

Deployment of sources of cowpea root rot (*Macrophomina phaseolina* and *Rhizoctonia solani*) resistance to improve cowpea in Ghana.

Mr Salim Lamini

PhD student, University of Ghana; Supervisors: Dr Francis Kusi, CSIR-SARI, Dr Eric W. Cornelius, University of Ghana, Dr Agyemang Danquah, West Africa Centre for Crop Improvement.



Mr Salim Lamini

Background

Field surveys carried out in Northern Ghana during 2015 established that root rot, caused by one or both of the fungi *Macrophomina phaseoli* and *Rhizoctonia solani*, is an important constraint over cowpea productivity.

Objectives

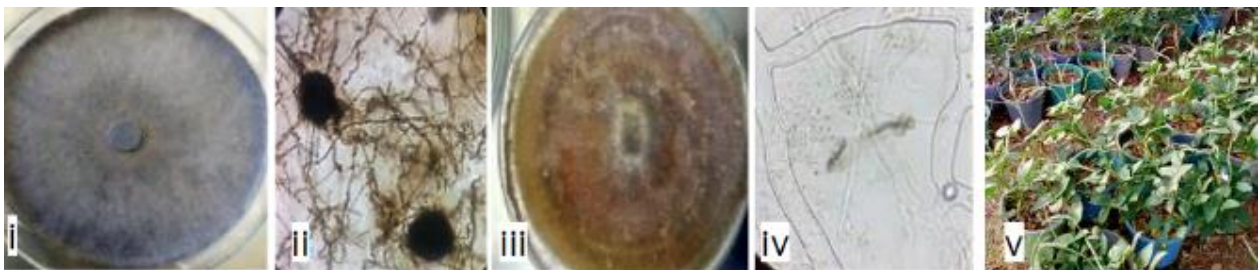
1. To incorporate resistance to *M. phaseolina* into the cowpea variety Songotra.
2. To determine the incidence and severity of *M. phaseolina* root rot across Northern Ghana through a survey.
3. To identify and characterise *M. phaseolina* isolates from samples collected from cowpea growing locations in Northern Ghana.
4. To identify cowpea genotypes with resistance to *M. phaseolina*.
5. To determine the genetics of inheritance of *M. phaseolina* resistance in cowpea.

Achievements

1. Cowpea plants showing symptoms of root rot infection were collected from sites in Northern, Upper East and Upper West Ghana. The pathogens were isolated and were identified on the basis of their morphology and genotype. The resulting strains were then back-inoculated into the susceptible cowpea variety Songotra. Re-isolated strains of *M. phaseolina* were used to screen a panel of 49 entries. A selection of three susceptible varieties (Songotra, Padituya and Zaayura) and seven resistant varieties (Suvita 2, Nhyira, Hewale, T2T4, AV2 3224, IT99K573-1-1 and Apagbaala) entries formed the basis of a diallele analysis. The resulting crosses were advanced to the F2 generation to determine the mode of inheritance of resistance. Resistance to *M. phaseolina* was shown to be conferred by two dominant complementary genes (both genes must be present in the dominant form, but not necessarily homozygous, for resistance to be expressed).

2. The IT99K573-1-1 variety, used as the donor of *Striga* resistance to derive Wang Kae, was crossed and back-crossed to Songotra, reaching the BC4F3 generation in 2020. A selection of 76 lines resistant to *M. phaseolina* were field-tested in 2020. All the lines expressed resistance to the *M. phaseolina* root rot disease and *Striga*.
3. A set of F7 recombinant inbred lines bred from the cross IT99K573-1-1 x Songotra was evaluated for their response to artificial inoculation with *M. phaseolina*, of which eight were selected for further evaluation. These lines were selected on the basis of their performance at F6 with respect to maturity time, seed coat and eye colour, and various podding traits.

Mr Lamini has successfully defended his PhD thesis and is awaiting his graduation.



Microscopic Identification of root rot pathogens: *M. phaseolina* in culture (i); *M. phaseolina* sclerotia (x40 magnification; ii); *R. solani* in culture (iii); typical *R. solani* mycelia (x 40 magnification; iv); advancement of recombinant inbred lines (v).