

INFLUENCING FACTORS AND SPATIAL PATTERNS OF SPRUCE BUDWORM INFESTATION IN EASTERN CANADA FORESTS

Application for the 2019 Esri Young Scholars Award



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General Background

Outbreaks of spruce budworm (*Choristoneura fumiferana* Clem.; SBW) are one of the predominant natural disturbances in North America. Outbreaks typically occur every 35 years [1], with the current SBW epidemic beginning around 2006 in Quebec, and populations increasing since 2014 in northern New Brunswick, causing large-scale mortality and economic losses. To better understand the initiation of a SBW outbreak and resulting defoliation, this study will address two questions: 1) what factors influence SBW outbreak initiation in northern New Brunswick, and 2) what are the spatial-temporal patterns of SBW defoliation of individual trees within plots in adjacent Gaspé, Quebec.

Sub-project A → Landscape

The first study area was in northern New Brunswick, covering about one-half of the province area (Fig.1). The study was based on the second-instar larvae (L2) per branch population data jointly collected by forest industries and New Brunswick Department of Energy and Resource Development from 2013 to 2018. During this period, the area experienced the initial stage of the outbreak. This study aimed to determine which factors are related to increased L2 population during this stage, and attempted to forecast the high L2 population region in New Brunswick in 2019, which benefits the early intervention against spruce budworm research project to protect the forest from SBW infestation.

What Factors Have Effects on Insect Population?

Based on the previous literature, four categories of environmental/site variables were hypothesized to affect SBW outbreak initiation: composition of tree species, climate conditions, topography/locations, and site quality. Spray treatment history and previous local SBW population were also included as predictors. 2013–2018 fishnet L2 data (i.e., response) were overlaid separately with other corresponding layers (i.e., predictors; Fig.2). The relative importance of predictors was estimated by Gradient Boosting Machine (GBM) analysis [2]. Spring temperature and degree days, previous local SBW population, and proximity to higher L2 sites were consistently the most important predictors among 2014 - 2018 GBM analyses.

