ABSTRACT

Common bacterial blight (CBB) of mungbean (*Vigna radiata* [L.] Wilczek var. *radiata*) is a major limitation to mungbean production in semi-arid areas of the world where mungbean is a major crop. Deployment of resistant varieties is a significant sustainable strategy for controlling CBB in marginal production systems. The objective of this study was to identify sources of resistance and the stability of mungbean landraces to CBB attack across drought-endemic environments. A total of 240 mungbean genotypes were evaluated for CBB resistance and performance of agronomic traits in an alpha lattice design at four locations for 2 years (2019, 2020). Data were subjected to residual maximum likelihood (REML) analysis to partition variance components attributed to main effects and interactions, respectively. REML analysis revealed significant main effects for genotype, environment (combination of cropping season and location) and genotype-by-environment interaction ($p < 0.01$), demonstrating the influence of environment on genotypic expression. A genotype main effect plus genotype-by-environment biplot was used to analyse the multi-location trial data based on CBB score to determine genotypic stability. The GGE analysis demonstrated that the Kambi Ya Mawe location in 2019 was the most suitable environment for the assessment of CBB resistance. Accessions GBK 004852, GBK 004789, GBK 026986, GBK 004970, GBK 004961, GBK 004882 and GBK 043573 were selected as having high and stable resistance across all environments. The identification of high and stable resistance sources is a first step towards deploying resistance in mungbean breeding programmes against CBB and the future deployment of resistant cultivars.