

Translating the genome and transcriptome in cardiovascular disease

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database in patients with cerebrovascular disease undergoing carotid endarterectomy we explored the detailed gene expression pattern related to disease phenotype.

Second, the translational step from identified disease modifying single nucleotide polymorphism (SNP) to affected gene has previously been difficult to complete. We utilized a novel approach of simultaneous SNP genotyping and expression measurement in the same patients to identify which genes are coupled to disease modifying SNPs. This method provided several novel gene targets.

Third, it has been speculated that gene expression measurements may reveal patterns of expression that could serve as diagnostic tool or prediction of disease progression. We developed this aspect in the cohort of patients with cerebrovascular disease and identified a set of genes which expression pattern contributed to increase the diagnostic accuracy of future cardiovascular events.

We conclude that genome wide nucleic acid sequence analysis is an important tool to identify novel genes and pathways related to clinical cardiovascular disease.

Biography

Anders Gabrielsen MD, PhD graduated from University of Copenhagen and continued with post-doctoral studies at Karolinska Institutet in the field of experimental cardiovascular research. Following the post-doctoral period he continued his medical education with board certification in Internal Medicine and Cardiology at Karolinska University Hospital where he is now working at Dept. of Cardiology. His previous academic training in integrative cardiovascular physiology and gene expression analysis in experimental models and clinical cardiovascular disease has aided in development of "omics" patient biobanks with a strong emphasis on translational medicine.