Chapter 1

Theoretical Framework for Crop Variety Trials

Key points

- The ultimate purpose of crop variety trials is to identify superior cultivars for a given target environment. The target environment is the sum of the environments that are likely to be encountered in a target region across years.
- The heritability of a trait obtained from a variety trial system is a measure of the system’s ability to reveal any genetic differences among tested genotypes for the trait.
- Heritability is a relative measure of the genetic variance (G) versus the genotype-by-environment interaction variance (GE), ignoring any experimental errors. So G and GE must be considered simultaneously in variety evaluation.
- Heritability must be estimated in the genotype–location–year framework because superior cultivars must be identified in test environments representative of the target environment.
- Heritability estimated in the genotype–location–year framework facilitates appreciation of the relative power of a single-trial, multilocation trials in a single year, and multilocation trials in multiple years.
- Variance components constituting heritability in the genotype–location–year framework can reveal possible approaches to improve the efficiency of variety trials, which are the topics of this book.

Variety trials are conducted every year in every geographical or administrative region for every major crop in that region. They are conducted by plant breeders to identify improved genotypes and/or by agronomists to identify superior cultivars to recommend to the growers. Despite the budget situation, variety trials are conducted every year and have rarely been discontinued, indicating their great importance to the agriculture and the economy. Variety trials are probably the best-funded applied research in agriculture.

The sole purpose of the whole book is to provide methods and techniques that can improve the efficiency of variety trials through variety trial design, conduct, data collection, data management, data analysis, and decision-making. This chapter is to set up the basic theoretical framework for crop variety trials.

The ultimate measure of the efficiency of a variety trial system is the predicted genetic gain, \( \Delta G \) for a trait or trait complex. According to the quantitative genetics theory, the predicted genetic gain

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is determined by three factors: the selection intensity \((i)\), the heritability of the trials \((h^2\) or \(H)\), and
the square root of the phenotypic variance \((\sigma_p)\) in the trials:

\[
\Delta G = ih^2\sigma_p. \tag{1.1}
\]

The selection intensity is the inverse of the proportion of the selection population that is selected; a higher intensity means a smaller proportion of the genotypes are selected. It is an arbitrary value set by the researcher. The heritability is the ratio of the genotypic variance \((\sigma_g^2)\) over the phenotypic variance,

\[
h^2 = H = \frac{\sigma_g^2}{\sigma_p^2}. \tag{1.2}
\]

It is the proportion of the observed variation among genotypes that is due to genetic differences for the trait of interest. Therefore, the heritability may also be understood as the “relative genetic variance” or “relative genetic variability” (Hanson and Brim, 1963). Equation 1.1 can also be rewritten as

\[
\Delta G = ih\sigma_g. \tag{1.3}
\]

Since the selection intensity is an arbitrary value, and the genotypic variance or its square root is supposed to be a constant for a given set of genotypes, the sole determinant of the predicted genetic gain in the variety trials is \(h\), i.e., the square root of heritability.

So, heritability is the single most important concept in quantitative genetics with regard to variety trials. All measures taken in variety trials, from design, conduct, to statistical analysis, have the same purpose, that is, to improve the heritability of the variety trials.

Another key concept regarding crop variety trials is that the heritability must be estimated under the genotype–location–year framework (Comstock and Moll, 1963). In this framework, each test environment or trial is viewed as a location-by-year combination and is determined and defined by both the year and the location factors, which have different biological implications. The main task of this chapter is to examine the definition of heritability and its variants under various scenarios.

### 1.1 Heritability under the genotype–location–year framework

Under the genotype–location–year framework, each observed value regarding the trait of interest corresponds to an experimental unit, i.e., a field plot, and is a combined effect of the genotype, the test location, the year, and their interactions, plus a random error:

\[
y_{ijkr} = \mu + \alpha_i + \beta_j + \gamma_k + (\alpha\beta)_{ij} + (\alpha\gamma)_{ik} + (\beta\gamma)_{jk} + (\alpha\beta\gamma)_{ijk} + \varepsilon_{ijkr}, \tag{1.4}
\]

where

\(y_{ijk} \) is the observed value of the trait in replicate \(r = 1\) to \(n_r\) for genotype \(i = 1\) to \(n_g\) at location \(j = 1\) to \(n_l\) in year \(k = 1\) to \(n_y\);
\(\mu\) is the grand mean of the trials;
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\( \alpha_i \) is the main effect of genotype \( i = 1, \ldots, n_g \);
\( \beta_j \) is the main effect of location \( j = 1, \ldots, n_l \);
\( \gamma_k \) is the main effect of year \( k = 1, \ldots, n_y \);
\( (\alpha\beta)_ij \) is the interaction effect between genotype \( i \) and location \( j \);
\( (\alpha\gamma)_ik \) is the interaction effect between genotype \( i \) and year \( k \);
\( (\beta\gamma)_jk \) is the interaction effect between location \( j \) and year \( k \);
\( (\alpha\beta\gamma)_{ijk} \) is the three-way interaction effect among genotype \( i \), location \( j \), and year \( k \);
\( \varepsilon_{ijkr} \) is the random error associated with the experimental unit in replication \( r \) for genotype \( i \) at location \( j \) in year \( k \).

In terms of variance components, the phenotypic variance is calculated as

\[
\sigma^2_p = \frac{\sigma^2_g}{n_l} + \frac{\sigma^2_y}{n_y} + \frac{\sigma^2_{gl}}{n_l n_y} + \frac{\sigma^2_{gy}}{n_l n_y} + \frac{\sigma^2_{gy}}{n_l n_y} + \frac{\sigma^2_{ijkl}}{n_l n_y n_r},
\]

where

\( \sigma^2_g \) is the genotypic variance,
\( \sigma^2_l \) is the location variance,
\( \sigma^2_y \) is the year variance,
\( \sigma^2_{gl} \) is the genotype-by-location interaction variance,
\( \sigma^2_{gy} \) is the genotype-by-year variance,
\( \sigma^2_{ly} \) is the location-by-year variance,
\( \sigma^2_{g} \) is the experimental error variance,
\( n_l \) is the number of locations,
\( n_y \) is the number of years, and
\( n_r \) is the number of replications within a trial.

Each of the items in Equation 1.5 corresponds to that in Equation 1.4 except for the grand mean, which is a constant for the trials and therefore has a variance of 0.

