



# Identification of peach accessions stability and adaptability in non-balanced trials through years

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## ABSTRACT

Identification of genotypes with acceptable yield and yield stability in different environments is an important issue in plant breeding. Genotype-by-environment interaction (GEI) can alter genotypes performances making the selection of superior material a tedious task for breeders. Consequently, it is necessary to assess the usefulness of different available methods and identify the most suitable for understanding GEI. The objectives of this work were to compare three methods to study genotype stability considering incomplete data sets: (i) Di Rienzo, Guzmán and Casanoves' test (DGC), (ii) relative yield (RY) and (iii) Piepho's method. In addition, AMMI (additive main effect and multiplicative interaction) analysis and eight AMMI stability measures SIPC, EV, ASV, Da, FP, B, FA and Za were computed to explore their advantages and disadvantages to select stable entries. The usefulness of the genotype selection index (GSI) and the rank-sum (RS) procedures to identify stable and high-yielding genotypes were evaluated and then compared with the superiority (P) and reliability indexes (I). The association between yield variation and climatic factors as frosts, chilling, heat, rainfall and the interactions among them were also analyzed. 29 peach entries were assessed in four to seven seasons in a completely randomized design with three replications. DGC and RY tests agreed on classifying Fireprince as a stable and high-yielding peach, RY classified 25 entries as stable, while Piepho's method did not separate the tested genotypes as DGC and RY did. The results of AMMI indicated that 25.06% of total variability was justified by genotypes, 9.76% by environments and 58.97% by GEI. The first five interaction principal components could explain 94.82% of GEI and showed the efficiency of AMMI model to study and understand GEI. The AMMI parameters showed no association with fruit yield, therefore, they could be useful to indicate stable entries but they would not be appropriate to select stable and high-yielding genotypes. The EV and Za indicated static stability while ASV, SIPC, Da, FA and FP pointed out the dynamic stability concept. The performance of the best entries selected by GSI, RS, P and I procedures were not different, therefore, any of them can be used to select superior peach genotypes. Rainfall during endodormancy, rainfall from floral bud endo- to ecodormancy - and heat accumulation during fruit development period showed significant correlation with yield variation across seasons.

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## 1. Introduction

Mean yield of genotypes obtained through years or locations has been regularly used as crop performance and adaptation in different environments. The genotype-by-environment interaction (GEI) reduces the association between phenotypic and genotypic values and complicates superior genotype identification because acces-

sions may have high yields in some environments and low yields in others (Cruz and Regazzi, 1997). The term stability is used to characterize a genotype that shows a relatively constant yield, independently of environmental conditions. This concept of stability is named biological or static (Becker, 1981). A genotype showing a consistent performance in all environments does not necessarily respond to improved growing conditions with increased yield. Plant breeders, therefore, prefer an agronomic or dynamic stability concept (Becker and Leon, 1988; Becker, 1981) by which genotypes are not required to respond equally to environmental fluctuations (Becker and Leon, 1988). These concepts represent different aspects

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of stability and do not always allow analyzing the problem as a whole.

Argentina is the ninth largest peach producer worldwide and the second in South America with 291 thousand tons (FAOSTAT, <http://faostat3.fao.org/>). In Argentina, the peach crop was recently expanded to regions as C3rdoba, Misiones, R3o Negro (middle and lower valley), Jujuy and Salta, whose microclimates allow obtaining fruits with specific organoleptic properties. The main peach-producing areas in Argentina are Mendoza, R3o Negro (high valley) and the northeastern of Buenos Aires province. San Pedro Agricultural Experimental Station of the National Institute of Agricultural Technology (INTA San Pedro) is located in this last region and has a wide peach and nectarine germplasm that is evaluated every season. Many of the peach varieties used in Argentina are initially selected in INTA San Pedro and final evaluation of genotypes is performed in each one of the geographic regions mentioned above. As peach varieties remain in production for many years, the selection of genotypes with high yield and stability through years would be critical for horticulturist, whose main concern is to avoid low production years and to prevent their incomes fall. Additionally, the production stability is also important to avoid disturbing the normal market supply.

Procedures based on analysis of the variance (ANOVA) are the most common approaches to study GEI and to determine genotype stability and adaptation (Huehn, 1996). Although there are well-recognized statistical and biological limitations in the regression approach (Crossa, 1990; Flores, 1993; Lin et al., 1986), it provides useful parameter estimates when the number of genotypes and environments are sufficiently large and when there are no extreme environments that bias regression slopes (Flores, 1993). ANOVA and regression methods are parametric and therefore, the assumption of normal data distribution and the homogeneity of variance are required. On the contrary, non-parametric stability measures are largely unaffected by data distribution. As these procedures are based on ranks and not on values, a genotype is considered stable if its ranking is relatively constant across environments (Huehn, 1979; Kang, 1988; Nassar and Huehn, 1987).