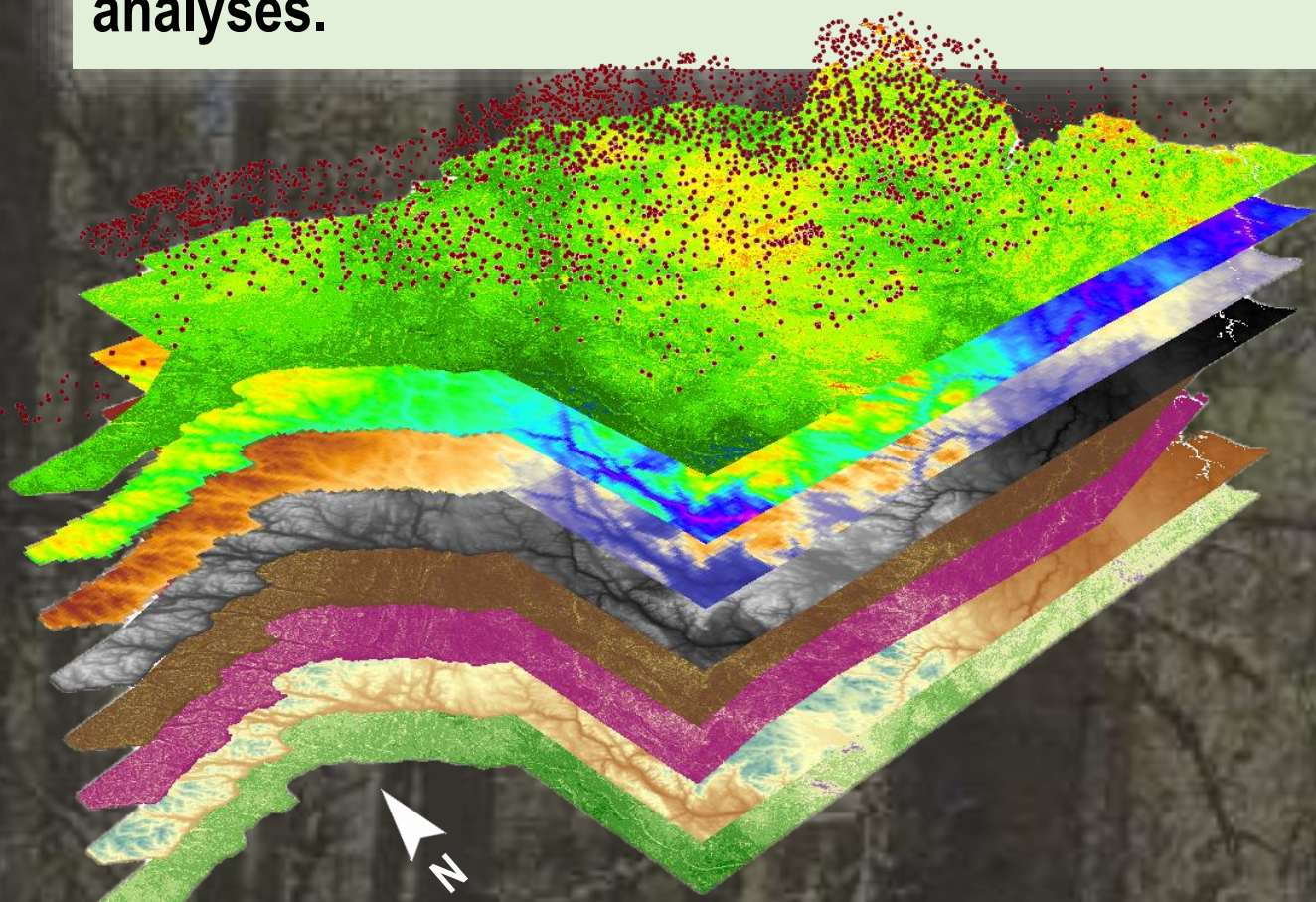


Fig. 2. An example of 2016 L2 raw sample points overlaid with all the other influencing factor layers.

Is Insect population predictable?

To encounter spatial autocorrelation processes in the ecological data, autocovariate regression (AC; [3]) models were fitted for further understanding of impacts from potential factors on L2 population, and to make an effort in forecasting spatial region with higher L2 population. Evidence showed that, compared with OLS models, AC models can reduce spatial dependence in residuals (e.g., Fig.3). Annual AC models can explain 77–82% of the variance in L2 population. Fitted models were also used to predict L2 population in the subsequent years, and the predicted population distribution were compared with the observed ones by interpolated raster layers (Fig.4). Results revealed that predicted distribution is highly correlated with the observed ones in most of years, although the observed L2 declined dramatically in 2018 and the reasons behind remain unknown.