The purpose of variety trials is to compare among the genotypes; the effects for year, location, and location–year interaction are the same for the tested genotypes (i.e., they are fixed), so their variance components \( (\sigma^2_l, \sigma^2_y, \sigma^2_{ly}) \) are all zero. When these terms are removed from the phenotypic variance, Equation 1.5 becomes

\[
\sigma^2_p = \sigma^2_g + \frac{\sigma^2_{gl}}{n_l} + \frac{\sigma^2_{gy}}{n_l n_y} + \frac{\sigma^2_{g}}{n_l n_y n_r}.
\]

Note that all variance components in this equation contain the letter “g” except for the error variance term. These are the variance components that must be considered in genotype evaluation and therefore in calculating the heritability.
According to Equation 1.2, therefore, the heritability under the genotype–location–year framework (Atlin et al., 2000) is

\[
H_{lyr} = \frac{\sigma_g^2}{\sigma_p^2} = \frac{\sigma_g^2}{\sigma_g^2 + \frac{\sigma_l^2}{n_l} + \frac{\sigma_y^2}{n_y} + \frac{\sigma_{ly}^2}{n_l n_y} + \frac{\sigma_{ln}^2}{n_l n_y} + \frac{\sigma_{lny}^2}{n_l n_y n_r}}. [1.7]
\]

From this equation, heritability \( H \) or its square root \( \hbar \) can take values from 0 to 1 inclusive. When \( H = 1 \), it means any observed differences among the genotypic effects are completely due to genetic differences and are absolutely reliable, no matter how small the differences may be. When \( H \) is close to 0, however, the observed genotypic differences, no matter how dramatic they may appear, are due to either genotype-by-environment interactions or experimental errors and therefore cannot be trusted.

Equation 1.7 is the most basic formula in quantitative genetics regarding variety trials, the subscript “\( lyr \)” here is used to indicate that it is based on replicated multiyear, multilocation data; all other forms of heritability, as will be discussed later, should be viewed as a special case of this form. The essence of improving the efficiency of variety trials is to increase the heritability so that superior genotypes can be effectively identified. This equation shows not only how heritability is estimated but also possible approaches to improve it.

Equation 1.7 shows that the concept of heritability is consistent with the concept of mixed models, in which the environmental main effects (L, Y, and LY) are considered fixed while the genotype and its interactions with the environments (GL, GY, GLY) plus the experimental error are random. It is also consistent with the concept of GGE biplot analysis (Yan et al., 2007) in that both G and GE are integral part of heritability and must be considered simultaneously in genotype evaluation.

### 1.2 Possible approaches to improve the variety trial efficiency

#### 1.2.1 Increase the genotypic variance

From Equation 1.7, it is obvious that increase in the genotypic variance \( \sigma_g^2 \) of the variety trials can lead to a higher heritability. However, increasing the genotypic variance is the task of the breeding stages prior to variety trials. Furthermore, it is easy to increase the genotypic variance by including exotic and unadapted genotypes in the trials but such increase will not help in identifying superior genotypes. At the variety trial stage, the genotypic variance is supposed to be a fixed value for a given set of genotypes. Similarly, for a well-defined target environment, the variance components due to GL, GY, and GLY are also supposed to be fixed and are characteristic of the target environment. This leaves the only feasible way to improve the heritability by increasing the denominators under these variance components, i.e., the number of years, locations, and replicates within trials, as discussed below.

#### 1.2.2 Increase the number of years

Equation 1.7 may be rewritten as follows:

\[
H_{lyr} = \frac{\sigma_g^2}{\sigma_p^2} = \frac{1}{1 + \frac{\sigma_l^2}{n_l} + \frac{\sigma_y^2}{n_y} + \frac{\sigma_{ly}^2}{n_l n_y} + \frac{\sigma_{ln}^2}{n_l n_y} + \frac{\sigma_{lny}^2}{n_l n_y n_r}}. [1.8]
\]
Based on Equation 1.8, increase in the number of years \( n_y \) can reduce \( \frac{\sigma^2_{gy}}{\sigma^2_g} \) and \( \frac{\sigma^2_{gy}}{n_y \sigma^2_g} \), and thereby increase the heritability. The effectiveness of increasing the number of years is dependent on the magnitude of \( \sigma^2_{gy} \) and/or \( \sigma^2_{gl} \) relative to the genotypic variance, i.e., \( \frac{\sigma^2_{gy}}{\sigma^2_g} \) and/or \( \frac{\sigma^2_{gl}}{\sigma^2_g} \) (Equation 1.8). The larger these ratios the more effective it will be. However, increasing the number of years in variety trials is extremely costly, not only in terms of money and resources, but more importantly, in the time required to release or recommend a cultivar. Breeding efficiency per unit of time is the ultimate criterion for the success of a breeding program. In reality, the longevity of a cultivar in the modern times is fairly limited, due to the frequent change of biotic and abiotic stresses in the target environment and due to the release of newer and better cultivars. So there is little space to increase the number of years in the variety trials beyond 2 or 3 years in order to increase the trial heritability. Currently most variety trial systems require data from 2 to 3 years of test to decide if a new genotype should be supported for registration or if a cultivar should be recommended to the growers. It is hardly feasible to either increase this number or reduce it. Theoretically, an optimum number of years can be determined based on the \( \frac{\sigma^2_{gy}}{\sigma^2_g} \) ratio, as will be discussed in section 1.4.1 in relation to the optimum number of test locations.

The \( \frac{\sigma^2_{gy}}{\sigma^2_g} \) ratio may be used to calculate an upper limit of achievable heritability. Assuming that the number of years is fixed at \( n_y = 3 \), then Equation 1.8 becomes

\[
H_{byr} = \frac{\sigma^2_g}{\sigma^2_p} = \frac{1}{1 + \frac{\sigma^2_{gy} / \sigma^2_g}{n_y} + \frac{\sigma^2_{gl} / \sigma^2_g}{3 n_l} + \frac{\sigma^2_{gl} / \sigma^2_g}{3 n_y n_r}} \tag{1.8a}
\]

The maximum heritability possible would be that when all items other than the \( \frac{\sigma^2_{gy} / \sigma^2_g}{3} \) term are set to 0. That is

\[
H_{\text{max}} = \frac{1}{1 + \frac{\sigma^2_{gy} / \sigma^2_g}{3}}
\]

For example, if \( \frac{\sigma^2_{gy}}{\sigma^2_g} = 0.5 \), then the maximum achievable heritability would be 0.86. If \( \frac{\sigma^2_{gy}}{\sigma^2_g} = 1 \), then the maximum achievable heritability would be 0.75. If \( \frac{\sigma^2_{gy}}{\sigma^2_g} = 3 \), the maximum achievable heritability would be 0.5. The achievable \( H \) would be 1.0 if \( \frac{\sigma^2_{gy}}{\sigma^2_g} = 0 \), of course.

