Identification of new antimicrobial resistance genes in *E. coli* through network diffusion

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Antimicrobial Resistance (AMR) is an emerging issue, related to the massive use of antibiotics in the last century for health and food safety, causing significant economic costs and probably becoming one of the first causes of death in the next decades. It is thus mandatory to better understand the AMR mechanisms within pathogens, possibly to develop novel drug and multidrug strategies involving novel targets. In our work, we used a systems biology approach consisting of a combination of network diffusion and gene set enrichment analysis to discover putative and new AMR-related genes in *E. coli*. Starting from 53 AMR-related genes known from literature (CARD, ResFinder and PointFinder databases) we could identify a list of 61 genes potentially associated with antimicrobial resistance, involved in known pathways but also related to other biological mechanisms. We used an in-house *in vitro* validation protocol to test the growth of seven mutants on eight different antibiotics. The primary results are very promising. A more conventional validation protocol is being performed to confirm the involvement of these new genes in anti-microbial resistance and the final findings will be shared soon. This work will contribute to a better understanding and characterization of AMR in *E. coli* to better control the spread of this phenomenon.