

Can Environmental Characteristics of the European beech (*Fagus sylvatica* L.) on Mount Vogelsberg be Detected by its Genetic Characteristics?

Introduction

European beech (*Fagus sylvatica* L.) has been greatly studied regarding its genetic variability among regions and the plausibly affecting role of the ecological environment (Sander *et al.* 2000). Two such studies on Mount Schauinsland and Mount Vogelsberg in Germany of European beech have intrigued studies for further investigation of this genetic variability. The study on Mount Schauinsland documented changes in allele frequencies of beech on an altitudinal transect from bottom to top, and suggest causes made by climatic adaptations by the beech as it moved along the transect (Sander *et al.* 2000). In conjunction with this study, Mount Vogelsberg also demonstrated similar changes in European beech genotypes while performing inventory studies (Sander *et al.* 2000). In the midst of these studies and many others alike, further investigations of the European beech were provoked.

Among genetic variability, tree-specific forest management can be improved when investigating environmental patterns of European beech along mountain transects. Since higher elevation prompt shallower soils and reduce water uptake (Grayston & Rennberg 2006), precipitation reductions by global warming will cause an effect on European beech populations (Peuke *et al.* 2002). In fact, European beech has been deemed drought-sensitive and therefore requires more attention in sustaining its forests (Grayston & Rennberg 2006). Information pertaining to the environmental characteristics of European beech may be obtained by observable patterns within genetic make-up; and therefore, assist in proper forest management.

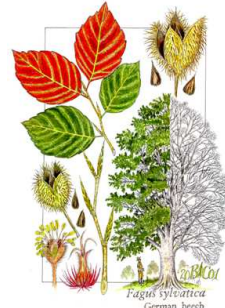
In the present study, allele and genotype frequencies of 5 enzyme loci from six forest areas on Mount Vogelsberg in Germany were employed from Sander *et al.* 2000. An analysis of genetic variability and differentiation will be performed to gain insight of the environmental characteristics of the European beech.

Methods

A data set was obtained from a journal article by Sander *et al.* (2000) which discussed the genetic variation of European beech trees on Mount Vogelsberg in Germany. Six forest areas on Mount Vogelsberg were analyzed (Table 1). Allele and genotype frequencies from five enzyme loci for the six different forest areas were taken for analysis and used to infer any patterns among environmental characteristics (Table 1).

Table 1 Characteristics of the six forest areas on Mount Vogelsberg in Germany (Sander *et al.* 2000)

Forest Area	Elevation (m above sea level)	Age (years)	Precipitation (mm per year)	Temperature (°C per year)
A	150-180	114	680	8.8
B	172-203	160	610	8.7
C	210-260	120	736	8.5
D	280-310	135	970	7.0
E	360-400	108	970	8.0
F	600-660	131	1050	6.8



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Results

Table 2 Observed and expected (using Hardy-Weinberg proportions) heterozygosities of all five enzyme loci for all forest areas on Mount Vogelsberg. Number of alleles is given in parentheses

Forest Areas on mount Vogelsberg	Enzyme Loci						Mean
		Locus 1	Locus 2	Locus 3	Locus 4	Locus 5	
		(2)	(3)	(3)	(2)	(2)	
A	Ho	0.46	0.01	0.22	0.20	0.38	0.25
	He	0.48	0.01	0.22	0.28	0.38	0.27
B	Ho	0.41	0.11	0.30	0.41	0.43	0.33
	He	0.48	0.10	0.34	0.43	0.38	0.35
C	Ho	0.46	0.06	0.33	0.27	0.33	0.29
	He	0.47	0.06	0.30	0.32	0.36	0.30
D	Ho	0.36	0.06	0.27	0.38	0.26	0.27
	He	0.42	0.06	0.26	0.38	0.27	0.28
E	Ho	0.39	0.02	0.28	0.47	0.30	0.29
	He	0.41	0.02	0.26	0.44	0.30	0.29
F	Ho	0.53	0.03	0.37	0.35	0.28	0.31
	He	0.46	0.03	0.42	0.42	0.34	0.33
Mean	Ho	0.44	0.05	0.30	0.35	0.33	
	He	0.45	0.05	0.30	0.38	0.34	

