



Jeanette Erdmann

Coordinator:

 Jeanette Erdmann
University Hospital Schleswig-Holstein (UKSH), Institute for Cardiogenetics, Luebeck, Germany

Contact:

jeanette.erdmann@uni-luebeck.de

Partners:

 Lucian Itu, Transilvania University of Brasov (UTVB), Automation and Information Technology, Romania

 Baiba Vilne, Rīga Stradiņš University (RSU), Bioinformatics Research Unit, Latvia

 David-Alexandre Tregouet, University of Bordeaux (UBx), Bordeaux Population Health Research Center, France

Partners without funding:

 Niels van Royen, Radboud umc, Nijmegen, Netherlands

PROGRESS

PRecisi**O**n medicine in CAD patients: artificial intelli**G**ence for integ**R**ated g**E**nomic, functional and anatomical a**S**essment of the coronary collateral circulation

Coronary artery disease (CAD) is a major burden for patients and healthcare systems worldwide. The most common cause of CAD is atherosclerosis, an inflammatory disease on with life-threatening effects in the coronary circulation. Often, the circulation adapts through collateral artery formation, leading to significantly improved long-term post-ischemic outcome.

Hence, timely determination of the collateral profile presents a pivotal factor in the personalised treatment of CAD.

However, the coronary collateral circulation (CCC) development is not well predicted by traditional CAD risk factors. Moreover, manifold inconsistencies are still apparent in CCC research, mainly associated with the difficulty of quantifying CCC accurately and reproducibly. Therefore, the overarching objective of PROGRESS is to develop a tool for more accurate, reproducible and automated prediction of patients’ potential to develop CCC, which could be used for a more efficient CAD patient management.

We will harness Artificial Intelligence (AI)-based angiogram image and genetics analyses aiming to improve risk stratification and management of CAD patients, based on their CCC formation profile. This will be followed by timely application of therapeutic approaches in order to stimulate CCC formation and thus improve survival rates of patients after diagnosis.

We have collected well-powered CAD cohorts with genetic and imaging data. AI-based image analysis will aid in phenotyping CCC and also in generating post-hoc surrogate functional parameters (validated against a cohort of invasively phenotyped patients) in an unbiased fashion. This provides the basis for a genome-wide association study (GWAS) on CCC performed in large detection and validation cohorts.

