

European College of Neuropsychopharmacology – press release

[Study shows DNA of people with childhood abuse or depression ages faster](#)

For immediate release, Sunday 7th October 2018

*Type of study: case-control study/peer reviewed/people*

**Barcelona, 7th October:** DNA from people who suffer from major depression is biologically older than that of healthy people by on average 8 months, suggesting that they are biologically older than their corresponding calendar age. This effect was greater in people who have had childhood trauma, such as violence, neglect or sexual abuse, who show a biological age around a year older than their actual age. This work is presented at the ECNP conference in Barcelona\*.

There is increasing evidence that serious depression and trauma is associated with shorter life-spans. Now an international team of researchers has shown that major depression causes measurable changes in the in the DNA of sufferers, giving values which correspond to those of older people.

Working with 811 depressed patients and 319 control subjects from the Netherlands Study of Depression and Anxiety, the team studied how their DNA extracted from blood samples was changed with age. The genetic material DNA is often processed in the body by *methylation*, which is when a methyl group (CH<sub>3</sub>) is added to the DNA. DNA methylation is a way the body allows gene function to be modified without changing the DNA sequence itself.

According to lead researcher, Laura Han (from the Amsterdam UMC, Amsterdam), *“What we see is in fact an ‘epigenetic clock’\*\*, where the patterns of modification of the body’s DNA is an indicator of biological age. And this clock seems to run faster in those who are currently depressed or have been stressed”*.

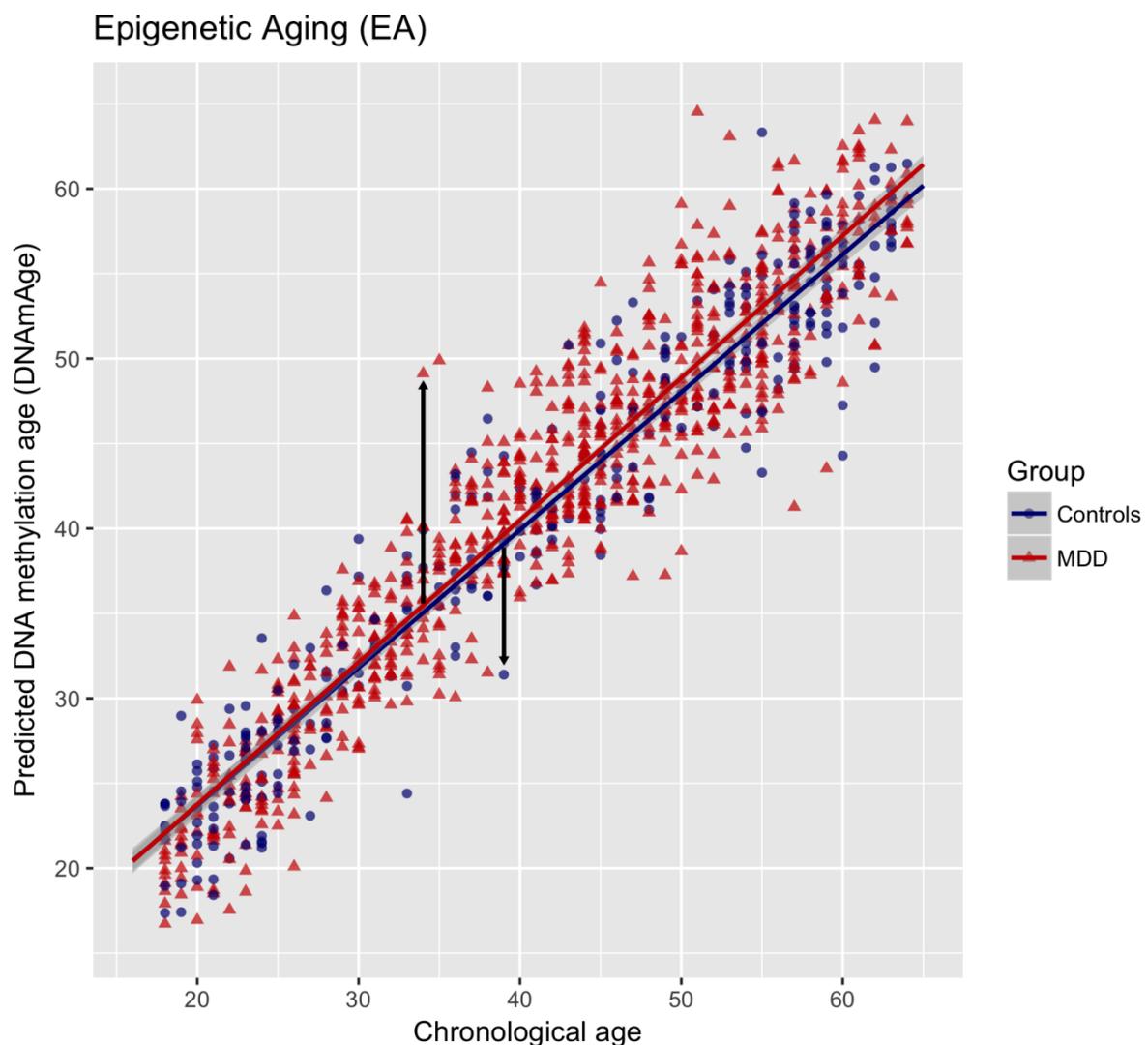
On average the team found that patients with Major Depressive Disorder (MDD) showed a degree of DNA methylation which corresponded to an increased age; biologically, they were on average 8 months older than healthy control subjects. In some cases of extreme depression, patients were found to have a biological age of 10 to 15 years older than the chronological age. The team checked the finding by examining post-mortem brain samples, of 74 depressed patients and 64 control subjects, and found similar results in brain tissue.

