Abdominal aortic aneurysm (AAA) is a common and potentially life-threatening medical condition with substantial economic consequences for the health system. The underlying problem of this disease is constant weakening of the aortic wall, which left untreated can result in progressive dilatation and eventual rupture, being responsible for about 2% of deaths worldwide. Surgical procedure is the only efficient treatment for patients with aneurysms; however, it is still associated with high risk of major perioperative complications, including stroke, cardiovascular events and death. On the other hand, at the moment there is no evidence that any specific treatment (drug, diet, or exercise) can inhibit AAA enlargement.

Pathogenesis of AAA is still unclear, however recent studies indicate possible role of dysregulated systemic immune response in this process. Some evidence even suggest that aneurysms could be treated as a systemic autoimmune disease. Therefore, the aim of this proposal is to clarify the possible role of lymphocytes associated traditionally with autoimmune processes (Th17 and Treg) in the formation of aneurysms. Moreover, we would like to investigate if regulation on posttranscriptional level mediated by microRNA molecules could affect differentiation Th17 lymphocytes from naïve CD4+ cells obtained from AAA patients. Especially, we assume that:

1. There is an imbalance between proinflammatory Th17 cells and regulatory T cells among patients with AAA.
2. Level of Th17 cytokines is elevated in aneurysmal tissue compared to unchanged one.
3. Induction of miR-21 overexpression in naïve lymphocytes causes differentiation to Th17 phenotype.

To verify hypotheses mentioned above, series of experiments will be performed using serum, peripheral blood cells (PBMC) and aortic tissue obtained from patients with AAA. This approach will allow us to construct a model of Th17 and Treg contribution in pathogenesis of abdominal aortic aneurysm, including epigenetic regulation mediated by microRNA. In addition, we will be able to indicate pathways which could be a target for novel therapies for AAA.