

Researchers one step closer to preventing preeclampsia

March 14 2024



Credit: *Physiological Genomics* (2024). DOI: 10.1152/physiolgenomics.00058.2023



Researchers have identified several differences in DNA methylation in people who experienced preeclampsia during pregnancy, according to a new study from Oregon Health & Science University. The study also revealed these differences appear to occur in connection to genes relevant to the disease. The <u>study</u> is published in *Physiological Genomics*.

DNA methylation is a chemical modification of the DNA in which <u>methyl groups</u> (a combination of atoms) are added to the DNA molecule. Methylation can change the activity of a gene without changing its sequence, basically acting as a "light switch." If you think of genes as light bulbs, DNA methylation is the on/off switch. When and where in the body this switch is turned on/off will impact development, aging and occurrence of diseases.

Preeclampsia is a hypertensive disorder of pregnancy that affects approximately 2%-5% of all pregnancies. The disease contributes to four of the top 10 causes of pregnancy-related deaths and remains a long-term risk factor for cardiometabolic diseases. Yet, little is still known about the <u>molecular mechanisms</u> that lead to <u>preeclampsia</u>.

The study's purpose was to determine to what degree pregnant people with preeclampsia showed differences in the makeup of inherited genes compared to those with normal pregnancies. Researchers analyzed global DNA methylation among three groups:

- Individuals who experienced early-stage preeclampsia (less than 32 weeks).
- Those with late-stage preeclampsia (greater than 37 weeks).
- Those with no complications during their pregnancies.

The researchers also studied DNA from the children born from these



three groups. They found significant differences in regions near or within genes that are important for placentation, <u>embryonic development</u>, <u>cell adhesion</u> and inflammation between women who experienced preeclampsia compared to those with no complications.

"People who have had preeclampsia have greater risks for <u>cardiovascular</u> <u>disease</u> after the pregnancy, and their offspring are more likely to have cardiovascular conditions and die of stroke," said Kent L. Thornburg, Ph.D., a professor emeritus and one of the study's authors.

"If we can identify DNA methylation patterns in genes associated with the disease, we will have much clearer strategies to prevent the disease. Moreover, we might be able to develop biomarkers that can help preventative intervention. Our next step is to determine which of these genes were altered before pregnancy and which are the result of the disease itself."

More information: Cora E. Layman et al, High-throughput methylome analysis reveals differential methylation for early and late onset preeclampsia for mothers and their children, *Physiological Genomics* (2024). DOI: 10.1152/physiolgenomics.00058.2023

Provided by American Physiological Society

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