Stellingen

Behorende bij het proefschrift

"Dissection of the Complex Genetic Architecture of Human Stature and Osteoporosis"

1. A strong and common genetic factor for fracture risk is located at the novel 18p11.21 BMD locus in the *FAM210A* gene. (This thesis)
2. At least 180 common genetic variants, clustered in biological pathways and in genes underlying skeletal growth defects, explain approximately 10% of human stature. (This thesis)
3. Allelic heterogeneity is a common feature of highly polygenic traits such as height and BMD. (This thesis)
4. Common variation in the C-type natriuretic peptide-signaling pathway plays a major role in the biology of human stature, especially in north-western Europeans. (This thesis)
5. Grid-computing will be required for the expedited analysis of large-scale genetic epidemiology datasets. (This thesis)
6. Analyzing and interpreting genome sequence data will be more important than generating the data.
7. "Omics" technology will rationalize and revolutionalize the way medicine is currently practiced which is mostly inadequate.
8. The required sample size to find new genetic loci associated with a human trait has created the need for an unprecedented level of worldwide scientific collaboration.
9. The balance between common regulatory and rare coding variants in explaining genetic variance of a phenotype depends on evolutionary pressure.
10. Humans can have normal lives with approximately twenty completely inactivated genes (MacArthur, 2012).
11. Life is like a box of chocolates, you never know what you're gonna get. (Forrest Gump, 2004)

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