Title: NON-SPECIFIC RESPONSES SYSTEM FROM STRAINS OF *Escherichia coli* K-12 TO INDUCED TOXICITY BY THE HERBICIDES PARAQUAT, 2,4-D AND ATRAZINE

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Abstract:

Microorganisms are essential in the maintenance of biogeochemical cycles. The continuous use of herbicides to minimize the productivity loss in agricultural environments can lead to damage in microbiota. One reason for this is the increase in production of reactive oxygen species (ROS), which may lead to oxidative stress. The magnitude of this stress can be conditioned by the kind of herbicide. The cell responses against ROS involve an increase in the expression of enzymes such as SOD (superoxide dismutase), responsible for the dismutation of $O_2^{\bullet-}$. The objective of this study was to evaluate the responses of different SOD isozymes from *Escherichia coli* K-12 by treatments with different herbicides. The herbicides studied were 2,4-D, paraquat and atrazine, and *E. coli* K-12 strains were knockouted for Mn-SOD (*sodA*) and Fe-SOD (*sodB*) genes. These herbicides promoted the imbalance of redox potential, increasing the production of H_2O_2 and MDA (malondialdehyde). After the paraquat treatment, which produces redox cycling, the strains *E. coli wt* (wild type) and *ΔsodB* showed increased production of H_2O_2 and Mn-SOD activity, probably as a consequence of activation of SoxR, which promotes the transcription of the gene *sodA*. In *ΔsodA*, rates of toxicity with paraquat were not higher than the control, indicating a possible regulation of the expression of Fe-SOD by the transcriptional factor OxyR. Our results indicate that *ΔsodB* and *ΔsodA* have time specific responses, demonstrating the role of isozymes in the defense against oxidative stress in different stages of bacterial growth. Despite the observed toxicity induced by herbicides, the strains were able to grow at rates close to those observed in control, mainly *ΔsodA.* Bacteria having a polymorphic system for SOD may enhance their cell viability in an environment containing toxic molecules. It is suggested that mechanisms for herbicide tolerance, even without selection, is widespread in bacteria, as it was found in *E. coli* K-12, a strain developed in a laboratory, and probably with low survivability in natural environment. Such phenotypic plasticity model could be found in other bacteria of agricultural soil under intense use of herbicides, which indicates a quick response potential. Differently, a considerable impact could be expected on the diversity and functionality of this microbiota.

Keywords: environmental microbiology, oxidative stress, peroxide, response system, superoxide dismutase

Financial Support: Master Degree Grant, CAPES. Universal, CNPq. Science without Borders, Special Visitor Researcher, CNPq