27th ECCMID Vienna, Austria 22 – 25 April 2017
The congress of ESCMID

Session: P030 Colistin resistance: detection, mechanisms and synergy

Category: 3d. Resistance mechanisms

23 April 2017, 13:30 - 14:30
P0658

A snapshot of the COL-R Acinetobacter baumannii comparative transcriptome by RNA-seq

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Background
Colistin (COL) is the last-resort treatment for Multi-Drug-Resistant (MDR) *Acinetobacter baumannii*, thus COL-resistance represents a concern for the *A.baumannii* infection management.
Materials/methods
The small-RNA and mRNA comparative transcriptome of two Italian clinical COL-R/COL-S isogenic isolate pairs were investigated by Illumina-RNAseq, bioinformatics (Rockhopper) and computational filtering analysis for sorting, first, the differentially expressed sRNAs and mRNAs in the COL-R strains versus their COL-S counterparts and, thus, only those present in both COL-R isolates.
Results
Small-RNAome of the same pairs, showed: i) in 1-R, **211** 5'-UTRs and **94** 3'-UTRs, **1499** sense- and **1411** antisense-small-RNAs, **77** differentially- expressed protein coding genes, **331** likely operons and **279** multigene-operons *vs* 1-S; ii) in 2-R, **94** 5'-UTRs and **48** 3'-UTRs, **1165** sense- and **743** antisense-small-RNAs, **27** differentially-expressed protein coding genes, **334** likely operons and **280** multigene-operons *vs* 2-S.
COL-R *vs* COL-S isolate **mRNAome** evidenced: i) in 1-R strain, **55** 5'-UTRs and **18** 3'-UTRs, **14** sense- and **19** antisense-mRNAs, **47** differentially-expressed protein coding genes, **343** likely operons and **286** multigene-operons *vs* 1-S; ii) in 2-R strain, **277** 5'-UTRs and **152** 3'-UTRs, **32** sense- and **85** antisense-mRNAs, **73** differentially expressed protein coding genes, **404** likely operons and **325** multigene operons *vs* 2-S.
Statistically significant (*qValue*≤ 0.01 for the differential expression after read-count normalization by the upper-quartile-gene-expression level) filtering-analysis of the data sorting for small antisense non-coding RNAs (sRNAs) and coding mRNAs of the COL-R isolates versus their COL-S counterparts showed: i) **2** up-regulated sRNAs, for the 16S rRNA and for a soluble cytoplasmatic-protein (A1S_2505), as well as **1** down-regulated sRNA for a signal peptide, involved in the cytokinin

biosynthetic process (A1S_3097) (Biological Process GO:0009691); ii) 5 up-regulated coding mRNA for a lipoprotein involved in the polysaccharide metabolic process (A1S_0938) (Biological Process GO:0005976), for two hypothetical proteins (A1S_2027 and A1S_2230), for a peptide synthetase involved in metabolic process (A1S_2651) (GO:0008152) and for Lipid A phosphoethanolamine transferase involved in metabolic process (A1S_2752) (GO:0008152).

Conclusions

Our study, first, took a snapshot of the COL-R comparative *A.baumannii* RNAome.