Meta-analysis of differentially expressed genes in ankylosing spondylitis

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ABSTRACT. The purpose of this study was to identify differentially expressed (DE) genes and biological processes associated with changes in gene expression in ankylosing spondylitis (AS). We performed a meta-analysis using the integrative meta-analysis of expression data program on publicly available microarray AS Gene Expression Omnibus (GEO) datasets. We performed Gene Ontology (GO) enrichment analyses and pathway analysis using the Kyoto Encyclopedia of Genes and Genomes. Four GEO datasets, including 31 patients with AS and 39 controls, were available for the meta-analysis. We identified 65 genes across the studies that were consistently DE in patients with AS vs controls (23 upregulated and 42 downregulated). The upregulated gene with the largest effect size (ES; -1.2628, P = 0.020951) was integral membrane protein 2A (ITM2A), which is expressed by CD4+ T cells and plays a role in activation of T cells. The downregulated gene with the largest ES (1.2299, P = 0.040075) was mitochondrial ribosomal protein S11 (MRPS11). The most significant GO enrichment was in the respiratory electron transport chain category (P = 1.67 x 10^-9). Therefore, our meta-analysis identified genes that were consistently DE as well as biological pathways associated with gene expression changes in AS.

Key words: Ankylosing spondylitis; Gene expression; Meta-analysis; Pathway analysis