assess the ability of the insect to complete its life cycle on each beech genotype and to quantify the degree of susceptibility of non-resistant individuals. Genomic DNA will be extracted from leaf tissue of the phenotyped progeny to undergo genomic sequencing. The sequence data will then be used to construct a linkage map and perform QTL analysis to identify loci associated with beech bark disease resistance in this family. These loci will be compared against QTLs derived from a previously mapped family (unpublished). A BLAST search will be performed with the identified loci against relevant genomes in an attempt to reveal potential gene function.

While this work is still underway, this research intends to identify additional genomic loci in American beech that contribute to quantitative resistance to beech bark disease.

Knowledge of genomic markers that confer resistance can be used to develop marker assisted selection strategies to identify resistant parents and progeny increasing the efficiency of breeding efforts and accelerating the development of improved seed sources that can be used for reforesting areas affected by beech bark disease. Additionally, understanding the genomic basis of resistance can be used to predict the vulnerability of American beech populations naïve to beech bark disease.

## Exploring genotype-by-environment interactions: impacts on genome-wide association and genomic prediction for 30 white spruce traits related to productivity, defense, and climate-adaptability

Eduardo Pablo Cappa

**Background:**
White spruce (*Picea glauca* (Moench) Voss) is considered a keystone species in boreal forest ecosystems and a valuable resource for the commercial timber industry. White spruce is also known for its adaptability to diverse environments. Understanding the genetic basis of traits related to productivity, growth, and stress resilience is essential, especially in the context of a changing climate. Genome-wide association studies (GWAS) and genomic prediction (GP) are potent tools for understanding complex traits in forest trees. However, their application to genotype-by-environment interactions in white spruce remains limited, highlighting a research gap in forest tree genetics. We conducted a comprehensive multi-environmental GWAS and GP analysis for 30 productivity, defense, and climate-adaptability traits assessed on 1,540 white spruce trees from central Alberta, Canada, genotyped for 467,224 SNP markers, and growing across three environments.

**Methods:**

Multi-environment GWAS was performed to obtain estimates of marker effects, and their associated p-values were obtained by back solving for SNP effects based on the breeding value predictions. A ten-fold cross-validation analysis was conducted on 30 traits using a multi-environment model. Predictive ability (PA) was assessed by correlating predicted breeding values obtained by fitting the full data set with those from validation set values, accounting for narrow-sense heritability, while prediction bias (PB) was determined through regression coefficients.

**Results:**

A total of 563 significant associations (p-value $< 1.07 \times 10^{-05}$) were found across the 30 traits and three environments. Among them, 105 SNPs showed overlapping associations over two or three environments. Wood density, myrcene, total monoterpenes, α-pinene, and catechin had the highest overlap (>50%) across environments. Gas exchange traits, intercellular $CO_2$ concentration, and intrinsic water use efficiency had the highest number of significant associations (>38%), while showing less stability across environments (<1.2%). Among the 30 traits, 20 showed a significantly different PA (0.03-0.41) across environments. Stable carbon isotope ratio had the highest average PA (0.36), while gas exchange traits had the lowest PA (0.07). However, only two traits showed differences in PB across environments. The majority (80%) of the site-trait PB values fell within a narrow range (0.90 to 1.10), indicating low bias across traits and sites.

**Conclusions:**

We demonstrated that the integration of GWAS and GP techniques offers valuable insights into the complex interplay between genotype, phenotype, and environment in white spruce trees grown in central Alberta, Canada.

## Conservation genomics in a pine species: *Pinus chiapensis* (Martínez) Andresen

Karla Vianey Martínez Conde

*Pinus chiapensis* (Martínez) Andresen plays a crucial role in the canopy of Mesoamerican cloud forests. Nevertheless, its conservation status is cause for concern due to its limited genetic variation. Recently, there has been a growing interest in developing strategies and tools for the conservation and sustainable management of *P. chiapensis*. However, the conservation and management of natural resources are intricate processes that necessitate integration of diverse information and analytical tools. Presently, genomic analyses provide insights into the variability and genetic structure of populations and species, aiding in forecasting and detecting signs of local adaptation to environmental