

Gonçalo Pereira<sup>1</sup>, João Pereira<sup>1</sup>, Rita B. Santos<sup>1</sup>, Andreia Figueiredo<sup>1</sup>

<sup>1</sup> BioISI - Biosystems & Integrative Sciences Institute, Faculdade de Ciências da Universidade de Lisboa, Lisboa, Portugal

## Background

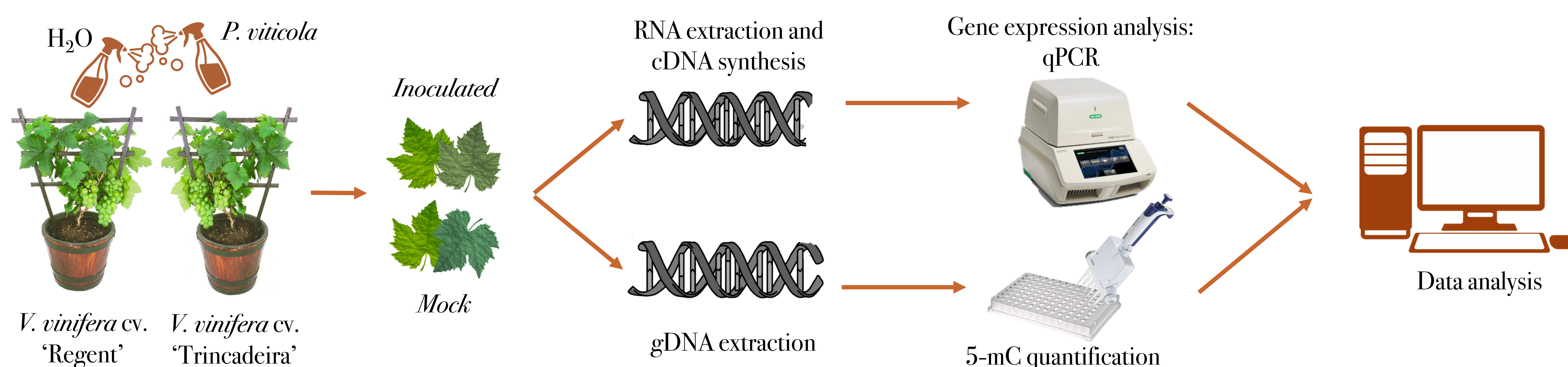
*Vitis vinifera* L. cultivars are of great economic and cultural significance, as they are widely used for wine production across the world. These cultivars are, however, susceptible to many diseases, including downy mildew, caused by the biotrophic oomycete *Plasmopara viticola* (Berk. et Curt.) Berl. & De Toni, leading to significant productivity losses and widespread agrochemical usage<sup>[1]</sup>.

The field of epigenetics deals with the changes that occur at the DNA level that don't alter its sequence but are responsible for shifts in gene expression. Recently, epigenetic changes have linked to plant immunity. Several studies have shown that global genome hypomethylation in cytosine (5-mC) is a common feature of incompatible interactions<sup>[2]</sup>, possibly through the activation of key defence genes that help the plant fend off the infection. Thus, gathering more knowledge in this rapidly-growing field of research could be key to better understand grapevine immunity to *P. viticola*.

