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Biosorption potential of *Azolla* and *Hydrilla* for the removal of heavy metals

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Background: Heavy metal removal from aquatic system is deemed to play significant role in human health. Conventional methods to remove hazardous heavy metals viz. chromium, copper, lead, arsenic include chemical and physical methodologies which are usually expensive non-eco viable. Therefore it is imperative to search for novel eco-friendly and economical alternative. *Azolla* and *Hydrilla* as adsorbents to remove chromium and copper has been well established and studied. However a deeper understanding of the mechanism involved in adsorption needs to be elucidated for its utmost exploitation.

Methodology: Batch adsorption technique and equilibrium kinetics were studied under different conditions of initial metal ion concentration, adsorbent dose, solution pH and shaking speed (rpm).

Results: The adsorption isotherm data of chromium and copper were fitted well to the Langmuir model. The maximum adsorption capacities of chromium and copper by *Azolla* and *Hydrilla,* calculated using the Langmuir equation, ranged from 35.70 to 65.50 mg g−1. The adsorption of chromium and copper by *Azolla* and *Hydrilla* was essentially due to presence of electrostatic forces on powdered biosorbent of *Azolla* and *Hydrilla* which was characterized by FTIR.

Conclusion: The experimental results suggest a better efficacy of *Azolla* over *Hydrilla* as an adsorbent in the removal of heavy metals from waste water which might be further tailored for its industrial applications.

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Anti-proliferative molecular mechanisms modulated by the synergistic interaction of epigallocatechin gallate and hydroxychavicol on human glioma cell lines: A transcriptomic approach

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The concept of multi-target therapeutic is to obtain highly effective and safe therapy with low side effects. Epigallocatechingallate (EGCG) displays many therapeutic effects, including antioxidant, anti-inflammatory, anticancer and immunomodulatory effects. Meanwhile, hydroxychavicol (HC) selectively kills cancer cells via ROS generation without affecting normal cells. Combining these bioactives yield synergistic interaction. Thus, this study focuses on unraveling the molecular mechanism that contributes to the synergistic effects of bioactive mixtures using the "omics" technology. High-throughput RNA sequencing (RNA-seq) was performed to explore the transcriptomic changes of human glioma 1321N1 and LN18 cell lines treated with combined EGCG+HC bioactives. Approximately 30-50 million high-quality reads were generated for each sample. A total of 2103 and 2442 genes were differentially expressed in 1321N1 and LN18 cells respectively (FDR P<0.05, fold-change>1.5), when treated with combined EGCG+HC, where 1025 genes were found to be commonly expressed in all treatments. Only 26 genes were commonly expressed in both cell lines treated with EGCG alone, whereas 268 genes were commonly expressed in both cell lines treated with HC alone. The genes induced by EGCG+HC treatment were grouped into functional networks such as apoptosis, cell cycle regulations, axon guidance, cytoskeleton organization, response to endoplasmic reticulum stress, inflammatory response, DNA repair, and telomere maintenance by bioinformatics analysis. Furthermore, subnetwork analysis of differentially expressed genes in 1321N1 and LN18 cells revealed five similar central genes, AKT1, ATF4, EIF2AK3, HIF1A, and NFE2L2. Taken together, the data provide evidence that the synergistic anticancer effect of EGCG+HC are influenced by both common and unique genes and pathways, that perhaps depend on the mutational status of each cell lines tested. Furthermore, combined EGCG+HC treatment was shown to enhance the effects of each individual bioactive by increasing the expression of genes present in EGCG or HC treatment alone, and/or by inducing the expression of other genes.

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