PRELIMINARY REPORT ON THE INCIDENCE OF POSTHARVEST PATHOGENS IN SUGARBEET

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In the red river valley of Minnesota and North Dakota, postharvest sugarbeet roots require storage as the high tonnage of the crop exceeds immediate sugar factory processing capabilities. Sugarbeet roots are piled in factory yards, piling stations, or ventilated sheds to allow the industry flexibility in sugar processing. Maintaining healthy sugarbeet roots in storage is essential to limit storage loss. Root pathogens in the production field, environmental conditions during harvest, varietal differences, and mechanical injuries from harvest and downstream operations all contribute to postharvest losses (Bugbee 1979; Klotz and Finger 2004; Strausbaugh 2018). Postharvest pathogens predominately infect injured sites on the root and can rapidly rot roots depending on environmental conditions in the piles causing elevations in respiration rate and temperature inside the pile (Campbell and Klotz 2006; Mumford and Wyse 1976). These postharvest pathogens not only decrease sugar yield but also increase costs, as severely decayed roots may need to be disposed without processing. Also, the roots that are processed typically might have higher concentrations of contaminants that can increase sucrose loss to molasses. Genetic resistance to storage diseases may alleviate postharvest losses, however, such resistance in sugarbeet cultivars has not been explored. The lack of knowledge on the predominant pathogens causing postharvest sugarbeet disease in each factory district have slowed the development of host resistance to storage diseases. Multiple fungal and bacterial strains are reported as causal agents for storage rots in sugarbeet growing areas in the US. However, limited information is available on the spectrum of postharvest pathogens in sugarbeet piles throughout the storage duration or if the factory districts have unique storage pathogens. Scientific understanding of the identity and abundance of postharvest pathogens will be the first key step to implement management strategies to minimize postharvest losses in sugarbeet storage. This study was conducted to understand the incidence of plant pathogens infecting sugarbeet roots in storage.

Materials and Methods

Symptomatic sugarbeet roots with microbial infestation or suspected roots in the vicinity of symptomatic roots were collected from factory yards and non-ventilated piles. Samples were collected from top, middle, and bottom of both non-ventilated piles and randomly from different points of the factory yard. A total of 150 sugarbeet roots comprising of 50 each from top, middle and bottom of the non-ventilated piles of Southern Minnesota Sugar Cooperative (SMBC) on Dec. 8, 2021 and on 14, 2021 from Raymond, MN. Nearly 40 infected roots were collected on June 02, 2022 from the factory yard of SMBC, Renville MN. A total of 150 roots were collected on March 29, 2022 from the factory yard of East Grand Forks factory of American Crystal Sugar Company. Samples were transported to the USDA-ARS facility, Fargo, ND, and stored at 4˚C until processing. Root tissues were thoroughly washed with sterile distilled water and incubated on the potato dextrose agar (PDA) amended with antibiotics using the protocol of Woodhall et al. (2020). Microbial isolates were further grown on the PDA or water agar until a pure culture of single isolates were received. The pure cultures of individual microbes were transferred into 15% glycerol in 2-mL cryovials and stored at -80°C.

The representative pathogen isolates were used to amplify and sequence ITS or 16S rRNA gene for fungi and bacteria, respectively, using sanger sequencing platform (Azenta Life Sciences, South Plainfield, NJ; Molecular Cloning Lab, South San Francisco, CA). The ITS or 16S rRNA gene sequences were submitted for BLASTN search into the National Center for Biotechnology Information nucleotide database to identify the pathogen isolates.

Results and discussions

The pure cultures of fungal and bacterial isolates were recovered from sugarbeet root tissues displaying the microbial invasion. Fungal and bacterial species were identified by sequencing of internal transcribed spacer regions and 16S rRNA genes in fungi and bacteria, respectively. A total of 35 fungal and 18 bacterial isolates were identified in root samples received from storage piles and factory yards. Fungal species; *Penicillium* spp., *Mucor* spp., *Hypocrea*/*Trichoderma* spp., *Fusarium* spp., and bacterial species; *Gluconobacter* spp., *Pseudomonas* spp., and *Rahnella* spp. were found primarily associated to infected tissues in postharvest sugarbeet roots (Figs. 1 and 2). The study is ongoing to characterize additional isolates and assess pathogenicity tests in sugarbeet cultivars. Furthermore, analysis of more DNA barcoding genes such as beta-tubulin, translation elongation factor 1 alpha gene etc., for fungal isolate characterization will be completed later in 2023.

