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Researchers define two categories of multiple sclerosis patients

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There are approximately 400,000 people in the United States with multiple sclerosis. Worldwide, the number jumps to more than 2.1 million people. Rather than a one-size-fits-all approach to treating the millions with multiple sclerosis, what if doctors could categorize patients to create more personalized treatments? A new study by researchers at Brigham and Women's Hospital (BWH) may one day make this idea a reality in the fight against the debilitating autoimmune disease.

A research team led by Philip De Jager, MD, PhD, BWH Department of Neurology, senior study author, has found a way to distinguish patients with multiple sclerosis into two meaningful subsets. The ability to categorize patients with multiple sclerosis may open new doors for treatment development.

The study will be electronically published on September 26, 2012 in *Science Translational Medicine*.

"Our results suggest that we can divide the multiple sclerosis patient population into groups that have different levels of disease activity," said De Jager. "These results motivate us to improve these distinctions with further research so that we may reach our goal of identifying the best treatment for each individual who has multiple sclerosis."

De Jager and his team extracted RNA—key molecules involved in making proteins from the instructions found in the DNA sequence—from blood cells of patients with multiple sclerosis. After

analyzing the samples, they found distinct sets of RNA molecules among the patient samples. These unique sets formed a transcriptional signature that distinguished two sets of multiple sclerosis patients—MSa patients and MSb patients—with those in the MSa group having a higher risk for future multiple sclerosis relapse.

According to the researchers, knowing the category a person with multiple sclerosis is in may help doctors make more informed treatment decisions. For instance, since a patient who falls into the MSa category is more likely to experience relapse, her doctor may consider a stronger treatment for the patient.

In light of the discovery, the researchers remain cautious about the findings.

"Our study is an important step towards the goal of personalized medicine in MS, but much work remains to be done to understand under which circumstance and in combination with which other information this transcriptional signature may become useful in a clinical setting," said De Jager.

However, from the pre-clinical perspective, the researchers recognize that the findings are essential because they build on earlier studies that had suggested that this structure might be present.

"The study will further enable the community of MS researchers to build upon this transcriptional signature with other data in order to enhance patient care in the future," said De Jager.

Provided by Brigham and Women's Hospital