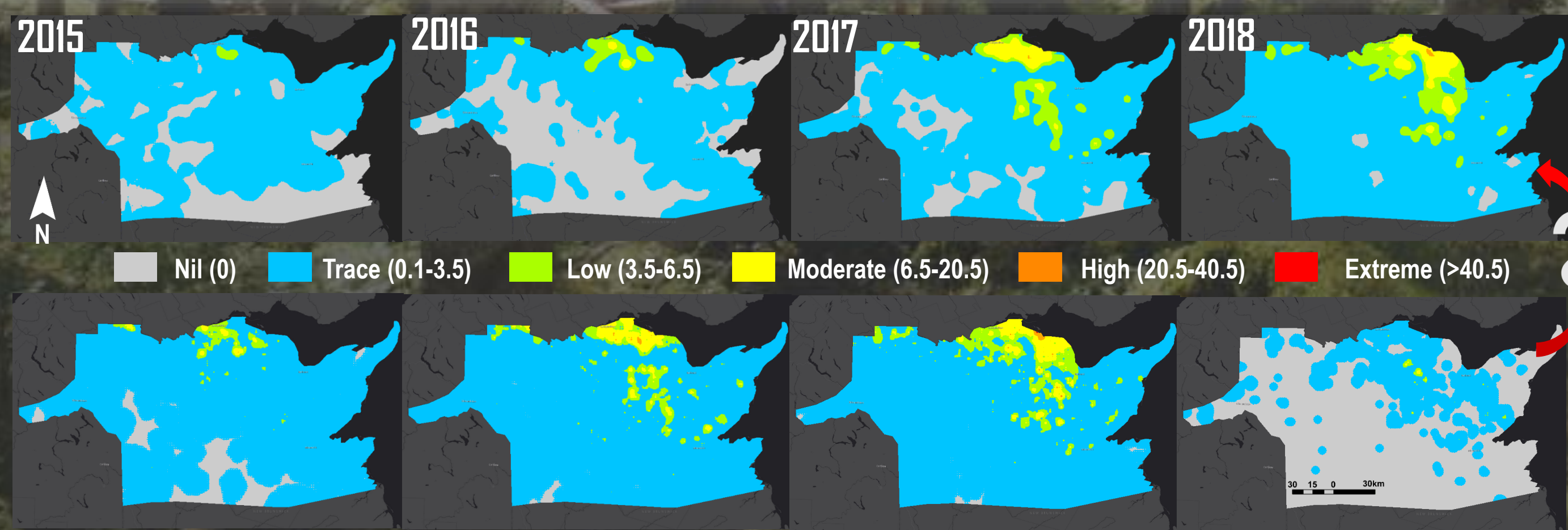


Fig. 4. Comparison between the predicted L2 spatial distribution by annual autocorrelation models and the observed spatial distribution among 4 years. The L2 population has been classified into six levels according to the average L2 per branch.

ACKNOWLEDGEMENTS

This research was funded by the Spruce Budworm Early Intervention Strategy project supported by Atlantic Innovation Fund and Natural Resources Canada. I thankfully acknowledge contributions from my committee members on the project: Dr. David MacLean, Dr. Chris Hennigar and Mr. Jae Ogilvie. I sincerely thank the New Brunswick Natural and Resource Development, Spruce Budworm Early Intervention Strategy Research group, and the Forest Watershed Research Centre at the University of New Brunswick for providing the research data for the first project. I also appreciate the excellent work of all field assistants involved in the data collection for the second project: Shawn Donovan, Sean Lamb, Rebecca Landry, Bo Zhang, Maggie Brewer, Jessica Cormier, Olivia Doran, David Alton, and Kerrstin Trainor.

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Sub-project B → Local Plots

The second study area was in the central Gaspé Peninsula region of Québec (Fig.1). The 57 plots at two sites, Amqui and Causapschal, were measured from 2014 to 2018. Annual defoliation was measured on individual tree within plots by ocular estimation. The area was at the developing stage of the outbreak, and the defoliated area was expanding continuously according to the annual report of SBW infestation in Québec [4]. The objectives were to evaluate spatial patterns of defoliation within plots, and to predict the defoliation on the target balsam fir (*Abies balsamea* L. Mill.) by surrounding trees' characteristics. This part of work has been published recently (i.e., [5]).

Is Defoliation of Individual Trees Clustered?

Global Moran's I analyses [6] were used to determine patterns of defoliation of trees (clustered, dispersed, or random). Results showed 28–47% of plots had significantly clustered defoliation during the 5 years (Table 1), while none of these plots had clustered tree stem distributions based on average nearest neighbor analyses. Plots with clustered defoliation generally had higher mean defoliation per plot and higher deviation of tree defoliation within plots (Fig.5).

Table 1. Number and percentage of plots with significantly clustered tree defoliation, based on global Moran's I analyses among years, all host species included.

Year	2014	2015	2016	2017	2018
Clustered # (%)	27(47)	16(28)	20(35)	17(30)	19(33)

Are There Any Hot or Cold Spot Trees?

At the tree level, 'hot spot trees' (highly defoliated trees surrounded by other highly defoliated trees) and 'cold spot trees' (lightly defoliated trees surrounded by other lightly defoliated trees) were determined within each plot using Getis-Ord G_i^* analysis [7]. Results revealed that plots with severe defoliation generally tended to exhibit cold spots, and plots with light defoliation tended to have hot spots, because whether defoliation was high or low enough to be a hot or cold spot depended on the defoliation level of the entire plot (e.g., Fig 6).