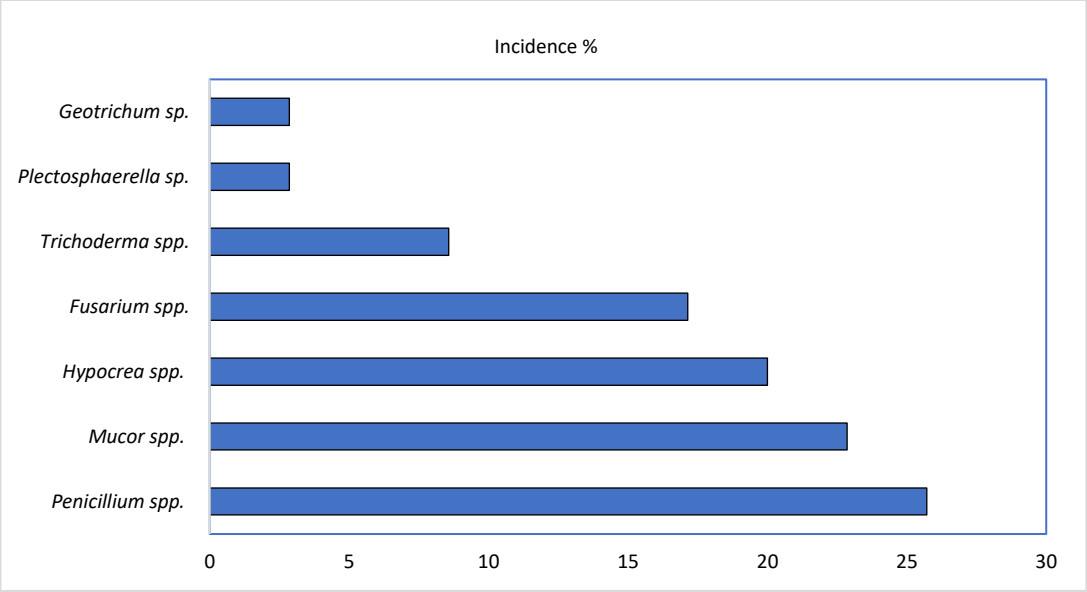

Fig. 1. Incidence of fungal isolates associated with the decaying tissues of sugarbeet roots from storage piles and factory yards.

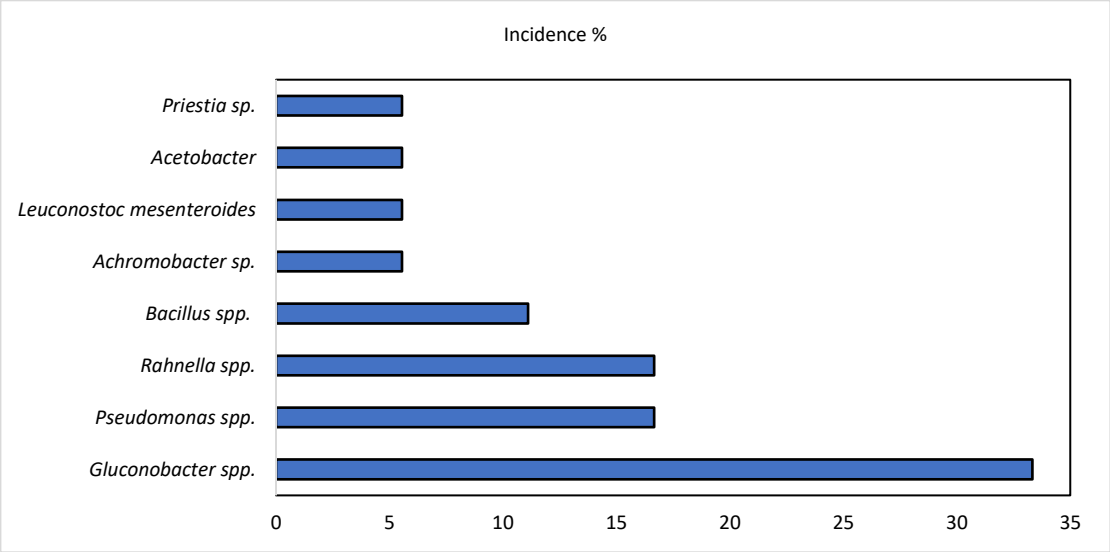

Fig. 2. Incidence of bacterial isolates associated with the decaying tissues of sugarbeet roots from storage piles and factory yards.

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