

New endophytic fungal species of Chaetomiaceae (Ascomycota) in Iraq

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Abstract. Al-Rifaie AA, Ameen MKM. 2023. New endophytic fungal species of Chaetomiaceae (Ascomycota) in Iraq. *Biodiversitas* 24: 5270-5277. The present study was conducted to isolate and identify some endophytic fungi from vegetable crops in Iraq. Samples of eight vegetable plants, namely *Abelmoschus esculentus*, *Mentha piperita*, *Vicia faba*, *Petroselinum sativum*, *Ocimum basilicum*, *Lawsonia inermis*, *Beta vulgaris* and *Apium graveolens* were collected from three regions in Basrah (Abu Al-Khaseeb, Karmat Ali and the Centre of Basrah). Isolation was done by solid culture method and moist culture method. The recovered endophytic fungi were purified and axenic cultures of each isolated species were then identified on the basis of their macro and micro-morphological features. Morphological identification was further confirmed by molecular analysis through DNA extraction and sequencing by PCR amplification of the ITS4 and ITS5 gene primers. Phylogenetic examination revealed that five novel endophytic fungal species related to the family Chaetomiaceae were isolated from vegetable plants, including *Chaetomium cucumericola*, *C. madrasense*, *Amesia atrobrunnea*, *A. cymbiformis* and *Botryotichum verrucosum*. Three species, including *C. cucumericola*, *A. cymbiformis* and *B. verrucosum*, were documented for the first time in the Iraqi mycobiota. To the best of our acknowledgment, this study is the first to investigating endophytic fungi from vegetables in Iraq.

Keywords: Ascomycota, *Chaetomium*, endophyte fungi, Iraq, vegetables

INTRODUCTION

Endophytic fungi are organisms that inhabit all healthy plant tissues throughout at least a portion or the entire life cycle of the plant without causing disease or noticeable morphological alterations (Wen et al. 2022). The presence of fungi within plant tissues has been recognized since the late 19th century, and the term “endophyte” was introduced by de Bary in 1866. Generally, endophytic fungi can colonize within intracellular and/or extracellular spaces of the plant tissues as a host. Some of these fungi are considered a serious plant pathogen such as *Fusarium* and *Aspergillus* species (Al-Rifaie and Al-Maqtoofi 2018; Minati and Mohammed-Ameen 2019a; Minati and Mohammed-Amee 2019b). Endophytic fungi typically can transmit into inside plant’s hosts through two main modes of transmission: vertical transmission via host seeds and horizontal transmission through air and soil microorganisms for colonization (Tian et al. 2022). However, these microorganisms have a significant ability to promote the host plants growth via capability of producing secondary metabolites resulting in enhancing the plant’s resistance to biotic and abiotic stresses (Rashmi et al. 2019). For this reason, the research community over the last three decades has expanded the efforts to get the advantages of endophytic fungi considering them valuable putative sources of bioactive compounds that have medicinal properties for plants, animals and humans that have antibacterial, antifungal, antiviral, anti-inflammatory, antitumor, antimalarial activity (Singh and Kumar 2023). Meanwhile, investigation wide resources for isolation and characterization of endophytic fungi can enrich providing

fungal species with a putative ability for production valuable metabolites and discovery the biodiversity of those microorganisms is needed (Gupta et al. 2023). One of the most common endophytic fungi is the genus *Chaetomium* that have a wide application in the field of healthcare and agriculture (Hashem et al. 2023).

The Chaetomiaceae is a large family that was identified by Winter (1885). This family is exemplified by *Chaetomium* Kunze. It belongs to the order Sordariales (Ascomycota) and currently comprises 25 genera (Alidadi et al. 2020). The Chaetomiaceae family is widely recognized for its saprophytic nature and showcases a remarkable diversity, encompassing more than 400 documented species (Rao et al. 2023). Members of the genus *Chaetomium* occupy various ecological niches, frequently being isolated from sources such as soil, seeds, decomposing plants, herbal drugs, sugarcane, and dung (Moya et al. 2020). Species of the genus *Chaetomium* are distinguished morphologically by its superficial ostiolate ascomata, which are adorned with terminal and terminal hairs and connected to the substrate via rhizoidal hyphae (Fortes and Vitoria 2023). The asci within this genus are typically clavate to fusiform, occasionally cylindrical, and possess thin walls without apical structures, ultimately fading away. Ascospores found in *Chaetomium* are aseptate and feature one or two germ pores, displaying hues ranging from brown to grey-brown (Asgari and Zare 2011). Morphological identification of the genus *Chaetomium* is highly limited due to extreme similarities with closely related genera, such as *Thielavia* and *Humicola* (Wang et al. 2022). For this reason, identification on the base of molecular and sequence analysis is needed as some species