

Misconceptions Regarding Heritability in Plant Breeding: An Overview Article

Temesgen Teressa

Ethiopian Institute of Agricultural Research (EIAR), Ethiopia
Email: temesgenteressa2013@gmail.com

Abstract—Heritability allows comparing the relative contributions of genes and environment to trait variation both within and between populations. Geneticists and plant breeders frequently use heritability as a measure for how accurate a trial or set of trials. Sewall Wright and Ronald Fisher established the idea of heritability almost a century ago, defining it as an estimable, dimensionless population quantity. Heritability is still essential to the response to selection in evolutionary biology and agriculture, particularly in plant breeding, despite ongoing misconceptions and disputes regarding its usage and application. The importance of heritability in the genomics era is demonstrated by recent reports of significant heritability for gene expression and novel estimation techniques utilizing marker data. Understanding the common misconceptions surrounding the use of heritability is crucial to minimize confusion during selection in plant breeding.

Keywords—heritability, environment, additive, genotype, phenotype, error, plant breeding

I. INTRODUCTION

Heritability is a ratio of variances; more precisely, it is the percentage of total variance in a population for a given measurement taken at a given time or age that can be attributed to variations in additive genetic or total genetic values, which are known as the broad sense heritability (H^2) and the narrow-sense heritability (h^2), respectively [1, 2]. It estimates, from a single value, the proportion of individual variance in a population that results from genetic differences. The majority of relatives share only one or no identical by descent copies; identical twins and full siblings (sibs) are the most notable exceptions. Dominance and other non-additive genetic effects that are based on sharing two copies do not contribute to their phenotypic resemblance. This is because individuals only transmit one copy of each gene to their offspring. This enlightens that h^2 is the typical parameter and the majority of relatives' selection response and correlation depend on it rather than H^2 [3].

Heritability is often computed in plant breeding in order to assess trial precision and determine the response to selection. Since the phenotype is typically an

aggregate value due to genotype replication in trials, it is typically approximated on an entry mean basis.

Geneticists and plant breeders usually use heritability as a gauge for how accurate a trial or set of trials and computing the reaction to selection is its primary application. The majority of heritability calculation formulas implicitly rely on balanced data and separate genotypic influences. In plant breeding studies, both of these presumptions are frequently broken [4].

Plant breeders frequently utilize heritability to measure the accuracy of a single field experiment or a set of field trials. It is sometimes referred to as heritability in the restricted sense, and it is defined as the percentage of phenotypic diversity across individuals in a population that is caused by heritable genetic factors. Similarly, the percentage of phenotypic variance that can be attributed to an impact on the entire genotype, which includes the total of additive, dominant, and epistatic effects, is known as heritability in the broad sense [5, 6]. Because it dictates how the population will react to selection, heritability is a crucial parameter in quantitative genetics.

The initial definitions of heritability were put forth in the context of animal breeding, where one individual animal is typically the fundamental unit of observation and selection. On the other hand, there are a plethora of distinct mating designs in plant breeding, and the observational units used in these experiments range from single plants to genotypes that have been evaluated in a variety of settings. This complicates both the concept and the measurement of heritability, as noted by [7].

One significant challenge is that almost all heredity models assume balanced data, even though most trials show some sort of imbalance. More specifically, in designs with incomplete blocks, big genotype sets are typically examined, and standard heritability criteria do not hold true. Additionally, the usual definitions presume that models with independent random effects for blocks, plots, plants, etc. are used to evaluate the trials, while spatial models which imply complex variance covariance structures pertaining to observational units are frequently used to analyze field trials [8].

Heritability measures in plant breeding have a fairly straightforward concept: they express the fraction of total phenotypic variance that can be attributed to the average effects of genes, which in turn establishes the degree of similarity between relatives [9]. It is defined as “the extent to which a phenotype is genetically determined”

by Costa-Lourenço *et al.* [10]. The combination of an organism's observable qualities is called a phenotype. It is the outcome of (i) the genotype of the organism being expressed, (ii) environmental influences having an impact, and (iii) the interactions between the two.

The link between observed/phenotypic values with phenotypic variance and the corresponding real genotypic values with genotypic variance that underlie them is thus examined via heritability. We refer to either narrow-sense heritability or broad-sense heritability, depending on whether breeding values or genotypic values are taken into account [11]. As a result, H^2 and h^2 may be distinguished clearly. However, keep in mind that the methodology discussed in this article applies to both measures, which is why, unless it becomes specifically important to refer to one of the two, we shall speak to heritability generally throughout this article. Although the actual genotypic and breeding values as well as their variances are unknown, phenotypic data can be used to approximate or predict them.