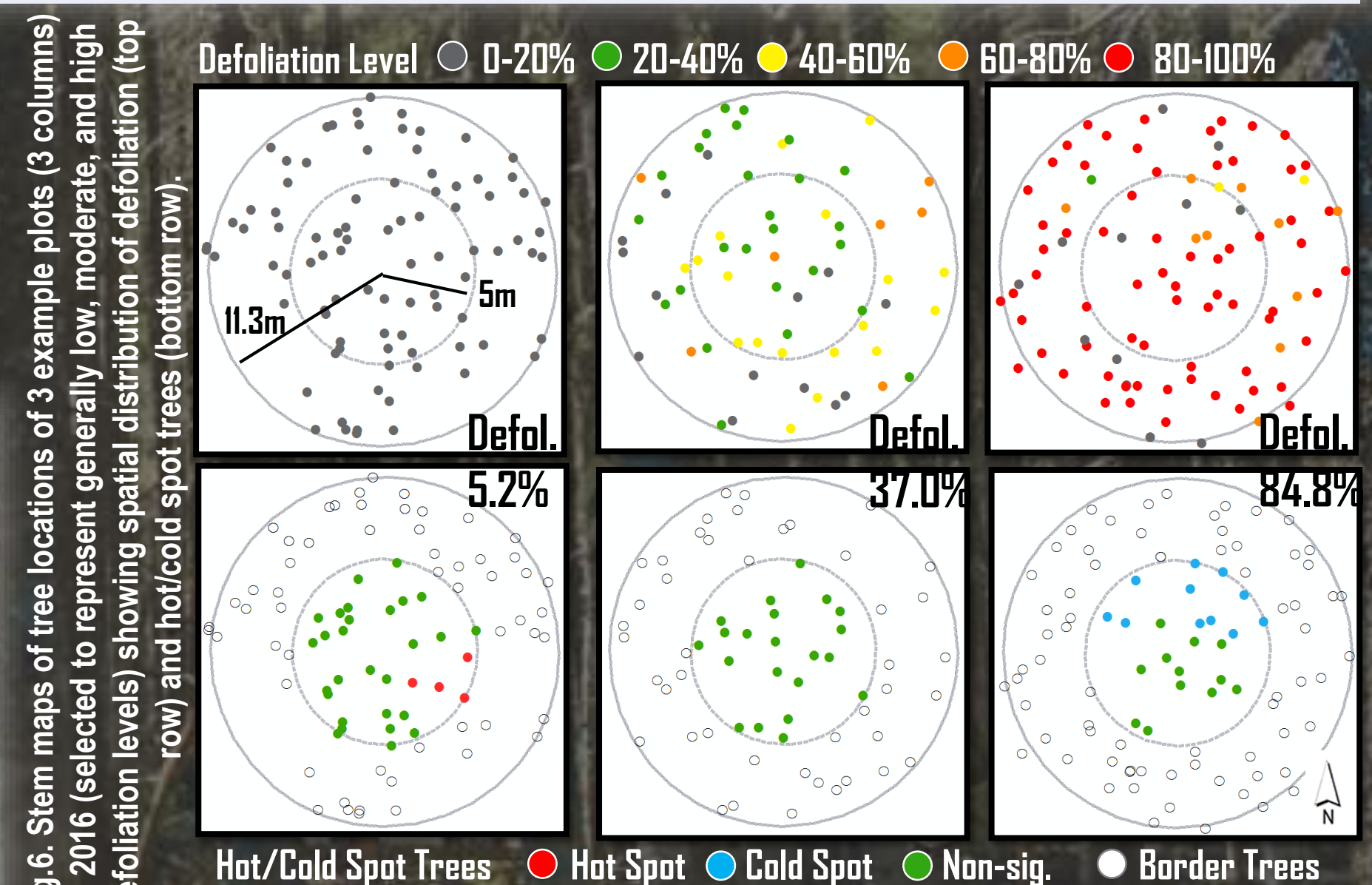


Fig. 6. Stem maps of tree locations of 3 example plots (3 columns) in 2016 (selected to represent generally low, moderate, and high defoliation levels) showing spatial distribution of defoliation (top row) and hot/cold spot trees (bottom row).

Can Subject Tree Defoliation be predicted?

Individual balsam fir defoliation models were fitted as a function of plot and surrounding tree characteristics (using search radii of 3–5 m). The best model contained plot average balsam fir defoliation and subject tree basal area, and these two variables explained 80% of the variance, which was 2–5% higher than the variability explained by the neighboring tree defoliation, over the 3–5 m search radii tested. It was concluded that plot-level defoliation and basal area were adequate for modeling individual tree defoliation, and although clustering of defoliation was evident, larger plots were needed to determine the optimum neighborhood radius for predicting defoliation on an individual.