

HERITABILITY AND ITS GENETIC WORTH FOR PLANT BREEDING

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INTRODUCTION

- The heritability of a metric character is one of the most important properties. It is the proportion of total variance that is attributable to the average effects of genes and this is what determines between relatives the degree of resemblance between relatives.
- It expressing the reliability of the phenotypic value as a guide to the breeding value. Only the phenotypic value of the individual can be directly measured, but it is the breeding value that determines their influence on the next generation.
- Therefore, if the breeders or experimenters choose individuals to be parents according to their phenotypic value, his success in changing the characteristics of the population can be predicted only from the knowledge of the degree of correspondence between phenotypic value and breeding value. This correspondence measured by the heritability.

WHAT IS HERITABILITY?

- The extent of contribution of genotypes to the phenotypic variation for a trait in a population is ordinarily expressed as the ratio of genetic variance to the total variance, i.e., phenotypic variance, for the trait; this ratio is known as heritability.
- Thus heritability denotes the proportion of phenotypic variance that is due to genotype i.e., heritability.
- Heritability may be expressed as a fraction or may be multiplied with 100 and expressed as percentage.

TYPES OF HERITABILITY

Heritability basically classified into two groups basing on their variance component taken into account and they are:

1. Broad sense heritability
2. Narrow sense heritability

1. Broad sense heritability:

- The ratio of genetic variance to that of phenotypic variance (or total variance) is called as broad sense heritability.
- In a cross between pure line parents P_1 and P_2 , broad sense heritability may be estimated by utilizing the F_2 population as phenotypic variance V_p .

- It is expressed as follows:

$$\text{Heritability}(H_{BS}) \text{ or } h^2_{bs} = V_g/V_p = V_g/(V_g + V_e)$$
$$h^2_{bs} (\%) = (V_g/V_p) \times 100$$

where, V_g , V_p and V_e are genetic, phenotypic and environmental components of variances respectively.

- The broad sense heritability can be determined by the following three ways:
 1. From analysis of variance table of a trial consisting of a large number of genotypes.
 2. Estimation of V_g and V_e from the variance of F_2 , P_1 , P_2 and F_1 generation of the cross.
 3. Parent offspring regression (b) provides an estimate of heritability. Here, b is the regression of the progeny means on parental values.

2. Narrow sense heritability:

- The ratio of additive genetic variance to total phenotypic variance is called narrow-sense heritability.
- A more restrictive and often more useful method of heritability estimation.
- It is calculated as follows:

$$\text{Narrow sense heritability } (H_{NS}) \text{ or } (h^2_{ns}) = V_A/V_P$$
$$h^2_{ns} = (V_A/V_P) \times 100$$

where, V_A and V_P are the additive genetic variance and phenotypic variance respectively.

Note: The symbol h^2 stands for the heritability itself not for the square. The symbol derives from Wright's (1921) terminology, where 'h' stands for the corresponding ratio of standard deviation.

RELATIONSHIP BETWEEN HERITABILITY AND REGRESSION OF BREEDING VALUE

- At equivalent meaning of the heritability is the regression of breeding value on phenotypic values. It can be represented as :

$$h^2 = b_{AP}$$

Where, h^2 = heritability

b_{AP} = regression of breeding value on phenotypic value

- If we split the phenotypic value into breeding value (A) and a remainder (R) consisting of the environmental dominance and interaction deviation, then $P = A + R$. Since A and R are uncorrelated, $Cov_{AP} = V_A$ and so

$$b_{AP} = V_A/V_P = h^2_{ns}$$

- We may note also that the correlation between breeding value and phenotypic values, r_{AP} is equal to the square root of the heritability. This follows from the general relationship between correlation and regression coefficient which gives,

$$r_{AP} = b_{AP} \cdot V_P / V_A = h^2_{ns} \cdot 1/h_{ns} = h_{ns}$$

This is how, the heritability, correlation and regression coefficients of breeding value are related.

- By regarding the heritability as the regression of breeding value on phenotypic value we see that the best estimate of an individual's breeding value is the product of its phenotypic value and the heritability:

$$A \text{ (expected)} = h^2 \cdot P$$

where, A = breeding value
 h^2 = heritability
 P = phenotypic value

- Breeding value and phenotypic values both are reckoned as deviations from the population. In other words the heritability express the reliability of the phenotypic values as a guide to the breeding value or the degree of correspondence between phenotypic value and breeding value.

ESTIMATIONS OF HERITABILITY

Let us first compare the merits of the different sorts of relatives for estimating either the additive genetic variance from the covariance or the heritability from the regression or correlation coefficient.

