Novel biomarker approach suggests new avenues to improve schizophrenia disease management

January 9 2014, by Eric Peters

Karolina Aberg, Ph.D., is the associate director of the VCU School of Pharmacy's Center for Biomarker Research and Personalized Medicine. Credit: Virginia Commonwealth University

Environmental effects of events such as oxygen deprivation and infections may be preserved as markers in blood that are associated to schizophrenia, according to an international study led by the Virginia

Commonwealth University School of Pharmacy's Center for Biomarker Research and Personalized Medicine.

"These markers, possibly from as early as embryonic development or birth, could be of considerable clinical importance as they could allow for identification of distinct schizophrenia subtypes or help predict treatment responses," said Karolina Aberg, Ph.D., associate director of the Center for Biomarker Research and Personalized Medicine and first author of the study.

Schizophrenia is a devastating psychiatric disorder. Although there is strong support for the involvement of DNA sequence variation in the development of the disorder, other factors such as environmental influences are also likely to play a major role.

The research team performed one of the first large-scale, methylome-wide association studies (MWAS) of schizophrenia, as detailed online in the January issue of *JAMA Psychiatry*, the JAMA Network journal.

"Methylation is a specific modification to the DNA molecule that could potentially reflect environmental events," said Edwin van den Oord, Ph.D., director of the Center for Biomarker Research and Personalized Medicine and senior author of the study. "Therefore, DNA methylation studies are very promising complements to traditional genetic studies that potentially can give us a deeper understanding of the schizophrenia disease etiology."

In this study, researchers investigated approximately 27 million DNA methylation markings in blood samples from 1,497 schizophrenia cases and controls.

This methylome-wide screening was performed by extracting the methylated portion of the genome and then investigating this portion

with massively parallel next-generation sequencing. To ensure that the findings from this screening were not false findings caused, for example, by method-specific artifacts or statistical errors, researchers used a different technology to follow up the critical top findings in independent subjects who were not part of the initial screening step.

The study identified 139 highly significant methylation sites. Many of the replicating markings could be linked to hypoxia, immune response and neuronal differentiation, which are risk factors previously associated with schizophrenia development.

Provided by Virginia Commonwealth University