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New Records of Entomopathogenic Fungi from Oak Lace Bug, *Corythucha arcuata* (Say) (Hemiptera: Tingidae) with Emphasis on the Genus *Cordyceps*

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ABSTRACT

Entomopathogenic fungi (EPF) are natural pathogens of arthropods that can be used widely as environmentally friendly biological control agents. The process of infection by EPF is initiated when the conidia attach to the epicuticle of the host, whereas other agents must be ingested to cause an infection. EPF can infect all developmental stages of insects, which makes them ideal candidates for controlling sap-feeding insects like the oak lace bug *Corythucha arcuata* (OLB). Several species of EPF have already been found on OLBs in Croatia, including *Beauveria pseudobassiana* as the most common one. In this research, we confirm the presence of EPF on OLB found at different locations of lowland oak forests in Croatia and report, for the first time, natural fungal infections of OLB by *Cordyceps fumosorosea*, *Cordyceps farinosa*, *Cordyceps cateniannulata*, and *Akanthomyces muscarius*. To recommend these fungi as potential biocontrol agents towards OLB, their pathogenic ability still needs to be evaluated.

Keywords: natural enemies; morphology; DNA analysis; *Akanthomyces muscarius*; *Cordyceps fumosorosea*; *Cordyceps farinosa*; *Cordyceps cateniannulata*

INTRODUCTION

Entomopathogenic fungi (EPF) are important natural pathogens of arthropods and have a broad host range, with a wide variability within and among species in terms of virulence and ecological features. More than 750 fungal species from over 100 genera are currently known to be pathogenic to insects (Hibbett et al. 2007). Some of the EPF belonging to the order Hypocreales, such as *Beauveria* spp., *Akanthomyces* spp. and *Metarhizium* spp., have been well-studied and used widely as environmentally friendly biological control agents (Faria and Wraight 2007, Humber 2008). EPF have certain advantages in pest control programs over other insect pathogens since they infect directly through the cuticle by penetration of the fungal propagules (Ortiz-Urquiza and Keyhani 2013), while other agents need to be ingested, and they also infect all stages of insects. That makes them ideal candidates for the control of sap-feeding insects that cannot be effectively controlled by microbial control agents that infect via ingestion.

The oak lace bug (*Corythucha arcuata*, Say 1832 - Heteroptera: Tingidae, OLB) is a sap-feeding insect native to North America (Barber 2010), and since its first appearance in Europe (Bernardinelli 2000, Bernardinelli and Zandigiacomo 2000) has spread rapidly, causing foliage damage primarily of oak trees.

Several species of EPF have already been found on OLBs in Croatia (Kovač et al. 2020). Among those, *Beauveria pseudobassiana* S.A. Rehner & Humber (2011) proved to be the most common fungus found, and its pathogenic potential has been evaluated (Kovač et al. 2021a).

Herein, we confirm the presence of *B. pseudobassiana* at different locations of lowland oak forests in Croatia and report for the first time natural fungal infections of OLB by the fungi *Cordyceps fumosorosea*, *Co rdyceps farinosa*, *Cordyceps cateniannulata*, and *Akanthomyces muscarius.*

MATERIALS AND METHODS

Collection of Samples and Isolation of Fungi

OLB samples were collected in March and April 2021 at the Spačva basin area: 45°08'45.7"N, 18°48'16.6"E (Privlaka); 44°59'41.1"N, 18°48'33.6"E (Posavski Podgajci); 45°02'22.5"N, 18°53'16.4"E (Vrbanja), and clone seed plantation Petkovac (Forest Office Otok, UŠP Vinkovci), and in March 2022, at the management unit Jastrebarski lugovi: 45°38'05.3"N, 15°41'15.2"E (Point 1); 45°38'28.3"N, 15°43'25.0"E (Point 2) and 45°37'32.3"N, 15°41'40.8"E (Point 3), as well as at the area of Našice (45°33'58.3"N, 18°18'17.2"E). OLB overwintering adults were collected from the bark and moss of pedunculate oak (*Quercus robur* L.) trees by using the same method described in Kovač et al. (2021a), and were transported to the Croatian Forest Research Institute for further analysis.

Dead OLB individuals or those exhibiting mycosis were separated and placed in the moist chamber for 1 week to stimulate potential fungal growth. Fungi were isolated by taking small pieces of mycelium from cadavers with a sterile needle and placing them onto the Potato Dextrose Agar medium. The petri dishes were incubated for 2 weeks at 25°C for further growth and sporulation. Each isolate was subcultured from a single colony to obtain pure cultures.

