An Analysis of Mortality Inventory Tally Using Large Plots Compared to Tally Using Small Plot Clusters

Vernon J. LaBau and John W. Hazard

Abstract.—During an inventory to assess spruce bark beetle impact on the Kenai Peninsula in south-central Alaska, 5-year mortality estimates were made for all growing-stock trees on 0.6 ha areas, on 0.4 ha areas, and on a cluster of four 1/60-ha subplots. The analysis of the results of the comparison between cluster data and the larger plot data highlighted some of the problems associated with trying to assess tree mortality from small plots. Based on the large chi square values observed in these tests, there seems to be a strong case for taking a mortality plot that is larger than the four 1/60-ha plots tested here. For the population under study, the smaller plots do not capture the highly variable distribution nature of mortality as well as the two larger plots evaluated.

BACKGROUND

During the summer of 1997 and 1998, the University of Alaska-Anchorage (UAA), through the Environment and Natural Resources Institute (ENRI), funded a study to evaluate the spruce bark beetle (*Dendroctonus rufipennis* (Kirby)) impact on the forests of the Kenai Peninsula in south-central Alaska (LaBau, in press). As a result of the forest stands reaching old age, the spruce bark beetle is the force behind one of the largest current and ongoing insect epidemics in the United States. It impacted over 1.3 million acres of Alaska white spruce (*Picea glauca* (Moench) Voss) and Lutz spruce (*Picea* x lutzii Little) during the spring and summer of 1996 (Boughton 1996).

OBJECTIVES

One of the objectives of this study was to evaluate how well the four-point cluster of subplots captured the highly variable nature of the mortality population of interest. It was felt that some measure of that could be obtained by comparing the four-point cluster mortality data set with the data set found on the .6-ha sample. The .6-ha plot completely encompasses the four-point cluster, so it is possible to compare these two samples. A second point of focus for the study was to evaluate how well the four-point plot evaluated for mortality compared to the .4-ha plot, and how well the .4-ha plot evaluated mortality compared to the .6-ha plot.

The null hypothesis was that for each of the four strata under test: "*there is no significant difference between the* ***Expected*** *tally of mortality trees on the .6-ha sample and that of the* ***Observed*** *tally of mortality trees on the four-point cluster sample*." It was decided that the occurrence of a chi square value larger than that at the 0.05 level would be considered sufficient to reject the null hypothesis. The tests were made for each of four mortality intensity strata, with each stratum having 10 plots, resulting in a total of 40 data sets over the four impact strata, and resulting in 10 degrees of freedom in the test for each stratum.

METHODS

Employing a two-phase (double) sampling methodology for stratification (Bickford 1952), ENRI evaluated 1,078 photo sample points at the first (photo interpretation) phase and established 40 phase 2 ground plots in four strata classes as identified in phase 1. The strata in this study were based on spruce bark beetle attack intensities as derived from annual aerial insect damage survey maps prepared by the USDA Forest Service's office of State and Private Forestry (S&PF) (Holsten *et al.* 1996) in cooperation with the State of Alaska's Division of Forestry, (Alaska Department of Natural Resources 1995). The four strata used in this study were "High," "Moderate," "Low," and "None," indicating the level of bark beetle attack in the immediate vicinity of the photo sample points. A study plan is available describing in greater detail how the strata were classified during phase 1 of the sample process.

Data were collected on the ground plots, using standard forest inventory methodologies (Larson 1987) and standard forest health evaluations (Conklin 1996) as set forth by the Forest Service in its Forest Inventory and Analysis (FIA) and Forest Health Monitoring (FHM) programs.

The standard FHM ground sample unit is four 1/60-ha subplots, resulting in a sample of 1/15-ha at each ground plot cluster for growing-stock trees (see figure 1). Data

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Senior Research Associate, University of Alaska, Anchorage, AK, USA, Environment and Natural Resources Institute, and Partner, Statistical Consulting Services, Bend, OR, USA, respectively.