### 1.2.3 Increase the number of test locations

Similarly, increasing the number of test locations \( n_l \) can improve the trial heritability (Equation 1.7), and the effectiveness of this depends on the magnitude of the variances of GL and GLY relative to that of G, i.e., \( \frac{\sigma^2_{gl}}{\sigma^2_g} \) and/or \( \frac{\sigma^2_{gy}}{\sigma^2_g} \) (Equation 1.8). Again, there is a cost with any increase in the number of test locations. It is important to determine an optimum number of test locations for a given target region for the crop of interest, which should be the minimum number of locations to achieve a certain level of heritability. Increase in the number of test locations or of test years also contributes to increased trial heritability through reducing the relative error variance (\( \frac{\sigma^2_{\varepsilon}}{n_l n_y n_r} \)).
Equation 1.8). However, increase in the number of locations is more affordable and feasible than increasing the number of years. To decide how many test locations are needed to achieve certain level of heritability, the ratio of $\sigma^2_{gl}/\sigma^2_g$ may serve as an important reference. For example, one may use a formula like Equation 1.9 to decide the minimum number of test locations:

$$n_l = 1 + k \sigma^2_{gl}/\sigma^2_g,$$

where $k = H/(1 - H)$ is a constant determined by the expected level of heritability. When $H = 0.75$ then $k = 3$, and 4 test locations would be needed at $\sigma^2_{gl}/\sigma^2_g = 1$, and 10 locations would be needed if $\sigma^2_{gl}/\sigma^2_g = 3$, and so on. Only one location is needed if $\sigma^2_{gl} = 0$, of course. See more discussion in section 1.4.1 on this topic.

1.2.4 Increase the number of replicates in each trial

Increasing the number of replicates in each trial can reduce the adverse effects of experimental errors on the trial heritability (Equation 1.8). However, with each increased replication also comes considerable experimental cost. Most variety trial systems uses two to four replications depending on factors such as the number of entries to be tested, seed availability, and resources available, etc.; again there is limited space to change the number of replications. From Equation 1.8, it can be seen that increasing the number of test locations may be more effective than increasing the number of replications within trials. At the same amount of additional cost (measured by the number of additional plots), increase in $n_l$ only reduces $\sigma^2_{\varepsilon}/n_l n_y$, while increase in $n_l$ reduces $\sigma^2_{gl}/n_1 n_y$, $\sigma^2_{el}/n_1 n_y$, and $\sigma^2_{\varepsilon}/n_1 n_y$. Accordingly, for the same number of plots, testing at more locations with fewer replications per location is clearly more effective than testing at fewer locations with more replications per location (Sprague and Federer, 1951). The cost for the former test scheme is usually greater than the latter, however, even when the total number of plots is the same. The number of replicates needed to achieve a within trial heritability 0.75 can be determined by the formula $n_t = 3(\sigma^2_{gl}/\sigma^2_g)$. If the ratio $\sigma^2_{gl}/\sigma^2_g = 1$, then three replicates would be needed.

1.2.5 Reduce the experimental error

Compared to above discussed approaches, reducing the experimental error does not involve additional cost and can lead to a “pure” gain in heritability. This can be achieved through improvements at various stages of variety trials, from experimental design, implementation, to data analysis. This will be an important topic in later chapters (Chapters 7 and 16).

1.2.6 Make use of any repeatable genotype-by-location interaction

In addition to reducing the experimental error, another possible approach to achieve a “pure” gain in trial heritability without additional cost is to try to utilize any GL that is repeatable across years. This approach is out of the box of the Equation 1.7 and is another important topic relative to variety
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trials. It requires the introduction of the concept “mega-environment,” as will be discussed in section 1.5. Methods for delineation of mega-environments based on variety trial data will be discussed in detail in Chapters 8 and 12.

1.3 Heritability under various scenarios and their interpretations

1.3.1 Unreplicated data from multiyear, multilocation variety trials

If the trials are not replicated, i.e., \( n_r = 1 \), Equation 1.7 becomes

\[
H_{ly} = \frac{\sigma^2_g}{\sigma^2_y} = \frac{\sigma^2_g}{\sigma^2_y + \frac{\sigma^2_g}{n_j} + \frac{\sigma^2_g}{n_y} + \frac{\sigma^2_g}{n_l n_y}} \tag{1.10}
\]

Compared to Equation 1.7, the heritability from unreplicated trials should be lower as the error term in the denominator will be greater. In practice, since the experimental error \( \sigma^2_e \) is not estimable with unreplicated data, \( H \) is usually estimated using the following equation:

\[
H_{ly} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_j}{n_j} + \frac{\sigma^2_y}{n_y} + \frac{\sigma^2_l}{n_l n_y}} \tag{1.10a}
\]

It is important to understand that various variance terms in the full model (Equation 1.7) always exist even when they are not estimable, so they should always be presented in the heritability formula. Omission of any variance term will lead to inflated estimation of the heritability. Therefore, \( H_{ly} \) based on unreplicated trials (Equation 1.10a) is inflated compared to \( H_{ly} \) based on Equation 1.10. However, if the experimental errors are well controlled and if the number of years and locations are many enough, the term \( \frac{\sigma^2_e}{n_l n_y} \) may be sufficiently small so that the \( H_{ly} \) based on unreplicated trials may be reasonably close to \( H_{ly} \). Testing at more locations at the expense of fewer replicates within locations is usually more informative and more cost-effective.

1.3.2 Multilocation trial data from a single year

It is common practice to analyze the multilocation variety trial data separately for each year, as opposed to analyze multiyear data jointly. There are two main reasons for this. First, variety trial data from multiple years are often highly unbalanced due to changes in genotypes and/or test locations in different years. This makes analysis and interpretation difficult. Second, researchers conducting variety trials have to make a decision every year; they cannot wait to make a decision until multiyear data become available. (They do have the option to make decisions based on data from the current year plus those from recent years, however. See Chapter 14 for an example.) Although this may not be the best practice from the viewpoint of the genotype–location–year framework, data from a single-year multilocation test are usually sufficient if the decisions are restricted to discarding poor genotypes as opposed to promoting superior cultivars (see Chapter 8 for single-year data analysis).
For a single-year dataset \((n_y = 1)\), Equation 1.7 becomes

\[
H_{lyr} = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gy}}{n_t} + \frac{\sigma^2_{gy}}{n_l} + \frac{\sigma^2_{gy}}{n_t n_l}}. \tag{1.11}
\]

No doubt that the heritability so estimated will be lower than that based on data from multiyear, multilocation trials; the extent to which the heritability is lowered depends on the magnitude of the \(\sigma^2_{gy}/\sigma^2_g\) and \(\sigma^2_{gly}/\sigma^2_g\) ratios in the target region. In practice, since the variance components involving the year factor (\(\sigma^2_{gy}\) and \(\sigma^2_{gly}\)) are not estimable using single-year data, Equation 1.11 is often reduced to

\[
H_h = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gy}}{n_t} + \frac{\sigma^2_{gy}}{n_l}}. \tag{1.11a}
\]

Apparently, the \(H_h\) so estimated is inflated relative to \(H_{lyr}\) due to its omission of \(\sigma^2_{gy}\) and \(\sigma^2_{gly}\).

1.3.3 Multiyear data at a single location

This situation is similar to that where heritability is estimated across locations in a single year, and all discussions regarding Equation 1.11 apply if the word “location” is replaced by the word “year.” This situation is rare in plant breeding programs aiming at genotype evaluation. However, it becomes meaningful when test location evaluation is a focus. This is a very important issue in variety trial data analysis but has largely been neglected so far. The heritability estimated for a given test location across years may be viewed as the repeatability of the test location in genotype evaluation. This topic will be discussed in detail in Chapter 13.

