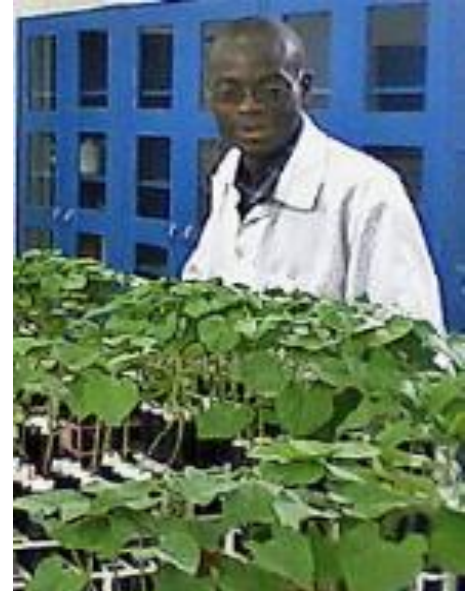




Ms Miyoba Sansala infecting different cultivars for the characterisation of ANT isolates.

Race characterization of *Colletotrichum lindemuthianum* in Zambia and identification of new sources of resistance to anthracnose in common beans



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Abstract

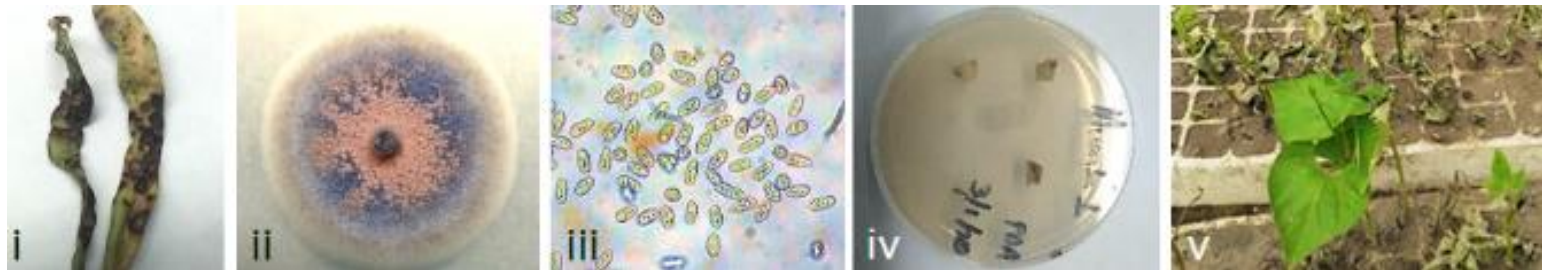
Sansala, M., Hamabwe, S., Kuwabo, K., Kachapulula, P., Parker, T., Mukuma, C., and Kamfwa, K. 2023. Race Structure and Molecular Diversity of *Colletotrichum lindemuthianum* of Common 22 Bean in Zambia. *Plant Dis.* (XX:XX-XX). Anthracnose, caused by the fungus *Colletotrichum lindemuthianum*, is a major disease of common bean (*Phaseolus vulgaris* L.) worldwide. *C. lindemuthianum* is genetically highly variable and understanding the pathogen's diversity and distribution is a key step in developing common bean varieties with durable anthracnose resistance. The objectives of this study were to (i) characterize the race structure of *C. lindemuthianum* in Zambia, and (ii) assess the molecular diversity of *C. lindemuthianum* in Zambia. A Field survey was conducted in 20 bean growing districts in Zambia to collect anthracnose symptomatic bean plants. A total of 103 *C. lindemuthianum* isolates were collected and characterized based on their reactions on 12 common bean race differential cultivars. RAM and ERIC-BOX DNA markers were used to assess molecular diversity of 60 isolates. A total of 58 races were characterized from the 103 isolates. Race 5 was the least virulent, and race 1631 was the most virulent based on their reaction on the 12 race differential cultivars. Race 19 had the highest recovery frequency (11%) and was the most extensively dispersed among the 22 bean-growing districts from where the isolates were collected. Only six races had previously been reported in Zambia, and 52 races were identified as new races reported for the first time in Zambia. Two races were virulent only on Andean cultivars, 11 races were virulent only on Middle American cultivars, and 45 races were virulent

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Middle American cultivars. No individual isolate showed pathogenicity on all the differential cultivars, and no isolate overcame the Co-4, Co-5, and Co-7 resistance gene 42 pyramid that naturally exists in G2333. Phylogenetic analysis categorized the 60 isolates in six major clusters and six sub-clusters. The 60 isolates showed high genetic heterogeneity among and within a race of same virulence. The study has revealed the existence of both Andean and Middle American races, and extensive molecular diversity of *C. lindemuthianum* in Zambia. The knowledge on the race structure of *C. lindemuthianum* that this study has provided will be valuable for making breeding decisions on the host plant resistance genes required for developing common bean varieties with durable resistance to anthracnose in Zambia.

Publication

Sansala, M., Kuwabo, K., Hamabwe, S., Kachapulula, P., Parker, T., Mukuma, C. and Kamfwa, K., 2023. Race Structure and Molecular Diversity of *Colletotrichum lindemuthianum* of Common Bean in Zambia. *Plant Disease*, (ja).



The lesion interphase of infected beans (i) collected during field surveys are cut into small pieces, surface sterilised and base plated (ii). The plates are incubated until sporulation (iii). A single spore is excised and plated to obtain a pure isolate (iv), which was characterised using a set of differentials to identify resistant genotypes (v).