

## Diversity of leaf functioning under water deficit in a large grapevine panel: high throughput phenotyping and genetic analyses

<u>Eva Coindre</u><sup>1,2\*</sup>, Laurine Chir<sup>2</sup>, Maxime Ryckewaert<sup>3</sup>, Romain Boulord<sup>2</sup>, Mélyne Falcon<sup>2</sup>, Thomas Laisné<sup>2</sup>, Gaëlle Rolland<sup>2</sup>, Maëlle Lis<sup>2</sup>, Llorenç Cabrera-Bosquet<sup>2</sup>, Agnès Doligez<sup>1</sup>, Thierry Simonneau<sup>2</sup>, Benoît Pallas<sup>2</sup>, Aude Coupel-Ledru<sup>2</sup>, Vincent Segura<sup>1,4</sup>

<sup>1</sup> AGAP Institut, Univ Montpellier, CIRAD, INRAE, Institut Agro, Montpellier, France

<sup>2</sup> LEPSE, Univ Montpellier, INRAE, Institut Agro, Montpellier, France

<sup>3</sup> Inria, LIRMM, Univ Montpellier, CNRS, Montpellier, France

<sup>4</sup> UMT Geno-Vigne, IFV, INRAE, Montpellier, France

\*Corresponding author: eva.coindre@umontpellier.fr

## Abstract (250 words)

Water resource is a major limiting factor impacted by climate change that threatens grapevine production and quality. Understanding the ecophysiological mechanisms involved in the response to water deficit is crucial to select new varieties more drought tolerant. A major bottleneck that hampers such advances is the lack of methods for measuring fine functioning traits on thousands of plants as required for genetic analyses. This study aimed at investigating how water deficit affects the trade-off between carbon gains and water losses in a large panel representative of the Vitis vinifera genetic diversity. 250 genotypes were grown under 3 watering scenarios (well-watered, moderate and severe water deficit) in a high-throughput phenotyping platform. To assess traits related to carbon and water functioning on the whole panel, we deployed an original approach where 120 leaves of 40 genotypes were phenotyped combining low-throughput devices to precisely measure ecophysiological traits, as well as innovative, portable high-throughput devices to measure near infrared reflectance, porometry and chlorophyll fluorescence. These data allowed us to build cutting-edge statistical models, such as multiblock models, which jointly use data from different devices, for predicting ecophysiological traits. Models for predicting photosynthesis and transpiration were accurate enough to be applied on the entire panel, only measured with high-throughput devices. Such predictions highlighted a wide range of genotypic variability and contrasting responses to water deficit. Multi-traits and Multi-Environment Genome Wide Association Studies further revealed genomic regions associated with these responses, and underlying candidate genes are being investigated.

**Keywords:** water deficit, high throughput phenotyping, prediction, photosynthesis/transpiration coupling, GWAS.