Factor analytic biplot in multienvironment trials with incomplete data

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In multi-environmental trials, the additive main effects and multiplicative interaction models (AMMI) are used to explore the genotype by environment interaction (GEI) based on a complete dataset where all genotypes were evaluated in all sites. The biplot from principal component analysis of residuals from the additive model (AMMI-biplot) allows us to visualize the ordination of the genotypes (G) according to their performance across environments (E), *i.e.*, locations and years combination. In incomplete datasets, the linear mixed models (LMM) using factor analytic (FA) covariance structure arise as an alternative to predict the GEI effect. Then, an FA-biplot could be obtained by plotting the G and E scores derived from the FA-LMM. The aims of this work were: 1) to quantify the consensus about G ordination achieved from the AMMI-biplot with the ordinations of G built from the FA-biplot obtained from complete multi-location and multi-year testing by the linear mixed model using FA covariance structure, and 2) to assess the impact of the increasing levels of missing G, discarded at a third year of testing due to low performances, on the final G ordinations. The G ordinations were assessed on four datasets from wheat testing with different arrangements of the number of G and E: 10G×15E, 15G×15E, 10G×30E, and 15G×30E. We started with complete datasets where all G had been evaluated in all E for three consecutive years. Then, to generate different levels of incompleteness, we eliminated the G with the worst performance in the last year of evaluation. Thus, we eliminated G simulating the selection of G in the Argentinean wheat plant breeding programs until we reached 50% of the missing genotypes in each database. To measure consensus we used a Generalized Procrustes Analysis. Despite applying two different procedures to obtain the biplots, one based on a fixed effects AMMI model and the other based on a random effects FA model, the biplots showed the same GEI pattern. With increasing levels of missing G, the consensus between the interaction patterns was also statistically significant demonstrating that FA-biplots are robust tools for ordering G under the studied mechanism of missing data.

Keywords: Genotype by environment interaction, Additive main effects multiplicative interaction (AMMI), Factor analytic covariance structure.