Risk gene for severe heart disease discovered

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Research led by Klaus Stark and Christian Hengstenberg of the University of Regensburg identified a common variant of the cardiovascular heat shock protein gene, HSPB7, which was found to increase risk for dilated cardiomyopathy by almost 50%. Their paper appears on October 28 in the open-access journal *PLoS Genetics*.

Per year, about 6 in 100,000 individuals develop dilated cardiomyopathy (DCM), with a higher prevalence in men. This disease is characterized by an enlarged, weakened heart, subsequently affecting the pumping capacity and often leading to chronic heart failure.

Those cases of DCM that occur in certain family groups are associated with a number of mutations affecting muscle cells. However, most cases are of unknown cause. To identify risk alleles for non-familial forms of DCM, an international collaboration of scientists analyzed the contribution of common gene variants to the more frequent, sporadic form of dilated cardiomyopathy, by conducting a large-scale genetic association study with more than 5,500 subjects. Different study groups from Germany and France contributed both well-characterized DCM patients and healthy controls. The HSPB7 gene was strongly associated with susceptibility to DCM.

The researchers concluded that, while genetic testing for this variant is not suitable to date, the findings are a first step towards supporting future preventive measures for this severe form of heart muscle disease.

More information: Stark K, Esslinger UB, Reinhard W, Petrov G,

Winkler T, et al. (2010) Genetic Association Study Identifies HSPB7 as a Risk Gene for Idiopathic Dilated Cardiomyopathy. *PLoS Genet* 6(10): e1001167. doi:10.1371/journal.pgen.1001167