

Bacterial Blight Occurrence and Resistance in Cowpea (*Vigna unguiculata* (L.) Walp.) Genotypes in Uganda

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Abstract

Cowpea bacterial blight (CoBB) disease, caused by *Xanthomonas axonopodis* pv. *vignicola* (*Xav*), is a constraint to cowpea production in Uganda. This study assessed CoBB occurrence and predicted environmental suitability, characterized the diversity of *Xav* isolates, identified cowpea genotypes with field resistance, and determined the mode of inheritance of resistance.

CoBB disease incidence and severity were assessed in two survey phases in 2019, each covering 420 farms in 42 sub-counties across 14 districts. Maximum entropy (MaxEnt) models were used to predict environmental suitability for disease occurrence. Sixty-nine bacterial isolates from symptomatic leaves were characterized using morphological and biochemical tests and molecular methods. Sixty-four cowpea genotypes were evaluated over two field seasons using an alpha lattice design. Nine selected parents and their F₂ progenies were then evaluated in a diallel experiment to estimate combining ability and genetic parameters for resistance.

CoBB disease incidence and severity varied among districts and survey phases and were strongly positively correlated in both phases ($r = 0.829$ in Phase 1; $r = 0.760$ in Phase 2). In Phase 2, incidence ranged from approximately 27% in Lira to 60% in Soroti and Yumbe. Precipitation was the strongest contributor to predicted environmental suitability, and the MaxEnt models achieved areas under the receiver operating characteristic curve of 0.814 and 0.848 in Phases 1 and 2, respectively. The *Xav* isolates showed biochemical and molecular variation, with molecular clusters containing isolates from different regions.

Disease levels in the genotype trial were higher in the second season. NE 32, WC 32A and NE 44 maintained moderately resistant responses across both seasons. Relative area under the disease progress curve (rAUDPC) was not significantly correlated with grain yield. For resistance, general combining ability effects were significant, whereas specific combining ability effects were not, indicating that additive gene effects were more important than non-additive effects in the parents and progenies studied. Reciprocal effects were also significant, suggesting that the direction of a cross influenced resistance. WC 26 and NE 31 were favourable general combiners for resistance. The broad-sense and narrow-sense coefficients of genetic determination for rAUDPC were 44.3% and 29.1%, respectively, and Baker's ratio was 65.8%.

The study identifies variation in CoBB disease occurrence and predicted environmental suitability in Uganda, documents diversity among *Xav* isolates, and identifies moderately resistant genotypes and useful parents for breeding. The predominance of additive effects supports selection for CoBB disease in progenies derived from the parents studied, while significant reciprocal effects should be considered in resistance breeding.