GENERALIZED PROCRUSTES ANALYSIS FOR DESCRIBING RELATIONSHIPS BETWEEN MAIZE HYBRIDS FROM MULTI-ENVIRONMENT YIELD TRIAL AND MOLECULAR DATA

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Maize breeding is based on selection of parents, making hybrids and selection through stages that typically culminate in multi-environment yield trials due to the omnipresence of genotype-byenvironment interactions. Besides that, molecular markers are used to characterize the new hybrids. Ordination methods used to understand germplasm relationships better require combining agronomic and molecular data. However, available information for commercial hybrids is usually incomplete, i.e. agronomic data at some environments and molecular data for some markers may be missing. This study investigated a multivariate approach for combining two-way tables (not necessary complete) of hybrid-by-environment yield data and hybrid-bymarker data. We studied the relationships between 23 hybrids of maize by the simultaneous use of genotype-by-environment interaction data (estimated by the residuals from the additive model for the agronomic trait) and genotype molecular characterization obtained from 52 polymorphic SSR bands. Generalized Procrustes Analysis (GPA) was used to transform, through iterative algebraic steps, agronomic and molecular configurations derived from Principal Coordinate Analysis on the corresponding distance matrices. The consensus configuration, obtained as the average of the two transformed configurations, explained a large proportion of the hybrid differences, which allowed us to establish the concordance between interaction and molecular data.