Several authors write articles related to heritability however, they do not consider the misconception regarding heritability and its application. So, this is to over view the misconception related to the use and application of heritability in plant breeding.

II. WHAT HERITABILITY IS AND NOT

According to <https://www.nealelab.is/blog/2017/9/13/heritability-201-types-of-heritability-and-how-we-estimate-it>, heritability is the percentage of trait variation that can be attributed to inherited genetic variants. Stated differently, it is a means of quantifying the extent to which variations in an individual's DNA can account for variations in their phenotypes. Between 0 and 1 (genetics explains nothing about the characteristic) is the range of heritability (genetics explains everything). According to Ref. [12], the heritability of height is approximately 0.80, while the heritability of the number of hours slept per night is between 0.15 and 0.20.

Heritability calculates the degree to which we could use genetics to predict a trait (assuming we fully understood all the relevant genetic factors). In a similar vein, it indicates the degree to which we could anticipate the trait in you from the trait in your parents. It is quite unlikely that this prediction could be made from your DNA since it would require exact knowledge of the impact of each genetic variation. However, when we get more insight into the genetics of the trait, the heritability places a ceiling on how accurate that forecast might be possibly [13].

Heritability quantifies the contribution of genetics to a trait. When the heritability of a trait is high, meaning it's close to 1, it means that most of the variation between individuals can be explained by genetics; when it's low, meaning it's close to zero, most of the variation cannot be attributed to genetics. A trait's high heritability does not imply that a single gene causes it in a clear biological way; rather, it indicates that the trait's total contribution from all direct and indirect causal effects as well as other

correlations between distinct DNA variants and the trait are sufficient to be informative [13, 14].

Heritability is a population level characteristic rather than an individual's. The degree to which genetic variables contribute to population variability is indicated by a trait's heritability. It doesn't "explain" why a plant has a certain infection. A trait's heritability depends on the method used to test it. Since random measurement error isn't genetic, traits that are more difficult to measure and have more of it will be less heritable. Additionally, this may result in variations in heritability depending on who measures the trait or between a simplified measure and the intended trait [8, 13].

Heritability varies depending on the subject of the measurement. It concerns which population you compare the genetic influences to, as heritability encompasses the complete variation of the characteristics in the population. But, heredity is not destiny. You are not destined to have a trait just because it is heritable and appears in your parents. Although it might be more likely, it's not a given. There are changes to heritability. Because heredity is a measure of how genetic and environmental influences balance out, altering one's environment can alter a trait's heritability.

High heritability does not imply a genetic basis for group differences. There is a concerning history of linking claimed racial inequalities in IQ scores and other observable group characteristics to genetics. As previously said a trait's heritability is not constant and depends on the measurement method, population, and environment. Therefore, using the estimated heritability of a trait as proof of "inherent" variations between groups is invalid [15].

III. HERITABILITY IN THE GENOME-WIDE ASSOCIATION ERA

Numerous traits across a variety of populations, animals, and time periods have had their heritability the percentage of phenotypic variation accounted for by genetic variation estimated. Researchers are attempting to use GWAS to directly identify the genetic variations responsible for the genetic component of phenotype, thanks to the recent development of rapid genotyping and sequencing technology. The "missing heritability problem" refers to the discrepancy between the phenotypic variation estimated from classical heredity methods and that explained by GWAS results. In this work, we analyze state-of-the-art heritability estimation techniques that directly utilize genotype and sequence data. We explore their implications for comprehending the genetic architecture of complex traits and address them in relation to standard heritability methods and the missing heritability dilemma [16].

Heritability is a commonly used statistic in quantitative genetics, yet it may be the most readily misconstrued statistic when studying human variation. We cannot easily discount the role that genetic inheritance plays in complex biological and behavioral phenotypes, but we still don't fully understand how that legacy manifest itself in any given environmental setting.

It cannot, in fact, be boiled down to a single figure. Nor does the anthropologists' inclination to focus on biological rather than behavioral characteristics when studying heredity make a more compelling case for the origins of human variety. The definition of heritability, measurement techniques, fallacies surrounding its misuse, and application to epidemiological and evolutionary anthropological research are all covered in this study [16].