Morphological Identification of the Isolates

For morphological identification of the fungal strains, the macroscopic traits of the colonies, such as the shape, form (fluffy, firm), the colour on the upper and lower sides of the plates, growth rate, and pigment production were observed first. Microscopic observations were also made based on the morphology of the hyphae, conidiophores and conidia (Humber 2005, Humber 2012, Zhang et al. 2024). The fungal cultures were deposited in the collection of entomopathogenic fungi of the Laboratory for Phytopathology Analyses at the Croatian Forest Research Institute (Jastrebarsko, Croatia). Morphologically identified species were confirmed molecularly for exact determination. Morphological observations were made using the Olympus SZ51 stereomicroscope and photographed by a DPX IM200-4K digital microscope. The fungal structures, such as conidiogenous cells and conidia, were observed with a phase-contrast microscope (Olympus, model BX53) and photographed using DeltaPix InSight modular software.

Molecular Identification of the Isolates

The DNA was extracted using a DNeasy Plant Mini Kit (QIAGEN) following the manufacturer's instructions. The concentration of nucleic acid extracts was estimated by spectrophotometry (Biospec-nano, Shimadzu). The DNA concentration in the extracts ranged from 1.58 to 29.43 ng·µl^{-1} (USA). The four DNA barcoding regions (ITS—Internal Transcribed Spacer, TEF1—Translation Elongation Factor 1-alpha, RPB2—second largest (RPB2) subunits of RNA polymerase II, and Bloc-Bloc intergenic region) were amplified according to the references (Table 1). The PCR product was electrophoresed in a 1.8% agarose gel and visualized by staining with Midori Green Advance (Nippon Genetics Europe). PCR products were purified by the Monarch DNA Gel Extraction Kit (NEB). PCR-amplified products were sequenced in both forward and reverse directions using PCR primers (Macrogen Europe, Amsterdam, the Netherlands). The sequence identification was performed using BLAST (Basic Local Alignment Search Tool). DNA sequences were deposited to GenBank (NCBI, Bethesda, MD, USA) under accession numbers PX457297- PX457318.

RESULTS

From the fungi collected from overwintering OLB adults, 25 fungal strains showing typical characteristics of entomopathogenic fungi were isolated. The morphological identification (employing macroscopic and microscopic information) allowed the identification of the strains to the genus and species level. Of these fungi, 10 strains belonged to *Beauveria* species (coded as JL2_1, JL2_2, PR1, PP1, VR1, NA1, NA3, NA4, ZD1 and ZD2), six strains corresponded to *Akanthomyces muscarius* (Petch 1932), Spatafora, Kepler & B. Shrestha (2017) (coded as JL1_2, JL2_3, PR3, PET1, PET3 and PET5), and nine strains belonged to *Cordyceps* species, of which five strains corresponded to *Cordyceps fumosorosea* (Wize) Kepler, B. Shrestha and Spatafora 2017 (coded as JL2_5, PR4, VR4, PET4 and NA2), two to *Cordyceps farinosa* (Holmsk.) Kepler, B. Shrestha and Spatafora 2017 (JL2_4, JL2_6), and two to *Cordyceps cateniannulata* (Z.Q. Liang) Kepler, B. Shrestha and Spatafora 2017 (JL1_1, JL1_4). In the case of fungi of the *Beauveria* genus, 10 strains showed white to cream colonies with irregular edges and a powdery appearance, typical macroscopic traits of the

Table 1. PCR data (DNA barcoding region, Primer pairs data, References).

DNA barcoding region	Primer Pairs	Primer Sequences (5′ → 3′)	References
ITS	ITS1	TCCGTAGGTGAACCTGCGG	White et al. (1990)
	ITS4	TCCTCCGCTTATTGATATGC	
EF1α	EF1-983F	GCYCCYGGHCAYCGTGAYTTYAT	Rehner and Buckley (2005)
	EF1-2218R	ATGACACCRACRGCRACRGTYTG	
RBP2	RPB2-5F1	GAYGAYMGWGATCAYTTYGG	Liu et al. (1999)
	RPB2-7cR	CCCATRGCTTGYTTRCCCAT	
Block	B5.1F	CGACCCGGCCAACTACTTTGA	Rehner and Buckley (2006)
	B3.1R	GTCTTCCAGTACCACTACGCC	

Beauveria genus. After 14 days, colonies of 9 strains changed color of the medium to light purple, which, together with the morphology of conidia and conidiogenous cells, indicated that the species might be *Beauveria pseudobassiana*, which was confirmed after molecular analysis. The remaining strain (JL2_1) belonged to *Beauveria bassiana* (Bals.-Criv.) Vuill. 1912 (Table 2).

