Differential DNA Methylation as a Predictor of Tocilizumab Response in Rheumatoid Arthritis Patients

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THU0022

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Background: Early diagnosis of axial Spondyloarthritis (axSpA) represents a major clinical challenge nowadays. Increasing evidence has determined that early diagnosis, prompt treatment initiation and early achievement of remission are the best predictors of long-term clinical, functional, and radiographic outcomes. New tools to support the diagnosis are needed.

Objectives: This study aims to identify differentially expressed genes that may improve the current clinical diagnosis approach for early axSpA.

Methods: A cross-sectional study was conducted on 50 participants, 25 patients with axSpA (according to ASAS criteria) and 25 Healthy Controls, matched by gender, age, and levels of physical activity. Peripheral blood samples were collected and RNA-Seq technology was performed. Normalization of raw data, and identification of differentially expressed genes was obtained using edgeR and limma. Genes were classified as Gene Set Enrichment Analysis (GSEA) and Functional Enrichment analysis using Gene ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) annotations were also performed. A number of Differently Expressed Genes were highlighted.

Results: 311 genes were identified as being significantly differentially expressed between patients and controls. In details, 129 downregulated (7 genes have fold change more than 1) and 182 upregulated genes (3 genes have fold change more than 1) are highlighted. These genes are mostly involved in Myogenesis, Innate Immune Signalling and JAK/STAT pathways. Several genes with functions of skeletal muscle development and muscle contraction were identified.

Conclusion: The evidence disclosed that regulation of muscle development and contraction may be also engaged in pathophysiology mechanisms of axSpA. These new cues open new perspectives for diagnosis and therapeutic approaches in axSpA.

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THU0023

Detailed Profile of Co-Occurrence of Relapsing Polychondritis and Autoimmune Thyroid Disease

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Background: Relapsing polychondritis (RP) is a rare inflammatory disease, which is characterized by recurrent inflammation and destruction of cartilage tissues. RP also has the profile of autoimmune disease and is often complicated with other autoimmune disease. Autoimmune thyroid disease (AITD) is one of common autoimmune diseases, which consists of Graves' disease (GD) and Hashimoto's thyroiditis (HT). While RP is reported to be complicated with AITD1, there has been no study on detailed profile of co-occurrence of RP and AITD.

Objectives: We aimed to reveal whether there is common (statistically significant) co-occurrence of RP and AITD. We also analyzed clinical and genetic profiles characterizing the co-occurrence.

Methods: We recruited 117 patients with RP and checked their medical records in order to obtain the information about complication of AITD and clinical features. In addition, we genotyped Human Leucocyte Antigen (HLA) A, B, Cw, DRB1, DQB1 and DPB1 alleles for 88 of the 117 patients. Co-occurrence ratio was compared with prevalence of AITD in the Japanese population. Associations of co-occurrence of AITD with clinical manifestations or HLA alleles were analyzed among the patients.

References:

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