

## GENES AND PATHWAYS ALTERED BY GLYPHOSATE EXPOSURE: AN INTEGRATIVE BIOINFORMATIC STUDY

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**INTRODUCTION:** Despite previous reports on gene disruption by glyphosate in human and animal models, reports remain scattered, with little understanding of long-term risks and lack of integrative analysis yielding meaningful findings. In this context, bioinformatics tools such as gene interaction network analysis and functional enrichment (GO, KEGG) can reveal the biological mechanisms underlying glyphosate toxicity. **OBJECTIVE:** To identify and characterize human genes associated with glyphosate exposure using a bioinformatics approach. **MATERIALS AND METHODS:** Multiple bioinformatics platforms were consulted -Comparative Toxicogenomics Database (CTD), GeneShot and GeneCards-complemented with artificial intelligence-assisted information retrieval strategies using the term “Genes and Glyphosate”. Genes present in at least two of the four sources consulted were selected. Subsequently, using the STRING tool, gene interaction and functional enrichment analyses were performed to identify biological processes, molecular functions and potentially altered metabolic pathways. The results were expressed in bubble plots for each of the enrichment criteria. **RESULTS AND CONCLUSION:** Forty genes were selected for analysis. In the functional enrichment of biological processes (GO), the term “response to xenobiotic stimulus” had the highest number of genes (n=18), an enrichment strength of 1.32, and an FDR of 2.64e-16. Another relevant process was “Response to toxic substance” with 12 genes and an enrichment strength greater than 1.41 (FDR=2.0e-11). In the KEEG pathway analysis, the most enriched pathways were “Colorectal cancer,” “Endocrine resistance,” and “Breast cancer,” all with FDR values between 2.56e-11 and 4.03e-11 and an enrichment strength of 1,73 in colorectal cancer. The gene-disease association analysis showed that the term “carcinoma” was the most representative (“liver cancer,” “hepatobiliary system cancer,” “endometrial carcinoma”), with high enrichment intensity and a significant FDR (7.71e-9; 7.39e-8; 1.62e-6, respectively). These findings suggest that exposure to glyphosate shows a strong involvement of genes related to cellular processes in response to xenobiotics, oncogenic pathways, and endocrine diseases.**Keywords:** Pesticide; Network Toxicology; Human. **Source of funding:** Minciencias-University of Cartagena (Grant 041/2023).