



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

Dr Salim Lamini

Dr Salim Lamini

PhD student, University of Ghana

Abstract:

A new cowpea root rot disease was reported across cowpea growing locations in northern Ghana in 2014. Efforts to control the disease using chemical and cultural methods were expensive and often failed to meet expected results. This study was therefore undertaken to determine the importance of the disease, identify the causal organism and to genetically improve a farmer preferred cultivar (Songotra) which is susceptible to the disease. A field survey was conducted in 17 cowpea growing locations in northern Ghana under both rain fed and irrigated conditions in 2016 and 2017 to determine disease prevalence, incidence (DI) and severity (DS). Diseased cowpea plants were collected from fields for identification of the causal organism using morpho-cultural characteristics, PCR and DNA sequencing. Forty-nine cowpea genotypes were screened to identify lines resistant to the disease using a completely randomised design (CRD) with five replications. Eight resistant cowpea genotypes (Suvita 2, Apagbaala, Hewale, AV2 3224, Nhyira, IT99K573-1-1, IT93K303-1 and T2T4) and a susceptible check (Songotra) were screened against 10 isolates of the *Macrophomina* root rot pathogen collected from 10 different locations using a nine (9) × ten (10) factorial experiment in CRD with five replications. A total of 109 to 250 F2 progenies developed from the hybridization of five *Macrophomina phaseolina* resistant cowpea genotypes (Suvita 2, Apagbaala, AV2 3224, IT99K573-1-1 and T2T4) and Songotra were screened for levels of resistance to *Macrophomina* root rot disease in the determination of genetics of inheritance of cowpea to the *Macrophomina* root rot pathogen. Allelism study, was then undertaken with 201 to 369 F3 progenies developed from resistant × resistant crosses of the five resistant cowpea genotypes and screened for disease resistance. A chi-square test of goodness of fit was used for data analysis. Two hundred and seventy-three F6 RILs developed

from IT99K573-1-1 × Songotra were screened for disease severity in an augmented design with two checks. Duncan's multiple range test at $P \leq 0.05$ was used for mean separation. The new root rot disease was prevalent in all the 17 locations surveyed. Under rain fed production for 2016, DI was 17.8%–43.8% whilst DS was 2.1–4.3. Under irrigated conditions for the same year, DI was 11.4%–44.5% whilst DS was 2.1–3.8. DI under rain fed conditions in 2017 was 8.7%–47.7% whilst DS was 1.6–4.3. Under irrigation in 2017, DI was 7.0%–64.8% and DS was 2.3–4.2. DI and DS for the root rot pathogen was similar under rainfed and irrigated conditions for both years. The causal organism of the root rot disease was identified as *M. phaseolina* and isolates were confirmed to be monotypic based on molecular characterisation. Ten cowpea genotypes (Suvita 2, Apagbaala, Hewale, AV2 3224, Nhyira, IT99K573-1-1, IT93K303-1, Marfotuya, Asetenapa and T2T4) out of the 49 were identified as resistant to the disease. Isolates from Manga, Feo, Silbelle Arigu and Asumsapeliga induced significantly higher disease severity of 3.8, 3.6, 3.4, 3.2 and 3.4, respectively compared with the six isolates. Eight genotypes which were further screened against 10 isolates of *M. phaseolina* for resistant stability were found near constant in their disease resistance (stable) regardless of the variant of the pathogen isolates. A 9:7 resistant: susceptible ratio was observed for T2T4 × Songotra; Suvita 2 × Songotra; Apagbaala × Songotra and IT99K573-1-1 × Songotra whilst AV2 3224 × Songotra recorded a 15: 1 resistant: susceptible ratio in mode of inheritance study. The genetic relatedness study revealed a resistant: susceptible ratio of 27: 37 for Suvita × T2T4 whilst all the other populations were resistant. 120 out of 273 RILs developed from IT99K573-1-1 × Songotra were resistant to the disease. It can therefore be concluded that the root rot disease of cowpea caused by *M. phaseolina* was prevalent in all the 17 locations surveyed at varying levels of DI and DS for 2016 and 2017. Ten cowpea genotypes out of 49 were resistant to the disease. Two dominant complementary genes confer resistance of cowpea to the disease. Cowpea genotypes (Apagbaala, T2T4, IT99K573-1-1 and AV2 3224) were allelic whilst Suvita 2 was non-allelic. Macrophomina root rot resistance was introgressed from IT99K573-1-1 into cowpea genotype Songotra through a RIL method.

Publication

Lamini, S. 2020 Deployment of sources of cowpea root rot (*Macrophomina phaseolina* and *Rhizoctonia solani*) resistance to improve cowpea in Ghana.



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).