Greater complexity in study designs, such as the measurement of environmental (physical and sociocultural) variation and the careful selection of phenotypes for study, will be necessary to advance anthropological genetics. Understanding the development of human biological variety requires a specific focus on clarifying the ontogenetic mechanisms that underlie adaptive plasticity. These developments will also clarify if genotype-targeted biomedical treatments are feasible. Ignoring the limitations of these methods can cause funds to be diverted from environmental health programs that have been shown to be beneficial to entire populations. We should question oversimplified ideas of genetic determinism for the benefit of our theories and the health of wider communities. Anthropological genetics excels when it integrates anthropology into the investigation of human phenotypic diversity, as demonstrated by the work of Frank B. Livingstone (<https://www.thessgac.org/faqs>).

IV. MISCONCEPTIONS RELATED TO HERITABILITY

- **Misconception (1) A heritability of 0.40 indicates that 40% of the trait is determined by genetics.**

This is a relatively widespread misperception that stems, in part, from a misreading of the definition. When a trait's heritability is 0.40, it means that genetic variation accounts for 40% of the trait's phenotypic variance. Compared to the definition that states that in every animal, genes account for 40% of the trait's expression and external factors account for the remaining 60%, this definition is far different (<https://www.youtube.com/watch?v=hunPN1PEucw>).

- **Misconception (2) A low heritability means that traits are not determined by genes.**

Genes always impact the expression of the phenotype when the heritability is greater than zero. The ratio of the genetic variance to the phenotypic variance establishes the heritability. Thus, a low heritability may suggest a low level of genetic variety. For instance, the majority of people have five fingers on each hand; hence there is very little genetic diversity in the number of fingers on a hand, even though this is highly genetically fixed.

- **Misconception (3) A low heritability means that genetic differences are small.**

It is not always the case that a low heritability means a minimal genetic variance. It could also indicate a high error variance. Additionally, faulty phenotypic recording may also play a role in this. The environment might have a significant influence. For instance, an individual's genetic susceptibility to a particular infection determines their level of resistance to it. The challenge is in

quantifying that potential. You can identify the sheep that are affected at that moment if you walk into the field and measure each sheep to see if they are contaminated with nematodes, for example. However, it is impossible to identify among the remaining sheep which ones are resistant to nematode infections, have already recovered, or have not yet contracted the infection. Put differently, a great deal of error exists in your observations.

The inability to accurately attribute a phenotype to every animal will lead to a comparatively high error variance and, thus, a poor heritability. A more accurate assessment of the sheep's ability to resist nematode infection and, consequently, a more accurate estimate of the genetic and environmental variance for this trait can be obtained if you enhance the recording of nematode infection, for instance by going into the field more frequently and/or improving the measurement technique. If there is little genetic diversity, the heritability may still be low, but at least the cause is no longer erroneous phenotypes (<https://www.youtube.com/watch?v=hunPN1PEucw>).

- **Misconception (4) Heritability is a fixed value.**

Heritability is a measure of how much the genetic variance component contributes to the phenotypic variance in a population, based on observations made at a certain point in time. In addition to genetic variance within a population, environmental factors and observation accuracy also play a role in determining the heritability of a population. One population's genetic variation may differ (to a certain extent) from another population's. In particular, if the other group belongs to a distinct breed. However, over time, heritability can also vary within a group. For instance, if a more precise recording technique had been used to gather the new set of phenotypic observations and alternatively, the impact of the environment may have changed if the structure has changed since the last recording. Therefore, it makes sense to periodically reevaluate the heritability.

- **Misconception (5) Heritability varies from individual to individual.**

One measure of the population is heritability. In the population, it is an estimate. It could differ depending on the population (<https://www.youtube.com/watch?v=hunPN1PEucw>).

- **Misconception (6) Heritability varies is the proportion of a phenotype that is passed on to the next generation.**

Heritability, in a restricted sense, is the portion of variance attributable to additive genetic effects. Half is passed on to the following generation. But the real half is different for every child (<https://www.youtube.com/watch?v=hunPN1PEucw>).

V. SUMMARY AND CONCLUSION

Heritability is the degree to which the additive genetic variance, for a given population in a given environment, determines the phenotypic variance. The amount of environmental variance is determined by the particular environment, the population under consideration, and the accuracy to which phenotypes are recorded to identify

genotype differences. Comparing the relative contributions of environment and genes to trait variation within and between populations is made possible by heritability. Almost a century ago, Sewall Wright and Ronald Fisher originated the idea of heritability and defined it as an estimable, dimensionless population characteristic. Population parameters include heritability and the variations that contribute to it. Since estimates are all we really know about these parameters, confusion has resulted from the fact that parameter and estimate are frequently used interchangeably. Based on empirical data pertaining to observed and expected similarity between relatives, heritability can be evaluated. The anticipated similarity between relatives is predicated on the conjecture of the underlying genetic and environmental factors. These assumptions can be simple or complex.

