Q5(c)

Heritability and its estimation

UPSC Civil Services Mains 2024 · Anthropology GS 1 · 10 marks · Mendelian genetics in man-family study, single factor, multifactor, lethal, sub-lethal and polygenic inheritance in man.

9.2 Mendelian genetics in man-family study, single factor, multifactor, lethal, sub-lethal and polygenic inheritance in man.

Core demand of the question

- Define heritability as a population statistic
- Distinguish broad-sense and narrow-sense heritability
- Explain estimation through relatives, twins, adoption and variance components
- State the assumptions and limits of interpretation

Revision summary

Heritability is a population-and-environment-specific share of phenotypic variance.

Broad H^2 includes all genetic variance; narrow h^2 includes additive variance.

Fisher's variance partition underlies the concept.

Twin, adoption, pedigree and parent-offspring designs estimate familial resemblance.

Equal-environment assumptions and gene-environment correlation limit twin estimates.

High heritability does not mean immutability or explain group differences.

Introduction

Heritability is the proportion of observed phenotypic variance in a specified population and environment attributable to genetic variance. It does not measure how genetic an individual's trait is, nor does a high value make a trait unchangeable.

Body

Concept and estimation

Quantitative genetics partitions phenotypic variance as **V(P) = V(G) + V(E) + interactions**. Broad-sense heritability, **H^2 = V(G)/V(P)**, includes additive, dominance and epistatic variance. Narrow-sense heritability, **h^2 = V(A)/V(P)**, retains additive variance and best predicts response to selection; **R. A. Fisher** supplied the variance framework.

Estimation uses resemblance among relatives:

- parent-offspring regression and sibling correlations estimate additive familial resemblance;
- classical twin studies compare monozygotic with dizygotic twins, often using **$h^2 \approx 2(rMZ - rDZ)$** under restrictive assumptions;
- adoption studies separate resemblance to biological and rearing relatives;

- pedigrees and modern genomic relatedness methods estimate variance components in large samples.

Height is highly heritable in many well-nourished populations, yet mean stature can rise rapidly with nutrition. IQ estimates similarly vary by age, class and environment. Twin estimates assume comparable environments and may be inflated by gene-environment correlation, assortative mating or shared prenatal conditions. Population stratification can also distort genomic estimates.

Thus heritability is local to population, age, environment and measurement. It says nothing directly about between-population causes.

Flow diagram

Phenotypic variance -> Genetic variance

Phenotypic variance -> Environmental variance

Genetic variance -> Additive

Genetic variance -> Dominance and epistasis

Additive -> Narrow h squared

Genetic variance -> Broad Narrow h squared squared

Conclusion

Heritability converts family resemblance into a variance estimate. Used carefully, it clarifies polygenic variation; used as destiny, it revives biological determinism. The anthropological answer must always specify whose population and which environment.

Facts & figures

R. A. Fisher

Reconciled Mendelian inheritance with continuous traits through additive effects and analysis of variance.

Narrow-sense h²

Additive genetic variance divided by phenotypic variance; it is the quantity most relevant to selection response.

Twin design

Compares resemblance of monozygotic and dizygotic pairs, subject to equal-environment and representativeness assumptions.

Secular height change

Population means can shift with nutrition and disease even where rank-order variation is highly heritable.

ask@wrapexams.com · wrapexams.com