

The Role of Complement Cascade in Abdominal Aortic Aneurysms

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Abdominal aortic aneurysm (AAA) is a dilatation of the infrarenal aorta and typically affects individuals over the age of 65. AAA is considered a complex genetic disorder with many genetic and environmental risk factors. Mechanisms known to be involved include: inflammation, extracellular matrix degradation, oxidative stress, and vascular smooth muscle cell apoptosis. To identify biological mechanisms leading to the development of AAA, pathway-based analysis was carried out. Results of the genome-wide microarray expression profiling showed 3,274 differentially expressed genes between aneurysmal and control aortic tissue. Interestingly, numerous genes in the complement cascade were differentially expressed. The complement cascade is a known modulator of inflammatory pathways, which have been strongly implicated in AAA pathogenesis in previous studies. *In silico* analysis demonstrated that the promoters of these genes have binding sites for transcription factor STAT5. Immunohistochemical analysis showed strong staining for complement factor 2 (C2) protein in AAA tissues. These results combined with previously published animal studies by other investigators suggest that complement cascade plays a role in AAA.