

TFM proposal

Genome sequencing and multiomics integration to study the unknown metabolic pathway leading to the production of the alkaloid boldine in *Peumus boldus*

About the project

We propose to combine newly generated genome sequencing data with multiomics approaches (including transcriptomics, metabolomics, and comparative genomics) to uncover the currently unknown biosynthetic pathway responsible for boldine production in *Peumus boldus*. Publicly available datasets, together with tissue-specific expression profiles, will be used to construct and inspect gene co-expression and metabolite–gene correlation networks to pinpoint candidate structural genes involved in alkaloid formation. In parallel, pathway reconstruction will be guided by genomic context analyses, enzyme family mining, and correlation of gene expression with boldine accumulation across tissues and conditions. The student will be responsible for integrating these datasets, prioritizing candidate enzymes, and helping to assemble a coherent biosynthetic pathway model for boldine, thereby enabling functional validation in future work.

We hope to hear from prospective 1st and 2nd year students looking for a lab to carry out a final year master’s project. Feel free to contact us with any questions you may have!

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