ABSTRACT

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DNA metabarcoding is a high-throughput sequencing-based molecular approach that is effective for simultaneously identifying fungal communities in plant tissues. This study aimed to analyze fungal communities associated with symptomatic and asymptomatic potato (Solanum tuberosum) stems in Central Java, Indonesia. Stem samples were collected from Kejajar District, Wonosobo Regency, and subsequently analyzed using DNA metabarcoding targeting the ITS2 gene region and sequenced on the Illumina MiSeq platform. Bioinformatic analyses were performed using QIIME2 with the DADA2 pipeline to generate Amplicon Sequence Variants (ASVs) and to assign taxonomic classifications based on the UNITE database. The results showed that fungal communities in both sample types were dominated by the phylum Ascomycota, with a higher proportion of Incertae sedis taxa observed in symptomatic stems. Symptomatic stems exhibited a higher number of ASVs and greater fungal diversity and were dominated by opportunistic and potential pathogenic fungi such as Fusarium, Alternaria, Diaporthe, Nigrospora, and Itersonilia. In contrast, asymptomatic stems displayed a more stable fungal community structure and were dominated by non-pathogenic taxa such as Tetragoniomyces, Sporobolomyces, Papiliotrema, Torula, and Symmetrospora. These findings indicate that ITS2 metabarcoding effectively reveals differences in fungal community structure and has potential as a complementary approach for the early detection of potato plant pathogens.

Keywords: metabarcoding; fungi; potato stem.