

P1394 **Metabolic profiles of *Klebsiella pneumoniae* strains in basal conditions and under 'antibiotic stress'**

Claudio Foschi¹, Melissa Salvo¹, Luca Laghi², Simone Ambretti³, Antonella Marangoni*¹

¹Microbiology, DIMES; University of Bologna, Bologna, Italy, ²Centre of Foodomics, Department of Agro-Food Science and Technology; University of Bologna, Cesena, Italy, ³Microbiology Unit; S.Orsola-Malpighi Hospital, Bologna, Italy

Background: The global spread of carbapenemase-producing *Enterobacteriaceae* is of great concern to health services worldwide. In particular, multi-drug resistant *Klebsiella pneumoniae* (KP) harbouring KPC enzymes has been causing epidemics of international proportions.

The analysis of the metabolic profiles of KP strains could represent an intriguing approach to obtain useful information to set up new diagnostic methods and to develop new antimicrobial strategies. The aim of this study was to characterize the metabolic profiles of several KP strains, characterized by specific resistance pattern.

Materials/methods: A total of 59 KP strains, isolated from clinical samples submitted to the Microbiology Unit of S.Orsola-Malpighi Hospital of Bologna (Italy) for diagnostic procedures, were included in the study. In particular, 27 carbapenemase-negative and 32 carbapenemase-positive strains were analyzed. For each strain, bacteria were grown overnight in Mueller-Hinton (MH) broth. Afterwards, the suspension was standardized (2.8 McF) and centrifuged to separate the cell pellet from the supernatant. The metabolomic analysis was performed by means of ¹H-NMR spectroscopy analysis (Avance III Spectrometer; Bruker), starting from 700 µL of filtered supernatants ('external metabolome') and 100 µL of cell lysates ('internal metabolome').

The same protocol was used to study the metabolic profile of 8 KP strains (4 wild-type and 4 KPC-producing) under 'antibiotic-stress', allowing the bacteria to grow in MH broth with a meropenem concentration corresponding to 1/8 of the MIC value.

Results: A total of 44 and 32 molecules, mainly belonging to organic acids, amino acids and alcohols, were detected in the external and the internal metabolome, respectively. In basal conditions, we found 6 metabolites (acetate, isobutyrate, lysine, phenylacetate, hydroxybutyrate) whose concentration was

significantly different between carbapenemase-positive and carbapenemase-negative KP strains. The Table shows the molecules that differed between carbapenemase-positive and carbapenemase-negative strains under 'meropenem-stress'.

Conclusions: The metabolomic analysis allows to detect molecules that significantly differed between carbapenemase-positive and carbapenemase-negative KP strains, both in basal conditions and under 'antibiotic stress'.

Metabolites	Carbapenemase-positive strains	Carbapenemase-negative strains	<i>P</i> value
Urocanate	-0.0002 mM	-0.012 mM	0.01
Pyroglutamate	0.073 mM	0.163 mM	0.01
Succinate	1.46 mM	2.25 mM	0.03
Pyruvate	-0.81 mM	-1.03 mM	0.03
Alanine	-0.05 mM	0.168 mM	0.03