.