25èmes rencontres HélioSPIR

Montpellier, 11 & 12 juin 2024

Résumés des communications

Association HélioSPIR
Réseau de spectroscopie proche infrarouge
www.heliospir.net

HelioSPIR est l'association francophone dédiée à la spectrométrie dans le proche infrarouge.

HelioSPIR a vocation à fédérer les scientifiques et les utilisateurs de la technologie SPIR au sein d'un réseau et à promouvoir l'utilisation de la spectroscopie proche infrarouge. Fondée en 2004 autour de la communauté scientifique d'Agropolis à Montpellier, l'association dépasse maintenant les contours de la région Occitanie et de l'hexagone. C'est un pôle de compétences à dimension internationale dans le domaine de la spectroscopie proche infrarouge.

HélioSPIR organise chaque année une ou deux sessions de rencontres scientifiques. C'est un moment privilégié d'échanges autour de diverses thématiques autour de la spectroscopie proche infrarouge et de découverte des derniers travaux de la communauté. C'est également l'occasion de découvrir ou redécouvrir les équipements de spectroscopie et d'imagerie hyperspectrales des principaux fabricants du secteur.

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NIRS as a high-throughput phenotyping tool for assessing the diversity of leaf functioning under water deficit in a large grapevine panel

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***Mots-clefs** : High-throughput phenotyping, Near-infrared spectroscopy (NIRS), PLS Regression, Ecophysiological traits, Water deficit, Model robustness*

Water resource is a major limiting factor impacted by climate change, threatening the yield and quality of grapevine production. Understanding the ecophysiological mechanisms involved in 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 functioning traits on thousands of leaves as required for genetic analyses. Recent studies have highlighted the interest of near-infrared spectroscopy (NIRS) and chlorophyll fluorescence for high-throughput evaluation of leaf functioning traits. The aim of this study is to develop these methods, and test their robustness to facilitate their deployment for phenotyping the genetic diversity of grapevine.

246 genotypes, representative of the genetic diversity of the species Vitis vinifera, were phenotyped over two consecutive years. In 2021, the genotypes were grown in pots outdoors under non-limiting irrigation conditions, while in 2022, the same potted genotypes were subjected to three different water scenarios (i. Well-watered, ii. Moderate water deficit, iii. Severe water deficit) in a greenhouse (PhenoArch high-throughput phenotyping platform).

To evaluate traits related to carbon and water functioning across the entire panel, a subset of genotypes were phenotyped by combining i/ low-throughput devices to precisely measure ecophysiological traits, and ii/ innovative high-throughput portable devices to measure NIRS, porometry and chlorophyll fluorescence. These data enabled the creation of partial least squares regression (PLSR) models using both low- and high-throughput data to predict ecophysiological traits. Leaf mass per area and leaf water content were well predicted by spectrometers ($R^2 > 0.7$). Photosynthesis, on the other hand, was well predicted by chlorophyll fluorescence and porometry data.

The robustness of the predictive models was tested between experiments by comparing models calibrated with data from one experiment to predict data from the second one. The robustness of the models was dependent on the trait and the high-throughput device used. The prediction of leaf mass per area, using NIRS, appeared to be accurate and stable between experiments. Intra-experiment robustness analysis showed that water deficit can impact the quality of trait predictions, particularly those related to water, such as water content and water use efficiency. The R^2 and RMSE parameters provided additional information, especially as water deficit affected trait variability. The prediction of these traits was less accurate when applied on a plant that had been grown under severe water deficit. Compelling models will be employed to predict these traits across the entire panel, enabling their use in genetic analysis.