1.3.4 Data from a single trial

Although researchers are fully aware that data from a single trial (a single location in a single year) have limited power in genotype evaluation, particularly for traits highly subjective to GE, it is also very common that data from a single trial are analyzed as soon as they become available. When data from a single trial \((n_y = 1, n_l = 1)\) are analyzed, Equation 1.7 becomes

\[
H_{lyr} = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gy}}{1} + \frac{\sigma^2_{gy}}{1} + \frac{\sigma^2_{gy}}{1} + \frac{\sigma^2_{gy}}{n_t}}. \tag{1.12}
\]

No doubt that the heritability based on a single trial will be much lower than that based on multiyear, multilocation data. Because \(\sigma^2_{gy}\), \(\sigma^2_{gy}\), and \(\sigma^2_{gly}\) are not estimable from a single trial, the
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heritability is estimated in practice by

\[ H_t = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_e}{n_t}} \]

[1.12a]

Apparently, the \( H_t \) so estimated will be severely inflated relative to the \( H_{lyr} \) based on Equation 1.12; it can be misleading when used in making decisions about the genotypes. However, the heritability estimated for a single trial is a useful measure of the relative magnitude of the experimental error in the trial and may be used to decide how informative a trial is. The trial heritability or its square root is often used to weight the trial in joint multi-environment trial analysis (Chapter 5).

1.4 Heritability estimated in the genotype–environment framework

The \( H \) defined in Equation 1.7 implied that G, GL, GY, and GLY are all considered as random factors. Under this assumption, the G-L-Y three-way data can be arranged into a genotype-by-environment (G-E) two-way table (each environment being a year–location combination), a genotype–location (G-L) two-way table averaged across years, a genotype–year (G-Y) two-way table averaged across locations, or even a location–year (L-Y) two-way table averaged across genotypes, depending on the research focus (see section 17.4 for a complete list of possible two-way tables from a multiyear, multilocation dataset). Arranging the G-L-Y three-way data into two-way tables is useful because the data can then be studied using the biplot methodology, which is an important subject of this book (see Chapters 3–6 for theoretical description and Chapters 8–14 for applications in variety trial data analysis). This section describes the heritability estimation under the G-E two-way table framework.

1.4.1 Replicated genotype–environment data

When a year–location combination is viewed as a random sample in the population of the target environment (i.e., target region), the G-L-Y three-way data may be viewed as G-E two-way data. Thus, the phenotypic variance of Equation 1.6 becomes

\[ \sigma^2_p = \sigma^2_g + \frac{\sigma^2_{ge}}{n_e} + \frac{\sigma^2_e}{n_en_r} \]

[1.13]

where \( \frac{\sigma^2_{ge}}{n_e} = \frac{\sigma^2_{gn_e}}{n_e} + \frac{\sigma^2_{yn_e}}{n_e} \) and \( n_e = n_l n_y \) if location and year are factorial or \( n_e = \sum n_l \) if locations are nested within years. And, Equation 1.7 becomes

\[ \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_e}{n_e} + \frac{\sigma^2_e}{n_e}} \]

[1.14]
Equations 1.7 and 1.14 are equivalent for multiyear, multilocation trial data. However, Equation 1.7 is more informative and allows the possibilities for identifying and utilizing repeatable genotype–location interactions (section 1.5), whereas the use of Equation 1.14 assumes that the target region is a single mega-environment. Equation 1.14 is more flexible, however, as it does not require the same locations in all years.

Equation 1.14 may be used to estimate the number of test environments required to achieve a certain level of heritability in the target region. Equation 1.14 may be rewritten as

$$H_{lyr} = \frac{1}{1 + \left(\frac{\sigma^2_ge + \sigma^2_\varepsilon}{\sigma^2_g} \cdot \frac{1}{n_r}\right) / \sigma^2_e}.$$  \[1.14a\]

Define “noise quotient” or $Q$ as:

$$Q = \frac{\sigma^2_ge + \sigma^2_\varepsilon}{\sigma^2_g \cdot \frac{1}{n_r}}.$$  \[1.15\]

We have the following linear relationship between the number of test environments or year–location combinations and $Q$:

$$n_e = Q \cdot \frac{H_{lyr}}{1 - H_{lyr}}.$$  \[1.16\]

Two important relationships can be made from Equation 1.16. First, at a given level of $Q$, the number of needed test environments is a curvilinear function of the heritability; second, the needed number of test environments is a linear function of the $Q$ given a target level of heritability. The first relationship is depicted in Figure 1.1, assuming $Q = 1$.

Figure 1.1 shows that heritability ($H$) is roughly a linear function of $n_e$ when $H$ is less than 0.65. This means that within the range of [0, 0.65], $H$ can be effectively improved by increasing $n_e$. When $H > 0.8$, the cost to improve $H$, in terms of the number of test environments, increases quickly. For example, from $H = 0.65$ to $H = 0.75$ it takes only 1.1 additional environments; from $H = 0.75$ to $H = 0.85$, it takes 2.7 environments; from $H = 0.85$ to $H = 0.95$, it takes as many as 13.3 environments (Figure 1.1, Equation 1.2). $H = 0.75$ appears to be the upper limit that $H$ can be effectively improved by increasing the number of test environments.

Assuming a target heritability of 0.75, Equation 1.16 becomes

$$n_e = 3Q.$$  

$Q$ is composed of two parts (Equation 1.15). In cases when the term $\frac{\sigma^2_\varepsilon}{\sigma^2_g}$ in Equation 1.15 is not estimable (i.e., if replicated data are not available), it may be supplied with an empirical value, say, 1/3. Then, the number of test environments needed to achieve a heritability of 0.75 can be determined by the following equation, similar to equation [1.9]:

$$n_e = 1 + 3 \left( \frac{\sigma^2_ge}{\sigma^2_e} \right).$$
When $Q$ can be estimated, Equation 1.16 can be used to more accurately estimate the number of test environments needed to achieve a certain level of heritability. For example, when $Q = 10$, i.e., when $\sigma^2_{ge} + \sigma^2_I/n_i$ is 10 times that of $\sigma^2_g$, the number of year–location combinations required to achieve an $H$ of 0.75 is 30. If a three-year test scheme is assumed, then 10 test locations per year would be needed to achieve this level of trial heritability. To achieve a heritability of 0.9, 90 year–locations, i.e., 30 test locations in each of 3 years, would be needed.

Different traits have different levels of heritability; hence, the number of test locations and environments needed to achieve certain level of heritability are also different. For example, oil concentration in the oat grain is a highly heritable trait and genotype ranking is rarely affected by GE. As a result, genotypes can be effectively evaluated for this trait from one to two environments. Other traits such as yield, however, are much more subjective to GE, and many more environments are needed to achieve the same level of heritability (unpublished data).

