

ABSTRACT

Maize is a strategic food crop that serves as an important source of carbohydrates and plant-based protein. Increased productivity must be accompanied by improvements in kernel nutritional quality (especially kernel protein content); therefore, understanding the relationships between agronomic traits and kernel protein content in maize genotypes is essential. This research aimed to evaluate the relationships between quantitative agronomic traits and kernel protein content in 30 maize genotypes, using descriptive and multivariate statistical approaches to identify the main traits contributing to increased kernel protein content. Thirty maize genotypes were evaluated using 14 traits, including kernel protein content, phenological traits, plant morphology, yield components, and production per hectare. The results of the research showed extensive genetic diversity among 30 maize genotypes, as indicated by a very significant genotype effect ($p < 0.01$) on all observed traits and a significant mean difference based on the 5% HSD test. Phenotypic correlations showed that production per hectare was strongly correlated with most of the tested traits, except for kernel protein content and number of leaves, whereas kernel protein content showed weak associations with several yield-related traits, suggesting a potential trade-off. PCA analysis showed that genotype diversity is explained by two main dimensions: the first, comprising 12 traits, and the second, comprising kernel protein content and the number of leaves. The mean performance and PCA–biplot mapping indicated that G28, G29, and G22 were selected as superior genotype candidates for variety assembly and as parents in the high-protein, high-yielding maize breeding program.

Keywords: maize germplasm, kernel protein content, phenotypic correlation, principal component analysis, agronomic traits