

Oxidative stress in patients with osteoarthritis with infectious urinary tract: Approach through gene network analysis, urinary myeloperoxidase activity, and the oxidant/antioxidant status

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Determining MPO activity and oxidant/antioxidant (MDA, SOD and CAT) levels in the urine of osteoarthritis patients with urinary infection was also performed for the first time to reveal the targets of gene enrichment network analysis of osteoarthritic and urinary system-related genes. In addition, our other main goal was to learn that the use of computer-aided designs in this study and other studies could help the target. Genes from patients with osteoarthritis and urinary infections were retrieved from DisGENET. A venn Diagram was drawn for genes from DisGENET, and gene network analysis for common genes was done with SRplot. 31 patients with concomitant osteoarthritis and urinary tract infection, 17 patients with osteoarthritis, 15 patients with urinary tract infection and 25 healthy controls were included in the study. Urinary MPO, catalase (CAT), superoxide dismutase (SOD), and malondialdehyde (MDA) levels were examined in a spectrophotometer as indicators of oxidant and antioxidant status. Gene network analysis was performed for the first time for urinary infection and osteoarthritis, and 50 common genes were found. These common genes appear to be associated with arthritis, according to the KEGG pathway result. In the osteoarthritis group, MPO activity and MDA levels were higher, and CAT and SOD levels were lower ($P < 0.001$). CAT, SOD, MPO activity and MDA levels were higher in the urinary tract infection group compared to the control group ($P < 0.05$). MPO activity, and MDA levels were found to be higher in patients with concomitant osteoarthritis and in the group with urinary tract infection, and CAT and SOD activities were found to be significantly lower in the group with only tract infection ($P < 0.001$). This study revealed that the group with osteoarthritis and urinary tract infection showed different inflammatory reactions and caused an imbalance in the oxidant/antioxidant status. In addition, it was evaluated for the first time by network analysis and it was determined that which genes it was associated with and that these genes would lead other studies within the scope of this target.

Keywords: Gene set enrichment analysis (GSEA), KEGG Pathway