

## **Closing the gap on “missing” heritability**

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“Missing” heritability – the gap between heritability estimates from twin/family studies and the variance explained by observed variants in molecular genetics studies – has been a constant concern throughout the GWAS era of psychiatric genetics research. This gap may be sensitive to model assumptions in defining “heritability”, but remains an important benchmark for understanding the role of genetics in psychiatric disorders. In this context, we reflect on two recent trends in complex trait genetics. First, large GWAS studies are enabling increasingly robust estimates of the total contribution of common genome-wide SNPs to heritable traits, both increasing precision and enabling better modelling of variation in effect sizes across the genome. Second, increasing sample sizes are closing the gap between the estimated SNP-heritability and the actual predictive accuracy of polygenic risk scores, with accuracy further accelerated by methodological improvements.