A systems genomics approach to identify risk loci and pathways to Candida infection

Matzaraki, Vasiliki

Stellingen behorende bij het proefschrift:

“A systems genomics approach to identify risk loci and pathways to *Candida* infection”

1. Genetic polymorphisms that regulate complement and blood coagulation determine susceptibility to candidaemia (chapter 2).

2. Rather than responding uniformly to all infections via regulation of the same cytokines, immune responses are organized to have specific responses to specific fungal pathogens, and adjuvant immunotherapy needs to take these pathogen-specific effects into consideration (chapter 3).

3. Increased risk to candidaemia is explained by the effect of disturbed lipid homeostasis on the regulation of pro-inflammatory cytokines in response to *Candida* infection (chapter 3).

4.The existence of distinct genetic contributions to inflammatory responses to *Candida* infection, susceptibility, and survival indicates that modulation of cytokine responses alone is not sufficient to treat all candidaemia patients (chapter 4).

5. The genetic architecture of infectious diseases, including candidaemia, is different from that of immune-mediated diseases, with low frequency variants showing an intermediate effect in infections.

6. Combining systems approaches with longitudinal, patient-specific clinical data and organ-on-chip technology will enable us to identify novel genes and molecular pathways and revolutionize the drug target discovery process.

7. Detecting true genetic associations in sepsis requires both increased sample sizes and accurate phenotype delineation.

8. [Locating the gene related to a disease from scratch is like] trying to find a burned-out light bulb in a house located somewhere between the East and West coasts without knowing the state, much less the town or street the house is on (Francis S. Collins).