In the microscopic observations, the six strains presented reproductive structures and conidia with the morphology, size, and color typical of *A. muscarius.* Colony on PDA was white, circular, fluffy and regular, with septate, branched, and smooth hyphae after 14 days. Conidiogenous cells are phialidic, singly or in verticels, swollen at the base and smooth, with conidia variable in size (2.4–7.2 × 1.7–2.6 µm), solitary, slimy, ellipsoidal, subcylindrical to cylindrical, apex rounded, 1-celled, smooth, hyaline to subhyaline. Conidiophores are septate, branched, erect and smooth (Figure 1).

Five strains had traits typical for *C. fumosorosea,* which included the smoky pink colour of the culture, with raised floccose overgrowth and powdery due to the conidia after 14 days of incubation. Conidial structures are mostly complex, consisting of erect conidiophores arising from submerged or laterally from aerial hyphae. Hyphae smooth-walled, hyaline, 1.5-3.5 µm wide, conidiophores mono- or synnematous, smooth-walled, hyaline, consisting of verticillate branches bearing whorls of 4 to 6 phialides, and conidia oval in shape, hyaline to slightly pink, measuring 2.8-3.8 x 1.5-2.5 µm (Figure 2).

Two strains identified as *C. farinosa* (JL2_4 and JL2_6) displayed white, fluffy colonies with length of a hyphae about 15 µm and round or spherical aseptate, hyaline, thin-walled, and smooth conidia, about 2.5-3.5 × 1.8-2.5 µm (length x width) grouped in a phialides with a wide globose basal portion at the apices of the branches of the conidiophore (Figure 3).

The remaining two strains (JL1_1 and JL1_4) exhibited white, velvety and dense colonies, with smooth, septate, 1–3 µm wide hyphae, and hyaline, smooth, ovoid or sub-globular conidia (4.2-5.8 x 2.5-5.2 µm), which, after molecular analysis, determined the species as *C. cateniannulata* (Figure 4).

Table 2. DNA barcoding data of isolates: reference sequence (GenBank accession number, NCBI) of DNA regions (EF1α, ITS, RPB2, and Block), collection site, and date. No data available is denoted by „-".

No.	Fungus isolate	Scientific name	Reference sequence (GenBank accession no., NCBI)				Collection site	Collection date
			ITS	EF1α	RPB2	Block		
1.	JL1_1	*Cordyceps cateniannula*ta	MH532847.1	KP743150.1	-	-	Jastrebarsko	March 2022
2.	JL1_2	*Akanthomyces muscarius*	MH858126.1	OQ338593.1	-	-	Jastrebarsko	March 2022
3.	JL1_4	*Cordyceps cateniannulata*	MH532847.1	MH532847.1	-	-	Jastrebarsko	March 2022
4.	JL2_1	*Beauveria bassiana*	MT533246.1	OQ067547.1	-	-	Jastrebarsko	March 2022
5.	JL2_2	*Beauveria pseudobassiana*	MK142275.1	MN523569.1	MN523614.1	MN868282.1	Jastrebarsko	March 2022
6.	JL2_3	*Akanthomyces muscarius*	MH858126.1	OQ338593.1	-	-	Jastrebarsko	March 2022
7.	JL2_4	*Cordyceps farinos*a	MH864784.1	JN998764.1	-	-	Jastrebarsko	March 2022
8.	JL2_5	*Cordyceps fumosorose*a	MH532834.1	XM_018849589.1	XM_018853140.1	PQ655117.1	Jastrebarsko	March 2022
9.	JL2_6	*Cordyceps farinos*a	MH864784.1	JN998765.1	-	-	Jastrebarsko	March 2022
10.	PR1	*Beauveria pseudobassiana*	-	MW245734.1	-	HQ880723.1	Spačva	April 2021
11.	PR3	*Akanthomyces muscarius*	MH858126.1	OQ338593.1	-	-	Spačva	April 2021
12.	PR4	*Cordyceps fumosorosea*	MH532834.1	XM_018849589.1	OP244390.1	PQ655117.1	Spačva	April 2021
13.	PP1	*Beauveria pseudobassiana*	MH185843.1	MN523546.1	-	HQ880722.1	Spačva	April 2021
14.	VR1	*Beauveria pseudobassiana*	MT239436.1	-	-	HQ880728.1	Spačva	April 2021
15.	VR4	*Cordyceps fumosorosea*	MH532834.1	XM_018849589.1	XM_018853140.1	-	Spačva	April 2021
16.	PET1	*Akanthomyces muscarius*	MN080299.1	XM_056193486.1	-	-	Spačva	April 2021
17.	PET3	*Akanthomyces muscarius*	MH858126.1	OQ338593.1	-	-	Spačva	April 2021
18.	PET4	*Cordyceps fumosorosea*	-	-	XM_018853140.1	-	Spačva	April 2021
19.	PET5	*Akanthomyces muscarius*	MH858126.1	OQ338593.1		-	Spačva	April 2021
20.	NA1	*Beauveria pseudobassiana*	-	-		HQ880722.1	Našice	March 2022
21.	NA2	*Cordyceps fumosorosea*	MT333241.1	-	XM_018853140.1	PQ655117.1	Našice	March 2022
22.	NA3	*Beauveria pseudobassiana*	MW940787.1	-	-	PQ655103.1	Našice	March 2022
23.	NA4	*Beauveria pseudobassiana*	MF872410.1	-	-	PQ655100.1	Našice	March 2022
24.	ZD1	*Beauveria pseudobassiana*	MF872410.1	MN523569.1	-	LC769336.1	Jastrebarsko	March 2022
25.	ZD2	*Beauveria pseudobassiana*	MT241786.1	MN523546.1	-	HQ880722.1	Jastrebarsko	March 2022