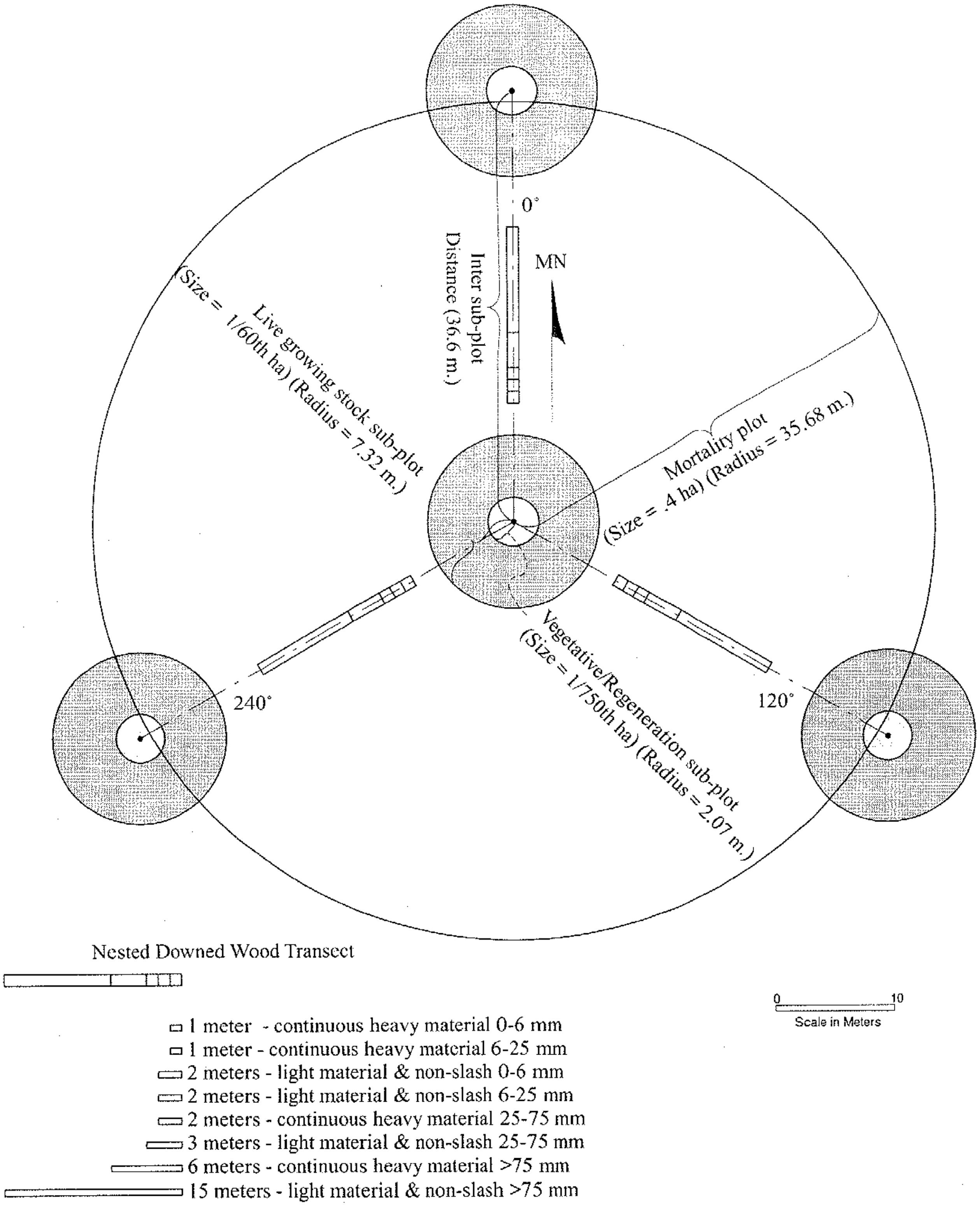

Figure 1.—*Standard FHM ground plot layout with the addition of the 0.4 ha mortality plot used in this study.*

were collected on growing stock, seedling and sapling regeneration, and understory vegetation at each subplot. Normally, FIA and FHM collect mortality tree data on those same clusters of subplots. This was also done in this study. However, in this study, an additional 0.6-ha mortality plot was laid over the cluster of subplots, and all growing-stock trees (all trees 12.7 cm and larger) that died within the last 5 years (guides in FIA procedures (Larson 1987)) were selected in the growing-stock mortality sample.

DATA ANALYSIS

During the course of the ground sample, more than 1,700, 1,100, and 200 mortality growing-stock trees were tallied respectively on the 40 0.6-ha plots, the 0.4-ha plots, and on the same 40 clustered subplots sets. Because the subplot clusters were only 1/9 the size of the 0.6-ha plot, the sample of mortality trees from the clusters were expanded accordingly to enable a valid comparison of tree tally on an area-by-area and tree per hectare basis. Table 1 summarizes the tree tallies by species for the 0.6-ha, 0.4-ha, and four-point cluster samples, with all scaled to a per acre basis for valid comparisons in the analysis.

The method chosen for comparing these data sets was the chi square analysis test of accuracy (Freese 1960), where the mortality tally on the 0.6-ha plot would be the *Expected* count and the mortality tally on the four subplots or the 0.4-ha plots would be the *Observed* count. Tests would be made for each of the four strata, since each stratum had different intensities of mortality tally.

