

Western Pine Beetle

Dendroctonus brevicomis LeConte
Coleoptera: Curculionidae, Scolytinae

Hayes, C. J.; Fettig, C. J.; Merrill, L. D. 2009. Evaluation of multiple funnel traps and stand characteristics for estimating western pine beetle-caused tree mortality. *Journal of Economic Entomology* 102: 2170-2182.

Objective: To determine the relationship between *D. brevicomis* trap catches and levels of tree mortality attributed to *D. brevicomis* attack.

Abstract: The western pine beetle, *Dendroctonus brevicomis* LeConte (Coleoptera: Curculionidae, Scolytinae), is a major cause of ponderosa pine, *Pinus ponderosa* Dougl. ex Laws., mortality in much of western North America.

This study was designed to quantify relationships between *D. brevicomis* trap catches and levels of tree mortality attributed to *D. brevicomis* at 44 trapping sites (stands) and within five general locations (forests) in California. Preliminary analyses were conducted by Pearson's correlation coefficient (r) using tree mortality/ha and % tree mortality and 10 potential predictor variables. All predictor variables that had significant correlations (*D. brevicomis* per day, *D. brevicomis*: *Temnochila chlorodia* [*D. brevicomis* predator] ratio, percentage of *D. brevicomis* [percentage of total trap catch, including predators, represented by *D. brevicomis*], trees per ha, basal area of all tree species, basal area of *P. ponderosa*, mean diameter at breast height [dbh] and stand density index) were considered for linear and multiple linear regression models for predicting levels of *D. brevicomis*-caused tree mortality.

Monitoring *D. brevicomis* populations through the use of pheromone-baited multiple funnel traps was not an effective means of predicting levels of *D. brevicomis*-caused tree mortality. However, levels of *D. brevicomis*-caused tree mortality can be efficiently predicted (Adj. $R^2 > 0.90$) at large spatial scales (forests; $\approx 3,000$ to 14,000 ha of contiguous host) by simply measuring stand density, specifically the basal area of all tree species or stand density index.

Sampling Procedure: In *P. ponderosa* and/or mixed conifer forests (area of concern must be at least 3,000 ha), containing $> 50\%$ *P. ponderosa*, establish ten 0.081-ha circular plots. Separate plots by a minimum of 800 m. On these plots record diameter at breast height (dbh, 1.37 m in height) and species of all live trees. With these data calculate stand basal area, stand density index, and mean dbh for each plot. Average these values across all plots and plug resulting value (replace "x") into one of the models (Table 1). Resulting y-value will be an estimate of *D. brevicomis*-caused tree mortality in each forested area.

Models may also be used to estimate basal area and stand density index targets to "beetle proof" forested areas. For example, if one desires a *P. ponderosa*-dominated forest that will only experience $\sim 2\%$ *D. brevicomis*-caused tree mortality in future

outbreaks, find 2% on the y-axis of Figure 1A or 1B, draw a line over to the linear model and then follow straight down to find the target basal area or stand density index, respectively. Remember, however, that this is a large scale model and individual stand site quality will vary and may impact stand susceptibility to *D. brevicomis* attack and associated levels of tree mortality. The target basal area or stand density index should be averaged over many stands (forested areas > 3,000 ha), with lower density targets for poor quality sites and higher density targets for higher quality sites.

Notes: These equations were developed during one *D. brevicomis* outbreak, and therefore the results should be interpreted with caution.

Tables and Figures:

Table 1. Five large-scale (forest) regression models relating percentage of *P. ponderosa* killed by *D. brevicomis* (WPB) in yr-1 (A-C), and yr-1 and yr-2 (combined, D and E) to various forest stand characteristics in California, 2003-2005.

