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A DIFFERENT DNA METHYLATION PROFILE IS OBTAINED FROM A RECENTLY PUBLISHED MZ STUDY OF PSYCHIATRY

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Aim: To get a more robust DNA methylation profile from the data given by a published article of a MZ study of psychiatry.

Method: Considering the relevance of birth weight with DNA methylation profiles, we reanalyzed the data from the paper of Mill etc. (DOI: 10.1002/ajmg.b.30316) with rearrangement of the group order within twin pair, prior if lighter in birth weight. Statistical methods used are including mean, correlation and paired-samples t-test (considering twins' particularity).

Results: We calculated twin difference by lighter twin's methylation percentage minus that of heavier twin. The mean of CpG1 methylation differences is -7.08% while -7.17% for CpG2. The two means have no statistical significant difference in a paired-samples t-test ($t=0.027$, $p=0.979$, 2-tailed). These results are different from the original paper: 10.3% for CpG1 and 16.1% for CpG2, which are statistical significantly different ($t=-2.792$, $p=0.018$, 2-tailed). Besides, we found that in the lighter twin group, the methylation percentage are statistical significantly different between CpG1 and CpG2 ($t=2.627$, $p=0.024$, 2-tailed). As to correlation analysis, we got a slightly different result: correlation between MZ differences in two sites is weaker after rearrangement ($r=0.875$, while $r=0.913$ before arrangement, both $p < 0.001$).

Conclusion: According to our study, the results imply that twin differences may not be the only thing worthy of investigation. Different patterns among CpGs in certain kinds of subgroups should also need attention. We need conduct a robust data analysis strategy in our researches on the epigenetic aspects of psychiatry, where monozygotic twins have a favorable utility.