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Perceptions about the nanoparticles interaction with wheat proteome

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To elucidate the role of Cu and Fe nanoparticles (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 of seeds in Pakistan 13. Protein abundance ratios of identified proteins were performed with Genesis software through cluster analysis. The cluster analysis indicated three clusters with contrasting behavior 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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