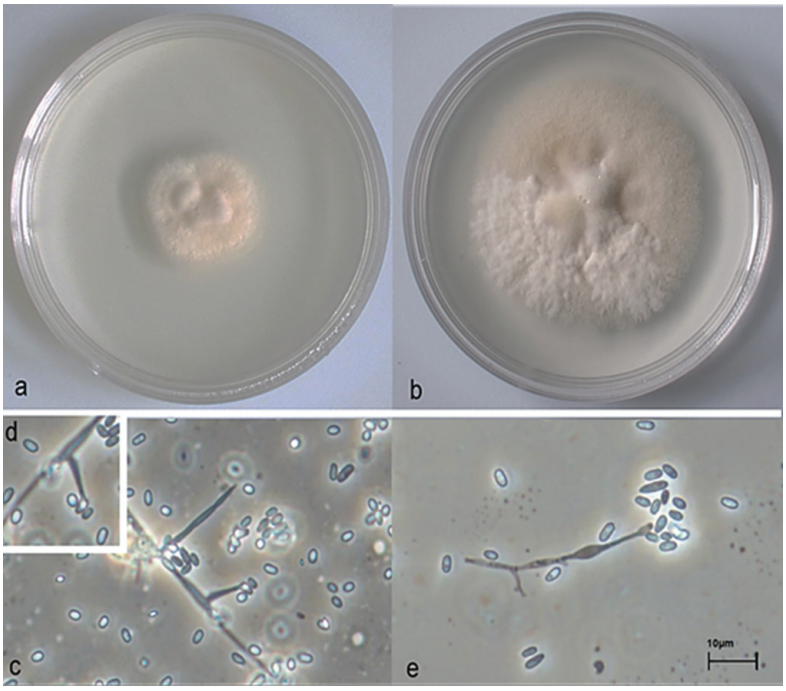

Figure 1. *Akanthomyces muscarius*: **(a, b)** Culture plate on PDA (upper) on the 7th day **(a)** and 14th day **(b)** at 25 °C; **(c-e)** Conidiophores, conidiogenous cells and conidia.

