Genetic properties of four types of stability parameter*

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Summary. The genetic properties of four types of stability parameter for individual genotypes were investigated using a set of diallel cross data (28 genotypes × four locations × 3 years). The specific parameters studied were: the variance of a genotype across environments (T1); the genotype × environment (GE) interaction effect for a genotype, squared and summed across all environments (T2); the residual mean square (MS) of deviations from the regression of a genotype on an environmental index (T3); and years within locations MS for a genotype, averaged over all locations (T4). Each stability statistic was fitted to the additive model, based on the assumption that if the stability parameter is heritable, stability of F1 is most likely to be the average stability of its parents. The results showed that T1 and T4 were additive, but T2 and T3 were not. A study of the consistency of stability rankings between two seeding rates over the same set of environments showed a similar pattern. It appears that stability parameters of types 1 and 4 are heritable, and thus useful for selection, while those of types 2 and 3 are nonheritable, and thus not useful.

Key words: Genotype-environment interactions – Regional trial – Diallel crosses

Introduction

Lin et al. (1986) studied the statistical relationship among nine conventional stability parameters and classified them into three types. A genotype is considered to be stable of type 1, if its variance over all environments is small; of type 2, if its environmental response is parallel to the mean response of all cultivars in the test; and of type 3, if its deviation mean square (MS) from the regression model (Finlay and Wilkinson 1963) is small. Lin et al. (1986) concluded that among these three types of stability, type 3 is the most problematical, because the residual MS from a regression model is merely an indicator of goodness of fit, and cannot be considered as a stability parameter. Their reason was that the regression model is a data-based descriptive model (not a predictive model based on external variables), and thus the residuals do not have a deterministic property that can be associated with genotypes.

Type 2 stability: since it uses the mean response as the standard, a stable genotype by this definition implies stability only with respect to the other genotypes in the test and it cannot be generalized. In contrast to both types 2 and 3, type 1 is a biologically meaningful parameter: it measures a genotype's homeostatic property to resist environmental change. However, this parameter has practical disadvantages. A breeder would like to find a genotype not only with good type 1 stability but also with high yield. However, type 1 stability is often associated with a relatively poor response in environments where other genotypes have high yields. Furthermore, although a high level of performance under a wide range of environments is desirable, this is difficult to achieve in practice. Even if it can be achieved, the effort is not entirely necessary, because several less widely adapted genotypes can be bred and then grown separately in different environments to achieve maximum production. Thus, the usefulness of type 1 depends largely on the range of environments under which the experiment is conducted. If the range is very large, such as a collection of sites from across the continental USA, type 1 stability may not be very meaningful, but if the range is small, such as a collection of sites from several counties within a state, then type 1 stability could be very important.

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In view of the theoretical and practical limitations of these three types of conventional stability parameters, Lin and Binns (1988) proposed a stability parameter (type 4) based on a genotype's years within location MS (as part of a genotype x location x year experiment). A genotype is considered to be stable if this MS is small. The idea is to separate environmental variation into predictable and unpredictable components, and then measure a genotype's stability with respect to the latter. Lin and Binns' (1988) reasoning was that predictable variation, such as genotype x location (mostly edaphic), can be controlled to some extent by selecting genotypes with specific adaptability to the region, while unpredictable variation, such as genotype x year (mostly climatic), cannot be controlled – one must rely on the homeostatic property of the genotype itself. Type 4 measures this property, which is independent of the regression analysis and also of the genotypic means.

Irrespective of how a stability parameter is defined, one of the most critical questions is whether it is genetic. If the characteristic measured by the parameter is nongenetic, it is not heritable and thus selection by such a parameter is fruitless. Lin and binns (1988) studied this problem for type 3 and type 4, using two sets of data collected from regional trials in which two seeding rates were used within the same set of locations. Their assumption was that if the parameter is genetic, the resulting stability ranking for each seeding rate should be approximately the same, since both rates were subject to the same environments. Spearman's ranking correlation between the two seeding rates was significant \( (p < 0.05) \) for type 4 but not for type 3. The inconsistency of type 3 was also confirmed by another set of data in which type 3 was assessed separately for each year. The resulting rank correlations among years were again not significant. These examples from both seeding rate and year studies support the theoretical argument that type 3 is only a measure of performance of the parameter. If such a test shows evidence of consistency, then the nonadditive genetic effect may be real, but if not, it is safe to conclude that the parameter is nongenetic.

The purpose of this paper is to investigate the additivity and consistency of four stability parameters, through crossed and non-crossed material, and to assess which of the four types of stability may be useful for breeding purposes. The validity of the conclusions for stability parameters of types 1, 2, 3 was further checked using diallel cross experiments reported in the literature. The merits of the type 4 stability parameter and the feasibility of breeding lines with high yield and high stability (of this type) are discussed.

### Methods

Forage yield of 28 genotypes of smooth bromegrass, consisting of the progenies of a 7 x 7 half-diallel cross plus parental lines, grown in four locations in western Canada for 3 years, was analyzed. The combining ability analysis of this set of data was reported by Tan and Tan (1980). The mean data averaged over six replications for a 28 x 4 x 3 (genotype x location x year) experiment (W. K. Tan, personal communication) were used for the present analyses. Four types of stability parameter were calculated for each genotype, and these were then treated as data (stability) values for additivity analyses.

Let \( Y_{ij} \) be the stability value of \( F_1 \) for a cross between line \( i \) and line \( j \). Then an additive genetic model can be written as:

\[
Y_{ij} = u + g_i + g_j + e_{ij},
\]

where \( u \) is the overall mean, \( g_i \) and \( g_j \) are the additive genetic effects of parental lines \( i \) and \( j \), and \( e_{ij} \) is the deviation assumed to be normally and independently distributed with constant variance. Note that expect for the assumption about \( e \), the above model is essentially the same as a combining ability model for a diallel cross: \( g \) represents the general combining ability (GCA) and \( e \) the specific combining ability (SCA) of the parents. Therefore, Grifling's (1956) method 2 can be used for the ANOVA.

The four stability parameters chosen for the present study are:

- **T1** – Variance of a genotype across environments (type 1).
- **T2** – Wricke's ecovalence (1962): the GE interaction effect for a genotype, squared and summed across all environments (type 2).
- **T3** – Eberhart and Russell's (1966) deviation parameter: the residual MS of deviations from the regression of a genotype on the environmental index, defined by the difference between location mean and the grand mean (type 3).
- **T4** – Lin and Binns' (1988) stability parameter: in a genotype x location x year experiment, the years within location MS for a genotype averaged over all locations (type 4).

Note that T1, T2, and T3 were calculated based on a 28 x 4 data structure (means over 3 years). Since the \( df \) associated with T1, T2, and T3 may be too small to give precise estimates, these three stabilities were also calculated based on a 28 x 12 data structure.