



Fundamentals of Genomic Prediction and Data-Driven Crop Breeding (August 4-8, 2025)



Heritability in Plant Breeding

Module 3
August 6, 2025

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Proportion of Variances

$$\text{Phenotype}(P) = \text{Genotype}(G) + \text{Environment}(E) + \text{Residual}(e)$$

$$V_P = V_g + V_e + V_{ge}$$


$$V_a + V_d + V_i$$

- Heritability is used to measure the proportion of variance
- The proportion of variation that is due to genetics is heritability

$$\text{Broad Sense heritability } (H^2) = \frac{V_g}{V_P}$$

Proportion of total genetic variance
Measures the role of the environment
Highly unpredictable-includes $V_d + V_i$

$$\text{Narrow Sense heritability } (h^2) = \frac{V_a}{V_P}$$

Proportion of additive genetic variance
Responds to selection
Predictive-includes V_a
Measures breeding Value

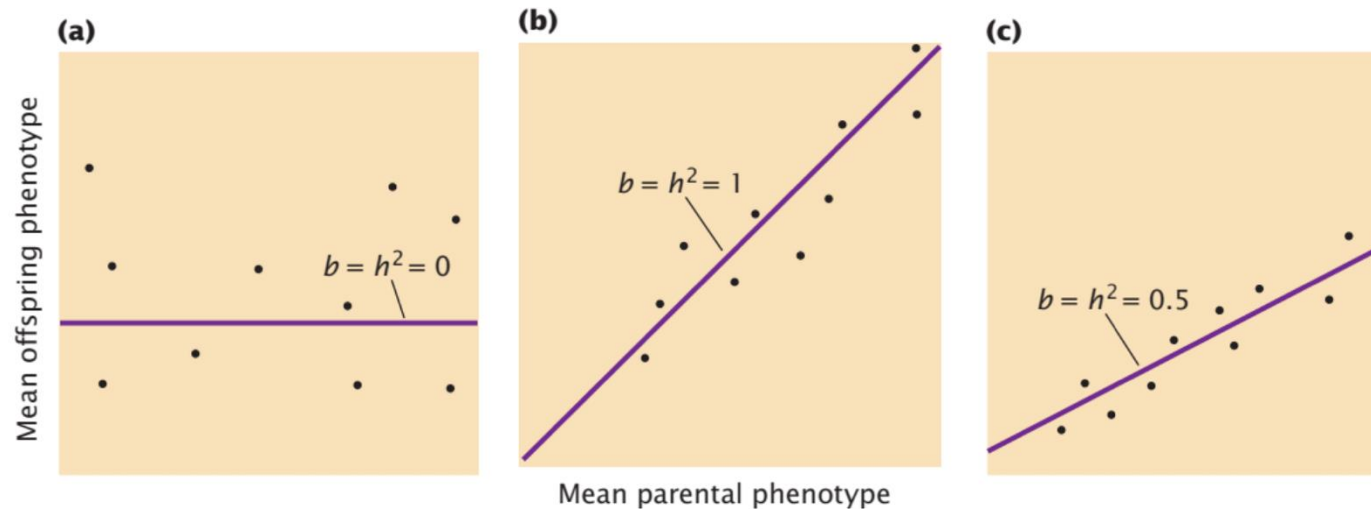
Misconceptions

- Heritability do not determine genetics
- Individuals do not have heritability.
- Heritability effected by genes and environment.

Narrow Sense Heritability

Heritability by parent-offspring regression

$$h^2 = b_{(\text{regression mean offspring against mean of parents})}$$



The h^2 is equal to the regression coefficient b .

- a) There is no relationship between parental phenotype and offspring
- b) Offspring phenotype is same as parental phenotype
- c) Besides genes some other factors contribute to difference between parent and offspring

Narrow Sense Heritability

Regression Coefficient of Breeding Values

$$P_i = A_i + \varepsilon_i$$

where P is phenotype value and A is breeding value and ε is residual

$$b_{PA} = \frac{\text{cov}(A, P)}{\text{var}(P)} = \frac{\sigma_A^2}{\sigma_P^2} = h^2$$

Accuracy, which is \sqrt{h} is a correlation between phenotype (P) and Breeding Value (A)

$$\text{Correlation coefficient } (r_{AP}) = \frac{\text{Cov}(A, P)}{\sqrt{\sigma_A^2 \sigma_P^2}} = b_{AP} \frac{\sqrt{\sigma_P^2}}{\sigma_A} = b_{AP} \frac{1}{\sqrt{h^2}} = \frac{h^2}{h} = h$$

Narrow Sense Heritability

Breeding Value is product of Phenotypic Value and heritability

$$A_{expected} = h^2 \times P$$

$$Phenotypic\ value\ (P) = \frac{A\ (breeding\ value)}{h^2}$$

If heritability is 1, the breeding value equals the Phenotypic value!!

Lower the heritability ; poor is to indicate the breeding value from phenotypic value

Measuring Heritability in Plant Breeding

For Balanced Data (MET data across locations)

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

Phenotype is mean of genotypes across l locations and r replication per trial, and this has variance (Entry mean based Heritability)

$$H^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_{ge}^2}{l} + \frac{\sigma^2}{lr}}$$

where, σ_{ge}^2 is variance due to genotype x environment,
 σ^2 is residual error variance

Under balanced Data, H^2 has simple and direct interpretations

- a) H^2 is the fraction of phenotypic variation that can be explained by the genotype, where the phenotype is taken to be the arithmetic entry mean.
- b) H^2 is equivalent to the coefficient of determination of a linear regression of the (latent) genotype on the observed phenotype
- c) H^2 is also the squared correlation between predicted (phenotypic) value and actual genetic or genotypic value
- d) H^2 can be used to predict the response to selection $R = h^2S$, where S

Measuring Heritability in Plant Breeding

What if we have these scenarios

- Data is Unbalanced (For example, missing or p rep-design)
- Genetic (Random) Effects are correlated, not independent
- Heteroscedastic (heterogeneity of variances)
- Complex variance-covariance structures (spatial variations)

Reliability (An Alternative Approach)

$$H_p^2 = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\bar{V}_{BLUE}}{2}} \quad (\text{Pheipho and Mohrang, 2007})$$

where, mean variance of difference of BLUEs and σ_g^2 is variance of genotypes

$$H_c^2 = 1 - \frac{\bar{V}_{BLUP}}{2\sigma_g^2} \quad (\text{Cullis et al. 2006})$$

where, \bar{V}_{BLUP} is mean difference of BLUPs and σ_g^2 is variance of genotypes

Underestimate or overestimate the variance components

<https://doi.org/10.1534/genetics.107.074229>

<https://doi.org/10.2135/cropsci2018.06.0376>