

## TFM proposal

### Using network theory to study non-coding RNA regulation of stilbenoid metabolism in *Vitis vinifera*

#### **About the project**

*Vitis vinifera*, grapevine, is a widely cultivated crop of high industrial importance given its essential role in wine and table grape production. Its rich specialised metabolism is not only an interesting field of study but a source of pharmacological potential as any beneficial effects of wine are often attributed to such compounds. Many land plant species produce phenylpropanoids, which are bioactive compounds related to plant defense and response to stresses and often have potential beneficial health effects in animals given their strong antioxidant activities. Nevertheless, grapevine is one of the few plant species known to produce stilbenoids, a class of compounds that encompass resveratrol and its derivatives or variants. The regulation of stilbenoid metabolism at the transcriptional level has been quite well-studied, by our lab and other labs, however, post-transcriptional regulation has not yet been reported. Preliminary evidence from gene co-expression networks points to a possible role of particular non-coding RNAs in regulating stilbenoid production.

We propose to dissect these potential roles through the study of gene co-expression networks based on the new T2T genome annotation, which includes long non-coding RNAs for the first time. This will require the application of network theory principles, specially regarding modularity, to obtain a broad functional classification of all annotated long ncRNAs. Moreover, transcriptomic data from elicited *in vitro* cultures of grapevine has already been generated in the lab. A reanalysis with the new annotation will be key to determine regulatory candidates. The use of public data will be also encouraged, as well as the improvement of ontology-based automatic classification pipelines of transcriptomic metadata developed by the lab. This is particularly relevant to unlock the possibility of building treatment-specific gene co-expression networks from public data, which will not only be useful for the project but a novelty in grapevine. The student will also have the opportunity to participate in the development of the VitViz module within the [PlantaeViz](#) platform, an omics web portal developed by the lab. Publications are expected by the end of the Master's project.

**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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