ABSTRACT

Stem rust, caused by *Puccinia graminis* f. sp. *tritici*, is a destructive fungal disease of bread wheat (*Triticum aestivum* L.) and poses a major challenge to wheat production in sub-Saharan Africa and Asia. The continuous evolution and variable nature of stem rust predispose wheat to serious genetic vulnerability, necessitating proactive incorporation of new and effective resistance sources into breeding lines. This study evaluated 25 wheat genotypes over three seasons at the Kenya Agricultural and Livestock Research Organization (KALRO), Njoro, to assess resistance mechanisms and yield stability under stem rust pressure. A 5 × 5 partially balanced alpha lattice design was employed. Disease progression was assessed using final disease severity (FDS) and area under the disease progress curve (AUDPC), alongside evaluations of agronomic performance. Statistical analyses revealed significant ($P \leq 0.001$) effects of genotype, season, and genotype × season interaction for AUDPC and agronomic traits. Grain yield (GY) was significantly ($P \leq 0.001$) negatively correlated with disease components, and positively correlated with kernels per spike (KS), biomass (BM), harvest index (HI), and thousand kernel weight (TKW). Broad-sense heritability (H^2) estimates ranged from 59.90% for grain filling period to 95.58% for FDS. Adult plant resistance genes *Lr34/Yr18/Sr57*, *Lr46/Yr29/Sr58*, *Sr2/Yr30*, and *Lr67/Yr46/Sr55/Pm46* were detected in various combinations across 21 genotypes. Based on disease response and yield performance, genotypes 8790929, 8790027, 8790948, and 8790935 exhibited the highest levels of resistance and superior grain yield. These genotypes represent valuable sources of stem rust resistance and are recommended for use in breeding programs for gene introgression and varietal development.