Then:

$$X^2 = \sum_{i=1}^{10} \left(\frac{(x_i - \mu_i)^2}{\sigma^2} \right).$$

where: χ_i = the ***observed*** value from the i^{th} cluster sample, or the 0.4-ha plots,

μ_i = the ***expected*** value from the i^{th} 0.6-ha sample, and

σ^2 = the required accuracy, which for this case is defined as

$$= \frac{(\text{10\% deviation from the average strata mortality tally})^2}{(\text{The standard normal deviation for a 0.05 two-tailed test})^2}$$

and for the "High" strata with an average tally of 52.1 trees per acre on the 0.6-ha sample is:

$$= \frac{(5.21)^2}{(1.96)^2} = 7.066 \text{ trees}$$

The required accuracy for the "Moderate," "Low," and "None" strata were 2.17, 2.11, and 0.06 trees, respectively.

RESULTS

Four chi square tests were run, one for each of the strata in the study; 10 pairs of data were tested in each stratum, providing 10 degrees of freedom for each stratum tested. For the 10 degrees of freedom in these tests, the chi square threshold for rejecting the null hypotheses at the 0.05 level is 18.31.

For all four of the strata evaluated, the null hypotheses were rejected at the 0.05 level, implying that the tally of mortality trees on the four-point cluster is significantly different from the tally on the 0.6-ha plot, and that neither the four-point cluster nor the 0.4-ha plot gives estimates of mortality as accurately as the 0.6-ha plot.

Results of the chi square evaluations for each stratum, as tested for the three combinations of plots, are shown in table 2.

DISCUSSION

The primary objective of this exercise focused on how the mortality tally on the four-point cluster and the 0.4-ha plot compared with the 0.6-ha plot. The 0.6-ha plot was used as our standard for comparison and provided the most information on mortality at each plot location. We were asking the question "Do the four-point cluster and the 0.4-ha plot provide estimates of the mortality on the 0.6-ha plots within an acceptable level of accuracy?". Freese's chi square test of accuracy was used to make this comparison. The Paired t-test and other comparisons of variance are not appropriate for this test, as explained in Freese (1960). Given the high chi square values observed in the test, it was concluded that the four-point cluster and 0.4-ha plot did not produce results within the acceptable level of accuracy.

Had it been established that the alternative methods (four-point cluster and 0.4-ha plot) reproduced the results of the standard method (0.6-ha plot), within the specified level of accuracy, then, it would have been appropriate to look at other characteristics, such as cost, convenience, quality control, and flexibility. However, this not being the case, these other characteristics were not evaluated.

Some additional comments need to be made about this study. First of all, results cannot be extended beyond the population tested, so it is not possible to extrapolate these results to all FHM plots in the United States, or the West Coast, or even to Alaska beyond the Kenai Peninsula. Second, the sample size (10 plots per stratum) is a smaller

Table 1.—*Summary of mortality tally for the three plot configurations under study, Kenai Peninsula, Alaska spruce bark beetle study, 1997 and 1998*

Beetle impact strata	Plot	Mortality tree tally 0.6 ha tally	Mortality tree tally 0 .4 ha tally	Mortality tree tally 4-point cluster tally	Plot	Trees per acre 0.6 ha	Trees per acre 0.4 ha	Trees per acre 4-point cluster
High	**7**	7	5	1	**7**	4.67	5	6
High	**52**	144	112	10	**52**	96.00	112	60
High	**63**	45	29	7	**63**	30.00	29	42
High	**75**	5	5	0.0	**75**	3.33	5	0.0
High	**82**	24	22	3	**82**	16.00	22	18
High	**89**	135	96	17	**89**	90.00	96	102
High	**92**	116	79	10	**92**	77.33	79	60
High	**111**	17	13	2	**111**	11.33	13	12
High	**124**	286	189	29	**124**	190.67	189	174
High	**129**	2	0.0	0.0	**129**	1.33	0.0	0.0
Low	**153**	42	22	13	**153**	28.00	22	78
Low	**160**	0.0	0.0	0.0	**160**	0.00	0.0	0.0
Low	**167**	4	2	2	**167**	2.67	2	12
Low	**176**	27	17	7	**176**	18.00	17	42
Low	**177**	11	11	3	**177**	7.33	11	18
Low	**188**	16	2	4	**188**	10.67	2	24
Low	**204**	152	101	18	**204**	101.33	101	108
Low	**214**	18	11	0.0	**214**	12.00	11	0.0
Low	**226**	61	37	1	**226**	40.67	37	6
Low	**248**	103	59	14	**248**	68.67	59	84
Moderate	**276**	0.0	0.0	0.0	**276**	0.00	0.0	0.0
Moderate	**283**	4	3	0.0	**283**	2.67	3	0.0
Moderate	**298**	49	35	5	**298**	32.67	35	30
Moderate	**313**	92	63	10	**313**	61.33	63	60
Moderate	**317**	0.0	0.0	0.0	**317**	0.00	0.0	0.0
Moderate	**337**	32	24	2	**337**	21.33	24	12
Moderate	**338**	1	1	0.0	**338**	0.67	1	0.0
Moderate	**343**	230	156	26	**343**	153.33	156	156
Moderate	**371**	12	12	1	**371**	8.00	12	6
Moderate	**374**	7	5	2	**374**	4.67	5	12
None	**386**	1	1	1	**386**	0.67	1	6
None	**389**	13	9	3	**389**	8.67	9	18
None	**407**	6	4	3	**407**	4.00	4	18
None	**409**	4	3	0.0	**409**	2.67	3	0.0
None	**414**	15	9	4	**414**	10.00	9	24
None	**417**	4	3	0.0	**417**	2.67	3	0.0
None	**428**	1	0.0	1	**428**	0.67	0.0	6
None	**438**	19	10	3	**438**	12.67	10	18
None	**448**	7	4	4	**448**	4.67	4	24
None	**461**	0.0	0.0	0.0	**461**	0.00	0.0	0.0
	TOTAL	1712	1154	206	**AVERAGE**	28.53	28.85	30.8:

