

Researchers identify epigenetic 'signatures' in immune cell populations

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Researchers based in the Keele University Research Institute for Science and Technology in Medicine and at the Haywood Rheumatology Centre in Stoke-on-Trent, in the UK, have identified fundamental differences between specific immune cell populations purified from whole blood.

These cells, known as B- and T-cells, are major contributors to both health and disease processes. Now, and for the first time, these findings provide a unique epigenetic "signature" in healthy, disease-free individuals, which will be key to the identification of [epigenetic changes](#) in disease, in particular for [rheumatoid arthritis](#) in which these cells play an important role.

These studies were performed by Dr John Glossop who examined more than 450,000 candidate sites in highly purified B- and T-[cell populations](#). In this way, Dr Glossop and colleagues were able to identify 250 genes that showed the same, highly consistent differences in each of the individuals investigated.

This ground-breaking work, funded by the Haywood Rheumatism Research and Development Foundation, has been published in the USA by a highly prestigious journal in this field, *Epigenetics*.

More information: Glossop, J. et al. Epigenome-wide profiling identifies significant differences in DNA methylation between matched-pairs of T- and B-lymphocytes from healthy individuals, *Epigenetics*, 2013 Sep 4;8(11).

Provided by Keele University

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