| Model | Independent variables (x_i) | | | | Model statistics | | | |
|--|---------------------------------|--------------------------------|-------------------|-------------|------------------|-----|--------|------------|
| | Variable | Range of values | Coefficient (SEM) | Partial P | F | df | P | Adj. R^2 |
| A. $y = \text{Yr-1 } \% P. ponderosa \text{ mortality } (n = 5) \text{ (range of values, 0.3-6.2 \%)}$ | | | | | | | | |
| | Constant | - | -6.28 (1.51) | 0.02 | 37.8 | 1,3 | 0.01 | 0.90 |
| | x_1 BAA ¹ | 23.4 – 46.8 m ² /ha | 0.27 (0.04) | 0.01 | | | | |
| B. $y = \text{Yr-1 } \% P. ponderosa \text{ mortality } (n = 5) \text{ (range of values, 0.3-6.2 \%)}$ | | | | | | | | |
| | Constant | - | -11.27 (1.01) | 0.002 | 197.6 | 1,3 | <0.001 | 0.98 |
| | x_1 SDI ² | 171.9 – 261.9 | 0.07 (0.004) | <0.001 | | | | |
| C. $y = \text{Yr-1 } \% P. ponderosa \text{ mortality } (n = 5) \text{ (range of values, 0.3-6.2 \%)}$ | | | | | | | | |
| | Constant | - | -5.37 (0.88) | 0.03 | 68.3 | 2,2 | 0.01 | 0.97 |
| | x_1 BAA | 23.4 – 46.8 m ² /ha | 0.37 (0.04) | 0.01 | | | | |
| | x_2 Mean dbh ³ | 19.5 – 75.4 cm | -0.11 (0.04) | 0.10 | | | | |
| D. $y = \text{Combined } \% P. ponderosa \text{ mortality } (n = 5) \text{ (range of values, 0.9-8.6 \%)}$ | | | | | | | | |
| | Constant | - | -7.60 (0.78) | 0.002 | 229.8 | 1,3 | <0.001 | 0.98 |
| | x_1 BAA | 23.4 – 46.8 m ² /ha | 0.34 (0.02) | <0.001 | | | | |
| E. $y = \text{Combined } \% P. ponderosa \text{ mortality } (n = 5) \text{ (range of values, 0.9-8.6 \%)}$ | | | | | | | | |
| | Constant | - | -13.20 (1.89) | 0.006 | 83.9 | 1,3 | 0.003 | 0.95 |
| | x_1 SDI | 171.9 – 261.9 | 0.08 (0.009) | 0.003 | | | | |

¹BAA; stand basal area of all tree species (m²/ ha)

²SDI; stand density index

³dbh; diameter at breast height (1.37 m above ground)

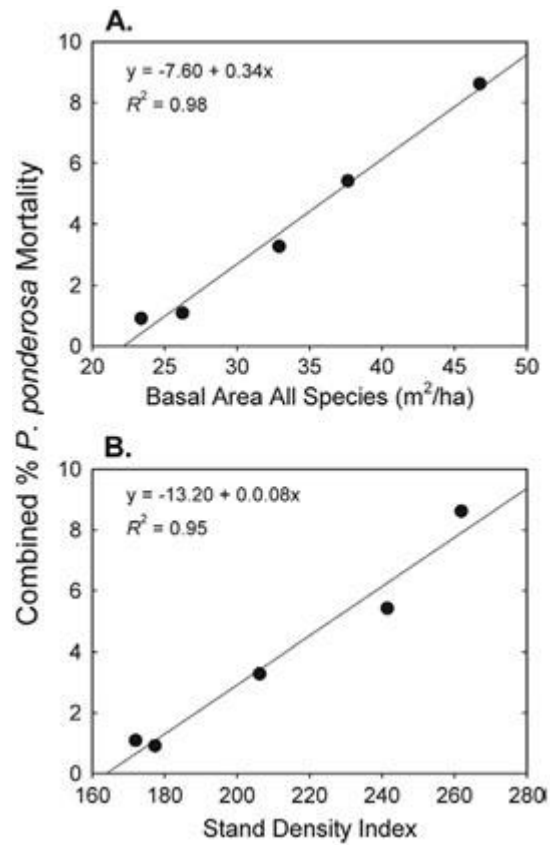


Figure 1. Linear regressions overlaid on observed data points for (A) basal area of all tree species and mean percentage of *P. ponderosa* killed by *D. brevicomis* in yr-1 and yr-2 combined (see Table 1, model D for additional statistics), and (B) stand density index and mean percentage of *P. ponderosa* killed by *D. brevicomis* in yr-1 and yr-2 combined (see Table 1, model E for additional statistics).