

# IDENTIFICATION AND CHARACTERIZATION OF TRUNK PATHOGENS ON OAK SEEDLINGS IN FOREST NURSERIES USING NGS SEQUENCING OF DNA

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## INTRODUCTION

Pathogens belonging to the complex of trunk diseases (TD) colonizing phloem and xylem were previously detected on a broad host range of economically and environmentally important woody plants, e.g. *Abies*, *Acer*, *Buxus*, *Fagus*, *Juglans*, *Picea*, *Pinus*, *Vitis* (Eichmeier, et al., 2019; Cochard, et al., 2015; Hofstetter, et al., 2012; Kobayashi, et al. 2005; Lee, et al., 1999; Magasi and Newell, 1983; Smahi, et al., 2017; Mahamedi, et al., 2020; Zolciak, et al., 2009). This study is focused on the identification of pathogens from the TD complex on 2-yr old oak seedlings of *Quercus* spp.

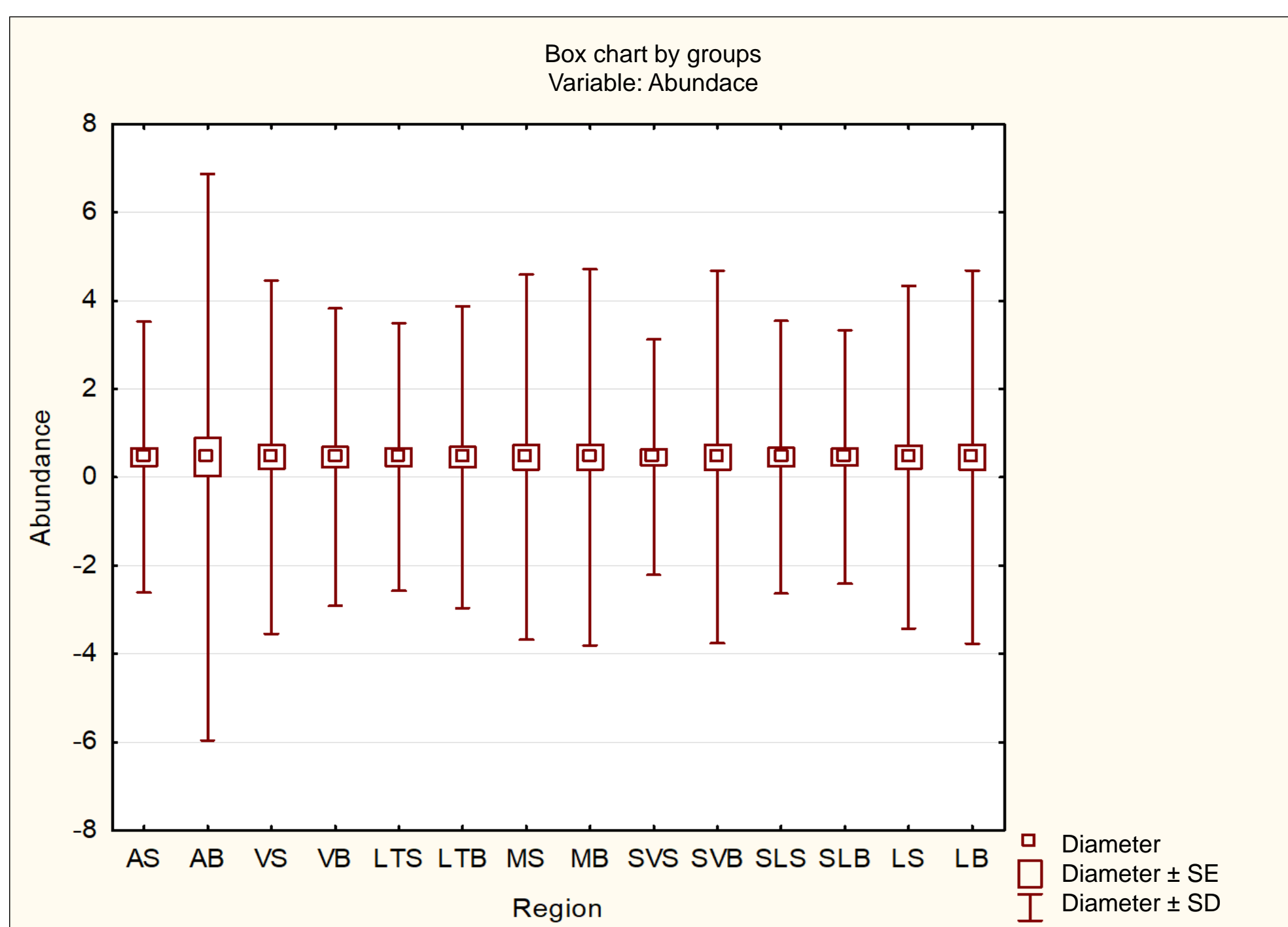


Fig. 2 Statistically significant differences between locations by Kruskal-Wallis test (STATISTICA): SL – Lescus Cetkovice; SV – Vlkov u Tišnova; ST – Lescus Nová Ves nad Lužicí; M – Miličovice; V – Višňová; A – ATRO Dlouhá Loučka; L – Svatopluk Lengál; S, B shortcut for S – stem, B – base

## RESULTS

Statistically significant differences were observed among forest nurseries Atro and Miličovice, Višňová and Lescus Třeboň, Višňová and Vlkov, Lescus Třeboň and Miličovice, Miličovice and Vlkov, Lescus Boskovice and Miličovice Fig. 2.

