Abstract

Bacterial wilt (Ralstonia solanacearum) is a major disease affecting global potato production. Host plant resistance has been proposed as the cheapest and most practical bacterial wilt management option. However, this management option has various limitations which has necessitated frequent screening of different potato germplasms to identify those with resistance traits for adoption and commercialization. A study was conducted for two successive seasons (October 2021 to August 2022) at Kiandu (Nyeri County) and Turi (Nakuru County) in Kenya to assess resistance levels of thirty potato genotypes against bacterial wilt. The experiment was laid down in 3 × 7 alpha lattice design with 3 replicates in season one and 3 × 9 alpha lattice design with 3 replicates in season two. Data were collected on disease severity, disease incidence and yield parameters. Scott Knott test ($p < 0.05$) was performed on AUDPC to rank resistance levels of potato genotypes per trial site using 'ScottKnott' package in R software. The study results ranked genotypes CIP 515008.530, CIP 515014.567, CIP 515004.535, CIP 515008.521, Sherekea, Kenya Karibu and CIP 515002.516 as the most resistant to bacterial wilt while Shangi, Asante, Tigoni and Arka were highly susceptible. However, all the resistant genotypes had very low yields [tuber weights (t/ha)] compared to commercialized varieties which may affect their future adoption and commercialization by farmers. Thus, to increase chances of adoption and commercialization, future studies should focus on integrating high yielding and resistance traits. Additionally, most of the tested genotypes displayed internal bacterial wilt symptoms from dissected tubers and hence can only be suitable for ware potato production as opposed to seed potato production.