Douglas-Fir Cone Moth

Barbara colfaxiana (Kearfott) Lepidoptera: Tortricidae

Sweeney, J. D.; Miller, G. F. 1989. Distribution of Barbara colfaxiana (Lepidoptera: Tortricidae) eggs within and among Douglas-fir crowns and methods for estimating egg densities. Canadian Entomologist 121: 569-578.

Objective: To develop a sequential sampling plan that predicts when *B*. *colfaxiana* populations are high enough to cause a 10% loss of Douglas-fir seed.

Abstract: The Douglas-fir cone moth, *Barbara colfaxiana* (Kearfott), is the most prevalent pest of Douglas-fir, *Pseudotsugae menziessi* (Mirb.) Franco, seed in British Columbia. The spatial frequency distributions of *B. colfaxiana* eggs in Douglas-fir trees and stands were determined by dissecting 13,262 conelets collected from 81 trees at three sites in 2 years.

Sampling Procedure: Collect Douglas-fir conelets after they have begun to turn down, following pollination and the oviposition period of *B. colfaxiana*, but before they become pendant. Sample at least 10 trees 4-14 m tall, collecting three conelets per tree. Consult the sequential sampling table (Fig. 2), and continue sampling until a decision is met. If the cumulative number of eggs exceeds the upper decision limit, then the population is expected to cause greater than 10% seed loss. When the number of eggs falls below the lower decision limit, damage is expected to be minimal. Sample a maximum of 59 trees, and calculate mean egg densities to compare with the critical density (10% seed loss). Sampling time ranges from 3 to 18 h.

Notes: The relationship between the mean and variance is similar in both natural stands and seed orchards. This sequential sampling plan is quite reliable for classifying *B*. *colfaxiana* egg density except when densities approach the critical level, which results in 10% seed loss.





FIG. 2. A two-stage sequential sampling plan for classifying the mean density of Douglas-fir cone moth eggs per conelet relative to a critical level defined as 0.6 eggs per conelet. Three conelets are sampled per tree, the minimum number of trees to sample is 10, and the maximum is 59. The nominal confidence level is 90% (but see Fig. 3).

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