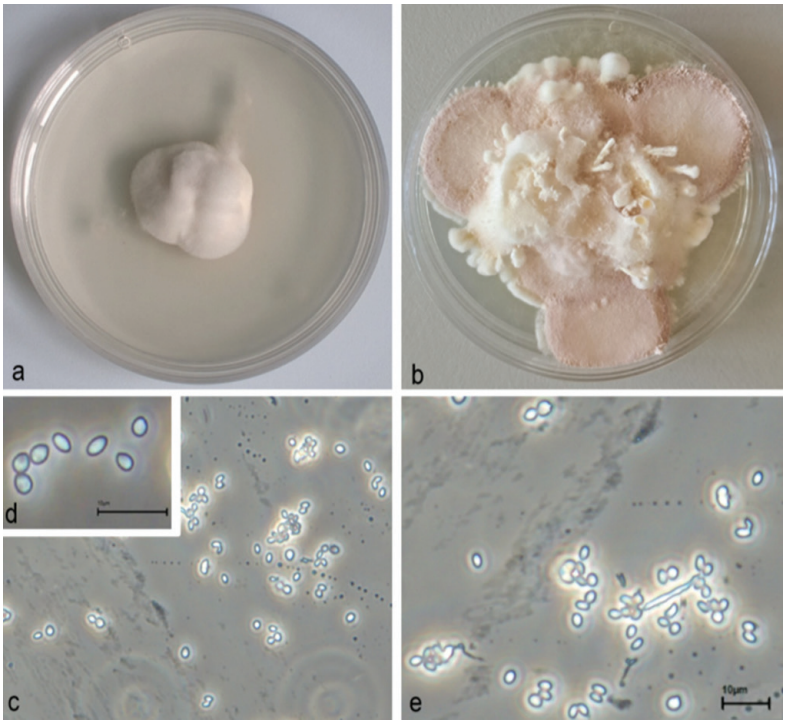

Figure 2. *Cordyceps fumosorosea*: **(a, b)** Culture plate on PDA (upper) on the 7th day **(a)** and 14th day **(b)** at 25 °C; **(c-e)** Conidiophores, conidiogenous cells and conidia.

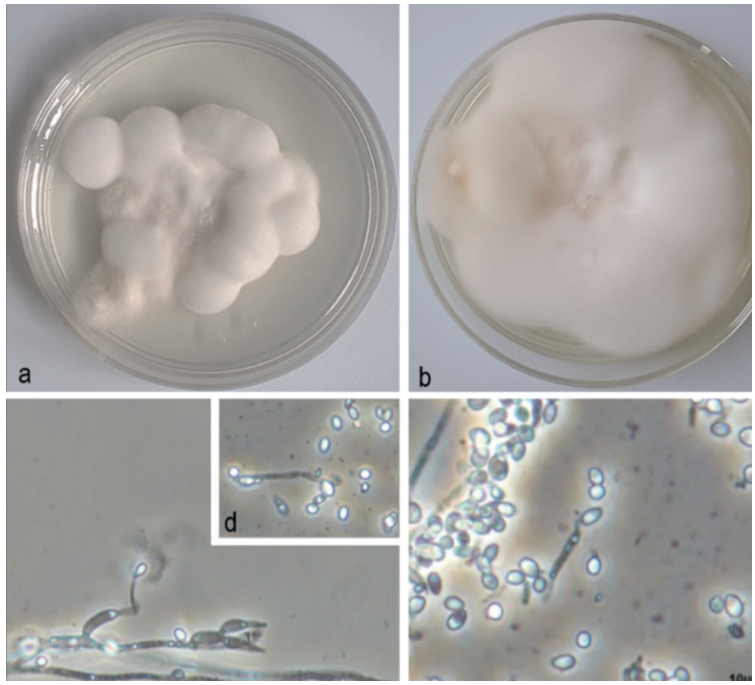

Figure 3. *Cordyceps farinosa*: **(a, b)** Culture plate on PDA (upper) on the 7th day **(a)** and 14th day **(b)** at 25 °C; **(c-e)** Conidiophores, conidiogenous cells and conidia.

