

EuroSciCon conference on Protein, Proteomics and Computational Biology

December 06-07, 2018 Amsterdam, Netherlands

Biochem Mol biol J Volume:4 DOI: 10.21767/2471-8084-C5-021

BIOINFORMATICS AIDED PROTEOMIC ANALYSIS OF WHEAT SEEDS EXPOSED TO COPPER AND IRON NANOPARTICLES

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To elucidate the role of Cu and Fe NPs on the proteomic variations in wheat, a gel-free proteomic technique was used. NPs were synthesized and characterized through zeta potential, EDX, and SEM. On treatment with 25 ppm Cu and Fe NPs, a total of 121 proteins were changed in abundance in seeds of Pakistan-13. Protein abundance ratios of identified proteins were performed with Genesis software through cluster analysis. The cluster analysis indicated three clusters with contrasting behaviour in Pakistan-13 wheat seeds treated with Cu and Fe NPs. Protein abundance was further visualized through MapMan software. In Pakistan-13, glycolysis- and starch degradation-related proteins were not significantly changed following treatment with 25 ppm Cu or Fe NPs. However, proteins related to the tricarboxylic acid cycle were increased in Fe NPs-treated seeds as compared to control and Cu NPs-treated seeds according to MapMan analysis. These results suggest that bioinfomatics tools enabled us to easily understand the huge proteomic data and can predict the changes brought by Cu and Fe NPs in wheat seeds.

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