# Genomics of atrial fibrillation

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Atrial fibrillation (AF) is a supraventricular arrhythmia characterized by an uncoordinated atrial activation and contraction. It represents a major clinical, social and economical burden, and its importance is expected to increase even more in the near future. Over the last seven years, data have emerged to support a genetic contribution to AF. New mutations and gene variants that may predispose to the development of familial AF and sporadic AF will be identified in two genome-wide association studies. For the first time, special ECG analysis methods will be applied for improved and more accurate phenotyping, driven by the hypothesis that different ECG phenotypes point to different underlying mechanisms. This work will be complemented by the exploration of the genetic contribution to novel ECG phenotypes, such as early repolarization syndrome and baseline or drug-induced right precordial ST segment/J point elevation. Furthermore, the hypothesis that gene variants modulate the outcome of therapeutic strategies in AF, i.e. response to catheter ablation will be investigated, thereby rendering an important contribution to individualized medicine.

**Projektbeteiligte**

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