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

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Introduction:

NPs were comprised and characterized through zeta potential, EDX, and SEM. To elucidate the role of Cu and Fe NPs on the proteomic variations in wheat, a gel-free proteomic technique was used. On treatment with 25 ppm Cu and Fe NPs, a total of 121 proteins were changed in abundance in seeds of Pakistan-13. NPs were comprised and characterized through zeta potential, EDX, and SEM. The cluster analysis indicated three clusters with contrasting behavior in Pakistan-13 wheat seeds treated with Cu and Fe NPs. Protein abundance ratios of identified proteins were performed with Genesis software through cluster analysis. Protein abundance was further visualized through MapMan software. Protein abundance was further visualized through MapMan software. The cluster analysis indicated three clusters with contrasting behaviour in Pakistan-13 wheat seeds treated with Cu and 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. In Pakistan-13, glycolysis- and starch degradation-related proteins were not significantly changed following treatment with 25 ppm Cu or Fe NPs. Advances in nanotechnology around the world fastly increased and focused the effects of nanoparticles (NPs) on plants mechanism. 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. Copper (Cu) and iron (Fe) NPs have stimulatory effects on the germination ratio and plant growth of wheat. Understanding the complex mechanisms involved in plant response to NPs is indispensable in approaching the ultimate impact of nano-pollutants on ecosystem. After researching of morphology of trees, proteins extracted from shoots were analyzed with gel-free/label-free proteomic technique. Wheat variety NARC-11 at early stage was treated with or without Cu and Fe NPs. Cu NPs increased the number and abundance of amino acid related to protein metabolism while Fe NPs increased photosynthesis related amino acid in NARC-11. The proteomic results were validated with bioinformatics analysis. Venn diagram analysis indicated marked increase in number of proteins on Cu and Fe NPs exposure. The number of proteins related to glycolysis and tricarboxylic acid cycle were increased on Cu NPs exposure while did not change on Fe NPs exposure in this wheat variety. Out of photosynthesis related proteins, light reaction was enhanced in NARC-11 on Fe NPs exposure while did not change on Cu NPs exposure. Protein abundance ratios of identified proteins were performed with Genesis software through cluster analysis. On treatment with 25 ppm Cu and Fe NPs, a total of 121 proteins were changed in abundance in seeds of Pakistan-13. To elucidate the role of Cu and Fe NPs

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