**Introduction**

Root rot of common beans in Puerto Rico is a significant issue, affecting production and yield. Understanding the causal agents of root and stem rots is crucial for effective screening and selection of disease-resistant common bean germplasm.

**Materials and Methods**

**Objective**

The objective of this study was to effectively screen and select disease-resistant common bean germplasm by utilizing molecular and microbiological techniques.

**Methods**

- **Materials:** Samples of symptomatic plants were collected in seed multiplication fields in Puerto Rico. These samples included diseased roots of common beans.
- **Methods:**
  - **DNA Isolation:** DNA was extracted from plant samples using the Powerplant	extsuperscript{TM} Pro DNA Isolation Kit.
  - **PCR Amplification:** The DNA of each sample was amplified using primers ITS4/ITS5.
  - **DNA Sequencing:** DNA sequences were classified using the Chromas Lite 2.1.1 software and compared with sequences from the NCBI database.

**Results**

- **Identification of Fungi:** Seven fungal colonies were isolated from infected plants, representing 17 culture isolates. These isolates were tested for pathogenicity using the straw test, leading to the identification of two or more fungal species in 5.8% of cases.
- **Pathogenicity Testing:** The isolates from culture were tested for pathogenicity on 143 old plants in the greenhouse. Plugs from isolated fungal cultures were placed in drinking straw sections and lesions in infected tissue were recorded after 48 hours of incubation in a humidity chamber.

**Conclusion**

The straw method was used to test for pathogenicity, and DNA bar coding was employed for the identification of pathogen races and related tools. This approach provides a synergistic method for effective screening and selection of disease-resistant common bean germplasm.

**References**


**Figures**

- **Fig. 1** Diseased roots of common beans.
- **Fig. 2** Isolated Cultures on PDA (Potato Dextrose Agar).