ASSOCIATION OF ALLELES FROM INFLAMMATORY, VASO-ARCHITECTURE, AND COAGULATION PATHWAYS WITH CLINICAL CHARACTERISTICS OF A DEEP VEIN THROMBOSIS

ACC Poster Contributions
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Background: There has been little research in determining the role genetics plays in the clinical presentation of a deep vein thrombosis (DVT). Characteristics such as pulsatility, thrombolysis, propagation and the potential for recurrence all affect the presentation, outcomes and risk of long term complications from a DVT. Genetic factors that affect vein architecture, flow rates, and platelet aggregation may play a role in the clinical presentation of this event.

Methods: Subjects were participants in the Marshfield Clinic's Personalized Medicine Research Project (PMRP) who experienced a DVT between 2003 and 2006 (n=1091). Individual chart review was performed to extract clinical characteristics of each thrombus including the location of the thrombus, pulsatility of the thrombus, if propagation of the thrombus occurred, whether there was spontaneous thrombolysis, and any previous or recurrent DVT events. Genotyping was performed previously on this population for a number of polymorphisms (n=51) including many involved in vasomotor tone, immune activation and coagulation.

Results: Polymorphisms in a number of genes were associated with clinical features of DVT. For instance, aggregation factor VWF (RS1093856), was associated with both propagation of DVT and recurrence. EDN1 (RS5370) and MMP2 (RS243865), both genes expressed in endothelial cells were associated with recurrence of DVT. Genes previously associated with cardiovascular disease such as APOE (E4 haplotype), APOB (RS1042031), and AGTR1(RS5186) were associated with pulsatility in DVT. Genes involved in inflammation such as CFTR (RS213950) and CTLA4 (RS231775) were also associated with the clinical presentation of the DVT.

Conclusions: This hypothesis generating study used multiple risk alleles from vaso-architecture, inflammatory, and coagulation pathways to identify genes that are important in the clinical presentation of DVT. This study represents one of the first steps toward incorporating alleles from all of these pathways to identify at risk individuals through multi-gene screens.