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Molecular markers-assisted selection of tomato genotypes for resistance to bacterial and fusarium wilt in Nigeria

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Bacterial wilt (caused by Ralstonia solanacearum, Rs) and fungal wilt (caused by Fusarium oxysporum (f.sp). lycopersici, Fol) are two major production constraints of tomato in Nigeria. The two diseases constitute 40-80% loss of yield in endemic areas. Single Nucleotide Polymorphism (SNP) marker, LEOH19, was used to screen for bacterial wilt resistance gene (bw) while Cleaved Amplified Polymorphic Sequence (CAPS) markers TAO1 and TG105 were used to identify the resistance gene (I2) to fusarium wilt in tomato. Fifty tomato genotypes within the country were screened. With LEOH19, the primer pairs produced amplification at 300 bp in 35 genotypes. Restriction enzyme digestion produced amplicons in four genotypes namely FUNAABTO09803, FUNAABTO0201, Tomachiva and Eyetom. Screenhouse experiment confirmed the resistance in the four mentioned genotypes. The primer pairs for TAO1 and TG105 produced amplification at 902 bp in 33 accessions and 450 bp in 38 accessions, respectively. The restriction enzymes Fok1 and Hinf1, for TAO1 and TG105 respectively, produced fragments at base pairs indicative of susceptible, homozygous and heterozygous resistant accessions to Fol. Restriction fragments from the two markers indicated that 11 accessions were homozygous resistant to Fol. Four of these accessions (Delila, Gem Pride, K-Small and Oxheart) occurred in the two molecular markers as homozygous resistant to Fol. The combined effect of the two markers enhanced precision in the identification of tomato accessions with resistance status to Fusarium vascular wilt. The resistant tomato genotypes against bacterial and fungal wilt had been recommended to farmers and researchers for further evaluation.

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