**Press release: European College of Neuropsychopharmacology**

# *Strict parenting may hard-wire depression risk into a child's DNA*

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Strict parenting can alter the way the body reads the DNA of the children. These changes can effectively become 'hard-wired' to the DNA of those children who perceive their parents as harsh, increasing their biological risk for depression in adolescence and later life.

Presenting the work at the ECNP Congress in Vienna, Dr Evelien Van Assche said:

*"We discovered that perceived harsh parenting, with physical punishment and psychological manipulation, can introduce an additional set of instructions on how a gene is read to become hard-wired into DNA. We have some indications that these changes themselves can predispose the growing child to depression. This does not happen to the same extent if the children have had a supportive upbringing".*

The researchers, from the University of Leuven in Belgium, selected 21 adolescents who reported good parenting (for example, the parents being supportive and giving the children autonomy), and compared them with 23 adolescents who reported harsh parenting (for example, manipulative behaviour, physical punishment, excessive strictness). All adolescents were between 12 and 16 years old, with a mean of 14 years for both groups. For both groups 11 adolescents were boys meaning that the two groups were comparable, with a similar age and a similar, boy-girl distribution. Many of those who had experienced harsh parenting showed initial, subclinical signs of depression.

The researchers then measured the range of *methylation* at more than 450,000 places in the DNA of each subject and found that this was significantly increased in those who reported a harsh upbringing. Methylation is a normal process which occurs when a small chemical molecule is added to the DNA, changing the way that the instructions written in your DNA are read: for example, methylation may increase or decrease the amount of an enzyme produced by a gene. Increased variation in methylation is known to be associated with depression. Evelien Van Assche said "*We based our approach on prior research with identical twins. Two independent groups found that the twin diagnosed with major depression also had a higher range of DNA methylation for the majority of these hundreds of thousands of data points, as compared to the healthy twin".*

Dr Van Assche (now working at the University of Munster, Germany) continued "*The DNA remains the same, but these additional chemical groups affect how the instructions from the DNA are read. Those who reported harsher parenting showed a tendency towards depression, and we believe that this tendency has been baked into their DNA through increased variation in methylation. We are now seeing if we can*

*close the loop by linking it to a later diagnosis of depression and perhaps use this increased methylation variation as a marker, to give advance warning of who might be at greater risk of developing depression as a result of their upbringing*".

*In this study we investigated the role of harsh parenting, but it's likely that any significant stress will lead to such changes in DNA methylation; so in general, stresses in childhood may lead to a general tendency to depression in later life by altering the way your DNA is read. However these results need to be confirmed in a larger sample".*

Commenting, Professor Christiaan Vinkers, Department of Psychiatry, Amsterdam University Medical Centre, said:

*"This is extremely important work to understand the mechanisms how adverse experiences during childhood have life-long consequences for both mental health and physical health. There is a lot to gain if we can understand who is at risk, but also why there are differing effects of strict parenting".*

Professor Vinkers was not involved in this work, this is an independent comment.

*This work is presented at the 35th European College of Neuropsychopharmacology annual conference, which takes place in Vienna and online from 15-18 October, see https://www.ecnp.eu/Congress2022/ECNPcongress. Up to 5000 delegates are expected to attend. The ECNP is Europe's main organisation working in applied neuroscience.*

*Press release labelling system for journalists, see https://tinyurl.com/3kww75hy for details.

## Notes for Editors

Abstract

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**Introduction:** Epigenome-wide DNA methylation studies are well suited to investigate the link between environmental exposure and the development of psychopathology, such as depression or depressive symptoms. Epigenome-wide studies can focus on specific differential methylation at loci or regions. Methylation can also be seen as a general genome regulation marker by looking at it as a whole and interpreting its genome-wide variability. Studies looking into depression, find consistently increased overall variability over methylation loci in the affected group, as compared to the non-affected group. We set out to investigate epigenome-wide DNA methylation levels in adolescents, relating those to a relevant, environment factor, i.e., perceived parenting. We compare perceived 'good' (authoritative) parenting to the generally more adverse and stressful perceived 'bad' (authoritarian) parenting.

**Aim:** Can exposure to a stressful everyday life-environment in adolescence can alter epigenome wide variability, as also seen at a depression diagnosis later in life? We hypothesize that DNA methylation variability can reflect current exposure to chronic stress, potentially acting as an endophenotype and preceding a formal diagnosis of depression in adulthood.

**Methods:** The study is part of the STRATEGIES cohort. A cluster analysis on 1,103 adolescents (Mean age = 13.79 (SD = 0.94); 51% Boys), identified two extreme perceived parenting conditions, authoritative ('good') and authoritarian ('bad') based on the four subscales of the Leuven Adolescent Perceived Parenting Scale (LAPPS), four subscales of

the shortened version of the Parental Behavior Scale (PBS-short), the hostility subscale of the Verbal Hostility Scale, and the Behavioral Control Scale. From these two clusters 45 adolescents were randomly drawn, balanced for age and gender, for a 450k epigenome-wide DNA methylation analysis with an Illumina Infinium HumanMethylation 450 BeadChip. After QC 465,031 probes were available on 44 individuals. Depressive symptoms were measured through the CES-D scale. DNA-wide methylation differences were calculated through a Wilcoxon Signed Rank test. Data were analysed using R (including package RnBeads).

**Results:** Depressive symptoms were significantly different between both parenting groups ($F(1,42) = 9.14$, $p=0.0042$). The variability of DNA methylation comparing both groups regarding the full set of CpGs, showed that there is a shift in variability between the two groups. Epigenome wide variability as measured by differences in standard deviations per CpG between the two groups were significant between the 'good' perceived parenting and 'bad' perceived parenting groups (Wilcoxon Signed Rank test: $V = 4.48\times10^{10}$; median estimate:$-5.84\times10^{-4}$; $p < 2\times10^{-16}$). The 'bad' parenting group showed higher overall DNA methylation variability than the 'good' parenting group.

**Conclusion:** We show that increased variability in DNA methylation is already present in adolescents experiencing adverse parenting and subclinical depressive symptoms, consistent with previous results. These findings can indicate that environmental stress can influence DNA methylation regulatory mechanisms which could lead to a higher overall variability for the chronic stress-exposed group. The results fit in the growing evidence that chronic adversity, such as perceived bad parenting, is associated with DNA methylation alterations. They also support the notion that epigenomic overall variability in DNA methylation itself could act as an endophenotype, reflecting chronic exposure to adverse circumstances in adolescence.

References

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