DESICCATION TOLERANT FUNGI IN CROATIAN FOREST ECOSYSTEMS

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INTRODUCTION

In accordance with their high biological diversity, fungi developed large scale of life strategies. Their life cycle is quite short and many species rapidly react on environmental changes (Matočec et al. 2000). Because of that several ecological groups of fungi are so far used as bioindicators and reflect reliably environmental health and quality (Kraigher et al. 1995), i.e. lichenized fungi are used as reliable indicators for some types of air pollution (Conti & Cecchetti 2001), same as ectomycorrhizal fungi (Fellner 1993). Desiccation tolerant non-lichenized fungi from the phylum *Ascomycota* are taxonomically very poorly known. They are very similar to lichenized fungi in ecological and physiological sense and live in aerophytic synusia (dead branches and bark still attached to plant individual) extremely exposed to atmospheric and cosmic influence. These fungi normally survive complete loss of their chemically unbound water and are capable to continue with all their metabolic functions after rehydration. Contrary to lichens, non-lichenized desiccation tolerant fungi are mainly saprotrophs on decaying woody substrate. The aim of this research is to explore biodiversity of desiccation tolerant fungi on pedunculate oak and to determine their possible bioindication value.

Fig. 1 Pedunculate oak forest, photo N. Matočec

Fig. 2 Branch after detaching from the tree, photo N. Matočec

Fig. 3 Marking of fragments, photo Z. Grgurić

Fig. 4 Part of the fragment 11 (plot 6), photo I. Kušan

MATERIALS & METHODS

Research of desiccation tolerant non-lichenized ascomycetous fungi was conducted in the Spačva basin, Slavonija region, Croatia, in forests with domination of pedunculate oak (*Quercus robur* L.) (Fig 1) . Sampling was done on selected trees of pedunculate oak, on 6 plots (1, 6, 7, 8, 9 and 10) after vegetation season. One branch, positioned at 6-12 m height, was taken on each plot (Fig 2). Collected branches were divided into 30 fragments in total (Fig 3). In the laboratory each fragment was characterized concerning its weight, length, and diameter and bark/lichen coverage. Fungi on the branch surface were detected using stereomicroscope (40×) and each fructifying unity (all fruitbodies confined to one supposed mycelium) was delimited and prepared for further analysis (Figs 5, 6 & 7). Bright field light microscope was used for identification of taxa. All fungi are identified to the genus level (Baral & Marson 2005, Dennis 1980, Munk 1957). Further taxonomic analysis is currently ongoing.

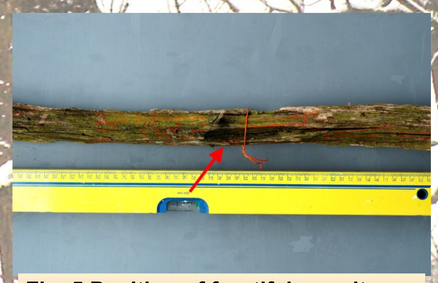

Fig. 5 Position of fructifying units on fragment, photo I. Kušan

Fig. 6 Marked fructifying units on fragment, photo I. Kušan

Fig. 7 Friutbodies of *Xylogramma* sp., photo I. Kušan

RESULTS

Preliminary results based on 6 plots in Spačva basin show relatively high biodiversity of desiccation tolerant fungi with 40 identified species from overall 760 collections. They belong to the orders *Helotiales*, *Orbiliales*, *Mycocaliciales*, *Rhytismatales*, *Dothideales*, *Lecanorales*, *Sordariales* and *Xylariales*. Some of the identified taxa are shown on Fig 8..