Laura Han commented, *“The fact that we saw similar results in both blood samples and post-mortem brain tissue helps support the belief that this is a real effect we are seeing”*.

Participants were also questioned about trauma, such as emotional neglect, sexual or physical abuse experienced before the age of 16. On average, those in the study who had undergone childhood trauma had a body clock 1.06 years older than the controls.

*“This work shows that methylation levels at specific loci increase and decrease with age, and so this pattern of methylation is a good indicator of biological age. This difference becomes more apparent with increasing age, especially once people move into their 50s and 60s. We also found that where people had been subject to stressors such as childhood trauma, or Major Depressive Disorder, they showed a degree of DNA methylation which corresponded to that of older people. ”*

*“When we look within the group of depressed individuals, we see that childhood traumas experienced before the age of 16 were associated with even more pronounced epigenetic aging later in life. Of course, these are associations, so we need long-term linked studies (longitudinal studies) to be able to draw any conclusions whether the trauma causes the epigenetic aging”.*



*Graph shows that DNA methylation age increases with chronological age, and increasing divergence of DNA methylation based age predictions between controls and depressed patients over time*

This discovery that DNA methylation changes with age may have several practical consequences. For example, it may be useful as an early-warning sign of risk for certain age-related diseases, especially with those at the extremes who show significant shifts in their epigenetic clock. However, the major use of this technique may be less to do with individual health, but more to do with how it might help us see ageing at a population (epidemiological) level.

Commenting, Professor Katharina Domschke, University of Freiburg, Germany (who was not involved in the work) said:

*“This work extremely important as it signifies the biological impact of trauma and depression on an epigenetic level and the necessity to employ preventive as well as early therapeutic interventions not only with regard to trauma-related depressive disorders per se, but also with respect to age-related somatic as well as mental disorders.”*

Notes:

\*A peer-reviewed paper based on this work was recently published, see Han, L et al. (2018). Epigenetic Aging in Major Depressive Disorder. *American Journal of Psychiatry*, *appi.ajp.2018.1*. <http://doi.org/10.1176/appi.ajp.2018.17060595>. None of the comments here are present in the published paper.

\*\* [Epigenetics](#) is the study of patterns of gene expression regulation that do not involve changes to the underlying DNA sequence.

For funding information, see Notes for Editors

## ENDS

### Notes for Editors

*Please mention the ECNP Congress in any story resulting from this press release.*

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#### **The European College of Neuropsychopharmacology (ECNP)**

The ECNP is an independent scientific association dedicated to the science and treatment of disorders of the brain. It is the largest non-institutional supporter of applied and translational neuroscience research and education in Europe. Website: [www.ecnp.eu](http://www.ecnp.eu)

The 31st annual ECNP Congress takes place from 6<sup>nd</sup> to 9<sup>th</sup> September in Barcelona. It is Europe's premier scientific meeting for disease-oriented brain research, annually attracting between 4,000 and 6,000 neuroscientists, psychiatrists, neurologists and psychologists from around the world. Congress website: <https://2018.ecnp.eu/>

Conference abstract (S.14.08)

**Epigenetic aging in major depressive disorder**

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Major depressive disorder (MDD) is associated with increased risk of mortality and aging-related diseases[1,2,3]. The authors examined whether MDD is associated with higher epigenetic aging (EA)[4] in blood as measured by DNA methylation (DNAm) patterns, whether clinical characteristics of MDD have a further impact on these patterns, and whether findings replicate in brain tissue.

DNAm age was estimated using all methylation sites in blood of 811 depressed patients and 319 control subjects from the Netherlands Study of Depression and Anxiety. The residuals of the DNAm age estimates regressed on chronological age were calculated to indicate EA. MDD diagnosis and clinical characteristics were assessed with questionnaires and psychiatric interviews. Analyses were adjusted for sociodemographic characteristics, lifestyle, and health status. Postmortem brain samples of 74 depressed patients and 64 control subjects were used for replication. Pathway enrichment analysis was conducted using ConsensusPathDB to gain insight into the biological processes underlying EA in blood and brain.

Significantly higher EA was observed in MDD patients compared with control subjects, with a significant dose effect with increasing symptom severity in the overall sample. In the depression group, EA was positively and significantly associated with childhood trauma score. The case-control difference was replicated in an independent dataset of postmortem brain samples. The top significantly enriched Gene Ontology terms included neuronal processes.

As compared with control subjects, MDD patients exhibited higher EA in blood and brain tissue, suggesting that they are biologically older than their corresponding chronological age. This effect was even more profound in the presence of childhood trauma.

## References

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