Genome-wide DNA methylation analysis of peripheral blood for psychological resilience

Andrew Ke-Ming Lu[a], Shulan Hsieh[b], Cheng-Ta Yang[b], Po-Hsien Huang[c], Sheng-Hsiang Lin[a]

[a] *Institute of Clinical Medicine, College of Medicine, National Cheng Kung University, Tainan, Taiwan*
[b] *Department of Psychology, College of Social Sciences, National Cheng Kung University, Tainan, Taiwan*
[c] *Department of Biochemistry and Molecular Biology, College of Medicine, National Cheng Kung University, Tainan, Taiwan*

Background

Resilience is a process associated with an effective capacity to recover from difficult life events. To establish DNA methylation changes for psychological resilience in the genome, biological markers of psychological traits have been tested to reflect how methylation signatures may influence brain or neural functions and to identify the potential mechanisms of resilience functionalities. We aimed to evaluate the discriminant abilities of DNA methylation signatures between the high resilience and low resilience individuals and explain the individual differences in resilience behaviors, providing a greater understanding of resilience's biological basis.

Methods

In this study, a total of 16 individuals (ages ranging from 20 to 30 years old) were recruited and the study subjects were divided into two groups (i.e., the subjects with high resilience scores versus low resilience scores) based on Connor-Davidson Resilience Scale (CD-RISC). Genomic DNA was isolated from whole blood samples and then bisulfite-conversion was following standard procedures. The methylation status of bisulfite-converted DNA samples was assessed using the human MethylationEPIC 850K BeadChip scanning of global DNA methylation pattern and DNA methylation β-values at individual candidate CpG sites. And then we conducted enrichment analysis to find potential biological pathways based on significant probes.

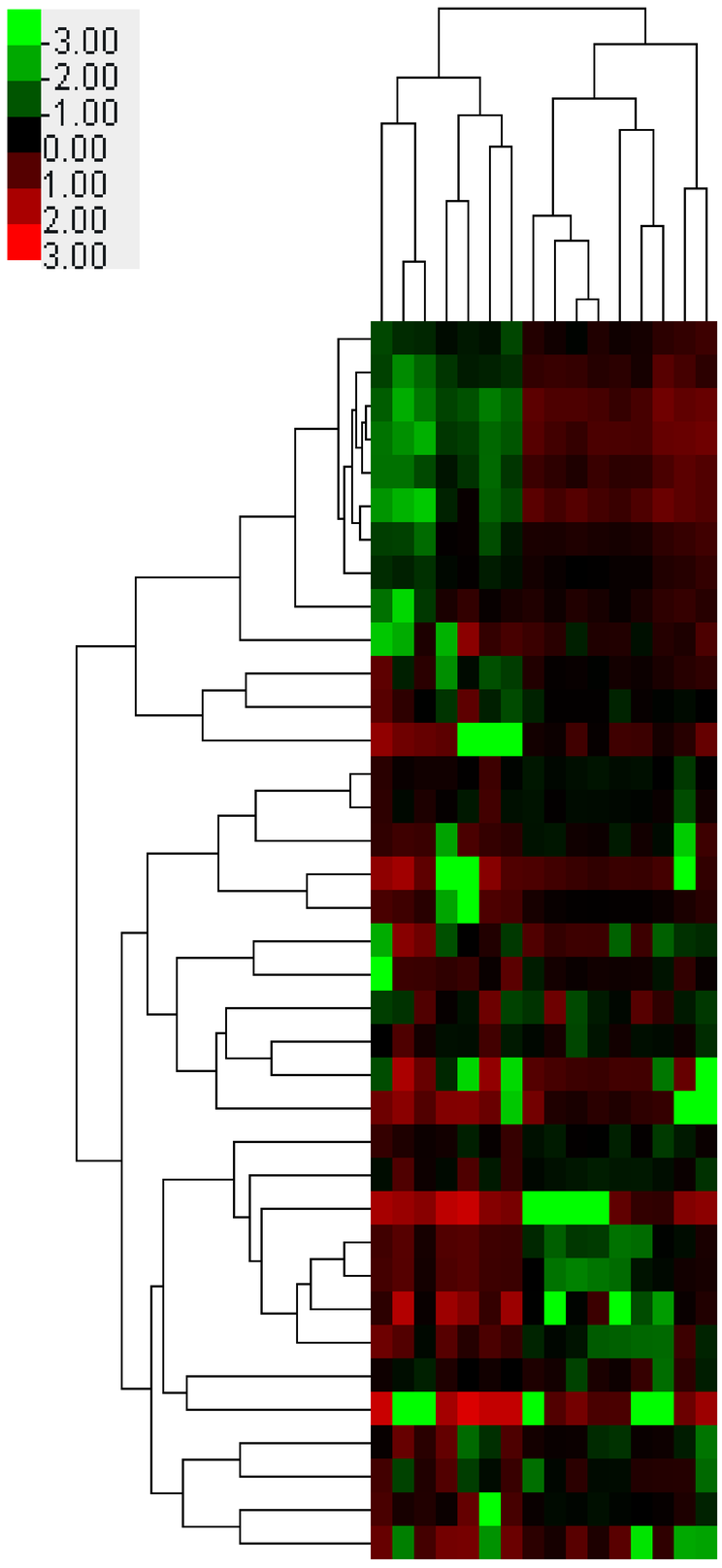

Figure 1. Heatmap of differentially methylated probes with >20% differences between the HR and the LR groups.

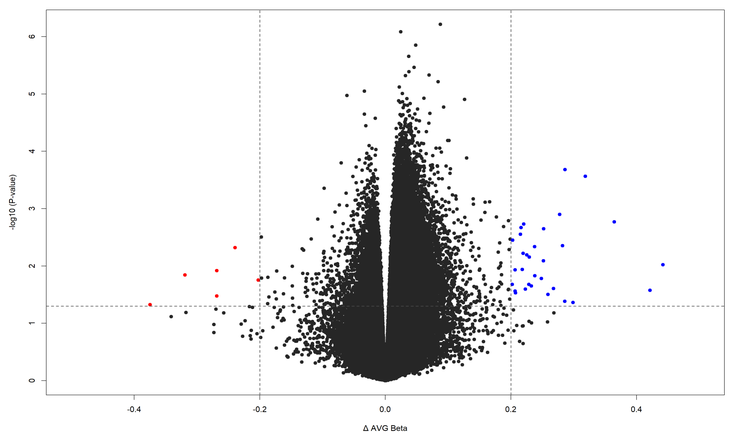

Figure 2. Volcano plot of differentially methylated probes with >30% differences between the HR and the LR groups.

Results

Based on genome-wide scans of 16 individuals (8 high resilience individuals versus 8 low resilience individuals), 37 differentially methylated probes were identified at FDR<0.05 and >20% differences in DNA methylation β-values. These differentially methylated CG probes and the CpG island-associated genes were analyzed with Enrichr databases. Our results identified five biological functional genesets that might associate with psychological resilience: (1) magnesium (P=0.003019); (2) brain (P=0.007519); (3) child behavior (P=0.016034); (4) positive regulation of oxidative stress-induced neuron death (P=0.004243); (5) regulation of oxidative stress-induced neuron intrinsic apoptotic signaling pathway (P=0.005936).

Conclusion

In the current analysis, the results showed DNA methylation differences between the high and low resilience individuals which may further affect pathways of neural functionalities. And these neural physiology functions may affect psychological resilience. In the future, discovering the physiological roles of candidate genes linked to psychological resilience may help to explore the association between psychological resilience and psychiatric disease.