

COI Species Report



Cell line: MB-04

ACC-No.: 122

Date of analysis: 13.10.2014

DNA processing number:

Method: DNA Barcoding by PCR amplification of 5' coding region of cytochrome c oxidase I (658 bp fragment size). Cycle sequencing of respective PCR products revealed following assignment upon submission to BOLD (Ratnasingham, S., Hebert, P. D. N. (2007) BOLD: The Barcode of Life Data System (www.Barcodinglife.org). Molecular Ecology Notes, 2007; 7(3): 355-364

Primer:

1x LepF1_t1: ATT TAG GTG ACA CTA TAG ATT CAA CCA ATC ATA AAG ATA TTG G

1x VF1_t1: ATT TAG GTG ACA CTA TAG TCT CAA CCA ACC ACA AAG ACA TTG G

1x VF1d_t1: ATT TAG GTG ACA CTA TAG TCT CAA CCA ACC ACA ARG AYA TYG G

3x VF1i_t1: ATT TAG GTG ACA CTA TAG TCT CAA CCA ACC ANA ANG ANA TNG G

1x LepR1_t1: TAA TAC GAC TCA CTA TAG GGT AAA CTT CTG GAT GTC CAA AAA ATC A

1x VR1d_t1: TAA TAC GAC TCA CTA TAG GGT AGA CTT CTG GGT GGC CRA ARA AYC A

1x VR1_t1: TAA TAC GAC TCA CTA TAG GGT AGA CTT CTG GGT GGC CAA AGA ATC A

3x VR1i_t1: TAA TAC GAC TCA CTA TAG GGT AGA CTT CTG GGT GNC CNA ANA ANC A

Sequence:

5'-TWWTTTTWRRGSGACACTATAGWYTCAACCAAYCAYAAAGAYATTGGTACATTATATTTT
ATTTTTGGGATTTGAGCAGGAATAGTAGGAACCTTCACTAAGTTTATTAATTCGAGCTGAA
TTAGGAAACCCTGGATCTTTAATTGGAGATGATCAAATTTATAATACTATTGTTACAGCT
CATGCTTTTATTATAATTTTTTTTATAGTTATACCTATTATAATTGGAGGATTTGGTAAT
TGA CTGTTCCATTAATGTTAGGGGCCCTGATATAGCATTCCCTCGAATAAATAATATA
AGTTTTTGACTTCTTCCCCTTCTTTAACTCTTTTAAATTTCAAGTAGAATCGTAGAAAAT

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GGAGCAGGAACAGGATGAACAGTGTACCCCCACTTTCATCTAATATTGCCCATGGAGGA
AGTTCAGTAGATTTAGCTATTTTTTCACTTCATTTAGCTGGTATTTCTTCAATTCTCGGA
GCTATTAATTTTATTACTACAATTATTAATATACGATTAAATAGTTTATCTTTTGATCAA
ATACCTTTATTTATTTGAGCTGTAGGAATTACTGCATTTTTATTATTATTATCTTTACCT
GTATTAGCTGGAGCTATTACTATACTTTTAAACAGATCGAAATTTAAATACATCTTTTTTT
GACCCTGCRGGRGGRGKTGWYCCAAWTTTWWTAYCAAMMWTTWATTKKTATTTYTKGACW CT-3`

Taxonomic Level Taxon Assignment Probability of Placement (%)
Phylum Arthropoda 100
Class Insecta 100
Order Lepidoptera 100
Family Noctuidae 100
Genus Mamestra 100
Species Mamestra brassicae 100

Identification Summary:

Search Result: The submitted sequence has been matched to **Mamestra brassicae**. This identification is solid unless there is a very closely allied congeneric species that has not yet been analyzed. Such cases are rare.