Study finds common genetic variants that double risk for blood clots in African Americans

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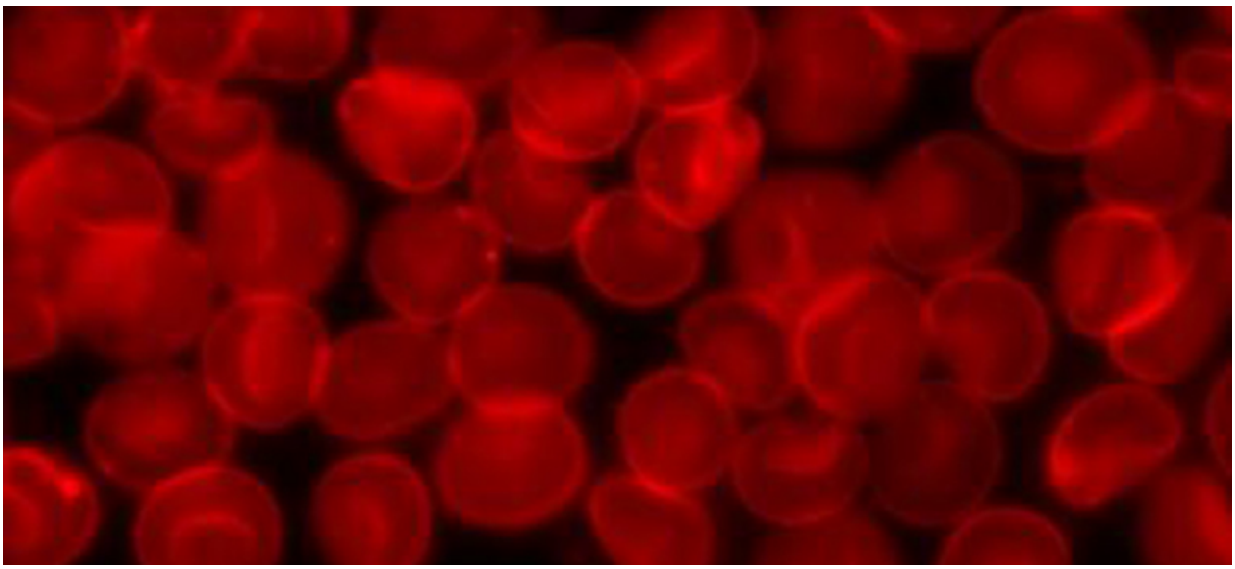

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New research published online today in *Blood*, the Journal of the American Society of Hematology (ASH), identifies common genetic variants predominantly found in African Americans that double their risk for blood clots.

Venous thromboembolism (VTE) is a disorder characterized by blood clots that form in the deep veins of the legs that can travel to the lungs

and become fatal. Those who suffer from VTE often have one or several alterations in their DNA that affect normal function of the blood's clotting process. Genotyping individuals to identify these genetic variants can help predict their risk. This study reports that the one-size-fits-all approach of looking for the same variants in all populations does not serve minorities, and the authors conclude that African Americans clearly require a specific approach when their risk for VTE is assessed.

In the United States, African Americans are 30 to 60 percent more likely to suffer from VTE than any other U.S. population. Despite this higher incidence, well-known genetic risk factors for VTE, such as factor V Leiden, are common in Caucasians but occur infrequently in African Americans with the disorder. This realization led researchers to hypothesize that there might be undiscovered genetic variants more specific to African Americans.

"While African Americans have a high risk for VTE, previous studies have not specifically focused on this population," said senior study author Minoli Perera, PhD, of the University of Chicago. "If we are not looking for the correct genetic mutations when we run a laboratory test, we are doing a disservice to minority populations."

To understand the genetic risk factors for VTE specific to African Americans, a team of researchers led by Dr. Perera conducted a genome-wide association study in which they genotyped DNA samples from 578 African Americans, 146 of whom had a history of unprovoked VTE. Next, they confirmed the variants deemed highly prevalent in the first group by genotyping the DNA of an additional group of 159 African Americans, including 94 with VTE.

Based on their analysis, researchers identified a link between VTE and three variants in a chromosome associated with decreased expression of thrombomodulin, a protein that regulates clotting: rs2144940,

rs2567617, and rs1998081. Investigators suggest that the presence of one of these three variants doubles the risk for VTE. Approximately 36 percent of African Americans have at least one of these variants. Surprisingly, these variants were found in much lower frequency in other ethnicities from previous studies.

"This study not only brings us closer to understanding the cause of VTE in African Americans, it demonstrates the importance of conducting population-specific research in precision medicine," said Dr. Perera. "Our next steps will involve investigating the predictiveness of these risk factors for VTE with the goal of reducing the high prevalence and burden of VTE in this disproportionately affected population."

Provided by American Society of Hematology