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Seed dispersal and realized gene flow of two forest orchids in a fragmented landscape

RNDr. Thesis

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Annotation

This thesis investigates the dispersal abilities of mycoheterotrophic plants represented by three orchid species. Seed trapping and gene flow study were used to examine this topic.

Declaration [in Czech]

I hereby declare that I am the author of this dissertation and that I have used only those sources and literature detailed in the list of references.

V Českých Budějovicích 25.1.2021

Milan Kotlínek

Author's contribution

Kotlínek M., Těšitelová T., Košnar J., Fibich P. Hemrová L., Ko utecký P., Münzbergová Z., Jersáková J., 2020. Seed dispersal and realized gene flow of two forest orchids in a fragmented landscape. *Plant Biology* 22, 522-532 (IF = 2.393).

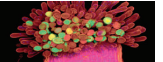
Milan Kotlínek was responsible for planning and conducting of the field sampling, part of the molecular analyses, analyzing the data and writing the manuscript. His contribution was 32.8 %.

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RESEARCH PAPER

Seed dispersal and realized gene flow of two forest orchids in a fragmented landscape

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Keywords

Cephalanthera rubra; *Epipactis atrorubens*; fragmented landscape; gene flow; microsatellite DNA markers; seed dispersal; seed traps.

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ABSTRACT

- Species with vast production of dust-like windborne seeds, such as orchids, should not be limited by seed dispersal. This paradigm, however, does not fit recent studies showing that many sites suitable for orchids are unoccupied and most seeds land close to their maternal plant. To explore this issue, we studied seed dispersal and gene flow of two forest orchid species, *Epipactis atrorubens* and *Cephalanthera rubra*, growing in a fragmented landscape of forested limestone hills in southwest Bohemia, Czech Republic.
- We used a combination of seed trapping and plant genotyping methods (microsatellite DNA markers) to quantify short- and long-distance dispersal, respectively. In addition, seed production of both species was estimated.
- We found that most seeds landed very close to maternal plants (95% of captured seeds were within 7.2 m) in both species, and dispersal distance was influenced by forest type in *E. atrorubens*. In addition, *C. rubra* showed clonal reproduction (20% of plants were of clonal origin) and very low fruiting success (only 1.6% of plants were fruiting) in comparison with *E. atrorubens* (25.7%). Gene flow was frequent up to 2 km in *C. rubra* and up to 125 km in *E. atrorubens*, and we detected a relatively high dispersal rate among regions in both species.
- Although both species occupy similar habitats and have similar seed dispersal abilities, *C. rubra* is notably rarer in the study area. Considerably low fruiting success in this species likely limits its gene flow to longer distances and designates it more sensitive to habitat loss and fragmentation.

INTRODUCTION

Gene flow is one of the main factors influencing genetic diversity of natural populations (e.g. Slatkin 1985). While most dispersal events occur over short distances, long-distance dispersal events are crucial for maintaining species, as well as their genetic diversity in fragmented landscapes (Malanson & Armstrong 1996; Cain *et al.* 2000; Baldauf *et al.* 2014; Helsen *et al.* 2016; Herrmann *et al.* 2016). Loss of genetic diversity due to limited gene flow and genetic drift leading to extinction of isolated populations is currently one of the main problems in conservation of endangered species (Coates & Dixon 2007). Understanding the patterns of seed dispersal, which together with pollen dispersal is responsible for gene flow among populations, is crucial for assessing the potential of a species to cope with habitat fragmentation.

Two main methods have been used in field studies focusing on gene flow realized through seeds: seed trapping experiments and plant genotyping using various molecular methods. Seed trapping primarily allows study of a species' short-distance dispersal (mostly dozens, rarely hundreds of meters; see e.g. Skarpaas *et al.* 2004; Skarpaas *et al.* 2011; Dauer *et al.* 2007). Information obtained from seed trapping relates to potential

area of plant recruitment, explains spatial genetic structure within populations and helps to understand seed dispersal as a template for subsequent processes, such as competition and mating (e.g. Skarpaas *et al.* 2011). Plant genotyping allows estimation of both short- and long-distance dispersal among populations (e.g. Cain *et al.* 2000; Jacquemyn *et al.* 2006). Long-distance dispersal is crucial to determining genetic structure, range expansion rates and other important features of populations that, like long-distance dispersal itself, cannot be explained from observations of common short-distance dispersal alone (see e.g. Hanson *et al.* 2007). Seed dispersion patterns far from sources can be qualitatively different from seed dispersion patterns near sources, because different dispersal processes can operate over different ranges of distances (Damschen *et al.* 2014; Heydel *et al.* 2014). However, estimates of short-distance dispersal by genotyping established individuals that do not show the real but the 'effective' seed dispersion, which is affected by plant establishment success rate (Cain *et al.* 2000; Nathan *et al.* 2003), and can also be confounded by pollen transport (Jordano 2010). For a comprehensive understanding of seed dispersion and its consequences, both methods should be combined to disentangle complicated interactions of the