RESISTANCE GENE POOL FOR BACTERIAL WILT OF TOMATO AMONG THE INTRODUCED GENOTYPES

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Bacterial wilt of tomato, caused among the most serious diseases of tomato in tropical and subtropical. It is now the major constraint on production of tomato in many parts of VietNam. Bacterial wilt is caused by the soil borne bacterium Ralstonia solanacearum. This oomycete pathogen attacks on leaves, stems, and roots of tomato. Introduction of resistant varieties is therefore the most effective measure to control this disease. However, conventional breeding approach for disease resistance is difficult, labor and cost time. The objective of this study is to research on genetic polymorphism using molecular marker SSR for identifying to tomato varieties so that resistant materials have been defined to Ralstonia solanacearum isolate that collected in Vietnam. The result of phenotypic evaluation by artificial infection showed that Vimina 1 and Vimina 2 varieties exhibited resistance to 3 isolates RsĐT6, RsĐT3 and RsĐD1. 3 isolates are exhibited the differential virulence. Varieties of Terminator, Tropic, Tomato and TN 323 are intermediate resistance to RsĐT3 isolate. 7 varieties which include Safina 404, Red Crown 250, Terminator, Mongal (T11), Tropic, Caribo and TN 323 are intermediate resistance to RsĐD1 isolate. Research also identify the marker SSR 306 on chromosome 4, ranged from 51 cM to 71 cM showing polymorphic between resistant varieties (Vimina 2) and susceptible variety (Seeda tomato) with band of 290bp and 258bp. This result opens up for marker assisted selection of bacterial wilt resistant improvement of tomato varieties in Vietnam.