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**Abstract Topic: -** Cancer

**Abstract Title: -** Altered cellular energetics in copper toxicity – A pathway towards cancer

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**Aims: -** Copper, an essential element vital for various biological processes, modulates enzymatic and molecular activities. However, excessive copper leads to cellular toxicity by triggering regulated cell death - apoptosis, paraptosis, pyropoptosis, ferroptosis & cupropoptotic and oxidative stress. Prior studies primarily focused on copper accumulation in the liver; nonetheless, recent research shows that due to the small size of copper nanoparticles, they have the propensity to accumulate in the lungs also. Within the lungs, significant gene expressions changes related to antioxidant defense, DNA damage and apoptosis by copper (II) sulphate (CuSO4) and copper oxide nanoparticles (CuO-NPs) was observed. These alterations underscore the potential of copper nanoparticles to induce oxidative stress through DNA damage in normal cells. Mitochondrial genes are impacted by copper toxicity which here we try to elucidate through computational tools and correlate the outcomes with cancer pathways.

**Methods: -** In this study, we performed a comprehensive analysis encompassing expression profiles of critical genes namely PMAIP1 and TXNRD1, within lung tissue exposed to varying copper conditions: normal copper levels, elevated copper concentrations, and copper nanoparticles. EnrichR-KG was done for understanding molecular pathways influenced by these genes. These genes were involved in mitochondrial energetics and apoptosis. Following the pathway analysis, we conducted mutation profiling of these genes to understand any potential genetic alterations. Further, we conducted drug sensitivity analysis to identify pharmaceutical agents that modulate the expression of these genes, and subsequently employed molecular docking techniques to elucidate the interaction between the identified drugs and the selected genes.

**Results: -** Our investigation revealed a discernible impact of copper on the selected genes associated with mitochondrial functioning. Notably, alterations in the expression of these genes were observed in response to varying copper levels. These findings underscore the influence of copper on genes crucial for mitochondrial functionality.

**Conclusions: -** The findings of this study shed light on the consequential role of copper-related genes in modulating mitochondrial functioning. The observed, disruption induced by copper on mitochondrial processes may induce cell death or initiate irreparable cellular mechanisms, hallmarks often associated with cancer pathogenesis. This emphasizes the potential significance of copper-induced mitochondrial dysfunction as a contributing factor in cancer development and progression.

**Keywords: -** Our investigation revealed a discernible impact of copper on the selected genes associated with mitochondrial functioning. Notably, alterations in the expression of these genes were observed in response to varying copper levels. These findings underscore the influence of copper on genes crucial for mitochondrial functionality.