Novel approach identifies unique DNA signature

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Researchers in Keele University's Research Institute for Science and Technology in Medicine and at the Haywood Rheumatology Centre, in Staffordshire, UK, and the University Hospitals of North Midlands NHS Trust, have for the first time identified disease-associated changes to the DNA epigenome in joint fluid cells from patients with rheumatoid arthritis.

These patients often develop swollen joints and the excess fluid represents an attractive source to harvest and study the cells that cause damage within the diseased joint without damaging the joint tissue itself.

The Epigenetics Research group used these cells to perform genome-wide profiling across more than 20,000 individual genes in these patients. This exciting new work has been published in the prestigious journal *Epigenomics*.

Dr John Glossop, first author of the publication, and colleagues identified a signature in these cells that uniquely distinguished patients with rheumatoid arthritis from those with other types of arthritis. Previous studies, where similar genes have been identified, have relied on cells from joint tissue obtained during joint replacement surgery. These important new data support the use of joint fluid as a readily available alternative to study the role of these changes in the onset of joint disease and in the clinical management of this condition.

Professor William Farrell, who led the study, said: "Many patients with rheumatoid arthritis have swollen joint and the fluid is taken off to relieve the symptoms of the disease. However, they provide a source for the collecting ("harvesting") of these cells surrounding the diseased joint.

"We are the first to publish these types of findings and, importantly it offers the opportunity to not only monitor the progress of the disease but also to determine if particular drugs/treatment are having an effect."

More information: "Genome-wide DNA methylation profiling in rheumatoid arthritis identifies disease-associated methylation changes that are distinct to individual T- and B-lymphocyte populations." *Epigenomics* 9(9):1228-1237 Sep 2014. DOI: 10.2217/epi.15.15

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