

Introduction Part 2. Consequences of Ash Dieback: Damage Level, Resistance and Resilience of European Ash Forests

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Global warming combined with increased risk of introducing new pests and pathogens through international trade is a global concern for forest health (Pautasso et al. 2010). The outbreak of ash dieback on European ash species (especially *Fraxinus excelsior*) is a recent example of a severe infectious pathogen that has developed into a major problem across the natural distribution of the host species within a few decades. The disease is caused by the fungus *Hymenoscyphus fraxineus* (Kowalski 2006, Bakys et al. 2009, Gross et al. 2014), which is native to Asia, but has been introduced to Europe – perhaps with plants of Mandschurian ash (Drenkhan et al. 2014). Later, dispersal of seeds, seedlings and timber products may have contributed to the rapid spread across Europe, in addition to long distance wind dispersal of ascospores (Solheim and Hietala 2017). Ash dieback is an example of an emerging infectious disease that challenges native tree species of large ecological and economical importance in the new environment. This new threat stresses the importance of forest assessment to determine the current severity of damage to our native ash forests and to foresee the damage caused in the decades to come. Another important aspect to clarify will be to what extent European ash trees will be able to respond to the new disease through selection and adaptation. Will ash populations be sufficiently resistant to survive in the short run, but only at specific habitats? Will European ash suffer severely in the short run, but be resilient and recover after generations of high selection pressure for trees with natural resistance? Previous examples of emerging infectious pest and pathogens have shown that forest trees species often possess evolutionary potential to respond to new diseases (Budde et al. 2016), but will this be the case for *Fraxinus*

excelsior challenged by *Hymenoscyphus fraxineus* across Europe?

Several studies report high mortality in young stands, but in general there is a fraction of trees that tends to remain healthy in areas that are otherwise heavily infected (Pliūra et al. 2011, Kjær et al. 2012, Enderle et al. 2013). The short term mortality of mature trees tends to be lower, and the situation can vary substantially among sites (Marçais et al. 2016). Studies of disease development among related trees (half sib families) in field trials have shown that phenotypic variation in susceptibility reflects genetically controlled resistance with moderate to high narrow sense heritability (reviewed in McKinney et al. 2014, Muñoz et al. 2016). The findings are supported by results from controlled infection assays (McKinney et al. 2012, Lobo et al. 2015) and recently from genomic and metabolomics studies (Harper et al. 2016, Sollars et al. 2016). The findings have led to optimism regarding presence of natural genetic resistance and to initiation of testing and breeding activities in several countries (see details in Vasaitis and Enderle 2017). But how will existing forests develop? Will damaged stands be regenerated by natural recruitment? A number of interesting studies that shed light on these important questions is included in the present issue of *Baltic Forestry*.

Highlights of this issue

Several studies deal with different aspects of the disease development from areas where the disease is relative new and areas where disease symptoms have been reported since the 90'ties. Solheim and Hietala (2017) document in detail how the disease has spread in Norway from the southeast towards the northwest with 25-78 km per year.

Norwegian regulations stopped movement of seedlings from infected areas, but the spread of the disease has continued showing the efficiency of dispersal by airborne spores. Timmermann et al. (2017) report how the disease has influenced the ash trees in different parts of Norway. High mortality was observed among young and intermediate sized trees, while the disease development has been slower in mature trees. A similar picture is presented by Marçais et al. (2017) based on results from a number of survey plots in different parts of France and Belgium. Besides the role of tree age, these studies shed new light on the role of environmental factors for the severity of the symptom development. Many details in this regard are also presented by Havrdova et al. (2017) based on a survey from the Czech Republic. Also here, the authors find damage level to be negatively correlated with tree height, and statistical correlations were observed with different environmental parameters, *i.e.* tree density, site class, species composition, presence of watercourses in the area, and distance to other ash stands. The role of other pathogens is also discussed in several of the papers. Pacia et al. (2017) studied damaged trees in the Wolica Nature Reserve in Poland and provide specific details on the presence and potential role of *Phytophthora* species. The ash trees in this Nature Reserve were genotyped with genetic markers, and the authors also report interesting genetic differences among trees in different damage levels. Similar results have previously been reported from Germany (Fussi and Konnert 2014) and Heinze and Fussi (2017) therefore present baseline information on genetic diversity in Austria based on seed samples collected prior to first observation of the disease in the country. The authors also describe how genetic markers can be an effective tool for monitoring the origin and level of diversity in seedlots.

Pušpure et al. (2017b) analyzed the natural regeneration in 90 different stands across Latvia. *Hymenoscyphus fraxineus* has probably caused significant health problems for at least 15 years in this region and therefore may already have triggered selection for more resistant trees and caused high level of damage on young trees. A very positive finding of the study was presence of relatively abundant healthy 2-6 years old ash seedling/saplings in many ash forests located on soils suitable for the species. The situation varied among sites depending on several factors and the authors note that further monitoring is required. Still, the results provide new optimism for the future of the species. Enderle et al. (2017) studied the situation in three stands in South West Germany, and based on their findings they also conclude that promotion of natural regeneration can prove an important supplement to breeding activities based on the presence of healthy individuals in the regeneration. The disease history is shorter at the German sites and the ash saplings were severely affected by the disease. However, a fraction of the recruitment remained healthy and even sap-

lings with some symptoms remained fast growing and so far survived competition in dense regeneration in the German sample plots.

Previous genetic studies have identified a statistical relationship between phenology and susceptibility to the disease. In this relation, Nielsen et al. (2017) report that *F. excelsior* seedlings inoculated with the pathogen prior to budburst developed stronger dieback compared to seedling inoculated after budburst. Diminic et al. (2017) provide results from an inoculation study of *F. angustifolia* clones and also find an apparent relationship between phenology and susceptibility where the early flushing also was associated with lower susceptibility. Only few studies have so far targeted the specific interaction between susceptibility and year-to-year variation in temperature and precipitation, but this aspect is addressed by Pušpure et al. (2017a), who compare increment cores from healthy and unhealthy trees at four sites in Latvia. They find that variation in annual fluctuations of temperature and precipitation in general has had higher influence on increment of unhealthy trees compared to healthy ones. Interestingly, the authors also find that the sampled unhealthy trees in general were older than the sampled healthy trees. The authors argue that older trees have higher maintenance cost making them more prone to damage by the fungus, and based on the increment patterns they also suggest that social status of the trees have had an effect. Given that older trees in general exhibited fewer symptoms compared to young trees in other studies (as discussed above), one can speculate if the result from Latvia also can be a result of higher past mortality among young trees compared to old trees in these stands given their relative long disease history. If so, old susceptible trees may remain longer in the studied stands. More studies are required to test such and other relevant hypotheses, but the findings indicate interesting on-going dynamics in the European ash forests. Many questions remain to be addressed regarding these dynamics and the short and long term consequences of ash dieback on the European ash trees are therefore still difficult to predict. However, the new findings presented in this thematic issue provide a valuable new contribution based on observations across Europe. The new knowledge will allow better prediction of disease development under various conditions, and thereby guide foresters in development of wise management and intervention activities.

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