### 1.4.2 Genotype–environment two-way table of means

Data from replicated multi-environment trials are often reported as a G-E two-way table of means, each value being a mean across replicates within a trial. When this type of data is used in estimating $H$, the term $\sigma^2_{n_i n_e}$ is not estimable, and Equation 1.14 is approximated by

$$H_{lyr} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_e}{n_e}}.$$

[1.17]
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The $H_{lyr}$ so estimated is inflated compared to that based on Equation 1.14. However, if $n_e n_r$ is large enough so that $\frac{\sigma_e^2}{n_e n_r}$ is negligibly small, the heritability estimation can be sufficiently accurate.

Equation 1.17 indicates that the number of environments needed for achieving a certain level of heritability is linearly related to the magnitude of $\sigma^2_{ge} / \sigma^2_g$. It also implies that the trial heritability is determined by two components: G and GE, omitting the experimental error. Therefore, for meaningful genotype evaluation, both G and GE must be considered at the same time. This is a basic and fundamental concept in variety trial data analysis. The G + GE or GGE biplot analysis, which is an important technique for variety trial data analysis, is in line with this concept. Genotype evaluation and test environment evaluation based on G-only, although acceptable, is incomplete use of the variety trial data; genotype evaluation and test environment evaluation based on GE-only is not only useless but also misleading (Yan et al., 2007). This point will be frequently emphasized in this book.

1.4.3 Genotype–environment two-way table of unreplicated trials

When the multi-environment trials are unreplicated, i.e., $n_r = 1$, Equation 1.14 becomes

$$H_{lyr} = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{ge}}{n_r} + \frac{\sigma^2_e}{n_e}}.$$  \[1.18\]

Furthermore, since $\sigma^2_e$ is not estimable with such data, the heritability is measured by:

$$H_{ly} = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{ge}}{n_e}}.$$  \[1.18a\]

Equation 1.18a takes the same form as Equation 1.17. However, the latter is more accurate because heritability estimated based on genotypic means across replicates ($H_{lyr}$) is more accurate. The role of replication in improving the variety trial accuracy does not diminish due to the rearrangement of the data.

1.4.4 Genotype–location table of means across years and replications

Data from multiyear, multilocation, replicated variety trials can be summarized into a G-L two-way table, in which each cell is the mean value across replications within trials and across years. Since the variances due to GY, GLY, and experimental error are not estimable, the heritability has to be estimated by

$$H_{lyr} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gl}}{n_l}}.$$  \[1.19\]
The heritability so estimated will be greatly inflated relative to Equation 1.7 due to the omission of some variance components, particularly when the GL variance is only a small portion of the total GE. Therefore it must be used with caution.

Equation 1.19 takes the same form as Equation 1.12a for a genotype by replication table from a single trial (\(H_r\)), Equation 1.17 for a G-E table of means (\(H_{lyr}\)), and Equation 1.18a for an unreplicated G-E table (\(H_y\)). The common point for these four equations is that they are estimated from a two-way table.

1.5 Heritability and target region subdivision

1.5.1 Heritability and variance component analysis

All discussions on heritability so far are under the unstated assumption that the target region belongs to a single mega-environment. A mega-environment is defined as a geographical region within which a single cultivar performs the best everywhere (Gauch and Zobel, 1997). A target region can be regarded as consisting of a single mega-environment in two scenarios. The first is when the heritability \(H_{lyr}\) is high such that all environments are closely correlated. In other words, the GE (consisting of GL, GY, and GLY) is small relative to G. The other is when the \(H_{lyr}\) is low but the GL is random and unrepeatable across years; that is, when the GE is mostly made of GY and GLY.

Therefore, a high \(H_{lyr}\) is an immediate indication that the target region is a single mega-environment. This is the ideal situation for a plant breeder. It means that the breeder can select the best cultivar by testing at a few locations for a few years, and the selected cultivar can be recommended with confidence to growers in the whole target region. The breeding program can be highly profitable if the acreage in the target region is large.

If the \(H_{lyr}\) is low, which means the GE is large relative to G, then the components of GE, i.e., the GL, GY, and GLY, need to be examined. If the GE is completely random and unrepeatable across years, then the breeder is dealing with a single, complex mega-environment. This is an unfortunate situation for the breeder. There is not much the breeder can do except to test at many locations for many years until the \(H_{lyr}\) becomes large enough (Equation 1.7 or 1.14). Only then will the breeder be able to identify with confidence the marginally better cultivars for the whole target region. When this is the case, the breeder should ask if his genetic base is too narrow and if it is possible to introduce new germplasm into his breeding program.

Among the components of GE, GY and GLY are apparently random, because it is not possible to “repeat” a year. The GL, however, is the component of GE that may be repeatable. Therefore, the variance ratio of GL/G, or \(\sigma^2_{gl}/\sigma^2_g\), becomes a key factor in mega-environment analysis. If this ratio is large, then the target region may be divided into subregions (mega-environments) so that some of the GL can be converted into G within subregions, thereby the overall heritability can be improved. On the other hand, if \(\sigma^2_{gl}/\sigma^2_g\) is small, then there is little merit to try to subdivide the target region.

1.5.2 Heritability and target region subdivision

When the \(\sigma^2_{gl}/\sigma^2_g\) ratio is large, subdivision of the target region may be worthwhile. According to Atlin et al. (2000), when the target region is to be divided into \(n_s\) subregions, the variance for
GL will be partitioned into the variance for genotype-by-subregion interaction (GS) and that for genotype-by-location interaction within subregions (GL(S)),

\[ \sigma^2_{gl} = \sigma^2_{gs} + \sigma^2_{g(l(s))} \]  

[1.20]

Likewise, the variance for GLY will be partitioned into variance for genotype-by-year-by-subregion interaction (GYS) and that for genotype-by-year-by-location within subregion interaction (GYL(S)),

\[ \sigma^2_{gl(y)} = \sigma^2_{gys} + \sigma^2_{gyl(s)} \]  

[1.21]

At the same time, the total number of test locations will also be divided among the subregions:

\[ n'_l = n_l / n_s \]  

[1.22]

assuming that the number of locations are equally divided into the subregions. Under this oversimplified framework, Equation 1.6 for the phenotypic variance becomes

\[ \sigma^2_p = \sigma^2_g + \frac{\sigma^2_{gs}}{n_k} + \frac{\sigma^2_{g(l(s))}}{n_l} + \frac{\sigma^2_{gys}}{n_y} + \frac{\sigma^2_{gyl(s)}}{n_l n_y} + \frac{\sigma^2_\varepsilon}{n_l n_y n_r}, \]  

[1.23]

and Equation 1.7 for heritability becomes

\[ H = \frac{\sigma^2_g}{\sigma^2_p} = \frac{\sigma^2_g}{\sigma^2_g + \frac{\sigma^2_{gs}}{n_k} + \frac{\sigma^2_{g(l(s))}}{n_l} + \frac{\sigma^2_{gys}}{n_y} + \frac{\sigma^2_{gyl(s)}}{n_l n_y} + \frac{\sigma^2_\varepsilon}{n_l n_y n_r}}. \]  