Interestingly, there were found no statistical differences between sampled organs – stem and root.

The most abundant potentially pathogenic species belong to genera *Dothiorella*, *Diplodia*, *Fusarium*, *Cladosporium*, *Diaporthe*, *Alternaria* Fig. 3.

## CONCLUSION

The pathogenicity of detected fungi and the ability to cause the TD symptoms must be confirmed by additional analyzes.

## ACKNOWLEDGMENT

This work was funded by the project IGA LDF\_VP\_2021028.

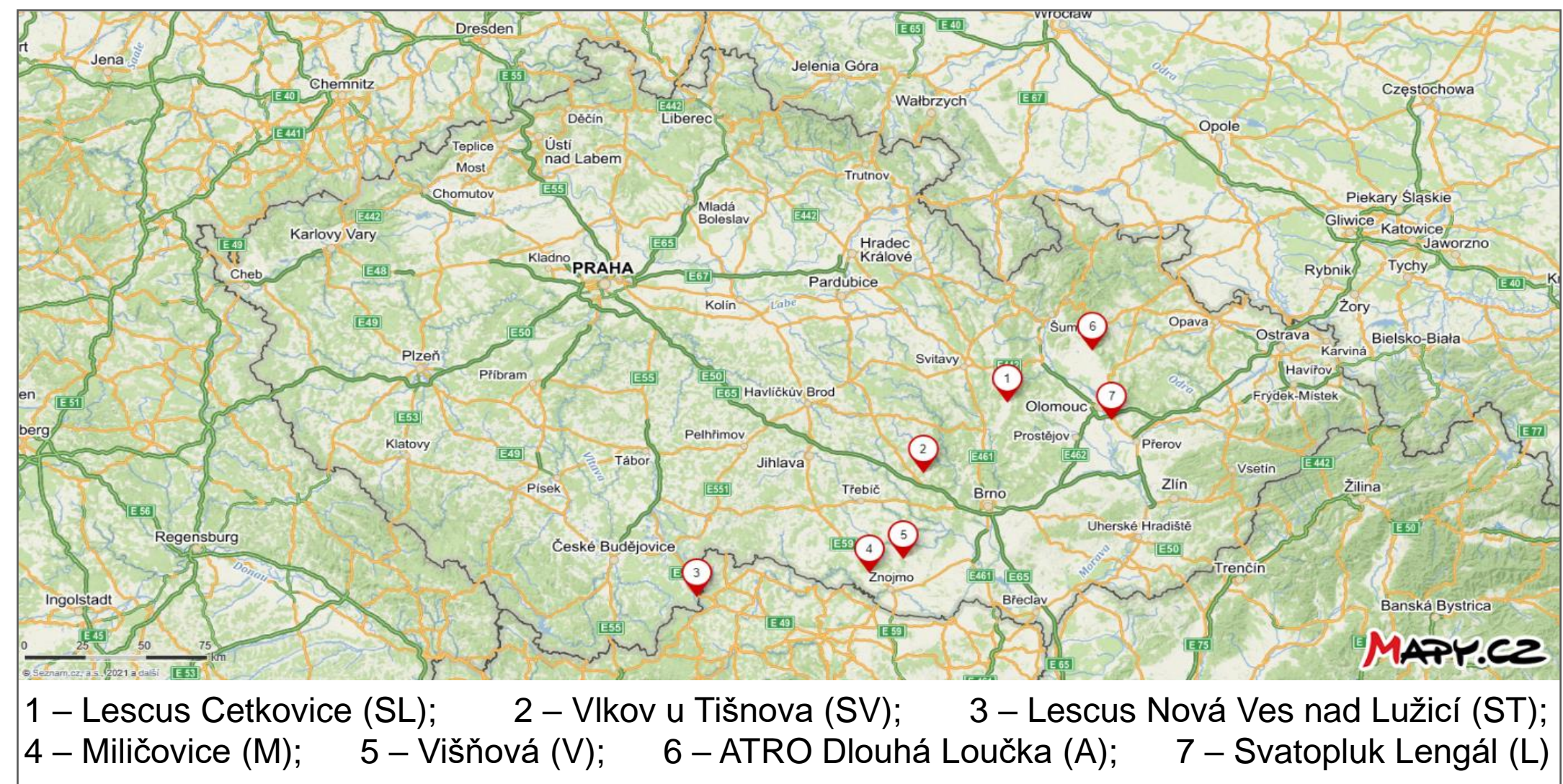


Fig. 1 Map of nurseries locations (www.mapy.cz)

## METHODS

During autumn 2020 and spring 2021 seven forest nurseries were visited. From each nursery were collected 10 seedlings, 70 plants in total.

