Pediatric Rheumatology

Oral presentation

14.4 Oligoarticular Juvenile Idiopathic Arthritis (JIA): can extension be predicted?

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Background

Oligoarticular JIA is presently unpredictable in its course and can become more severe after an initially mild onset. We examined the cellular and molecular composition of the first synovial fluid (SF) aspirates from oligoarticular JIA patients to discover markers that predict an increase in number of joints involved and thus, extension to more severe phenotype (extended oligoarticular JIA).

Methods

Flow cytometry was used to quantify T cells subsets, NK cells, B cells, dendritic cells, macrophages and other CD13+ cells in 33 (22 who had persistent outcome, 11 who later extended) synovial fluid mononuclear cell (SFMC) samples. From 22 of these (14 persistent, 8 who later extended) SFMC RNA were hybridized to Affymetrix U133v2 gene expression microarrays.

Results

Logistic regression produced a model that predicted extension correctly in 91% of the study group using CD8+ T cell, CD4+ T cell and CD19+ B cell proportions of the total live cells from each patient's SFMC. 62 genes were found to be 1.5-fold differently expressed between the two phenotypic groups with a significance of $p < 0.01$. A group of genes expressed in activated macrophages were among those more highly expressed in the extended outcome phenotype.

Conclusion

Our data suggest that in children with early oligoarthritis, deterioration of disease can be predicted by cell composition or gene expression from synovial fluid cells. If these findings are replicated in a new set of samples, they may represent a major step forward in our understanding of mechanisms governing severity in childhood arthritis.