DISTRIBUTION OF ATTACK BY BEECH SCALE *Cryptococcus fagisuga* IN BEECH PROGENY TRIALS[1]

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Abstract.--Surveys of beech scale infestation among progeny of single beech trees demonstrated significant variation in susceptibility between the progenies. Relative differences in susceptibility of some progeny were maintained on three different sites in southern England.

INTRODUCTION

At a previous beech bark disease symposium it was shown (Wainhouse and Deeble, 1980) that there were clonal differences in susceptibility of beech to beech scale *(Cryptococcus fagisuga* Lind.). The present paper is an extension of this investigation in which we were able to examine the progeny of single trees to determine their relative resistance to infestation by beech scale.

GENERAL METHODS

The progeny of trees of exceptionally good silvicultural characteristics ('plus' trees) had been established by the Genetics Department of the Forestry Commission in a series of trials to assess their survival, growth rate and form. When the trees had reached pole-stage, natural infestations of beech scale had developed in all the progeny trials and this provided an opportunity to determine their relative susceptibility to attack.

To establish the progeny trials, seed was collected from parent 'plus' trees or from their grafts or rooted cuttings. The trees were open pollinated with or without a pollen mixture supplement.

The data collected on the abundance of the scale or other beech bark disease symptoms from two trials (Arundel and Wendover) were analysed in detail. Data from a third, unreplicated trial were used in a between-trial comparison of the susceptibility of progeny to attack by beech scale.

The parent 'plus' trees were growing on various estates in the UK and the estate name and original Forestry Commission reference numbers were retained to simplify data handling.

Arundel Progeny Trial

This trial was situated in Arundel forest, Sussex. There were six replicates of each of ten progeny planted in 1964 in a randomised block design (Fig 2) with three surrounding guard rows. Each plot, originally contained 36 trees planted 1.5 x 1.5 m apart. The plots were unthinned with about 12% of trees missing through natural mortality.

Many trees within the plots had beech scale colonies on them but there were few other symptoms of beech bark disease present. In October/November 1980, the total number of colonies (discrete areas of wax) in a 3 cm x 3 cm quadrat placed at 0.8 m and 1.7 m above ground on the east and west side of each non-forked tree was determined. Counts were made by three different observers, each allocated two blocks at random. The total count for the four quadrats was used as an index of scale population on each tree. The girth of each living, non-forked tree at breast height (1.3 m) was measured in May 1981.

Results.--An analysis of variance of the girth of trees showed that there were significant

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[1] Paper presented at the IUFRO Beech bark disease Working Party Conference, U.S.A., September-October, 1982.

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differences ($P<0.001$) between the progeny. Furthermore mean counts of beech scale for the ten progeny and mean girth are significantly ($P<0.01$) positively correlated (Fig 1).

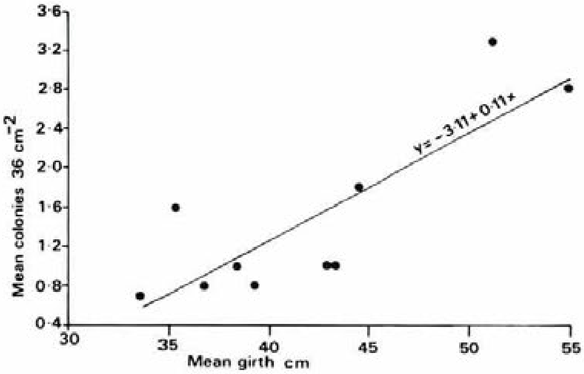

Figure 1.--Relationship between mean number of colonies 36 cm^{-2} and mean girth for progeny at Arundel.

Consequently in the analysis of variance of counts of beech scale (transformed to ln (count +1)), tree size was included as a covariate. Basal area calculated from the estimated mean girth of plots was used as an estimate of tree size. The analysis of variance results are shown in Table 1. The apparent difference between observers in the estimation of abundance of beech scale appears to be due to the significant ($P<0.05$) difference between blocks. Results show that there are highly significant ($P<0.01$) differences between the progeny in attack by beech scale, (Table 2) independently of the effects of tree size.

Table 1 Covariance analysis Table for number of beech scale colonies on progeny at Arundel

Source of Variation	D.F.	S.S.	M.S.	V.R.	Probability (P)
Between observers					
Covariate	1	0.923	0.923	2.934	
Residual	1	0.315	0.315	4.266	P <0.05
Total	2	1.238			
Between blocks within observers					
Covariate	1	0.572	0.572	1.970	
Residual	2	0.581	0.291	3.940	P <0.05
Total	3	1.154			
Between plots					
Progeny	9	2.242	0.249	3.378	P <0.01
Covariate	1	0.445	0.445	6.030	P <0.05
Residual	44	3.246	0.074		
Total	54	5.933			
Grand Total	59	8.324			

Table 2 Mean number of colonies of beech scale 36 cm^{-2} on progeny at Arundel.

