GENE EXPRESSION PROFILING AND INFLAMMATION BIOMARKERS IN BRAZILIAN MINERS OCCUPATIONALLY EXPOSED TO CRYSTALLINE SILICA

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INTRODUCTION: Two million workers are exposed to crystalline silica (CS) in Brazil. CS can trigger non-communicable chronic diseases such as silicosis, a progressive, incurable lung disease diagnosed by imaging tests, with no standardized biomarker of exposure or effect. **OBJECTIVE:** This study aimed to identify promising biomarkers by gene expression profiling and quantifying inflammation biomarkers in miners exposed to CS. **METHODS:** Subjects were divided into three groups: exposed to CS (n=42), workers with silicosis (n=41) and non-exposed to CS (n=30). Blood (5 mL) was collected, preserved in RNALater, stored at -80 °C, and sent to NIOSH for RNA extraction and sequencing. Data were processed with nf-core/RNAseq and Trimgalore. Genes with fold change >1.5 and FDR <0.05 were used for bioinformatic analysis. Malondialdehyde (MDA) plasma and vitamin C serum levels were quantified by high performance liquid chromatography. **RESULTS AND CONCLUSION::** Gene expression profiling of 25.834 genes revealed 491 significantly altered genes for those exposed to CS, 658 for those with silicosis, compared to the control group, and 17 genes for those exposed to CS compared to those with silicosis. Notable genes include ELANE, DEF4, and FAM20A (upregulated), and DSC1, SLC4A10, and NRCAM (downregulated). ELANE, DEF4, and FAM20A are associated with neutropenia, respiratory diseases, and calcification, respectively. DSC1 is related to autophagy, SLC4A10 to the inflammatory response, and NRCAM, a neuronal cell adhesion molecule, to lung cancer. Diseases and biological functions significantly enriched in the two groups (without and with silicosis) that are related to the genes are immune mediated inflammatory disease, inflammation of organ, cellular infiltration and inflammatory response. Considering that the genes are mainly involved in inflammation, we analyzed the inflammatory marker MDA and the antioxidant marker vitamin C. MDA levels in silicotic individuals were significantly higher compared to the exposed and control groups (p<0.0001). In contrast, vitamin C levels were significantly lower compared to the control group (p<0.0001). These findings suggest that inflammation plays a central role in the progression of silicosis. The altered expression of key genes and changes in inflammatory markers highlight potential targets for future therapeutic interventions.

Keywords: miners, crystalline silica, gene profiling, inflammation, biomarkers.