Genetic and methodological aspects of statin-induced lipid response

Smit, R.A.J.

Stellingen behorende bij het proefschrift

Genetic and methodological aspects of statin-induced lipid response

1. Genetic predisposition for fasting lipids may influence one's lipid response to statin therapy (*this thesis*).
2. *CETP* may be the only locus with common genetic variants that substantially influence HDL-C response to statins (*this thesis*).
3. The potential of Mendelian randomization as a pharmacovigilance and drug repurposing tool is unlikely to be fulfilled by proposing instruments on the basis of pharmacogenetic research (*this thesis*).
4. Survival bias is an underrecognized and realistic threat to Mendelian randomization studies (*this thesis*).
5. Despite being repeatedly linked to (sub)clinical outcomes, it remains unclear whether visit-to-visit lipid variability is either of etiological or prognostic significance (*this thesis*).
6. Violations of the assumptions necessary for the estimation of a causal effect should be regarded as second-order concerns (*Burgess S, Bowden J, Fall T, Ingelsson E, Thompson SG. Epidemiology 2017*).
7. That concentrations of HDL-C hold prognostic but no apparent etiological value results from grouping heterogeneous lipid subpopulations together.
8. Sample sizes of genome-wide association study meta-analyses exceeding a million participants has made the adage 'garbage-in-garbage-out' more relevant, not less.
9. Focusing on effect sizes and their uncertainty is but one alternative to lowering 'the' p-value threshold to 0.005 (*Ioannidis JPA, JAMA 2018*).
10. Save your scientific follies, pitfalls, and dead ends, for 'the manuscript in the drawer either rots or ripens.' (*Marie von Ebner-Eschenbach, Aphorisms, 1880*)
11. To paraphrase Bernard Le Bovier de Fontenelle: 'All [science] is founded on two things alone; an inquisitive mind, and poor eyesight.' (*Conversations on the Plurality of Worlds, 1686*)