[1.24]

This is the heritability when genotype evaluation is conducted across the whole target region. When the evaluation is conducted within subregions, the variance due to GS becomes part of G:

\[ \sigma^2_g' = \sigma^2_g + \sigma^2_{gs}, \]  

[1.25]

and the heritability for each subregion becomes

\[ H' = \frac{\sigma^2_g'}{\sigma^2_p} = \frac{\sigma^2_g' + \sigma^2_{gs}}{\sigma^2_g + \sigma^2_{gs} + n_s \left( \frac{\sigma^2_{ph}}{n_l} + \frac{\sigma^2_{ph(y)}}{n_l n_y} + \frac{\sigma^2_\varepsilon}{n_l n_y n_r} \right)} + \frac{\sigma^2_{g(l(s))}}{n_l n_y} \]  

[1.26]

Comparing this equation to that for the whole region (Equation 1.24), it can be seen that both the nominator and the denominator in Equation 1.26 become larger due to the introduction of \( \sigma^2_{gs} \) and \( n_s \), and \( H' \) may or may not be improved over \( H \). Subdivision of the target environment may be justified only when \( H' > H \). This requires that \( \sigma^2_{gs} \) is sufficiently large to more than offset the introduction of \( n_s \) in the denominator, which has to be 2 or greater, of course.
In Atlin et al. (2000), the justification of subregion division also inversely depends on the genetic correlation between the subregions and the undivided whole region, which is

\[
rg = \sqrt{\frac{\sigma_g^2}{\sigma_g^2 + \sigma_{gs}^2}}.
\]  

[1.27]

Apparently, the smaller the GS relative to the G, the greater the genetic correlation and the less justified the subdivision of the target environment. It can be seen that the genetic correlation is inversely related to the heritability for the whole region (Equation 1.24), so both the heritability before subdivision and the genetic correlation between subregions carry the same idea: if the heritability for the whole region is large, then GS must be small, and therefore no subdivision of the target environment is needed or justified. Note that this variance-based genetic correlation (Equation 1.27) does not allow negative correlations between the subregions and the whole region, however. A zero correlation means that the genetic variance is zero and is equivalent to a Pearson correlation of −1.0 (Equation 4.13, Chapter 4) between all pairs of subregions.

1.5.3 How to divide the target region

Subdividing the target region is the process to identify and utilize repeatable GE, i.e., the GS, in plant breeding. All other components of the GE, i.e., GL(S), GY, and GLY are unrepeatable and cannot be utilized. Repeatable GE are patterns while unrepeatable GE are noise. An important task of variety trial data analysis is to try to separate patterns from noise, and the best approach to this task is the GGE biplot analysis (Chapters 8 and 12).

1.5.4 The merging of different target regions

As discussed above, a target region may be subdivided to increase the heritability of each subregion, which will lead to the identification of specifically adapted cultivars for each subregion. Use of specifically adapted cultivars in different subregions will lead to increased overall productivity for the whole target region. For the same token, different target regions may be merged if a cultivar is identified to perform the best across target regions. Use of such cultivars across target regions is in fact merging of target regions into a single mega-environment. However, mega-environments are not only defined by the which-won-where pattern but also by the which-lost-where pattern (Chapter 12).

1.6 Genotype-specific heritability as a shrinkage factor

Heritability is usually used as a property of a trial or trials and measures the ability of the trial(s) to discriminate genotypes. In the discussions so far, the variety trial data are assumed to be balanced and complete. That is, it is assumed that the same set of genotypes is tested in the same set of test locations in the same years for the same number of replications within trials and there are no missing values. So the numbers involved in the heritability equations for \( n_y, n_l, \) and \( n_r \) are all the same for each of the genotypes. However, when the data are unbalanced, which is often the case, the
genotypes would have different values of \( n_y, n_l \), and/or \( n_r \). As a result, different genotypes will have different heritability values; this means that the trials have different power for different genotypes. In short, in balanced, complete variety trials, the trials have the same heritability or power for all genotypes. In unbalanced or incomplete variety trials, they have different heritability or power for different genotypes.

When the genotypic main effects are treated as fixed effects, the estimated genotypic main effects across trials are called the best linear unbiased estimates (BLUE). When the genotypic main effects are treated as random effects, the estimated genotypic effects are called the best linear unbiased predictors (BLUP). These values can be greater or less than 0, meaning above-average or below-average. The BLUP and BLUE values for genotype \( i \) have the following relationship (DeLacy et al., 1996a):

\[
\text{BLUP}_i = \text{BLUE}_i H_i \quad [1.28]
\]

where \( H_i \) is the heritability for genotype \( i \). For balanced variety trials, all genotypes have the same \( H_i \) value, so the BLUE and BLUP values are strictly proportional, and the genotypes are ranked exactly the same. For unbalanced variety trials, however, different genotypes have different heritability values, and therefore their BLUE and BLUP values are not exactly proportional. Since heritability is always less than 1.0, the BLUP are shrunk toward 0, relative to the BLUE, so the genotype-specific heritability serve as a shrinkage factor. Less tested genotypes have smaller heritability so they are more severely shrunk toward 0 as compared to more fully tested genotypes. Genotypes with values closer to 0 are less likely to be either selected or discarded, meaning that more tests are needed to decide whether they are promoted or abandoned. Therefore, there is an advantage to treat the genotype main effects as random when the variety trial data are unbalanced. Shrinkage toward mean (i.e., 0 for environment-centered data) is a major property of BLUP (Piepho et al., 2008).

### 1.7 Estimation of variance components and heritability

#### 1.7.1 Mean square, expected mean square, and variance components

To estimate the heritability, it is essential to obtain the variances of the various sources of variation in Equation 1.7. Under the setting that a set of genotypes are tested at the same number of test locations for the same years, variance components of each variation source can be obtained by a conventional analysis of variance (ANOVA). A regular ANOVA table presents the mean squares (MS) for each variation source. Variances for each variation source can be obtained from the MS values and their respective expected mean squares (EMS) (Kuehl, 1994) (Table 1.1).

