Biomarkers predict long-term outcomes in juvenile idiopathic arthritis

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Data presented today at the European League Against Rheumatism Annual Congress (EULAR 2014) demonstrate the possibility of using biomarkers (developed from whole blood gene expression profiles) in children with juvenile idiopathic arthritis (JIA) to predict the status of their disease at 12 months. The long-term disease status at 12 months was accurately predicted only after treatment had been initiated, in newly diagnosed patients.[1]

JIA is the most common childhood (under the age of 16) chronic rheumatic disease,[2] affecting 16-150 children in every 100,000. As indicated by the name, the cause of JIA is largely unknown.[3]

"By predicting disease progression in these young children we can better understand the course of the disease and how best to treat the individual," said lead author of the study Professor James Jarvis, from the Department of Paediatrics, University at Buffalo, Buffalo, New York.

Blood gene expression profiling has led to major advances in the field of rheumatology over the last decade but to date it has only been possible to predict therapeutic outcome at 6 months.[4]

"The challenge was to test the feasibility of using these prognostic biomarkers from whole blood gene expression profiles in children with newly diagnosed JIA to predict disease status at one year," explained Professor Jarvis. "Baseline expression profiles that could predict disease

status at six months could not predict status at 12 months. However, using four month data (the earliest point at which samples were collected from children on treatment) we were able to determine strong predictive properties for disease status at 12 months. Thus, after children had initiated therapy longer term outcome was predictable," Professor Jarvis said.

In this study, researchers also discovered the appearance of different mechanisms of response in Rheumatoid Factor (RF) positive† and RF negative patients after four months of therapy, a finding that could explain the relative refractoriness of RF positive patients to otherwise effective therapies.

Whole blood expression profiles were studied from children enrolled in the TREAT study, an NIH‡-funded clinical trial comparing methotrexate (MTX) with MTX + etanercept in children with newly-diagnosed JIA. Gene expression profiles were examined to determine those genes whose expression levels best predicted outcome (active vs. inactive disease) at 12 months.

Researchers have described seven types of JIA, which are distinguished by their signs and symptoms, the number of joints affected, the results of laboratory tests, and the family history.[3] In general, symptoms include joint pain, swelling, tenderness and stiffness that last for more than six continuous weeks; the condition can also affect the eyes and lymph nodes.[3]

More information: [1] Yao J, Jiang K, Franks MB et al. Developing prognostic biomarkers from whole blood expression profiling in Juvenile Idiopathic Arthritis: Influence of early therapy on treatment outcome. EULAR 2014; Paris: OP0187

[2] Ravelli A, Martini A. Juvenile idiopathic arthritis. *Lancet* 2007;369:767

[3] National Institute of Arthritis and Musculoskeletal and Skin Diseases. What Is Juvenile Idiopathic Arthritis? www.niams.nih.gov/Health_Info/… hritis/default.asp#2 [Accessed 05/06/2014]

[4] Jiang K, Sawle AD, Barton Frank M, et al. Whole blood gene expression profiling predicts therapeutic response at six months in patients with polyarticular juvenile idiopathic arthritis. *Arthritis Rheumatol* 2014; 66 (5): 1363-71

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