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## Identification of fungi isolated from the olive moth (*Prays oleae* Bern.) based on ITS region

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The internal transcribed spacer (ITS) region is one of the proposed DNA regions for barcoding fungal species. This region is extensively used for molecular systematic and identification of species, being probably the most widely sequenced DNA region in fungi. This fact arises from the simplicity of the amplification, related to the multicopy nature of the rDNA; the possibility of using universal primers; and the high level of sequence variation that occurs even between species closely related. Furthermore, a significant number of identified sequences is available for comparison in the GenBank database. However, some limitations can be pointed out, when using this region to perform species identification. Our work intends to exemplify the application of the ITS region in the identification of the fungal species associated to one of the major pests affecting the olive groves, the *Prays oleae* Bern., in the Portuguese region of Trás-os-Montes (Northeast of Portugal). For this purpose, larvae and pupae of the three annual generations (phyllophagous, antophagus and carpophagus) of *P. oleae* were collected from several olive groves from Trás-os-Montes region. When a fungus was associated to the cause of death of the moth, pure cultures of the fungus were prepared. Following DNA isolation, the corresponding ITS regions were amplified and sequenced, using the universal primers ITS1FO and ITS4RE. The obtained DNA sequences were analysed and fungal identification was performed by comparison with deposited sequences on NCBI database. Results concerning fungal species identification on different generation of olive moth will be presented. Overall results showed that from the total obtained sequences, 34.5% didn't allow identification to species level, only to genus level, when submitted to the NCBI database, and no further sequence handling was performed. However, as referred before, alignment comparison can provide useful information, which can, ultimately, allow the identification of all the sequenced fungal species, using the ITS region. In this work it will be discussed the percentage of sequences that were able to achieve identification to species level, the genera that demonstrated to be more difficult to disclose their species, as well as the limitations encountered will be discussed.

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