Parental 'plus' tree origin	Reference No.	Mean No. of scale colonies 36 cm^{-2} adjusted for covariate
West Dean	51	2.7
West Dean	52	2.0
Slindon	63	1.9
Slindon	65	1.7
Amberley	107	1.1
Pennwood	81	1.0
Pennwood	84	1.0
Brecon	100	1.0
Slindon	60	0.9
Maiden Bradley	90	0.9

The residual variation of counts of *C. fagisuga* after removal of the effects of progeny, girth and observers are plotted in Figure 2.

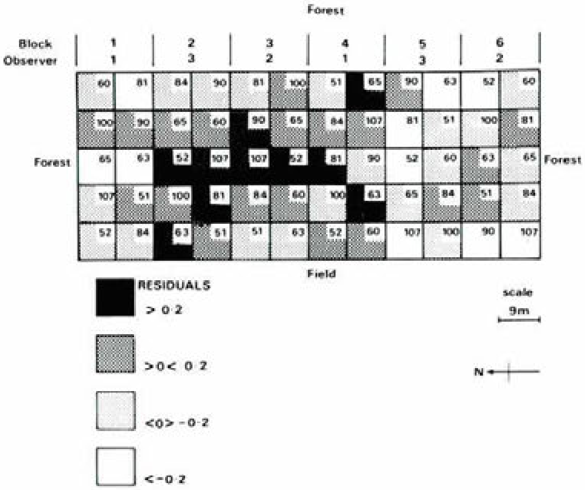

Figure 2.--Distribution of residual beech scale infestation (see text) among plots of progeny at Arundel.

Negative residuals indicate less and positive ones more beech scale infestation than the mean expectation. The results clearly illustrate the significant block effect in the analysis and show that the area in the centre of the trial has more, and the two ends less, beech scale infestation than the average.

Wendover progeny trial

This plot was situated in Wendover forest, Hertfordshire. There were three replicates of each of ten progeny in a randomised block design and one unreplicated block of a further twelve progeny. Each plot originally contained 25 trees, 1.2 m x 0.9 m apart planted in 1953. At the time of assessment, the plots were unthinned but about 50% of trees had died from either suppression or beech bark disease. In August 1979, the trees were assessed for severity of beech scale attack. It was not possible to use a quadrat counting method because of the high density of insects on some trees. Instead, a visual scoring (Table 3) of the insects' wax secretion was used. Two other disease symptoms, dimpling and tarry spots (Houston et. al. 1979) were also noted. Dimpling of the bark surface caused by beech scale feeding was assessed as light, moderate or extensive and tarry spots noted as present or absent. In addition to these disease symptoms the proportion of the basal circumference of trees damaged by the bark stripping activities of squirrels was assessed. Unlike the trial at Arundel, these plots were affected by fairly extensive bark stripping. In April 1980, the girth of trees at 1.3 m above the ground was measured.

Table 3 **Visual assessment scores for beech scale infestation at Wendover.**

Score	Description, applying to at least ¼ of main trunk
1	Up to 5 small colonies visible.
2	Some small colonies scattered over surface of bark. Few large colonies.
3	Moderate numbers of small colonies and large colonies present.
4	Many large and small colonies present.
5	Very many colonies, with large colonies coalescing.

Results.--Only data from the replicated plots were analysed. Analysis of variance of tree girth and squirrel damage showed that they did not differ significantly among the progeny. These two variables were used as covariates in the analysis of the three disease symptoms, beech scale wax cover, dimpling and tarry spots. The analysis of variance results for mean wax cover are shown in Table 4. As well as significant variation in beech scale infestation between blocks, there were highly significant differences between progeny (Table 5) supporting the results obtained from Arundel. However, no progeny differences were detected either for dimpling or for tarry spots.

Table 4 **Covariance analysis Table for beech scale wax cover on progeny at Wendover**

Source of variation	D.F.	S.S.	M.S.	V.R.	Probability (P)
Blocks	2	0.945	0.472	5.154	$P < 0.05$
Progeny	9	2.419	0.269	2.932	$P < 0.01$
Covariates	2	0.385	0.192	2.099	
Residual	16	1.467	0.092		
Total	27	4.271			
Grand Total	29	5.217			

Table 5 Mean infestation score of beech scale on progeny at Wendover

Parental 'plus' tree origin	Reference No.	Mean score adjusted for covariates
Goodwood	42	3.2
West Dean	51	3.1
Cirencester	30	3.1
Cowdray	71	3.0
Kingscote	3	2.9
West Dean	52	2.7
Kingscote	5	2.6
Slindon	61	2.6
Pennwood	83	2.3
Brecon	100	2.3

Comparisons between progeny trials

In addition to the progeny trials at Arundel and Wendover, one further trial was examined. This was an unreplicated trial at Alice Holt forest, Surrey planted in 1953. This had been visually assessed for beech scale infestation by E.J. Parker (unpublished 1975) using a scoring system similar to that described in Table 3.

The plot had been thinned in 1963 and 1968 and at the time of assessment in 1975 thinning and mortality had accounted for 80% of the trees which were originally planted at a spacing of 1.2 m x 0.9 m in plots of 25 trees.