Relatives	Covariance	Regression (b) or Correlation (t) in terms of heritability
Offspring and one Parent	$1/2 V_A$	$b = 1/2 h^2$
Offspring and mid Parent	$1/2 V_A$	$b = h^2$
Half-sibs	$1/2 V_A$	$t = 1/4 h^2$
Full-sibs	$1/2 V_A + 1/4 V_D + V_E$	$t > 1/2 h^2$

1. Intraclass correlation half-sib (t_{hs}):

$$\begin{aligned}
 t_{hs} &= V_{\text{between family half-sib}} / \text{Total variance} \\
 &= V_{\text{between family half-sib}} / (V_{\text{between family}} + V_{\text{within family}}) \\
 &= 1/4 (V_A / V_P) = 1/4 h^2_{ns} \\
 \text{Or, } h^2_{ns} &= 4 t_{hs}
 \end{aligned}$$

2. Intraclass correlation full-sib (t_{fs}):

If the ratio is very high then the between family variance is very high means each family individual resembling with each other and within family is negligible.

$$t_{fs} = \frac{V_{\text{between family full-sib}}}{(V_{\text{between family}} + V_{\text{within family}})} \\ = \frac{(1/2 V_A + 1/4 V_D)}{V_D}$$

- Intraclass correlation full-sib (t_{fs}) is more than heritability.
- If no dominance is present, then intraclass correlation full-sib is half of heritability, *i.e.*, $t_{fs} = 1/2 h^2$.

WHY BROAD SENSE HERITABILITY IS NOT MUCH USEFUL FOR THE PLANT BREEDERS?

- The degree of heterozygosity within segregating population will be related to the number of selfing generation.
- Maximum heterozygosity will be found in the F_1 family, and will be reduced by half in each subsequent selfed progeny.
- Similarly the dominance genetic variance will be dependent on the degree of heterozygosity in the population and will differ between filial generations.
- So, a more useful form of heritability for plant breeder narrow sense heritability (h^2_{ns}), which is the ratio of additive genetic variance (V_A) to total phenotypic variance (V_P).

WORTH OF HERITABILITY IN RELATION TO CROSS- AND SELF-POLLINATED CROPS

- In case of cross pollinated species, $H = 2b$, when the parents are non-inbreds. But in case of self-pollinated species, the correct estimate would be as follows: $H = b/2\gamma_{xy}$, where γ_{xy} is the coefficient of inbreeding of the progeny. The value of γ_{xy} will be 1/2, 3/4, 7/8, 15/16, 31/32 etc. for F_2 , F_3 , F_4 , F_5 and F_6 generations.
- The estimation of broad sense heritability is valid for homozygous lines or populations.
- But in case of segregating generations, genetic variance consists of additive and dominance components (assuming there is no epistasis).
- Since in self-pollinated crops we develop homozygous lines, the dominant component will not contribute to the phenotypes of the homozygous lines derived from a segregating generation.
- Thus in such cases only the additive component is relevant. So in segregating generation the narrow sense heritability is worthwhile.

HERITABILITY AND SELECTION

- Quantitatively inherited characters differ in heritability. A character such as yield greatly influenced by environment.
- Characters not influenced by environment are usually having high heritability. They may influence the choice of the breeding procedure used by the plant breeder.
- Selection in the F₂ of a cross between homozygous parents (F₁ if parents are heterozygous) will not be very effective for characters that have low heritability.
- Selection is effective in F₂ if the characters are highly heritable.
- Selection for a character with low heritability may be made more effectively if based on F₂ progeny performance. The net gain from selection depends upon the combined effect of the heritability, the amount of genetic variation present, the selection intensity and the cycle length (season per cycle).
- If heritability of a character is very high e.g., **0.8 or more**, selection for the character should be fairly easy because there would be a close correspondence between genotype and phenotype. But for a character with low heritability, say **less than 0.4**, selection may be considerably difficult or virtually impractical due to the confusing effect of the environment.
- The heritability values for different traits averaged over various crops, procedures of estimation, environments and cultivars have been approximately classified by **Robinson (1965)** as under:

Heritability (h^2 %)	Traits
1. Low heritability (5-10 %)	Yield, lodging resistance, winter survival, protein content
2. Medium heritability (10-30 %)	Components of yield, components of structures, quality traits
3. High heritability (30-60 %)	Maturity characters (flowering, heading, kernel size), chemical composition traits, developmental traits, heading date

PRINCIPAL USES OF HERITABILITY ESTIMATES

- To determine the relative importance of the genetic effects this could be transferred from parents to offsprings.
- To determine which selection method would be most useful to improve the characters.
- To predict the gain from selection (genetic advance).
- If meiosis is normal, only additive gene action can be passed from the parent to offspring. In this case the narrow sense heritability estimate would be particularly useful.

- However, if the plant breeder is working with clonally propagated crops such as sugarcane, banana, rubber or bermunda grass or if the crop reproduces apomictically, estimate of broad sense heritability would be more appropriate because vegetative propagation and apomixes fix both additive and non-additive (dominance plus epistasis) gene action and transfer if from parents to offspring.

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