

Genetic Variation in Susceptibility to Ash Dieback

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Abstract

In Denmark, assessment of clonal field trials indicated the presence of genetic resistance to ash dieback in some *F. excelsior* clones. Health score per clone (39 clones) was highly correlated between two study sites. Additionally, 101 families from open pollinated mother trees were tested at two sites (2008-2009) and initial results identify a low frequency of family groups showing significantly less symptoms. The results suggest that being a non-susceptible individual is genetically controlled. Recently initiated inoculation experiments will explore this further.

Keywords | *Chalara fraxinea*, genetic variation, susceptibility, resistance, *Hymenoscyphus pseudoalbidus*

Kurzfassung

Genetische Variation der Anfälligkeit gegenüber dem Eschentriebsterben

Felderhebungen von Klonversuchen in Dänemark haben gezeigt, dass bei einigen Klonen der Gemeinen Esche eine genetische Resistenz gegenüber dem Eschentriebsterben vorhanden ist. Die Gesundheitszustände gleicher Klone (50 Klonindividuen) auf zwei Versuchsflächen waren hoch korreliert. Zusätzlich wurden 101 Familien von frei bestäubten Mutterbäumen auf zwei Flächen getestet (2008-2009) und erste Ergebnisse zeigen Familiengruppen in geringer Häufigkeit, die signifikant weniger Symptome zeigen. Die Ergebnisse deuten darauf hin, dass Nichtanfälligkeit/Widerstandskraft/Resistenz von Individuen genetisch bestimmt ist. Mit kürzlich angelegten Inokulationsversuchen soll dies weiter untersucht werden.

Schlüsselwörter | *Chalara fraxinea*, genetische Variation, Anfälligkeit, Resistenz, *Hymenoscyphus pseudoalbidus*

Background

The health and viability of European common ash is presently threatened by a novel disease caused by the fungus *Chalara fraxinea* Kowalski (Kowalski 2006), the sexual form called *Hymenoscyphus pseudoalbidus* (Queloz et al. 2010). In Denmark the disease was first noted in 2002, and by 2005 it had become very common throughout the country causing devastating harm (Thomsen et al. 2007, Skovsgaard et al. 2009).

Materials and Methods

The project utilizes established seed orchards and progeny trials. The clonal seed orchards were

established in 1998 and consist of 39 clones each represented by 50 grafted ramets. Half of the ramets are grown at one site (Tuse Næs) and the other half at another site (Tapsøre). The progeny trials were established in 2002 with two-year old plants. The progeny trials include families from 101 open pollinated mother trees selected throughout Denmark. The families are likewise grown at two sites (Silkeborg and Randers). At each site the families are grown in four-tree-plots, and each family is replicated eight times in each trial (32 offspring per mother at each site).

We evaluated the health in the beginning of July over three years. The clonal trials were assessed in 2007, 2008, and 2009, while the progeny trials were assessed in 2008 and 2009. All living trees were assessed. However, in the clonal trials, trees with any dubious graftings in the clonal trials (potential rootstocks) were excluded from the analysis. Trees dead prior to the first assessment were also excluded as we could not determine if such trees had been killed by the fungus.

The health of each individual tree was scored according to defoliation of the crown. We used the following categories: Class 0: no symptoms, Class 1: 1-10 %, Class 2: 10-50 %, Class 3: > 50 %, Class 4: dead. Only results from the 2009 evaluation are presented below.

Data analysis

Presence of genetic variation within the seed orchards was tested by applying the model:

$D_{am,ij} = Y = c_i + B_j + \epsilon_{ij}$; where c_i is the effect of the clone (random effect $N(0, \sigma_g^2)$), B_j the effect of the block and ϵ_{ij} the residual assumed $N(0, \sigma_e^2)$.

The absence of genetic variation (corresponding to the null hypothesis $H_0 := 0$) was tested by a standard F-test in a generalised linear analysis of variance model.

The linear model was extended including plot variance (block x family interaction) in the analysis of the progeny trials and the family variation was tested with the plot variance.