Table 3 Pair wise genetic distances (Fst) between forest areas of European beech at Mount Vogelsberg using allele frequencies of five enzyme loci (distance matrix calculated using Philip 3.6.6). When all six forest areas were included $F_{5,30,0.05(1)} = 2.53, P > 0.05$

	A	B	C	D	E	F
A	0.0000					
B	0.0066	0.0000				
C	0.0011	0.0035	0.0000			
D	0.0070	0.0061	0.0044	0.0000		
E	0.0120	0.0055	0.0086	0.0020	0.0000	
F	0.0117	0.0030	0.0062	0.0072	0.0072	0.0000

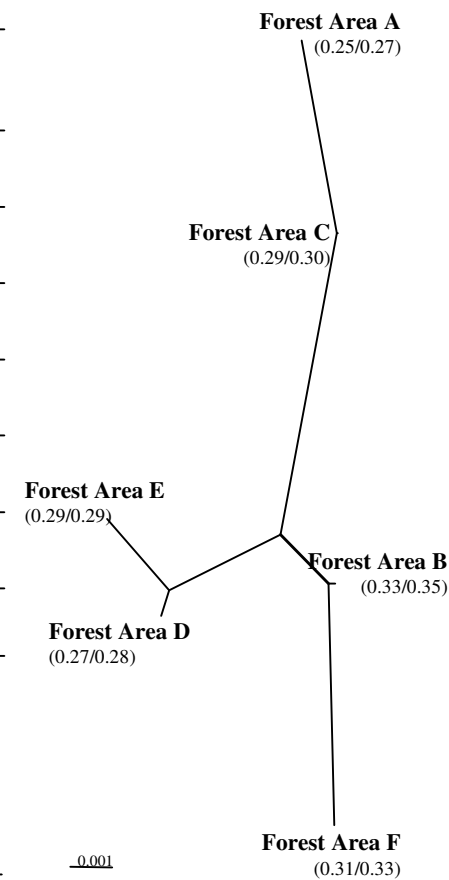


Fig. 1 Unrooted neighbor-joining tree of six forest areas on mount Vogelsberg based on pair wise genetic distances using the distance matrix calculated from Table 3 in Treeview. Parentheses are observed and expected heterozygosities, respectively.



Major Findings

- Overall, the observed heterozygosity was low for all forest areas and loci (0.29).
- Small genetic distances between forest areas correlated to similar levels of heterozygosity using an unrooted neighbor-joining tree; despite the non-significance of genetic distances ($F_{5,30,0.05(1)} = 2.53, P > 0.05$).
- In most cases, the further genetic distance between forest areas, the more different the level of elevation (m above sea level) and precipitation (mm per year).
- Forest areas with low elevation and low precipitation (such as A) are most different in pair wise genetic distance than forest areas with high elevation and high precipitation (such as E).

Discussion

Genetic differentiation of European beech along the altitudinal transect on Mount Vogelsberg is satisfied by: heterozygosity differences between forest areas (Table 2), and neighbor-joining relationships (Fig. 1) based on genetic distances (Table 3). Although no significance was detected between genetic distances ($F_{5,30,0.05(1)} = 2.53, P > 0.05$), it is suspected that the statistical test (ANOVA) accepted a false null hypothesis (Type II error) due to the clumped arrangement of the neighbor-joining tree. In fact, there may be significance between at least one of the forest areas.

Similarly depicted by the present study, Sander *et al.* (2000) concluded low genetic differentiation as well; however, some areas (such as Forest Area E and A) documented significantly different values regarding heterozygosity and population differentiation.

Based on the results from this experiment and Sander *et al.* (2000), the genetic characteristics of the forest areas can depict differences between the forest areas on Mount Vogelsberg. Not surprising are the distinct differences of environmental characteristics for Forest Areas A and E, such as: elevation and precipitation. With this information, it can be expected that European beech will be genetically variable along the altitudinal transect.

When considering forest management and predicting effects of global warming, genetic characteristics of European beech can assist in determining those trees that may suffer from reduced precipitation with decreasing global temperatures due to drought-sensitivity. Beech trees that reach levels significantly different from those below can be marked being at risk and monitored, assisting the survival of European beech.

References

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