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Craig G, Kenney H, Nilsson EE, Sadler-Riggleman I, Beck D, Skinner MK.

Epigenome association study for DNA methylation biomarkers in buccal and monocyte cells for female rheumatoid arthritis. Scientific Reports 2021 Dec 10;11(1):23789.

**Summary**

Genetics (i.e., mutations) has been assumed to be the major factor in rheumatoid arthritis (RA) etiology, but accounts for a minority of the variance in disease risk for RA. In contrast to genetics, the environment can have dramatic impacts on epigenetics that associate with disease etiology. The current study used buccal cells and purified blood monocytes from two different clinical cohorts involving Caucasian or African American female populations with or without arthritis. The differential DNA methylation regions (DMRs) between the control and RA populations were identified with an epigenome-wide association study. The DMRs (i.e., epimutations) identified in the buccal cells and monocytes were found to be distinct. The DMR associated genes were identified and many have previously been shown to be associated with arthritis. Observations demonstrate DNA methylation epimutation RA biomarkers are cell type specific and similar findings were observed with the two racial background populations. Rheumatoid arthritis susceptibility epigenetic diagnosis appears feasible and may improve the clinical management of RA and allowpreventative medicine considerations.