

Abstract

Maize is an important staple crop for millions of people in Sub-Saharan Africa. The crop grows in a wide range of environmental conditions. The present study was performed to analyze the genotype-by-environment (G×E) interaction for grain yield of forty two single cross hybrids grown in three environments located at different agro-ecological zones of Kenya. The maize genotypes were grown in randomized complete block design with three replicates in 2006 and 2007. Grain yield data of the single cross hybrids was analysed using the additive main effects and multiplicative interaction (AMMI) and GGE biplot methods. The additive main effects and multiplicative interaction model (AMMI) analysis of variance (additive main effects) showed significant effects for genotypes, environment and the genotype by environment interaction. The total proportion contributed by environment and G x E interaction accounted for 78% and 10% of the total variation. The results also showed that 64.5% of the total variation was contributed by the environment while the genotype and interaction was associated with 20.7% and 10.3% of the total variation, respectively. The most stable genotype in the high yielding group in this study was CML312/TZMI 711 (X20), followed by genotypes TZMI 102/CML384 (designated as X33), and CML312/TZMI 712 (X21). The genotype CML312/TZMI 711 (designated as X20) could be used for broad selection since it was found to be the most ideal genotypes with both high mean yield and high stability. In the biplot analysis, X20 was also close to the origin, had the shortest vector from the ATC and with large PC1 scores (high mean yield) and small (absolute) PC2 scores (high stability) implying it had the least contribution to genotype by environment interaction (GEI). Through the stability analysis, the superior genotypes identified could also be used as references for genotype evaluation and also included in further testing in both early and later stages of selection.