Narrow sense heritabilities were calculated from the estimated variance components (family variance,

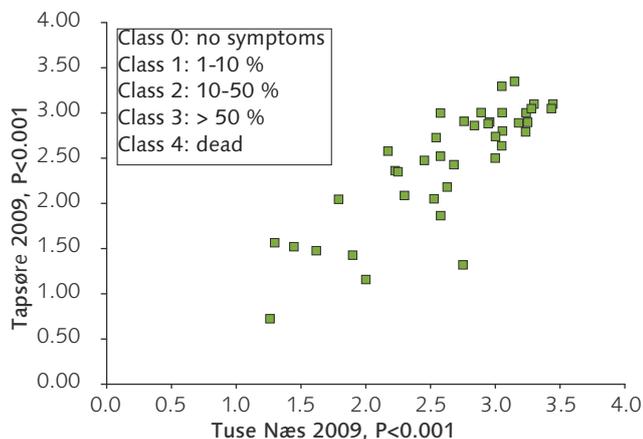


Figure 1: Correlation between the two clonal seed orchards (at Tuse Næs and Tapsøre in Denmark) in relation to health score. The tested clones are plotted by their average damage score at each of the two respective locations. Data from 2009.

Abbildung 1: Korrelation des Gesundheitszustandes zwischen zwei Klon-Samenplantagen (in Tuse Næs und Tapsøre in Dänemark). Für die untersuchten Klone sind die mittleren Schadensklassen der beiden jeweiligen Standorte dargestellt (Klasse 0: keine Symptome, Klasse 1: 1-10 %, Klasse 2: 10-50 %, Klasse 4: tot). Daten des Jahres 2009.

plot variance and residual variance) in the progeny trials assuming that the families were half sibs.

Results

The two clonal trials revealed highly significant effects among clones in all studied years ($P < 0.001$). The observed differences among clones were substantial indicating that the genetic variation is of large practical importance (2009; Figure 1). The correlations between sites were high even though the sites differed in ecological parameters (soil and precipitation). The same pattern was observed in the previous assessments (data not shown).

The two progeny trials revealed highly significant effects among families in both studied years ($P < 0.001$). Also here, the observed differences among families was substantial indicating that the genetic variation is of large practical importance (2009; Figure 2). Narrow sense heritabilities in 2009 were correspondingly high, $h^2 = 0.56$ (0.10) at Randers and 0.49 (0.09) at Silkeborg. The correlations between sites were also high (Figure 2) even though the sites differed in environmental conditions (mainly exposure to spring frost). The same pattern was observed in 2008 assessment (data not shown).

Conclusions and future work

The high correlations between sites both among ramets and half-sib families indicate that the genetically controlled resistance is consistent in different environ-

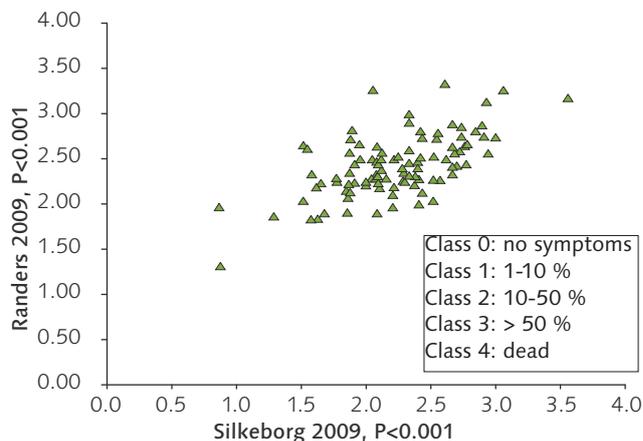


Figure 2: Correlation between the two progeny trials (at Silkeborg and Randers in Denmark) in relation to health score. The tested families are plotted by their average damage score at each of the two respective locations. Data from 2009.

Abbildung 2: Korrelation des Gesundheitszustandes zwischen zwei Herkunftsversuchen (in Silkeborg und Randers in Dänemark). Für die untersuchten Familien sind die mittleren Schadensklasse der beiden Standorte dargestellt (Klasse 0: keine Symptome, Klasse 1: 1-10 %, Klasse 2: 10-50 %, Klasse 4: tot). Daten des Jahres 2009.

ments. The moderate to high narrow sense heritabilities further suggest that the trait is inherited from one generation to the following and only moderately influenced by the environment.

The presented findings have recently been published (McKinney et al. 2011; Kjær et al. 2012).

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