ABSTRACT

The damage caused by cassava diseases has been on the rise in Africa in recent years. Most farmers obtain planting materials from their own fields or neighbours consequently enhancing the spread of the disease. The most feasible option of managing diseases is to improve existing cultivars through resistance breeding. This study was therefore conducted to evaluate the performance of cassava half-sib progenies arising from hybridization between diverse parental cassava germplasm deemed to be tolerant or resistant to that disease with the aim of determining their genetic inheritance. Five parental genotypes each with at least twelve progenies generated through polycross mating design were evaluated for agronomic and disease resistance. The half-sib families were developed from five elite parents selected based on their performance, disease resistance and farmers preferred traits. The experiments were established at the Kenya Agricultural and Livestock Research Organization (KALRO) at Kakamega and Alupe Research Stations from June 2016 to June 2017. Randomized completely block design was used. Data on emergence, plant height, height to the first branching, number of roots per plant, root yield, harvest index, dry matter, starch and cyanide content were recorded. Monthly assessment was done for cassava mosaic disease, cassava brown streak disease, cassava green mite and whiteflies infestation. Inheritance of agronomic traits and disease resistance was determined by calculating the general combining ability and estimating the heterosis between progenies and their best parents. There were high significant (P<0.01) differences in the reaction of genotypes to cassava mosaic disease and cassava green mite damages. Twenty three genotypes had a mean score of 1.0 to cassava mosaic disease and three to cassava green mite. Alupe site was observed to have high number of genotypes showing susceptibility compared to Kakamega, indicating the effect of the environment on the evaluated genotypes. Genotype, P4G1 followed by genotype P2G3 gave the highest fresh storage root yield across the study sites, while P3G6 and P5G9 recorded the lowest yield of 8.5t/ha. Significant correlation was observed among the agronomic traits, levels of cassava mosaic disease, green mite damage, fresh storage root yield, starch and cyanide content. Most parental cultivar expressed varying general combining ability effects in the two sites for most of the evaluated traits. Parental cultivars MM96/4271, MM96/0686, MM97/0293 and Kaleso had good general combining ability for cassava mosaic disease resistance. MM96/4271 was the most resistant parent among the five for cassava green mite with a negative general combining ability effect in both sites. Parental cultivar Kaleso had negative general combining ability effects for cassava mosaic disease and for the progression of the disease in both two locations. The progenies from Kaleso and MM96/4271 had high positive heterosis for fresh storage root yield, harvest index and storage root number, and the most negative better parent heterosis for cassava green mite and cassava mosaic disease incidence. Though there were significant differences between parents and their respective progenies in the reaction to cassava mosaic disease severity, there were a varying number of symptomless clones generated from different cassava families involved. This suggests that these genotypes may be suitable as genetic stock that could combine cassava mosaic disease and cassava green mite damage resistance in one background. Evaluation of new cassava varieties under local disease conditions would likely improve the productivity of cassava through selection of resistant clones. The parental cultivars and progenies identified here are potential candidates for producing a new generation of segregating progenies that could in future be released to farmers to increase the productivity of cassava in a number East African country.