

ABSTRACT

EVALUATION OF COMMON BEANS (*PHASEOLUS VULGARIS*) GERMPLASM FOR RESISTANCE TO *PYTHIUM* ROOT ROT DISEASE

By

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The common bean (*Phaseolus vulgaris* L.) is the second most important source of human dietary plant protein after Soybean and the third most important source of calories of all agricultural commodities grown in eastern and southern Africa after peanut and soybean. One of the major production constraints of this crop is the prevalence of bean root rot disease caused by the *Pythium* pathogen. This disease can result in yield losses of up to 70% to the farmers who cultivate most of the popular commercial common bean cultivars grown in Eastern Africa. The most effective, sustainable and environmentally safe management and control strategy of this *Pythium* root rot disease is the use of resistant common bean genotypes.

This study focused on ascertaining information on bean cultivation practices within the study area, morphological and molecular characterization and identification of *Pythium* species from infected bean plants collected from farmers' fields, determining the relationship between soil pH and the occurrence and distribution of *Pythium* species and the evaluation and selection of promising common bean genotypes for resistance to *Pythium* root rot disease under screen house conditions.

Infected plants showing root rot symptoms were collected from farmers' fields in Mbozi and Lushoto districts in Tanzania followed by aseptic pathogenic isolation in the laboratory. The pH of soils from the farmers' fields was determined. Pure cultures of *Pythium* isolates were used to identify the *Pythium* species based on morphological characteristics,

molecular characterization using Internal Transcribed Spacer conserved region and DNA sequencing. Screen house studies were conducted using two characterized *Pythium* isolates to evaluate the response of common bean genotypes for root rot disease resistance. Disease severity was determined using the CIAT disease rating scale of 1 – 9 with 1 being non-pathogenic and 9 being highly pathogenic.

Survey results indicated that most of the farmers (63%) practice sole bean cropping, 31.0% mixed cropping and 6.0% intercropping. 52.4% of farmers use farm saved seeds and 92.9% are not using fertilizer. Of the thirty two *Pythium* isolates sequenced eleven species were identified with *Pythium aphanidermatum* (31.25%) and *Pythium splendens* (28.13%) being the most widely distributed in the entire study area. Incidence and distribution of *Pythium* species from farmers' fields were dominant between soil pH of 5.03 – 5.95 with less incidence found between 6.05 – 6.41 pH indicating prevalence of root rot disease in more acidic soils. The study showed that, 5 bean cultivars (landraces) collected within parts of Tanzania were moderately resistant. From ADP's collections, 2 bean genotypes were resistant, 21 were moderately resistant and 12 were susceptible compared to CIAT bean genotypes of which from a total of 52 bean genotype population, 12 were moderately resistant and 40 were susceptible.

Identification of promising common bean genotypes with resistance traits can assist breeders on developing new common bean genotypes with resistance to *Pythium* root rot disease. This could potentially provide control of *Pythium* root rot disease through improved host resistance across the major common bean growing regions in Tanzania.

Key words: *Pythium*, identification, internal transcribed spacer (ITS), resistance, susceptible, common bean, genotypes, disease severity.