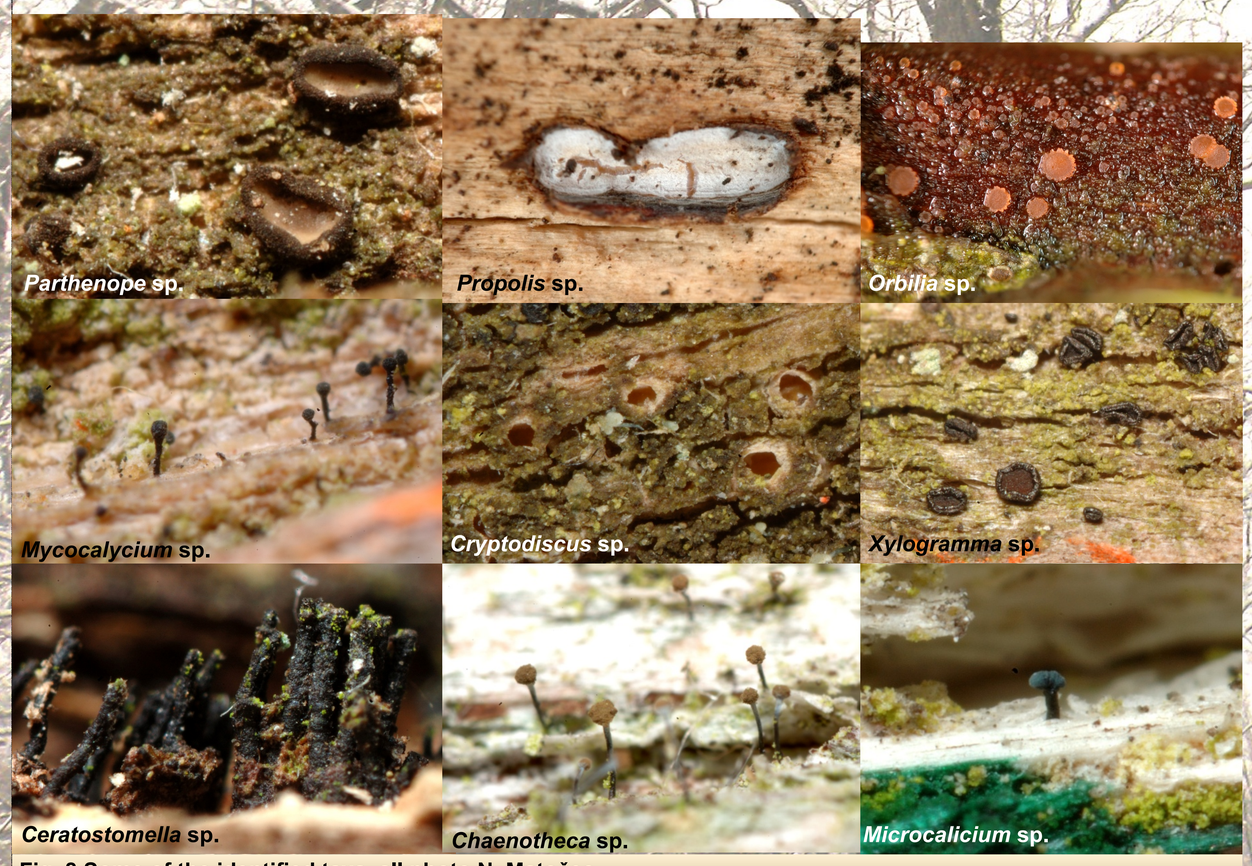

Fig. 8 Some of the identified taxa, all photo N. Matočec

DISCUSSION

Preliminary results show that only some species can be used in the analysis of bioindication value regarding the sampling system (one branch per plot). Our estimation is that this number should exceed 10 fructifying units (Fig. 10). Out of 40 identified species, the highest number was detected on the plot 6 (28 species), and the lowest on plot 10 (11 species) (Fig. 9). Plot 6 has the highest volume and weight of substrate and at the same time is in the best condition for colonization by desiccation tolerant fungi. Plots 8 and 10 have the lowest fungal diversity and as well the lowest volume and weight. We can determine 3 genera to be most abundant on investigated branches and they occur in more than 100 fructifying unit in total: *Orbilia* 185, *Xylogramma* 153 and *Mycocalicium* 103.

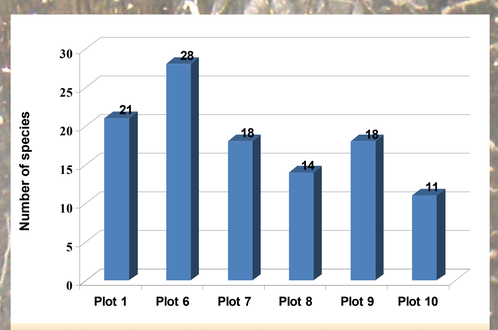

Fig. 9 Number of fungal species per plot

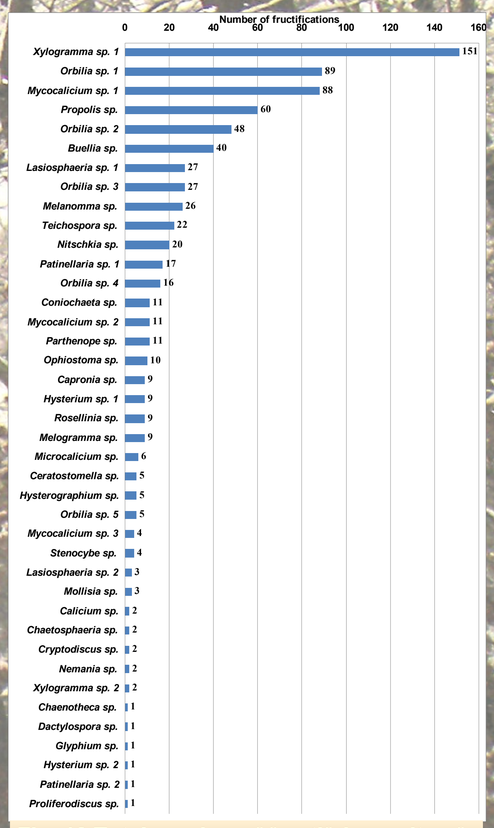

Fig. 10 Total number of fructifying units of all species on all plots

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