Stellingen

1. Selecting a study approach to investigate the role of SLC44A2 in the pathophysiology of venous thrombosis is challenging as this protein is present on both the endothelial and blood cells (this thesis).

2. Mass spectrometry based targeted proteomics is a compelling tool to measure proteins in multiplex with high precision (this thesis).

3. Targeting SLC44A2 as an antithrombotic therapeutic strategy would potentially eliminate the risk of hemorrhagic complications that are associated with current prophylactic anticoagulant therapies (this thesis).

4. It is fascinating that the contributing role of SLC44A2 to venous thrombotic disease can be allocated to three distinctive mechanisms. (This thesis, Constantinescu-Bercu et al. Elife, 2020, Bennett et al. Nat Commun. 2020).

5. Further standardization of microfluidic systems that mimic blood flow would highly advance thrombosis research.

6. The impact of sex on the plasma proteome in mice may be highly underestimated.

7. It is increasingly clear that bone marrow-derived cells are involved in different stages of deep vein thrombosis from thrombosis initiation to resolution. (Campos, Int J Biochem Cell Biol, 2020,).

8. Results from genomic association studies will be important not only for genetic risk profiling but also for directing future function-structure studies that will underpin understanding of the cause of disease at a molecular level (Adapted from Zöller, Blood, 2019).

9. The utilization of consumer-initiated health and ancestry genetic data in scientific research (as example “23 and me” as in Hinds et al, Hum Mol Genet, 2016) contributes to the already existing underrepresentation of ethical diversity in genome studies.

10. Animal experiments performed blinded for the researcher are a practical convention that can help to avoid unintentional bias.

11. Publishing all versions of a manuscript with its reviews is an interesting new idea (Rozendaal, J Thromb Haemost, 2018).

12. As humans struggle to comprehend our own massively complex genome and proteome, the emergence of the COVID-19 pandemic reminds us that we still have a lot to learn about the biology of far less complex elements (Adapted from Lilicrap, J Thromb Haemost, 2020)