Table 2.—*Summary of chi square computations for the three plot configurations under study, Kenai Peninsula, Alaska spruce bark beetle study, 1997 and 1998*

Chi Square test rejection value (0.05 level @ 10 df) = 18.31

Impact strata	Plot	0.6 ha Mort/Ac. U	0.4 ha Mort/Ac. Z	4 points Mort/Ac. X	A 0.6x4pt X-U	B 0.6x.4 Z-U	C 0.4x4pt X-Z	A2 0.6x4pt	B2 0.6x.4	C2 0.4x4pt		Chi sqrs.	Accuracy tolerance (tally trees)
high	**7**	4.7	5.0	6.0	1.3	0.3	1.0	1.8	0.1	1.0			
high	**52**	96.0	112.0	60.0	-36.0	16.0	-52.0	1,296.0	256.0	2,704.0	Acceptable U Miss (10%) =		5.21
high	**63**	30.0	29.0	42.0	12.0	-1.0	13.0	144.0	1.0	169.0	Acceptable Z Miss (10%)=		5.50
high	**75**	3.3	5.0	0.0	-3.3	1.7	-5.0	11.1	2.8	25.0	Chi Sq (.6x4pt.)=	309.1	
high	**82**	16.0	22.0	18.0	2.0	6.0	-4.0	4.0	36.0	16.0	Chi Sq (.6x.4)=	48.46	
high	**89**	90.0	96.0	102.0	12.0	6.0	6.0	144.0	36.0	36.0	Chi Sq (.4x4pt.)=	449.3	
high	**92**	77.3	79.0	60.0	-17.3	1.7	-19.0	300.4	2.8	361.0			
high	**111**	11.3	13.0	12.0	0.7	1.7	-1.0	0.4	2.8	1.0			
high	**124**	190.7	189.0	174.0	-16.7	-1.7	-15.0	277.8	2.8	225.0			
high	**129**	1.3	0.0	0.0	-1.3	-1.3	0.0	1.8	1.8	0.0			
	Totals	520.7	550.0	474.0	-46.7	29.3	-76.0	2,181.3	342.0	3,538.0			
	Means	52.1	55.0	47.4	-4.7	2.9	-7.6						
low	**153**	28.0	22.0	78.0	50.0	-6.0	56.0	2,500.0	36.0	3,136.0			
low	**160**	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Acceptable U Miss (10%) =		2.89
low	**167**	2.7	2.0	12.0	9.3	-0.7	10.0	87.1	0.4	100.0	Acceptable Z Miss (10%)=		2.62
low	**176**	18.0	17.0	42.0	24.0	-1.0	25.0	576.0	1.0	625.0	Chi Sq (.6x4pt.)=	2,331	
low	**177**	7.3	11.0	18.0	10.7	3.7	7.0	113.8	13.4	49.0	Chi Sq (.6x.4)=	107.4	
low	**188**	10.7	2.0	24.0	13.3	-8.7	22.0	177.8	75.1	484.0	Chi Sq (.4x4pt.)=	3,442	
low	**204**	101.3	101.0	108.0	6.7	-0.3	7.0	44.4	0.1	49.0			
low	**214**	12.0	11.0	0.0	-12.0	-1.0	-11.0	144.0	1.0	121.0			
low	**226**	40.7	37.0	6.0	-34.7	-3.7	-31.0	1,201.8	13.4	961.0			
low	**248**	68.7	59.0	84.0	15.3	-9.7	25.0	235.1	93.4	625.0			
	Totals	289.3	262.0	372.0	82.7	-27.3	110.0	5,080.0	234.0	6,150.0			
	Means	28.9	26.2	37.2	8.3	-2.7	11.0						
moder.	**276**	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			
moder.	**283**	2.7	3.0	0.0	-2.7	0.3	-0.3	7.1	0.1	9.0	Acceptable U Miss (10%) =		2.85
moder.	**298**	32.7	35.0	30.0	-2.7	2.3	-5.0	7.1	5.4	25.0	Acceptable Z Miss (10%)=		2.99
moder.	**313**	61.3	63.0	60.0	-1.3	1.7	-3.0	1.8	2.8	9.0	Chi Sq (.6x4pt.)=	79.85	
moder.	**317**	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	Chi Sq (.6x.4)=	18.38	
moder.	**337**	21.3	24.0	12.0	-9.3	2.7	-12.0	87.1	7.1	144.0	Chi Sq (.4x4pt.)=	117.3	
moder.	**338**	0.7	1.0	0.0	-0.7	0.3	-1.0	0.4	0.1	1.0			
moder.	**343**	153.3	156.0	156.0	2.7	2.7	0.0	7.1	7.1	0.0			
