The aim of the **TRANSCEND** project was to investigate the transcriptomic interaction between the host organism (*Drosophila melanogaster*), the pathogen (multiresistent ESKAPE bacteria) and last-resort antibiotics (colistin and meropenem). The main objectives included: i) evaluating the effect of ESKAPE bacteria and antibiotics on the *D. melanogaster* experimental model, ii) comparing the effect of *in vitro* and *in vivo* expression of antibiotic resistance genes, iii) identifying the clinical significance of the results by implementing bioinformatics analyses on the genetic expression profiles.

All objectives of the TRANSCEND project were meticulously achieved, with obtaining significant results, including: i) optimization of experimental infection protocols of ingestion on *D. melanogaster* model, as well as isolation and quantification of antibiotic resistant bacteria, sequencing experiments and development of 3 novel packages for bioinformatics analysis of sequencing and qRT-PCR data; ii) identification of *D. melanogaster* microbiota modification (increased of Proteobacteria/Firmicutes ratio in mutants, resulting in enhancing the pro-inflammatory status and horizontal transfer of antibiotic resistance genes) and eukaryotic genes modulated by the bacterial infection, depending on the studied genotypes, supporting the potential eukaryotic genes involved in transmembrane transport, activity of oxidoreductases and ubiquitination as markers for infection susceptibility in the studied genotypes or as markers for bacterial infection severity; iii) identification of eukaryotic modulated genes by colistin antibiotic administration, which stimulates processes associated with the endoplasmic reticulum and Golgi apparatus, highlighting the potential genetic compensatory mechanisms in the context of γCOP^{14a} mutation, and the potential use of these genes as markers of antibiotic toxicity; iv) expression differences in carbapenems resistance genes, depending on the bacterial strain and the genetic background of infected individuals, suggesting an unique competitional context caused by the immune vulnerability of *D. melanogaster* mutants.

The significant differences between the studied genotypes regarding the bacterial infections and antibiotics treatments have important clinical consequences, the data supporting a solid foundation for subsequent research with focus on the trialogue host – infectious agent – antibiotic, in order to develop the optimization and personalization of therapeutic strategies, based on the genetic background of patients.

The results have been disseminated by: publishing 7 ISI rated (Q1 and Q2) scientific papers, with one article currently in evaluation and one article currently in press; participation to 10 oral presentations in international (3) or national (7) conferences with acknowledge the TRANSCEND project; results publishing on the project's website (https://unibuc.ro/cercetare/promovarea-rezultatelor-cercetarii/proiecte-de-cercetare/proiecte-cu-finantare-nationala/transcend/; https://unibuc.ro/cercetare/promovarea-rezultatelor-cercetarii/proiecte-de-cercetare/proiecte-cu-finantare-nationala/transcend/?lang=en) and 3 original bioinformatics packages as open-source (https://github.com/DenisaConstantin/directRNAseqAnalysis; https://github.com/DL-UB/qDATA; https://github.com/DL-UB/RecoveryUnclassifiedReads).

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