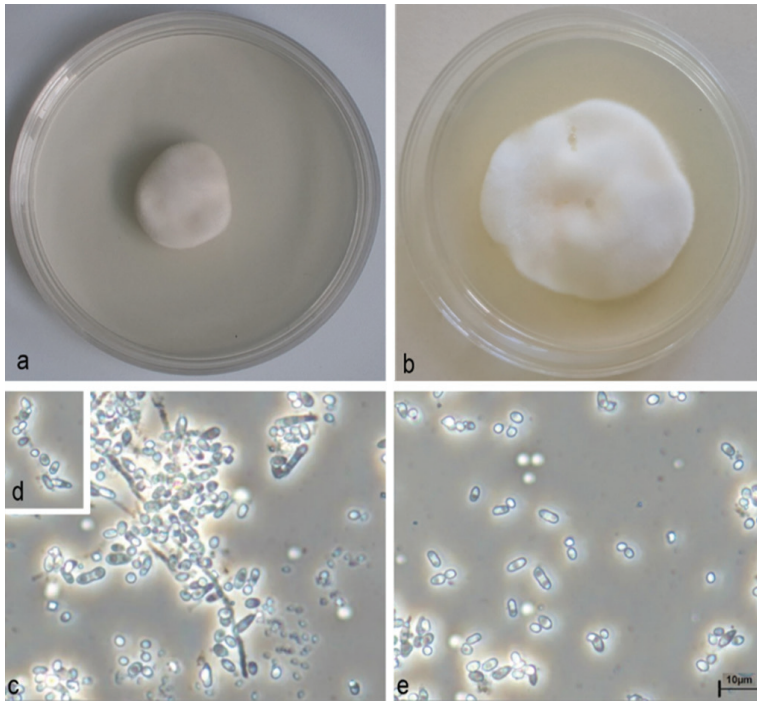

Figure 4. *Cordyceps cateniannulata*: **(a, b)** Culture plate on PDA (upper) on the 7th day **(a)** and 14th day **(b)** at 25 °C; **(c-e)** Conidiophores, conidiogenous cells and conidia.

DISCUSSION

In this work, we report four new EPF species found on OLB overwintering adults, found in pedunculate oak forests in different lowland areas of Croatia.

Cordyceps species are important species in the natural regulation of insect pest populations and have been considered for biological control of pests in several countries (Faria and Wraight 2007). *C. fumosorosea* (formerly *Isaria fumosorosea* or *Paecilomyces fumosoroseus*) has a global distribution and is used for the biological control of agricultural pests such as aphids, whiteflies, psyllids, mites, coleopterans and lepidopterans (Hussein et al. 2013, Mascarin et al. 2018, Maluta et al. 2022). Same as the fungus *B. bassiana,* it has been developed as a commercial mycoinsecticide and has attracted an increased interest from the biopesticide industry (Mascarin et al. 2019). *C. farinosa* (formerly *Isaria farinosa* or *Paecilomyces farinosus*) has a wide host range, strong lethality and is safe for mammals, so is often utilized as a biocontrol agent (Tong et al. 2022), same to *C. cateniannulata,* which has shown potential to control different pests and diseases, as well as the ability to promote plant growth (Zhang et al. 2014, 2024, Zhou et al. 2020).

Entomopathogenic fungi of the genus *Akanthomyces* (formerly *Lecanicillium*) are one of the most common and important fungal entomopathogens, which have been isolated from many different organisms like insects, mites and nematodes, and can also parasitize on phytopathogenic fungi like rust and powdery mildew (Kim et al. 2007, Askary and Yarmand 2007, Turco et al. 2024). *Akanthomyces muscarius* (Ascomycota, Cordycipitaceae) (previously known as *Verticillium lecanii*, *Lecanicillium lecanii*, or *L. muscarium*) can infect different groups of insects, but its entomopathogenic activity has been recorded mainly on species belonging to the order Hemiptera (Askary and Yarmand 2007, Broumandnia et al. 2021, Lopes et al. 2023). This is the first record of *A. muscarius* infecting OLB.

There is no doubt that entomopathogenic fungi are ubiquitous in the OLB population in Croatia, and so far, are the most investigated natural enemies of this invasive pest that show a great reduction potential. As in previous research (Kovač 2021a, Kovač et al. 2021b), fungi of the genus *Beuveria* have shown prevalence, with *B. pseudobassiana* as the most common one. This is also in accordance with the research in Kovač et al. (2021c), where the occurrence of EPF in the soils of different natural forest habitats in Croatia was investigated, and fungi from the genus *Beauveria* were the most frequent EPF found.

All the aforementioned together with this research confirms that entomopathogenic fungi may have an important and increasing role in the natural regulation of OLB populations, but evaluation of *C. fumosorosea, C. farinosa, C. cateniannulata*, and *A. muscarius* efficacy against OLB under laboratory and field conditions still needs to be conducted in order to determine the biocontrol potential of these fungi.

CONCLUSIONS

This study confirmed the presence of entomopathogenic fungi (EPF) as natural pathogens on the oak lace bug *Corythucha arcuata* in lowland oak forests of Croatia and, for the first time, recorded natural infections by *Cordyceps fumosorosea*, *C. farinosa*, *C. cateniannulata*, and *Akanthomyces muscarius*. Further work is required to evaluate the potential of these fungi as biocontrol agents against OLB. Future studies should investigate their pathogenicity, effectiveness under laboratory and field conditions, suitability for mass production, application methods, and long-term effects before they can be recommended for practical use.

Author Contributions

MK conceived and designed the research, and carried out the collection of samples, MK and NĆ performed laboratory analysis and processing of the data, MK wrote the manuscript.

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Conflicts of Interest

The authors declare no conflict of interest.

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