

# Introduction Part 1: New Insights into Disease Development and Control of Ash Dieback

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*Hymenoscyphus fraxineus*, the causative agent of ash dieback, has been spreading from east to west across continental Europe and the British isles during the course of the last two decades. The pathogen was presumably introduced from Asia, where it colonizes *Fraxinus mandshurica* asymptotically (Zhao et al. 2013). Proliferation of the disease is assumed to occur via ascospores, which develop on rachises of the previous year's leaves in early summer and infect young leaves (Gross et al. 2014). Molecular studies have shown that there is great molecular diversity of the individual strains of *H. fraxineus*, presumably due to its sexual mode of reproduction. Symptoms in *Fraxinus excelsior* include dieback of young shoots, necrotic lesions on the leaves and stems (Gross et al. 2014), and development of collar on the tree trunk (Langer 2017).

Whereas, sanitation measures can be useful in retarding disease progression in individual trees, especially in cities or parks (Thomsen, cited by McEwan 2015), there are presently no known measures for preventing disease due to *H. fraxineus* in forests or larger stands. Fungicides are effective against *H. fraxineus* (Hrabětová et al. 2016), but they obviously cannot be applied on a large scale, e.g. in forests. However, since individual trees of *F. excelsior* vary in their susceptibility to *H. fraxineus*, one approach to assure the survival of *F. excelsior* is to breed for relatively resistant phenotypes of the species (Enderle et al. 2015, Harper et al. 2016). Other potential approaches would employ biocontrol. For example, Schoebel et

al. (2014) elucidated the use of mycoviruses, which on the basis of their research suggested that they are not a promising option for controlling *H. fraxineus*. Initial experiments by Schlegel et al. (2016) are not optimistic regarding the use of endophytic fungi for biocontrol of ash dieback.

This special issue on *Hymenoscyphus fraxineus* presents results dealing with disease development and spread of *H. fraxineus* in species of *Fraxinus*, with physiology of the pathogen and with possible methods for controlling the disease.

## **Highlights of this issue**

Langer (2017) found that *H. fraxineus* and *Neonectria punicea* are the primary pathogens responsible for emerging collar rot of *F. excelsior*; secondary pathogens include *Phytophthora* and *Armillaria* species. Using highly sensitive real-time PCR of symptomatic bark sampled during all four seasons, Masiakh et al. (2017) showed that *H. fraxineus* is also the primary pathogen of bark lesions. One of the factors responsible for the success of this invasive pathogen may be its extreme phenotypic and molecular variability. Junker et al. (2017) found that each isolate of *H. fraxineus* has its own exoenzyme profile and that growth rates of the individual isolates also vary considerably. Stenlid et al. (2017) described the genomes of *H. fraxineus* and *H. albidus*, a native non-pathogenic sister species to *H. fraxineus*, showing that their genomes harbor similar and extensive Cell Wall Active Enzyme (CAZYme) repertoires and suggesting

that the prolonged saprotrophic growth phase on ash leaves of *H. fraxineus* and *H. albidus* has probably shaped their genomes.

Natural infection of *Fraxinus angustifolia* was found in Slovakia by Kádasi-Horáková et al. (2017) and of *F. excelsior* and *F. angustifolia* in Serbia by Keča et al. (2017). Results by Kirisits et al. (2017) demonstrated the relative resistance of *Fraxinus ornus* to *H. fraxineus*. In contrast, in Spain, Trapiello et al. (2017) found neither *H. fraxineus* nor other *Hymenoscyphus* species among the mycobiota of leaves of diseased *F. excelsior*. In New Zealand, where *F. excelsior* is an introduced species and *H. fraxineus* is not present, Power et al. (2017) showed that it has retained many of its native endophytes.

Other authors addressed potential biocontrol options for *H. fraxineus*. The option of using leaf litter of *Tilia* to accelerate decomposition of *F. excelsior* leaf litter was explored by Bartha et al. (2017). Most of the endophytic fungi isolated from healthy stems of *F. excelsior* inhibited growth of *H. fraxineus* in dual culture and thus may have biocontrol potential (Haňáčková et al. 2017). The group also showed that those with a presumed saprotrophic role in *planta* increased in the summer, those with a pathogenic role in the winter.

Čermáková et al. (2017) investigated mycoviruses in *H. fraxineus*, finding mycovirus HfMV1 and other putative double-stranded RNA mycoviruses in the isolates from central Europe.

And finally, Mitchell et al. (2017) investigated which tree or trees could assume the ecological functions of *Fraxinus excelsior* for organisms that in some way depend on it to complete their life-cycles, concluding that no one tree can substitute for the presumed future loss of *F. excelsior*.

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