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Chromatin Accessibility Patterns in Peripheral Blood Cells as Predictors of Opioid Dependence and Recovery

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In North America, opioid use disorder (OUD) is a critical public health crisis, linked to over 80,000 opioid-associated deaths annually and an estimated \$1 trillion in costs over the past decade. Chronic opioid use is associated with transcriptomic and epigenetic brain changes that drive craving and relapse, perpetuating OUD. Currently, no technique can longitudinally monitor brain epigenetic mechanisms across drug addiction phases or treatment responses in humans. However, evidence suggests a connection between blood-based epigenetic mechanisms and brain changes. Epigenetic modifications in blood have been found to mirror alterations in the central nervous system including those seen in neuropsychiatric disorders, suggesting the potential of blood-based epigenetic markers as indicators of brain-related conditions. To investigate this, we conducted an assay for transposase-accessible chromatin with sequencing (ATAC-seq) and RNA sequencing (RNA-seq) on peripheral blood mononuclear cells (PBMCs). Pilot analyses were run on PBMCs from 85 non-opioid substance users and controls with associated clinical information. We further analyzed PBMCs from 180 controls and opioid-dependent individuals, identified per DSM-IV, with subjects on either buprenorphine or methadone maintenance therapy, sourced from the NIDA Center for Genetic Studies. We report changes in chromatin and transcriptomic profiles linked to immune system dysregulation and assess the correlation with clinical measures of opioid use. The reported differentially expressed genes and accessible genomic regions could serve as potential biomarkers of opioid dependence, use, and recovery. These data provide a foundation for developing scalable, cost-effective blood-based biomarkers to refine OUD diagnosis and support patient monitoring through recovery.