

Epigenetics, gene expression, and stress in mothers and offspring in the Democratic Republic of Congo: A biocultural investigation of the intergenerational effects of stress

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The field of social and behavioral epigenetics examines how social and behavioral experiences can cause epigenetically-driven changes in gene expression that in turn influence health and well-being. We work in the eastern Democratic Republic of Congo, where 20 years of conflict and post-conflict violence have subjected women to extreme stress and sexual violence.

We collected blood samples from mothers and their offspring at birth, plus follow-up samples from offspring up to five years of age, in three cohorts (2010 cohort, n=25; 2013 cohort, n=103, 2015 cohort, n=77). Using DNA extracted from blood and placental samples, we assayed methylation using Illumina's 450K and EPIC chips, telomere length, and gene expression using the ClariomS chip. We also collected ethnographic and survey data on maternal stress, newborn health outcomes, and cortisol from offspring saliva and hair samples. Using these data, we tested for associations among maternal stress, DNA methylation, gene expression, and offspring health outcomes.

We find that epigenetic aging is accelerated in mothers relative to chronological age, but newborn epigenetic age appears unchanged. In contrast, telomere length is significantly shorter in offspring born to mothers with high levels of war stress, but this effect only emerges after birth. Analyses of epigenome and gene expression data are ongoing. Our study takes a biocultural perspective to understand the molecular, biological, and health effects of stress and violence, particularly from an intergenerational perspective.

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