

Abstract

This research was carried out to identify the root cause and crown root cause factors on some wild and wild grammars in Sistan region. Sampling from different parts of Sistan from plants with symptoms of wilting, jaundice and root and crown rot were done several times. PDAs were used to isolate the cultivars. Purification of isolates was done by single spore and tip method. The morphological characteristics of the cardiothoracic stem cell and the dye were studied using an Olympus CH^γ optical microscope. DNA extraction from selected isolates was performed by CTAB method and the ITS region of the ribosomal DNA was amplified using ITS^ϑ and ITS^ξ primers. PCR products were sequenced and the sequences were compared with similar sequences recorded at the Gene Bank (NCBI) using MEGA^ϑ software. If necessary, for final confirmation of the isolates, the nucleotide sequence of the ITS region was compared to the ribosomal DNA epinephrine and the sequences were compared and analyzed using the MEGA version ^ο software. Finally, with morphological characteristics and nucleotide sequencing information from the plant species studied, fungi: *Fusarium fujikuori*, *Bipolaris sorokiniana*, *Fusarium proliferatum*, *Fusarium thapsinum* were identified.

Key words: *Fusarium*, Birds family, Taxonomy, Plant diseases



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**Morphological and molecular identification of root and crown rot fungi of some
wild and cereals grasses in Sistan**

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