Most of these methods require the evaluation of genotypes in all environments. This condition is difficult to fulfill in practice since the germplasm evaluation is a dynamic process. Entries could be lost due to climatic factors, pest attack and continuous replacement of genotypes. If data sets are obtained from several locations, some genotypes may not be tested in all sites. Similarly, if yield tests are registered in different years, genotypes might not be tested yearly. Genotypes change from year to year as new genotypes become available and older ones become obsolete. Incomplete datasets require special analysis to consider all the information and minimize the chance of losing valuable genotypes. At the present time, several procedures that allow analyzing both yield and stability have been proposed. Some of them are easy to apply and can be used in non-balanced data sets. In the Fisher's protected LSD (least significant differences) test, the mean value of each varietal type in each environment is compared with the mean value of the highest yield varietal type in that environment using the LSD test of multiple comparisons (Steel and Torrie, 1980). Annicchiarico (1992) and Yau and Hamblin (1994) proposed the relative yield (RY) as a way to calculate stability parameters for stability evaluation, which eliminate the environment main effect. Piepho (1995) reported a procedure that can be considered in unbalanced data sets in which a value delta ( $\delta$ ) is used to compare the confidence intervals of each genotype to find differences between all entries and the best and to classify each genotype as adapted, non-adapted or unclassified.

The study of GEI in peach performed by Mauli3n et al. (2014a) has demonstrated that the crossover is predominant over non-crossover GEI. The crossover GEI is the main cause of erratic behavior of genotype performance among environments (Cruz and

Regazzi, 1997). Therefore, more sophisticated statistical techniques should be considered to establish the real response of genotypes in different environments. The trend in modern times is toward multivariate methods that can provide further information on the real response of genotype to environments. The three main purposes of multivariate analysis are to eliminate the noise from the data pattern, to summarize the data, and to reveal the structure of the data (Purchase et al., 2000). Becker and Leon (1988) defined the aim of various multivariate classification methods as to assign genotypes into qualitatively homogeneous stability subsets. Within subsets, no significant GEI occurs, while differences among subsets are due to GEI. The most refined multivariate method is the additive main effect and multiplicative interaction widely known as the AMMI model (Crossa, 1990; Gauch, 1988; Zobel et al., 1988). The AMMI model is a powerful statistical method that incorporates both additive and multiplicative effects of a two-way data structure, and therefore, is the most useful technique to target genotypes and to select materials that are affected by crossover GEI (Baker, 1988). Although AMMI analysis is performed using balanced dataset, however, various methodologies have been proposed in order to solve this lack of balance caused by missing values. One of it was performed by Freeman (1975), who suggested imputing the missing values in an iterative way by minimizing the residual sum of squares and then doing the GEI analysis. Gauch and Zobel (1990) developed this approach, doing the imputation by using the expectation-maximization (EM) algorithm and incorporating the AMMI model, now known as the EM-AMMI approach. Arciniegas-Alarcon et al. (2010), Bergamo et al. (2008) and Yan (2013) described imputation systems that involve the singular value decomposition of a matrix, and therefore, they can be applied in any incomplete multi-environment experiments. AMMI model provides a visual inspection and interpretation of GEI and genotype stability constructing biplots (Zobel et al., 1988). The first biplot or AMMI1 provides a means of visualizing the stability and yield of each genotype plotting the first interaction principal component (IPCA1) scores against the average genotype performance. In the second biplot or AMMI2 the IPCA2 scores are plotted against their respective IPCA1 scores. Biplot formulation of interaction will be successful only when significant proportion of GEI is concentrated in the first or first and second IPCA axes. When the F test suggests retaining more than two axes, the biplot formulation of interaction fails (Raju, 2002) and the use of parameters derived from the AMMI model is recommended.

Stability and adaptability of fruit yield are two characters closely associated with weather conditions. Dormancy is an important evolutionary mechanism that allows species to survive adverse environmental conditions during winter, and favors the synchronization of vegetative bud break and flowering in the spring (Carl, 1996). Each genotype requires a specific amount of chill and heat to exit the bud dormancy (Richardson et al., 1975). If these requirements are not completed properly, an irregular flowering will be obtained and fruit production will be erratic over years. Genotypes whose thermal requirements do not match with particular location climate cannot be recommended for successful production.

The objectives of this work were (i) to compare three different methods to study the stability of fruit yield in peach considering incomplete data sets throughout years, (ii) to explore the utility of AMMI model to study GEI and test some stability measures derived from AMMI model to select stable and high-yielding peach genotypes, (iii) to evaluate the efficiency of single indexes in the selection of superior genotypes and (iv) to associate fruit yield fluctuation with environment variables.

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