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Additive main effects and a multiplicative interaction (AMMI) model for analysis of *Musa* yield trials

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Plant breeders are interested in the selection of genotypes which perform well over a wide range of environments. To identify such genotypes, yield trials are carried out over years in the breeding station and at different locations. For *Musa* species the genotype-by-year (G x Y) interaction seems to be less important than the genotype-by-location (G x L) interaction, even in the same agroecological zone (Ortiz et al. 1993). In the presence of a significant interaction, both the stratification of environments according to agroclimatological similarities and the determination of stability parameters for genotypes across environments are important tools for the management of the genotype-by-environment (G x E) interaction.

Finlay and Wilkinson (1963) and Eberhart & Russell (1966) developed models to determine the most stable genotype in a set of replicated trials across years, locations, or combinations of both (namely environments). However, those postdictive models are not useful for the identification of genotypes and environments which contribute most to the G x E interaction. Moreover, a breeder may be interested in identifying which genotypes are adapted to specific environments and/or to predict their performance in a specific location.

The additive main effects and multiplicative interaction (AMMI) model (Gauch 1992) was developed to provide answers to such questions. AMMI uses analysis of variance (ANOVA) to study the main effects of genotypes and environments and principal component analysis (PCA) for the residual multiplicative interaction.

Five tetraploid hybrids, which are undergoing evaluation in the multilocation trials, were chosen to determine the validity of AMMI analysis of factorial (genotype-by-environment) designs for *Musa* yield trials. Data from early evaluation trials (EET) at Onne 1989/1990, preliminary yield trials at Onne in the plant crop (PYT-PC 1990/1991) and ratoon (PYT-R 1991/1992), and multilocational trials (MET) at Onne, M'Balmayo, and Ibadan (1992/1993) were used for this analysis. The most stable, but average yielding, genotype was the black sigatoka (BS) resistant TMPx 582-4. PYTs and METs at Onne and M'Balmayo differed only in interaction effects. The AMMI model equation provides the expected bunch weights for points of different kinds. For example, the AMMI expected yield for TMPx 548-9 in EET-Onne [TMPx 548-9 mean + EET-Onne mean − Grand mean + (IPCA1 EET)* (IPCA1 TMPx 548-9)] should be equal to 17.8 kg, which was not significantly different from the observed bunch weight (17.9 kg) of TMPx 548-9 in the EET-Onne. This means that the AMMI1 model left a residual of 100 g. It is also clear that the main effects for genotypes may indicate their reaction (susceptibility or resistance) to BS, with the smallest genotype mean for the BS susceptible tetraploid clone 597-4 (Fig. 1.). Similarly the main effects for environment represented overall site quality, with EET-Onne having the best weather and soil conditions in 1989–1990, while the poor results of the MET-Ibadan could be the result of its nonadaptability to the dry season of this location in the humid forest-savanna transition zone of Nigeria.

The AMMI2 model (interaction analysis) for bunch weight is illustrated in Figure 2. Points near the origin (such as TMPx 582-4 or MET-Onne) have little interaction and should be well fitted by the additive submodel. Points near each other have similar interaction patterns (the full-sib, BS-resistant TMPx 548-4, and TMPx 548-9) while points distant from each other are indeed different (the unrelated BS-resistant TMPx 2796-5 and 597-4). The IPCA 2 also helps in the identification of those trials or genotypes with the worse fit, i.e., farther from zero (origin). This is exemplified by TMPx 2976-5 in EET-Onne in the AAMI1 model; its expected bunch weight was 21.3 kg instead of the 25.9 kg observed in this trial. This also suggests that bunch weights from unreplicated EETs should be taken with caution.

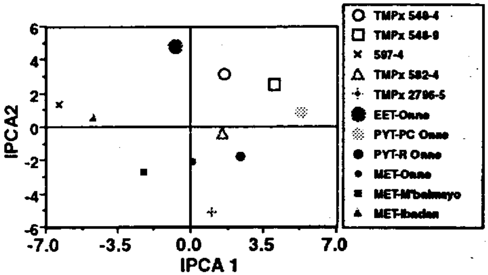

Figure 1. AMMI 1 Model for bunch weight in TMPx germplasm

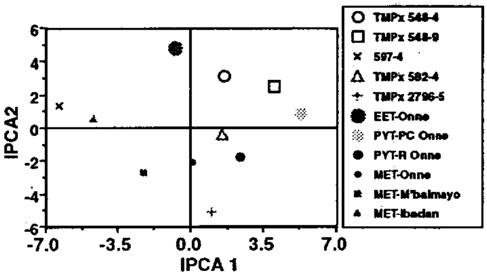

Figure 2. AMMI 2 model for bunch weight in TMPx germplasm

In conclusion, AMMI seems to be a powerful tool for the analysis of yield trials with a factorial structure such as location x genotypes. AMMI can analyze trials with within-site replications (METs) or trials with only 1 replication per location (International *Musa* Testing Program of INIBAP).

References

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