

Using Genomics to Control Spruce Budworm

Spruce budworm (SBW) outbreaks are the major natural disturbance affecting balsam fir stands in Canada. In Eastern Canada, the SBW destroys as many trees as fire. A new epidemic has been causing damage in Eastern Canada since 2006. In fact, areas defoliated by the SBW have been doubling every year, particularly on the North Shore, where 70% of Quebec's defoliated areas are found.

The current strategy for fighting the SBW is essentially aimed at protecting part of the foliage, to keep trees alive during an outbreak. Since the mid-1980s, a biological insecticide, *Bacillus thuringiensis* var. *kurstaki* (B.t.k.) has been used in aerial sprayings.

Here is a look at how the work in forest genomics conducted by the Canadian Forest Service (CFS) aims to overcome some of the limits of this strategy.

Journey into the heart of the genome

How many genes are contained in the SBW genome? Approximately 20,000. In order to develop new pest control products, we have to successfully target the genes that are specific to the budworm. This enormous task, which began in 2010, initially involved collaboration between researchers from Université Laval, the University of Alberta and the CFS. Genomics specialists from McGill University and Centro de Biologia Molecular e Engenharia Genética (Brazil) joined the team later on.

And what if this knowledge about the genome made it possible to increase winter mortality in the SBW? The researchers are exploring this strategy. To do this, they are working to identify the genes responsible for inducing diapause in the SBW. Diapause is a state of profound metabolic slowdown that allows the insect

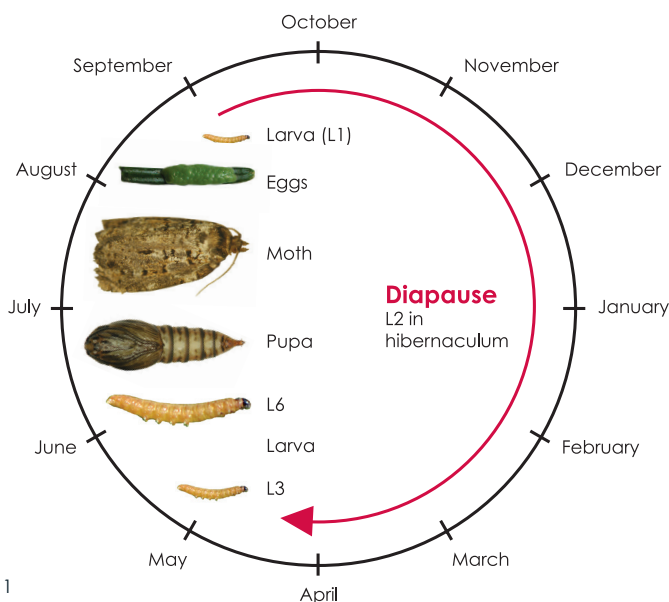


Figure 1
Photos: SOPFIM and NRCan



comparing the expression of all genes in budworms destined to enter diapause with other budworms selected because they "skipped" diapause, researchers are on the verge of identifying the factors that control its onset. There is much to indicate that the process is triggered in the egg stage. Therefore, if effective interventions aimed at blocking entry into diapause take place at the right time, this will lead to high winter mortality.

to live through the winter without feeding. In the SBW, this occurs during the second instar and lasts about 6 months (see Figure 1). By

Improving the arsenal

How do researchers develop new pest control products to target the SBW? The discovery of a gene responsible for the production of an enzyme vital to the insect's development provided them with a new avenue of research. In fact, blocking the activity of this enzyme could lead to severe physiological disturbances. In collaboration with a group from Université Laval, CFS researchers have determined the three-dimensional structure of this enzyme. Knowing this structure will facilitate the development of specific enzyme inhibitors with insecticidal properties.

Another avenue consists in discovering how to prevent the expression of essential genes. To do this, the researchers used a method known as RNAi¹. Here is how this process works. When a gene is "expressed", a copy of the gene is produced as "messenger RNA²". The RNAi destroys some of these RNAs, thereby blocking the expression of the corresponding genes. CFS researchers recently demonstrated that RNAi is effective in the case of the SBW. Work is ongoing to target the most promising genes and to identify a formulation for a sprayable, effective inhibitory substance.



Photo: NRCan

1. RNAi: ribonucleic acid interference.
2. RNA: ribonucleic acid.
3. To find out more: <http://cfs.nrcan.gc.ca/entrepotpubl/pdfs/35580.pdf>.



Photo: NRCan

Long-distance migrators in search of trees

SBW moths are capable of long migratory flights. The impact of their migration on the spread of outbreaks has long been considered as minor. However, CFS researchers suspect that migration plays an important role in this process. When it comes to early intervention (i.e. at the beginning of an outbreak) aimed at limiting damage within a given area³, it will be important to assess the likelihood that migrating moths would invade the area again.

That being said, more information is needed on the migratory movements of the SBW, both in terms of the migrants' origin and distances travelled. Genomics would make it possible to identify the origin of migrants using genetic markers specific to certain regional populations. Using these markers across Canada is currently under study by the CFS.



Photo: NRCan

The question: should we be reactive or proactive?

This work in forest genomics research adds to our knowledge about the SBW and the factors responsible for the onset and spread of outbreaks, and aims to mitigate the economic impacts caused by this major pest.

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