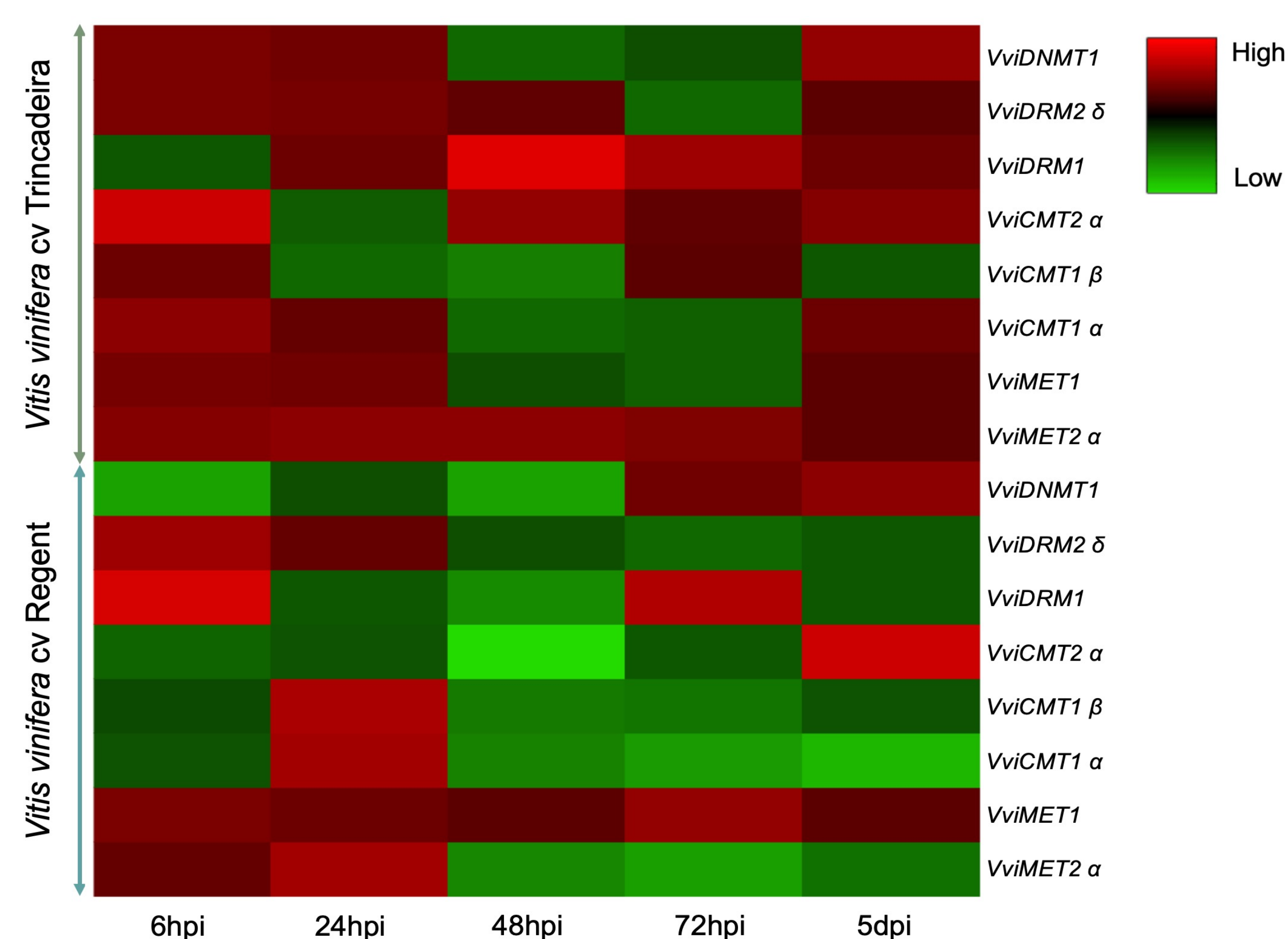
## Main Aim

Establish a connection between **global DNA methylation patterns** and **grapevine resistance to *Plasmopara viticola***, contextualizing it with the **expression of various DNA methyltransferases** during the progression of infection.