moder.	**371**	8.0	12.0	6.0	-2.0	4.0	-6.0	4.0	16.0	36.0			
moder.	**374**	4.7	5.0	12.0	7.3	0.3	7.0	53.8	0.1	49.0			
	Totals	284.7	299.0	276.0	-8.7	14.3	-23.0	168.4	38.8	273.0			
	Means	28.5	29.9	27.6	-0.9	1.4	-2.3						
none	**386**	0.7	1.0	6.0	5.3	0.3	5.0	28.4	0.1	25.0			
none	**389**	8.7	9.0	18.0	9.3	0.3	9.0	87.1	0.1	81.0	Acceptable U Miss (10%) =		0.47
none	**407**	4.0	4.0	18.0	14.0	0.0	14.0	196.0	0.0	196.0	Acceptable Z Miss (10%)=		0.43
none	**409**	2.7	3.0	0.0	-2.7	0.3	-3.0	7.1	0.1	9.0	Chi Sq (.6x4pt.)=	16,801	
none	**414**	10.0	9.0	24.0	14.0	-1.0	15.0	196.0	1.0	225.0	Chi Sq (.6x.4)=	166.6	
none	**417**	2.7	3.0	0.0	-2.7	0.3	-3.0	7.1	0.1	9.0	Chi Sq (.4x4pt.)=	21,712	
none	**428**	0.7	0.0	6.0	5.3	-0.7	6.0	28.4	0.4	36.0			
none	**438**	12.7	10.0	18.0	5.3	-2.7	8.0	28.4	7.1	64.0			
none	**448**	4.7	4.0	24.0	19.3	-0.7	20.0	373.8	0.4	400.0			
none	**461**	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0			
	Totals	46.7	43.0	114.0	67.3	-3.7	71.0	952.4	9.4	1,045.0			
	Means	4.7	4.3	11.4	6.7	-0.4	7.1						

sample than one would like to have to make statistical inferences from the study results. Given adequate funding, it would have been good to have been able to take at least four times as many plots (a minimum of 40 in each stratum). Third, the four-point cluster estimator should be unbiased, but from the results of this study, it seems that the smaller cluster plot size is not adequate for biologically describing what is on the ground, compared to the larger plots. A fourth point is that this test can be looked at as covering a spectrum of insect impact conditions ranging from endemic conditions (the "None" strata) to epidemic conditions (the "High" strata). This suggests that these results may have broader application to other similar conditions over the United States.

The four 1/60-ha cluster captures a very small sample of tree mortality, especially for endemic conditions. In view of the role of mortality as an indicator of forest health, it is very important to get the best possible data and information about what is causing trees to die. Mortality is not accurately assessed with the four-point cluster, thus making it difficult to find associations with stand characteristics (i.e., forest type, stand size, forest age, etc.), which are critical components for explaining forest health.

CONCLUSIONS

Based on the large chi square values observed in these tests, there seems to be a strong case for taking a mortality plot that is larger than the four 1/60-ha plots currently used by FHM. For the population under study, the smaller plots do not capture the highly variable nature of tree and plot mortality as well as the two larger plots evaluated.

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