Heritability is still essential to how organisms respond to selection in evolutionary biology and agriculture, despite ongoing misconceptions and disputes regarding its usage and implementation. The importance of heritability in the genomics era is demonstrated by recent reports of significant heritability for gene expression and novel estimation techniques utilizing marker data. To reduce misunderstandings about selection in plant breeding, it is essential to recognize the widespread fallacies surrounding the application of heritability.

CONFLICT OF INTEREST

The author declares no conflict of interest.

REFERENCES

- [1] S. Wright, "The relative importance of heredity and environment in determining the piebald pattern of guineapigs," *Proceedings of the National Academy of Sciences*, vol. 6, no. 60, pp. 320–332, 1920.
- [2] R. A. Fisher, "The detection of a sex difference in recombination values using double heterozygotes," *Journal of Theoretical Biology*, vol. 3, no. 3, pp. 509–513, 1962. doi:10.1016/S0022-5193(62)80042-3. hdl:2440/15164
- [3] D. Falconers, *Introduction to Quantitative Genetics*, Longman Group LDT, Longman House, UK, 1981.
- [4] P. Schmidt, J. Hartung, J. Bennewitz, and H. P. Piepho, "Heritability in plant breeding on a genotype-difference basis," *Genetics*, vol. 212, no. 4, pp. 991–1008, Aug. 2019. doi:10.1534/genetics.119.302134
- [5] W. E. Nyquist, "Estimation of heritability and prediction of selection response in plant populations," *Critical Reviews in Plant Science*, vol. 10, pp. 235–322, 1991. <http://dx.doi.org/10.1080/07352689109382313>
- [6] D. S. Falconer and T. F. C. Mackay, *Introduction to Quantitative Genetics*, 4th edition, Harlow: Addison Wesley Longman, 1996.
- [7] J. Holland, W. E. Nyquist, and C. T. Cervantes-Martinez, "Estimating and interpreting heritability for plant breeding: An update," *Plant Breeding Reviews*, vol. 22, pp. 9–111, 2003.
- [8] H.-P. Piepho and J. Möhring, "Computing heritability and selection response from unbalanced plant breeding trials," *Genetics*, vol. 177, pp. 1881–1888, 2007. doi:10.1534/genetics.107.074229
- [9] R. Thompson, *et al.*, "Estimation of quantitative genetic parameters," *Philosophical Transactions: Biological Sciences*, vol. 360, no. 1459, pp. 1469–1477, 2005.
- [10] A. P. R. D. Costa-Lourenço, K. T. B. D. Santos, B. M. Moreira, *et al.*, "Antimicrobial resistance in *Neisseria gonorrhoeae*: History, molecular mechanisms and epidemiological aspects of an emerging global threat," *Braz. J. Microbiol.*, vol. 48, no. 4, pp. 617–628, Oct.–Dec. 2017. doi:10.1016/j.bjm.2017.06.001
- [11] Xu, *et al.* (2013). *J. Infect. Dis.* [Online]. 208. pp. 528–538. Available: <https://academic.oup.com/jid/articlepdf/214/11/1785/7705773/jiw404.pdf>
- [12] D. J. Gottlieb, G. T. O'Connor, and J. B. Wilk, "Genome-wide association of sleep and circadian phenotypes," *BMC Med. Genet.*, vol. 8, suppl. 1, p. S9, Sep. 2007. doi:10.1186/1471-2350-8-S1-S9
- [13] A. Jacquard, "Heritability: One word, three concepts," *Biometrics*, vol. 39, pp. 465–477, 1983.
- [14] E. Turkheimer, "Three laws of behavior genetics and what they mean," *Current Directions in Psychological Science*, vol. 9, no. 5, pp. 160–164, 2000. <https://doi.org/10.1111/1467-8721.00084>
- [15] F. J. Meaney and C. Taylor. (2023). Heritability. *Encyclopedia Britannica*. [Online]. Available: <https://www.britannica.com/science/heritability>
- [16] P. M. Visscher, W. G. Hill, and N. R. Wray, "Heritability in the genomics era — Concepts and misconceptions," *Nature Reviews Genetics*, vol. 9, pp. 255–266, 2008.

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