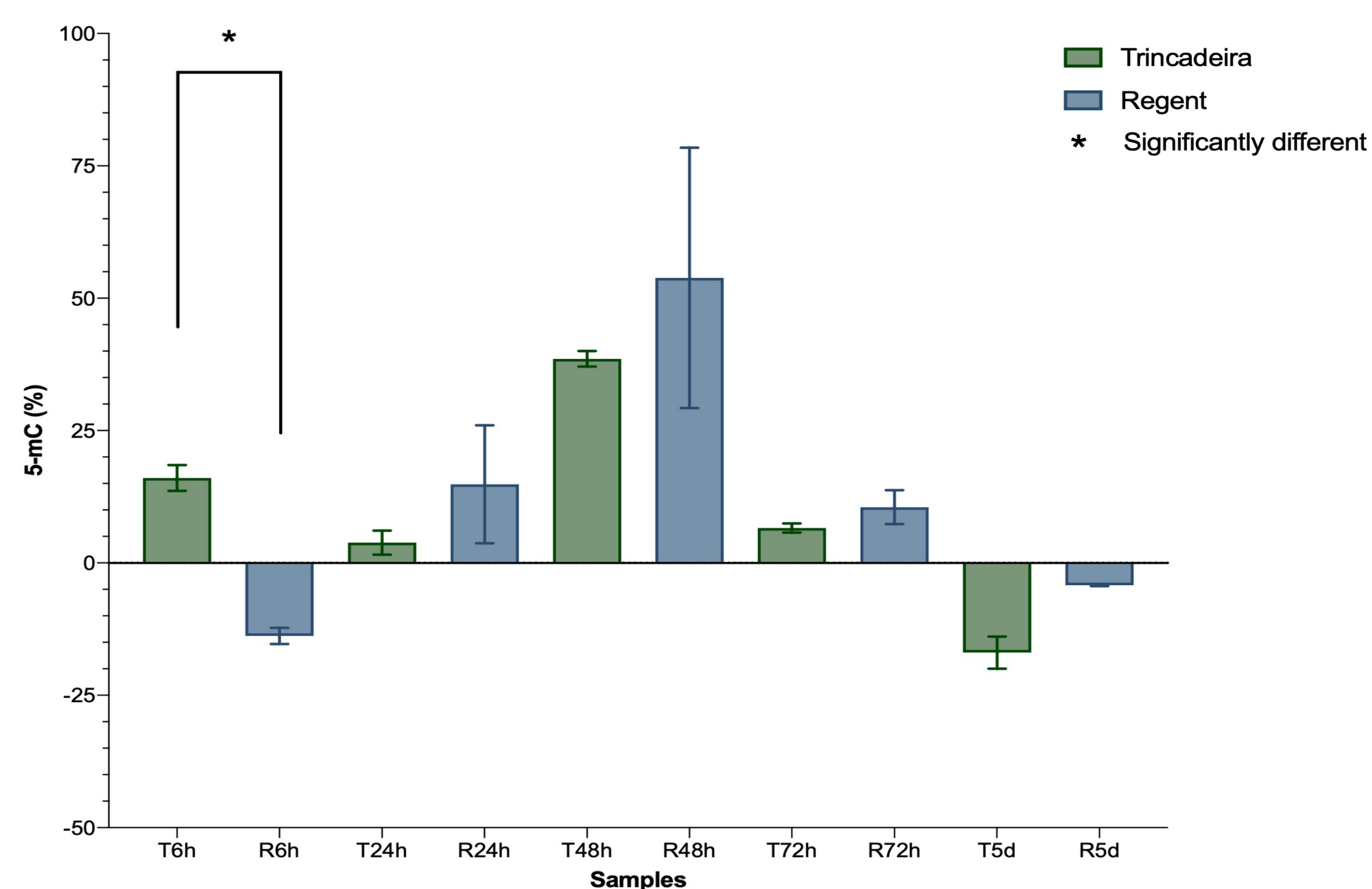
## Materials and Methods



## Results



**Figure 1** - Heatmap of 8 grapevine DNA C5-MTases expression in *V. vinifera* cv 'Regent' and *V. vinifera* cv 'Trincadeira' at 6, 24, 48, 72 hpi and 5 dpi with *P. viticola*. Each column indicates a time-point (6, 24, 48, 72 hpi and 5 dpi) and each row represents a MTase gene in the susceptible grapevine genotype ('Trincadeira') or in the tolerant grapevine genotype ('Regent'). Green indicates low expression levels, red indicates high expression levels. Asterisks (\*) represents significant difference ( $p \leq 0.05$ ) between target and control samples.



**Figure 2** - Global 5-methylcytosine (5-mC) variation between inoculate and mock in *Vitis vinifera* cultivars – 'Trincadeira' (susceptible) and 'Regent' (tolerant) at five different time points (6, 24, 48, 72 hpi, and 5 dpi). Asterisks (\*) represent a significant difference ( $p$  value  $\leq 0.05$ ) between susceptible and tolerant cultivars.

Differences in modulation of DNA MTase gene expression occurs during the infection progression

Hypomethylation occurs in the tolerant cultivar at 6 hpi. The maximum level of DNA methylation occurs at 48 hpi in both genotypes.

## Conclusions

- ✓ 'Trincadeira' 5-mC percentage results, revealed that inoculated samples present **higher methylation than the control samples**. Also, in 'Trincadeira', **DNA methyltransferases genes were mostly up-regulated**;
- ✓ 'Regent' gene expression analysis revealed that both the *CMT* and *DNMT1* genes are the **most down-regulated at both 6 and 48 hpi**, suggesting that the down-regulation of these enzymes **may be associated to the DNA demethylation pattern** observed at 6 hpi and after 48 hpi;
- ✓ Our results suggest that *CMT* and *DNMT1* genes **may be involved in the epigenetic modulation** associated to the establishment of the incompatible interaction.

### Acknowledgements

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### References

- [1] - Buonassisi, Daniele, et al. "Breeding for grapevine downy mildew resistance: a review of "omics" approaches." *Euphytica* 213.5 (2017): 103.
- [2] - Tirmaz, Soodeh, and Jacqueline Batley. "DNA methylation: toward crop disease resistance improvement." *Trends in plant science* 24.12 (2019): 1137-1150.