The total DNA was extracted from two organs of each plant – stem and root, 140 samples in total.

Amplicon libraries of the internal transcribed spacer 2 (ITS2) region were constructed indexed and high-throughput amplicon sequencing (HTAS) was carried out.

After bioinformatic evaluation of the raw data, statistically significant differences were assigned by the Kruskal-Wallis test.

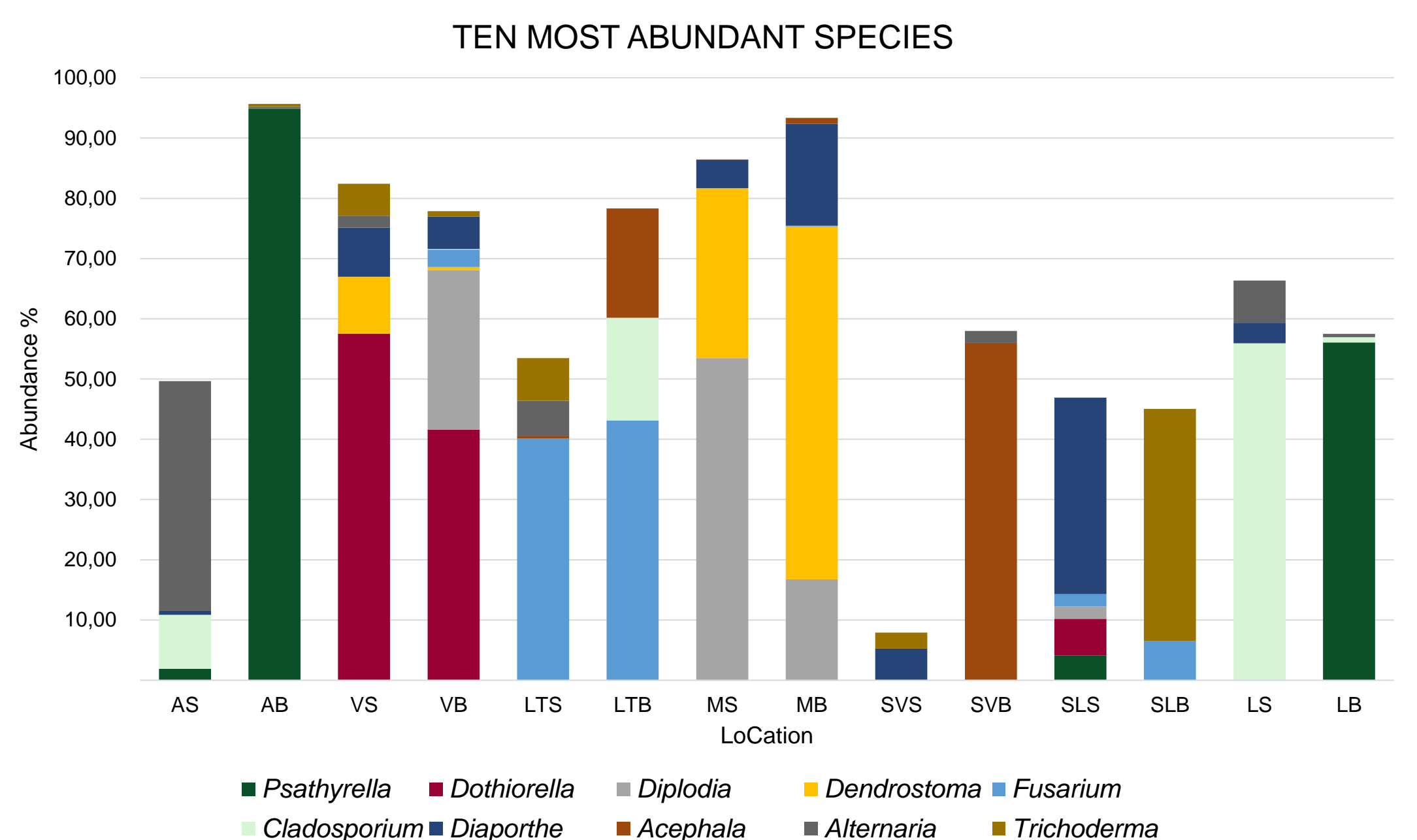


Fig. 3 Ten most abundant species, comparisons of locations and sampling sites on the plant (Shortcut in Fig. 2)

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