Of the large number of progeny planted in these trials, only five were present at all three sites. At each site these five progeny were ranked for mean infestation level and this forms the basis of the comparison in Table 6. The degree of association among the rankings was tested by the Kendall coefficient of concordance (W) (Siegel 1956). The result was non-significant indicating that the ranks did not agree closely at all three sites. However, the estimated value of W = 0.6 indicates some agreement between the rankings. Some progeny such as 51 and 52 were consistently the most heavily attacked whereas others such as 100 were apparently less susceptible.

Table 6 Ranks of mean scores of beech scale infestation on progeny at three sites in southern England

Parental 'plus' tree origin	Reference No.	Site		
		Arundel	Alice Holt	Wendover
West Dean	51	1	3	1
West Dean	52	2	1	3
* Slindon	60	3	2	4
* Maiden Bradley	90	4	5	2
Brecon	100	5	4	5

Kendall coefficient of concordance (W) = 0.6 (S = 54)

* Unreplicated at Wendover

DISCUSSION

At Arundel, the larger trees harboured greater populations of beech scale, supporting previous observations of this effect (Ehrlich 1934; Barter 1947; Wainhouse and Deeble 1980; E.J. Parker, D. Lonsdale and D. Wainhouse unpublished observations). The trees within each progeny trial were even-aged so the differences in tree girth are due to different rates of growth of the individual trees. The present observations therefore clearly separate the effect of tree size/growth rate from their age on the population development of beech scale. The differences in infestation between progeny at Arundel are nevertheless independent of variations in the size of trees.

The present results showing significant differences in beech scale infestation between progeny on at least two sites extend the previous results of Wainhouse and Deeble (1980). The trees are not grafted and are therefore free of possible rootstock effects on susceptibility so they are expressing presumed maternal variation in susceptibility to attack. A large amount of genetic variation is likely to exist between the trees within these open pollinated progeny. Nevertheless there is good evidence that relative susceptibility to infestation is consistently expressed independently of the site on which the trees are growing. That site may have some effect on host-plant susceptibility to this insect is suggested by the non-random distribution of residual variation in infestation level at Arundel and by the significant effect of blocks on infestation at Wendover.

The assessments were made at the three sites when the trees were 16 (Arundel), 22 (Alice Holt) and 26 (Wendover) years old, showing that differences between progeny are present at an early age and persist at least into the period when trees are considered maximally susceptible (Parker 1974). However, our results do not exclude the possibility that changes in relative susceptibility may occur during subsequent growth and development of the trees.

ACKNOWLEDGEMENTS

Our thanks to Angela Revett and Martin Jukes for assistance with fieldwork. David Lonsdale and Clive Carter made valuable criticism of the manuscript.

RÉSUMÉ

Les descendants d'arbres de caractéristiques sylvicoles exceptionnellement bonnes avaient été plantés dans le cadre d'une série d'essais sylvicoles, permettant ainsi de constater le degré d'invasion des descendants par la cochenille du hêtre et de déterminer leur sensibilité à l'attaque.

Nous avons pu démontrer des variations significatives de la sensibilité des descendants à l'invasion par la cochenille du hêtre. Il y avait aussi des indications que les mêmes différences relatives de sensibilité de certains descendants se retrouvaient a trois emplacements différents dans le sud de l'Angleterre.

ZUSAMMENFASSUNG

In einer Reihe von Versuchsanbauten mit Nachkommen von Bäumen mit außergewöhlich guten Eigenschaften bot sich die Gelegenheit, die Ausmaße eines Buchenwollschildlausbefalls aufzunehmen und die relative Anfälligkeit der Nachkommen festzustellen.
Wir konnten zeigen, daß bei den Nachkommen wesentliche Unterschiede in der Anfälligkeit gegenüber der Buchenwollschildlaus bestehen. Es zeigte sich auch, daß relative Unterschiede in der Anfälligkeit bei einigen der Nachkommen an drei verschiedenen Anbauorten in Südengland beibehalten wurden.

LITERATURE CITED

Barter, G.W. 1947 The beech scale. Forest insect investigations, Bimonthly progress report. Science service, Dept. Agriculture Ottawa 3 (4) 1.

Ehrlich, J. 1934 The Beech bark disease. A *Nectria* disease of *Fagus* following *Cryptococcus fagi* (Baer.) Can. J. Res 10 593-692.

Houston, D.R., Parker, E.J., Perrin, R., Lang, K.J. 1979 Beech bark disease: a comparison of the disease in North America, Great Britain, France and Germany. Eur. J. For. Path. 9 199-211.

Parker, E.J. 1974 Beech bark disease. Ph.D thesis. University of Surrey.

Siegel, S. 1956 Nonparametric statistics for the behavioural sciences. McGraw-Hill, New York 312 pp.

Wainhouse, D., Deeble, R. 1980 Variation in susceptibility of beech (*Fagus* spp.) to beech scale (*Cryptococcus fagisuga*). Ann. Sci. Forest., 37 (4) 279-290.