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).

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