



SCALLOP

SCALLOP consortium — *genetics of the proteome*

The SCALLOP consortium is a collaborative framework for the discovery and follow-up of genetic associations with protein expression data measured using the Olink Proteomics platform. To date, 25 PIs from 20 research institutions have joined the effort, which now comprises summary-level data on SNP to protein level associations from almost 65 000 patients or controls.

The aim of the SCALLOP consortium is to identify novel molecular connections and protein biomarkers that are causal in a broad range of diseases. This work starts with identification of so called protein quantitative trait loci, pQTLs, which are robust connections between a gene variant and the levels of a protein.

The SCALLOP consortium is currently mapping novel pQTLs for several hundreds of proteins in unprecedented numbers of samples. The pQTLs provide unique insights into protein regulation and causal role in disease.

Identify causal protein biomarkers

DISEASE

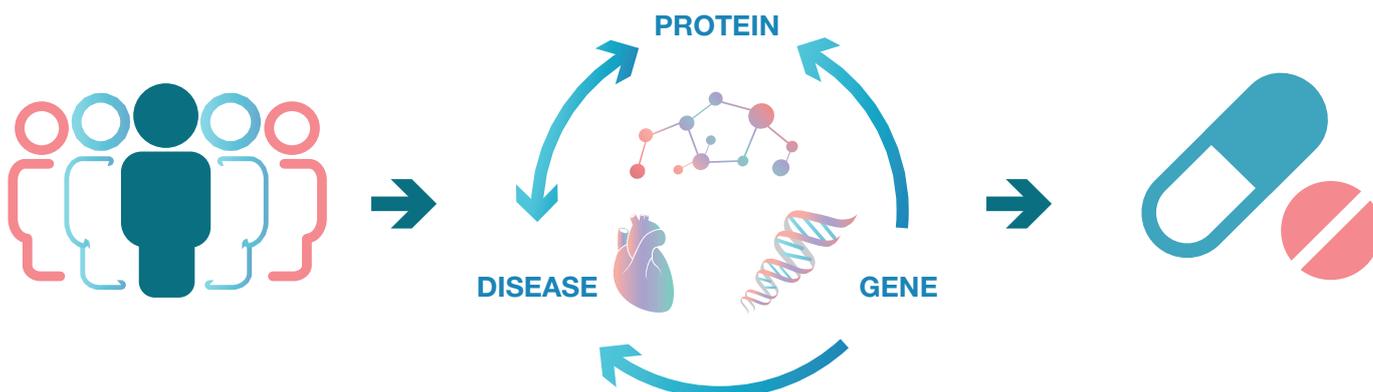
- What proteins are up/down regulated?
- Are they significantly associated with disease risk, progression or treatment response?
- Can we identify multi-marker diagnostic or prognostic protein signatures?

MENDELIAN RANDOMIZATION

- Combine data on genetics vs protein levels with data on genetics vs disease endpoints
- Identify proteins that are causal in disease (distinguish cause and consequence)

DRUG TARGETS

- Select proteins with established disease causality as new therapeutic targets
- Use the direction of effect shown in the Mendelian Randomization to design treatment modality
- Targets identified by plasma protein profiling may be more amenable to monoclonal antibody treatment



CVD study

using genetics and protein data

One SCALLOP study used 13 study cohorts with in total 21 700 subjects with genetics and Olink CVD I protein data.

SCALLOP analysis

- 27 million gene variants
- 90 CVD I proteins gave 2.43 billion data points
- 13 cohort studies gave 31.6 billion data points

Data was uploaded to the secure SCALLOP server for data harmonization and meta-analysis.

Findings

- 68 000 gene variants with genome-wide significant association to any CVD I protein
- 401 independent genomic loci
- 85 proteins with significant genetic regulation
- 7 proteins that were strongly causal in either RA, stroke, CHD or T2D

SCALLOP welcomes new members

To be a member of the SCALLOP consortium you have to be the PI of a study collection with participant health information and protein biomarker data obtained using the Olink platform.

Full details of the requirements and expectations for new consortium members can be found on our website at www.scallop-consortium.com. Any enquiries relating to joining SCALLOP should be addressed to Anders Målarstig (Anders.Malarstig@ki.se).



SCALLOP

Read more

www.scallop-consortium.com

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