TRANSCRIPTOMIC AND PROTEOMIC RESPONSE OF *ESCHERICHIA COLI* TO ZINC OXIDE

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Objectives: Zinc oxide (ZnO) is commonly used as a component of dyes, in cosmetics, as a food supplement and as a fertilizer. The interaction of ZnO with bacteria can alter cell metabolism and this can result in increased antibiotic resistance and virulence. Consequently, resistant bacteria can enter the human gut microbiome via the food chain and can cause difficult-to-treat infections. This study focuses on the interplay between the transcriptome and proteome that occurs in *Esherichia coli* after an extended exposure to ZnO.

Methods: *E. coli* was sub-cultured 40 times with the sub-lethal concentration of ZnO (ZnO40). RNA and proteins were extracted from bacterial pellets ZnO40 and the untreated control (C40). From RNA, cDNA libraries were prepared, transcriptome was sequenced by Illumina, processed by DESeq2, and analyzed. Proteins were isolated and processed by LC-MS. Final data were visualized by the ggplot2 package in RStudio. This study focused on genes with expression that changed significantly based on the proteomic and transcriptomic data together. Of these 75 genes, 37 with the common expression regulation were selected for STRING analysis.

Results: The selected genes were coding for various stress response to ZnO and most of them shared the same protein association networks. These pathways included nutrient uptake (carbon, nitrogen, and various metabolites) and oxidative stress (*dps, elaB, sufS, sufE, yjbJ, ybdgS, adhE*). There was also an increase in the production of proteins involved in cell membrane persistance (*skp, ompA*), lipid storage (*blc*), and nutrient transport (*otsA, otsB*). Production of several virulence factors, especially those involved in biofilm formation (*dosC, dosP*), also increased.

Conclusion: *Escherichia coli* stressed by an extended exposure to ZnO activated defense and virulence systems on several levels.