

VARIATIONS OF SPRUCE BUDWORM BACTERIAL COMMUNITIES OVER THE OUTBREAK LANDSCAPE

ABSTRACT

The eastern spruce budworm (*Choristoneura fumiferana*) is one of the most destructive forest pests in North America. It is a native moth in the Tortricidae family, belonging to the budworms species complex. Its larvae feed on the buds and young leaves of conifers, bringing about massive losses in wood production and harvesting. It belongs in a well-characterized complex food web comprising parasitoid wasps, hyperparasites and many competitors. Like all insects, the spruce budworm's gut contains a diversity of microbial taxa. However, the microbial communities associated with the spruce budworm have not been characterized in depth. The factors influencing those communities and the effects of those communities on the health of the budworm and on its food web have yet to be determined. This project aims to answer those questions and to give a clearer outlook on the spruce budworm microbiome role, composition and temporal evolution. We have one specific objective: determining how the composition of the microbiome of *C. fumiferana* varies depending on host tree and geographical location. Budworms will be sampled throughout the outbreak area in the Cote-Nord and microbial communities will be analyzed by 16S rRNA gene sequencing.

INTRODUCTION



Bacterial communities could have an impact on insect digestion and control agent (Bt) efficiency, so figuring out what drives community composition could be important in controlling outbreaks.

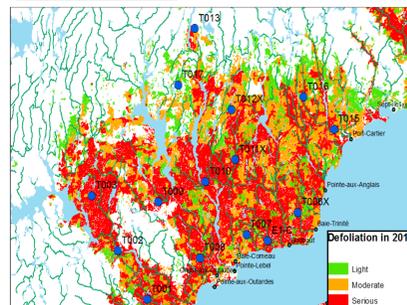
Objective

Determine which spatial factors drive taxonomic diversity in spruce budworm bacterial communities:

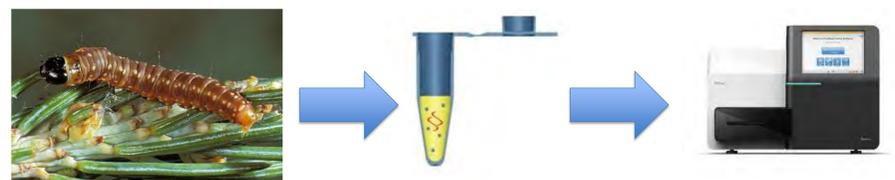
- At what scale (site, tree species, host-tree) is there the most variation?

METHODS

Sampling



Processing

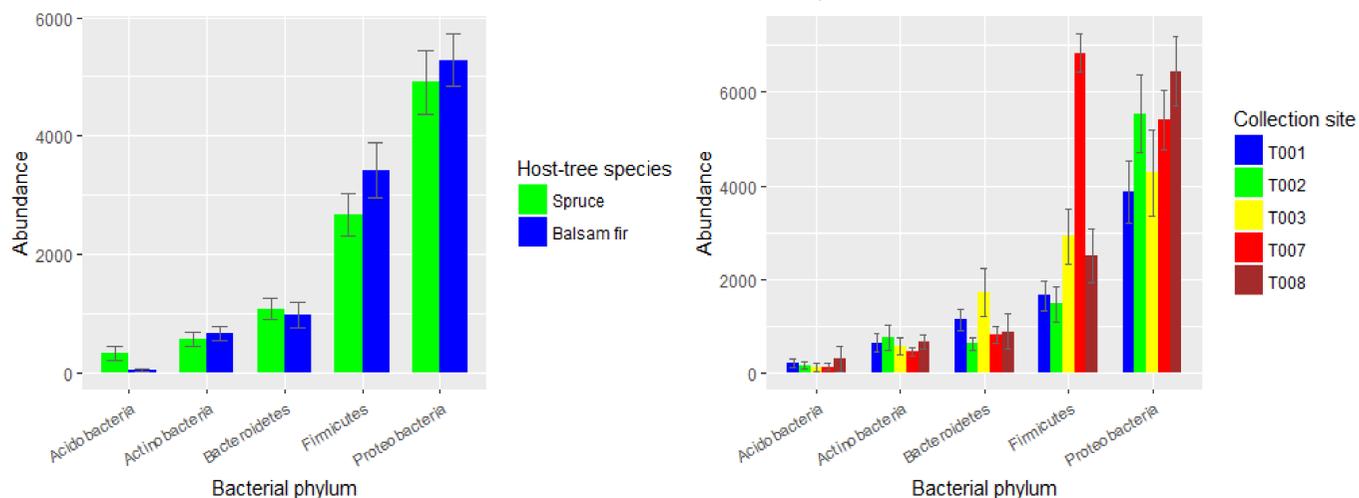


Sequencing of the 16S gene in environmental DNA extracted from larvae

- Extensive sampling area
- 2 host-tree species:
 - *Picea mariana*
 - *Abies balsamea*

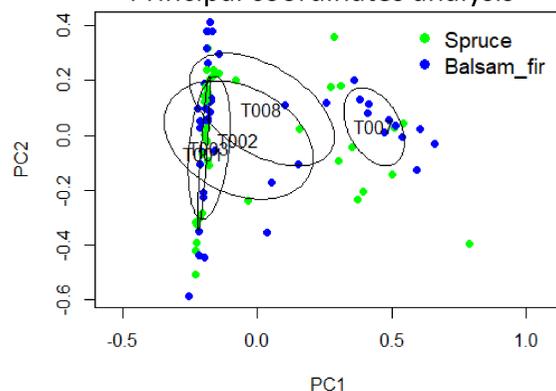
RESULTS

Relative abundance of most important taxa



At the phylum level, communities are very similar between spruce and fir trees, but differences can be seen between different sites.

Principal coordinates analysis



Samples cluster by site, but another factor is also clearly at play. Interestingly, site T007 was sprayed by Bt.

	PERMANOVA	Df	SS	MS	Fmodel	R ²	P-value
Site		4	4.275	1.06865	3.13106	0.13852	0.001
Tree species		1	0.417	0.41654	1.2188	0.01106	0.167
Site*Tree species		4	1.567	0.39174	1.1462	0.04162	0.158
Site*Tree species*Individual trees		20	7.559	0.37797	1.1059	0.20080	0.108
Residuals		55	18.798	0.34178		0.60799	
Total		84	32.615			1	

The only significant factor in our model is the Site, which explains for 13.85% of the variation.

CONCLUSION

We now know that:

- Most variation is between sites
- Bt application could impact the microbiome

Some other questions:

- Which factors (latitude, longitude, defoliation, climate) are responsible for inter-site variation?
- How correlated are the communities of the budworm and of the foliage it is feeding on?