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Aberrant Epigenomic Modulations of Glucocorticoids Receptor Gene (NR3C1) as Causal Inference in Major Depressive Disorders (MDD): Quantitative Evidence synthesis (QES)

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Background: Major Depressive Disorder (MDD) reflects substantial psychiatric condition in the US. However reliable risk determinants are not very fully understood, which reflects not merely DNA sequence, but specific gene and several environment interactions, hence aberrant epigenomic modulation. This study aimed at assessing data on specific environmental factors associated with MDD and the NR3C1 inverse correlation.

Rationale/Significance: MDD is indicative of several risk determinants, and the application of these risks in MDD narrowing and ultimate elimination. This assessment is indicative of a risk reduction in several communities, hence MDD as well as bipolar marginalization.

Hypothesis: Specifically, environment and gene interaction as epigenomic modulation reflects abnormal epigenomic modulation involving NR3C1 increases MDD. The QES design with Desermonian-Laid, and combined effect size (CES), heterogeneity effect and Confidence Interval (CI) were utilized.

Results: The NR3C1 hypermethylation was associated with MDD, CES = 2.12, 95%CI, 0.63-4.86. With respect to sex, females were observed with increased CES, 2.88, 95%CI,1.98-6.33, relative to males, CES,1.34, 95%CI, 0.97- 7.04. Additionally, childhood trauma and substance used disorder increased MDD due to hypermethylation of NR3CI.

Discussion: With respect to MDD, which is associated with several risk factors without substantial knowledge on the gene-environment interaction as epigenomic, this study very critically observed specific environment adversely influenced the glucocorticoid receptor gene by increasing MDD in the US population.

Conclusion: The NR3C1 indicative of hyperpolarization of the post-synaptic neuron reflects MDD, implying the understanding of MDD environment such as isolation, discrimination, racism and substance use disorders within the US population; and intervention mapping.