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Genotypic and virulence characterisation of *Xanthomonas axonopodis pv.phaseoli* and *Xanthomonas axonopodis pv.phaseoli var. fusca*ns, and reaction of the backcross four (BC4) common bean population to common bacterial blight (CBB).

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Abstract

Forty common bacterial blight isolates from seven localities were used for morphology, genotypic and pathogenicity/virulence characterizationstudy. Morphological and biochemical characterization showed that, 97.5% of the isolates wereXanthomonas axonopodis pv. phaseoliandXanthomonas axonopodis pv. phaseoli var. fuscans; from which 47.5% of them had diffusible brown, yellow pigment on yeast extract dextrose calcium carbonate agar media and were classified as Xanthomonas axonopodis pv. phaseoli var. fuscans and 50% of them had yellow pigment on yeast extract dextrose calcium carbonate agar.Isolates differed in aggressiveness on the common bean varieties (Red wolaita, Ibado and VAX6) had different level of resistance. 77.5%of isolates induced a slight reaction on variety Ibado and had rating of 1-2.67whereas Red wolaita andVax6 had (57.5%; rating=1-2.33) and (92.5%; rating=1-2.33), respectively. Isolates ET534, 516,517,515 and 504 were the most pathogenic/virulent and had mean severity of 3.67,3.33, 3.11, 2.89 and 2.78, and with mean incubation period of 18.6,19.11,19.33, 20.11 and 19.33 days, respectively. Three of the common bean lines (KT014, KT018 and VAX6) were resistant to all five (ET515, ET516, ET517, ET534 and ET504) virulent common bacterial blight isolates with a mean severity value of 2.89±1.26, 2.33±0.88, 2.00±1.00, 1.78±0.38, 2.00±0.34; 3.00±0.34, 2.66±0.67, 2.78±0.39, 2.88±0.39, 2.55±0.69; 2.33±0.58, 2.44±0.77, 1.00±0.00, 2.44±0.38 and 1.00±0.00 respectively. The remaining lines were assigned to two susceptibility groups (intermediate resistant and susceptible) based on Average Disease Severity Rating. Rep-PCR profiles generated a total of 62 clearly scorable bands out of which 48.71 (78.57%) were polymorphic and could distinguish

within common bacterial blight populations. The analysis of molecular variance shows a high level of genetic variation within population from different sampling areas (99%) but, there is only 1% of genetic variation between populations, suggesting the possibility of gene flow affecting populations. Results from this analysis showed that a significantly high ($p<0.0001$) PhiPT (0.021), indicating a high level of genetic differentiation within a population. In this experiment Shannon-wiener index(H) is greater for Sidama (2.565);Stoddart and Taylor's index(G) is also higher (13) thus, diversity is higher in Sidma population both by the Shannon-wiener index (H) and Stoddart and Taylor's index(G) test, which showed higher value compared to the other populations. Common bacterial blight isolates from the same geographical region often had different Rep-PCR profiles, revealing that the common bacterial blight pathogen is not clonal. Results suggest the existence of diverse isolates in single population that should be given prior attention in the future breeding programs. Similar studies should be carried out by collecting isolates from additional common bean producing areas representing the various agro-ecological zones to come up with an inclusive outlook of how the common bacterial blight population varies across the country.

Publication

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Mr Mitiku Shertore isolating and making pure cultures of Xanthomonas axonopodis, the causal agent of CBB (i); pure cultures of the pathogen (ii); during artificial infestation of plants in the greenhouse to test for disease-resistance (iii); symptoms of disease in susceptible plants after inoculation (iv).