#### 1.7.2 An example of heritability estimation

Here we will use a sample dataset to demonstrate heritability estimation. The sample dataset is a balanced subset extracted from the yield data (in kg/ha) of an oat registration trial conducted during 2010–2012 across Canada. It contains 6 oat genotypes tested at 8 locations in 3 years, with 3, 4, or 6 replications in different trials (year–location combinations). The original data contain more test locations and many more genotypes but most genotypes were tested only for 1 or 2 years at some of the locations.
Theoretical Framework for Crop Variety Trials

Table 1.1  Expected mean squares for the genotype–location–year factorial design with random effects

<table>
<thead>
<tr>
<th>Source of variance</th>
<th>Degree of freedom (DF)</th>
<th>Mean square (MS)</th>
<th>Expected mean square (EMS)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotype (G)</td>
<td>$n_y - 1$</td>
<td>MSg</td>
<td>$\sigma_g^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>Location (L)</td>
<td>$n_y - 1$</td>
<td>MSl</td>
<td>$\sigma_l^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>Year (Y)</td>
<td>$n_y - 1$</td>
<td>MSy</td>
<td>$\sigma_y^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>L*Y</td>
<td>$(n_y - 1)(n_y - 1)$</td>
<td>MSly</td>
<td>$\sigma_{ly}^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>G*L</td>
<td>$(n_y - 1)(n_y - 1)$</td>
<td>MSgL</td>
<td>$\sigma_{gl}^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>G*Y</td>
<td>$(n_y - 1)(n_y - 1)$</td>
<td>MSgy</td>
<td>$\sigma_{gy}^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>G<em>L</em>Y</td>
<td>$(n_y - 1)(n_y - 1)(n_y - 1)$</td>
<td>MSgly</td>
<td>$\sigma_{gly}^2 + n_x \sigma_y^2 + n_x n_y \sigma_n^2 + n_x n_y n_z \sigma_n^2$</td>
</tr>
<tr>
<td>Error</td>
<td>$n_x n_y n_z (n_y - 1)$</td>
<td>MSerror</td>
<td>$\sigma_e^2$</td>
</tr>
</tbody>
</table>

The dataset is stored in a Microsoft Excel spreadsheet, and when read using the GGEbiplot software it looks like Figure 1.2. The data are in five columns: in the order of the year, the location, the replication, the genotype, and the yield in kg/ha. Data on other traits can be added as additional columns. This is referred to as a “four-way data format” in GGEbiplot (see more in section 17.2.2).

The analysis was conducted using the ANOVA procedure of the GGEbiplot software. A snapshot of the interface of this procedure is shown in Figure 1.3.

This interface has four blocks. The first block is for assigning the columns in the data file to the appropriate factors. Thus, the “Rep” column in the data file was assigned to the “Rep” factor, the “Variety” column to the “Genotype” factor, the “Location” column to the “Site” factor, and the “Year” column to the “Year” factor.

The second block of this interface is to specify the experimental design. Options include Randomized Complete Blocks Design (RCBD), Incomplete Blocks Design (ICBD), Completely Randomized Design (CRD), and Row-Column Design. Here RCBD was used. See Chapter 16 for details on the various experimental designs.

The third block is the “By Options.” When a four-way data is read, the researcher has the option to conduct the ANOVA across all years and locations, for each year across locations, for each location across years, or for each location–location combination (that is, by trial). Here the “By Nothing” option is used to conduct a joint analysis (see Chapter 7 for single-trial data analysis using this procedure).

The last block is “Trait Selection.” When the file contains data for more than one trait, the researcher has the option to analyze all traits at a single click or choose a specific trait to analyze. When the “All Traits” option is selected, the ANOVA for traits will be conducted one by one. The “Spatial analysis” portion in Figure 1.3 will be described in Chapter 7.

Table 1.2 is the output of the joint analysis of variance for the sample dataset.

The first six columns in Table 1.2 are items in a regular ANOVA table from common statistical software packages such as SAS. The first column is the source of variation, it includes the genotype main effect (G), the environment main effect (E), which is partitioned into the year main effect (Y), the location main effect (L), and the year–location interaction (L*Y or LY), the genotype-by-environment interaction (GE), which is partitioned into GY, GL, and GLY, block within trials, and the experimental error. The second column is the number of degrees of freedom (DF) for each source of variation. These are followed by the sum squares (SS) (column 3), the MS (column 4), the $F$-values against the error mean squares (column 5), and the significance levels of the $F$-values.
Table 1.2 indicates that all effects except block within trials were highly significant when tested against the pooled experimental error. The Y, L, and LY had $F$-values many times greater than the other sources of variation. These sources of variation, however, are not pertinent to genotype evaluation. The pertinent ones are G and its interactions with the environment, including GL, GY, and GLY. The $F$-value for G (23.2) was greater than that for any component of the GE (Table 1.2). GL and GLY were the main components of GE, while the variance for GY was zero.

The variance components that are relevant in calculating the heritability are also included in Table 1.2. The second to last column contains the variances for G, GL, GY, and GLY, as well as that for the experimental error. They are calculated based on the MS values and their EMS.
Theoretical Framework for Crop Variety Trials

Figure 1.3  GGEbiplot interface for conducting analysis of variance for crop variety trial data.

shown in Table 1.1. The last column contains the variances divided by appropriate denominators (referred here as “Unit Variance”), which sum to the phenotypic variance (\( \sigma^2_p \)) (Equation 1.6), the denominator in the heritability Equation 1.7. So the genetic and phenotypic variances for this dataset were 34643 and 51161, respectively. Thus the heritability was \( \frac{34643}{51161} = 0.68 \). Note that the variance for GY was 0, while the MS for GY was found to be highly significant. This is because the MS for GY was significant when tested against the MS for the experimental error (MSe), but its variance was 0 because its MS was actually less than that for GLY, which is the term that GY has to be compared against (Table 1.1). So, the variance is more meaningful than the MS in indicating the importance of a particular source of variation.

The lower part of Table 1.2 contains some summary statistics for the sample dataset. They are

1. The heritability across the trials, as defined in Equation 1.7, which is 0.68 for this particular dataset as already mentioned. It means that 68% of the observed differences in mean yield among the 6 genotypes across the 3 years and 8 locations were due to genetic differences among them.
2. The grand mean, which is the mean of the trait, here yield, across the trials, which was 5146 kg/ha.
3. The standard error (SE, which equals to \( \sigma_e \)), treating GE as fixed effects. It was 439 kg/ha for this dataset.
## Crop Variety Trials

### Table 1.2

The ANOVA table for a multiyear, multilocation variety trial dataset

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>SS</th>
<th>MS</th>
<th>F</th>
<th>Probability</th>
<th>Variance</th>
<th>Unit Variance</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>536</td>
<td>2410592918</td>
<td>45161</td>
<td>51161</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotype (G)</td>
<td>5</td>
<td>22289602</td>
<td>4457920</td>
<td>23.2</td>
<td>0.00001</td>
<td>34643</td>
<td>34643</td>
</tr>
<tr>
<td>Environment (E)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Year (Y)</td>
<td>2</td>
<td>29587201</td>
<td>14793600</td>
<td>76.9</td>
<td>0.00001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Location (L)</td>
<td>7</td>
<td>1338194944</td>
<td>191170706</td>
<td>994</td>
<td>0.00001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>L*Y</td>
<td>14</td>
<td>812003187</td>
<td>58000228</td>
<td>301.6</td>
<td>0.00001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Block (L*Y)</td>
<td>66</td>
<td>28992962</td>
<td>439287</td>
<td>2.3</td>
<td>1</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GE</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>G*Y</td>
<td>10</td>
<td>7052633</td>
<td>705263</td>
<td>3.7</td>
<td>0.00001</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>G*L</td>
<td>35</td>
<td>51743213</td>
<td>1478378</td>
<td>7.7</td>
<td>0.00001</td>
<td>58293</td>
<td>7287</td>
</tr>
<tr>
<td>G<em>L</em>Y</td>
<td>70</td>
<td>57836111</td>
<td>826230</td>
<td>4.3</td>
<td>0.00001</td>
<td>169983</td>
<td>7083</td>
</tr>
<tr>
<td>Error</td>
<td>327</td>
<td>62893066</td>
<td>192334</td>
<td></td>
<td></td>
<td>192334</td>
<td>2149</td>
</tr>
</tbody>
</table>

