

GENETICS

# BIGGER IS BETTER

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John Todd has always been advocating that we should use larger sample sizes in our genetic association studies. I agree, it is also true that larger sample sizes will lead to smaller p-values. In his recent nature genetics comment he now suggest a p of less than  $10^{-8}$  to be relevant. Yes, all of his 6 examples show that significance level but only 1 provides functional evidence (the SLE study). All other studies including Todd`s own studies are number-crunchers. I fear that in the absence of functional data  $10^{-8}$  may not even be sufficient. Think of 500,000 SNPs, 20 possible traits, 5 genetic models and 20 competing groups - this multiplies to  $10^{-9}$ . Interestingly, the SLE study, showed a p of  $10^{-16}$ ! Having good functional evidence I would be even willing to accept  $10^{-2}$ . May I point you to an excellent study describing a new rSNP by means of CHIP and expression analysis of de Gobbi - using just a couple of families. Yea, yea.

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