### Summary statistics

- \( H = \frac{V_g}{V_p} = 0.68 \)
- Grand mean: 5146
- Standard error (fixed GE): 439
- CV\%: 8.52
- Standard error (random GE): 649
- LSD5\% (fixed GE): 644
- LSD5\% (random GE): 952
- \( G/GGE (SS) = 0.16 \)
- CORRg (variance based): 0.36
- CORRg (across locations): 0.61
- \( V_g/V_p = 1.68 \)
- Noise quotient: 8.08

DF, degree of freedom; SS, sum squares; MS, mean squares; CV, coefficient of variation; LSD, least significant difference.

4. The coefficient of variation (CV\%) of the trial, which is the ratio of SE over the grand mean. The CV can be viewed as the “relative standard error.” Just as heritability is more meaningful than the genotypic variance, CV is probably more meaningful than SE in describing the trials. The CV\% was 8.52\% for this dataset. The implications of heritability and CV in assessing the data quality of the variety trials are further discussed in Chapter 7.

5. The SE, treating the GE effects as random. It is 649 kg/ha for this dataset. This value was calculated by the following formula:

\[
SE' = \sqrt{\sigma_e^2 + \sigma_{ge}^2} = \sqrt{\sigma_e^2 + \sigma_{gl}^2 + \sigma_{gy}^2 + \sigma_{gly}^2}. \tag{1.29}
\]

This equation means that GE becomes a source of error when it is treated as random effect.

6. The least significant difference at 5\% probability (LSD5\%), treating GE as fixed. It is calculated based on SE and was 644 kg/ha for this dataset, meaning that two genotypes are considered to be significantly different in yield at 5\% probability level only if their mean yields across the trials differed by 644 kg/ha or more.

7. The LSD5\% treating GE as random effects. It was 952 kg/ha for this dataset. It is larger than the regular LSD value and therefore is more conservative in declaring a significant difference.

8. The \( G/(G + GE) \) ratio in terms of SS, which is commonly used as a measure of the relative magnitude of G versus GE in the trials. It was 0.16 or 16\% for this dataset.
9. The genetic correlation across the test environments, which is calculated by

\[ r_g = \sqrt{\frac{\sigma^2_g}{\sigma^2_g + \sigma^2_{ge}}} = \sqrt{\frac{\sigma^2_g}{\sigma^2_g + \sigma^2_{gl} + \sigma^2_{gy} + \sigma^2_{gly}}}. \]  

[1.30]

Note the similarity and difference between the definitions of heritability (Equation 1.7) and the genetic correlation. The genetic correlation was 0.36 for this dataset.

10. The genetic correlation across test locations, which is defined as

\[ r_g = \sqrt{\frac{\sigma^2_g}{\sigma^2_g + \sigma^2_{gl}}} = \sqrt{\frac{\sigma^2_g}{\sigma^2_g + \sigma^2_{gl}}}. \]  

[1.31]

This is similarly defined as Equation 1.27. It is a measure of similarity among test locations in their ranking of the genotypes, and it was 0.61 for this dataset.

11. The \( \sigma^2_{gl}/\sigma^2_g \) or \( V_{gl}/V_g \) ratio, which is a reverse way to look at the genetic correlation across test locations. This is a useful statistic in that it indicates the potential of improving the heritability through subdividing the target region. For this dataset, it was 1.68, meaning that the variance for GL is considerably larger than that for G, so it may be meaningful to subdivide the target region. See Chapters 8 and 12 for how to divide the target region into subregions or mega-environments.

12. The “noise quotient” (\( Q \)) as defined in Equation 1.15. This value represents the relative magnitude of the nongenetic variance relative to the genetic variance within the phenotypic variance and may be used to estimate the minimum number of year–locations needed to achieve a certain level of heritability (Equation 1.16). The \( Q \) was 8.1 for this dataset. According to Equation 1.16, 19 year–locations, or 6 to 7 test locations in each of 3 years, would be needed to achieve a heritability of 0.7. To raise the heritability to 0.8, 40 year–locations or 13 locations in each of 3 years would be needed.

1.8 Summary

In this chapter, we have discussed the concept of heritability under the multilocation, multiyear framework. The definition of heritability (Equation 1.7) has many implications and can serve as the general guidance in the design, conduct, and analysis of crop variety trials.

1. The heritability estimated under the genotype–location–year framework is a measure of the power of the variety trials in discriminating the genotypes.

2. The heritability also carries information on the power of a single trial or a multilocation trial in a single year in genotype evaluation. When the heritability is high (say, \( H > 0.8 \)), it implies that fewer test locations and years may be sufficient.

3. When the heritability is low (say, \( H < 0.5 \)), the relative magnitudes of the various variance components should be examined, which will provide clues on how to improve the trial heritability. If the GL/G variance ratio is large, subdividing the target region into subregions or mega-environments may be an effective way to improve the heritability.
4. When the heritability is low and the GL/G is small (say, less than 1), it means that the target environment is a single but complex mega-environment and that the only way to improve the heritability is to increase the number of test locations and years. The $Q$ as defined in Equation 1.15 may be used to determine how many more year–locations are needed to improve the heritability to a certain level. Alternatively, a high $Q$ may indicate that the genetic variability among tested genotypes is small and the germplasm base needs to be enriched.

5. When the heritability is low due to large error variances, it may point to problems or potential in the design (replication and local control), conduct (human error), and/or data analysis (spatial analysis) of individual trials (see Chapter 7 for single-trial data analysis).

6. The definition of heritability is consistent with the key concept in GGE biplot analysis, that is, both $G$ and $GE$ must be considered simultaneously in variety trial data analysis and genotype evaluation.

7. Finally, heritability is the fundamental concept in plant breeding and crop variety trials. However, it is only conceptually useful in diagnosing the problems but does not provide direct solutions. For example, it requires that both $G$ and $GE$ be considered simultaneously in genotype evaluation but it does not tell how this can be achieved; it may suggest subdividing the target region if the GL/G variance ratio is large but it does not tell how the target region should be divided. Other statistical tools, GGE biplot analysis in particular, are needed to achieve these objectives, which will be the subject matter of the next few chapters. Furthermore, the equations presented in this chapter are valid only for ideal situations, i.e., when balanced and complete data are available. For unbalanced data, the estimation of various variance components as well as the heritability has to resort mixed models, which are incorporated in major statistical software packages such as SAS, GenStat, ASREML, R, etc.