Title: Reflectance spectroscopy predicts leaf functional traits across wine grape varieties Running Title: Spectral reflectance and leaf economics in wine grapes **Authors Information:** Boya Cui ¹, Rachel Mariani ¹, Kimberley A. Cathline ², Gavin Robertson ², and Adam R. Martin ^{1,*} ¹ Department of Physical and Environmental Sciences, University of Toronto Scarborough, Canada ² Horticultural & Environmental Sciences Innovation Centre, Niagara College, Canada *Corresponding author: adam.martin@utoronto.ca

Summary

- Reflectance spectroscopy has emerged as a powerful tool for non-destructive and high-throughput phenotyping in plants. While the ability of reflectance spectroscopy to predict traits across diverse plant species and ecosystems has received considerable attention, whether or not this technique is able to quantify within species trait variation has not been extensively explored. Quantifying intraspecific variation in traits through reflectance spectroscopy is especially appealing in agroecology, where it may present an approach for better understanding crop performance, fitness, and trait-based responses to environmental conditions.
- We tested if reflectance spectroscopy coupled with Partial Least Square Regression (PLSR) predicts rates of photosynthetic carbon assimilation (A_{max}), Rubisco carboxylation (V_{cmax}), electron transport (J_{max}), leaf mass per area (LMA), and leaf nitrogen (N), across six wine grape (*Vitis vinifera*) varieties (Cabernet Franc, Cabernet Sauvignon, Merlot, Pinot Noir, Viognier, Sauvignon Blanc).
- Our PLSR models showed strong capability in predicting intraspecific trait variation, explaining 55%, 58%, 62%, and 64% of the variation in observed J_{max} , V_{cmax} , leaf N, and LMA values, respectively. However, predictions of A_{max} were less strong, with reflectance spectra explaining only 29% of the variation in this trait.
- Our results indicate that trait variation within species and crops is less well-predicted by
 reflectance spectroscopy, than trait variation that exists among species. However, our
 results indicate that reflectance spectroscopy still presents a viable technique for
 quantifying trait variation in agroecosystems.

Keywords: Agroecology, crop trait, functional trait, high-throughput phenotyping, reflectancespectroscopy.

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Societal Impact Statement

High-throughput phenotyping (HTP) is a key aspect of plant and agricultural science, being applied in crop improvement, crop selection, and in devising farm management strategies. Our research tested the ability of one HTP technique, reflectance spectroscopy, to rapidly and reliably phenotype wine grape varieties. Reflectance spectroscopy predicts important wine grape

leaf traits including photosynthesis and biochemistry with high accuracy, but in a fraction of the time compared to traditional techniques. Reflectance spectroscopy can therefore rapidly characterize wine grape phenotypes, and in doing so, inform predictions of how vines, clones, and varieties will respond to environmental change.

Introduction

In 2022 grape vines were the primary crop on an estimated 6.73 million ha of agricultural land globally, ranking grapes—which includes wine, juice, table, and dried grapes—as the world's 32nd most widespread agricultural crop species (Food & Agriculture Organization of the United, 2024). In this same year, the total economic production value for grapes was estimated at \$85.1 billion USD (Food & Agriculture Organization of the United, 2024), reflecting the high economic importance of this crop, particularly in the world's wine-producing regions of the world (Keller, 2020). In Canada for example, where our research is situated, wine production includes an estimated 12,600 ha of land distributed across 1,700 producers, while contributing ~\$9-11.5 billion to the Canadian economy annually (Hewer & Gough, 2020). However, wine grape production is increasingly being challenged by environmental change including increases in growing season temperatures (e.g., Liles & Verdon-Kidd, 2020), increases in the number of extreme temperature events (e.g., White et al., 2006), reduced water availability (e.g., Santillán et al., 2019), among others (e.g., Wolkovich et al., 2017). Such changes have complex and interacting effects on wine grape physiology, phenology, and growth, and are therefore individually and cumulatively expected to impact the viability and productivity of vineyards globally (reviewed by van Leeuwen et al., 2024). Quantifying and predicting the impacts of global change on wine grape production is therefore of tremendous agronomic and economic importance.

There exist a multitude of approaches for quantifying wine grape responses to abiotic stressors at genetic- through to whole-plant levels of integration (Cramer, 2010; Gambetta et al., 2020), which cumulatively underpin vineyard-scale responses to environmental change (e.g., Bernardo et al., 2018). One approach for understanding and predicting plant responses to environmental change, is through quantification of plant functional traits: the morphological, physiological, or phenological characteristics of plants that are readily measurable at an organismal scale, and influence the performance and response of individuals to environmental

75 changes (Díaz & Cabido, 1997; Lavorel & Garnier, 2002; Westoby & Wright, 2006; Funk et al., 76 2017). Indeed, a considerable amount of effort has been directed towards understanding the 77 extent, causes, and consequences of trait variation among plant species (Reich et al., 1999; 78 Westoby et al., 2002; Diaz et al., 2004; Wright et al., 2004; Wright et al., 2005; Díaz et al., 79 2016). This body of literature has led to a deeper understanding of the key dimensions of 80 functional trait variation that exist among the world's plant species (Díaz et al., 2016; Carmona 81 et al., 2021), and how these traits predict plant environmental responses (Lavorel & Garnier, 82 2002). 83 Among the most well-studied dimensions of trait variation employed to describe and 84 predict plant performance across environmental gradients, and the focus of our research here, is 85 the "Leaf Economics Spectrum" (LES) (Reich et al., 1999; Wright et al., 2004; Wright et al., 86 2005). The LES is a suite of six core leaf traits that covary among plant species including 87 maximum photosynthetic assimilation (A_{max}), leaf dark respiration rate (R_d), leaf nitrogen (N) 88 and phosphorus (P) concentrations, leaf mass per area (LMA), and leaf lifespan (LL). Taken 89 together, LES trait expression defines how species vary across a continuum of life-history 90 strategies, from fast-growing species characterized by rapid return on biomass investment, low 91 structural investment, high leaf nutrient concentrations, and relatively short lifespans on one end, 92 to resource-conserving species expressing the opposite suite of traits and by extension can be 93 more resilient to resource limitation. Variation in LES traits largely owes to evolved trade-offs 94 related to leaf biomechanics (Shipley et al., 2006; Blonder et al., 2011), as well as evolved or 95 plastic variation in physiological and leaf structural traits including stomatal and mesophyll 96 conductance (g_s and g_m, respectively), which in turn influence rates of maximum Rubisco 97 carboxylation (V_{cmax}), and electron transport (J_{max}) (Onoda et al., 2017; Onoda & Wright, 2018; 98 Xiong & Flexas, 2018): two traits that are explicitly important in wine grape responses to 99 temperature change (Greer & Weedon, 2012). 100 Much of the seminal work on trait variation is based on interspecific comparisons, though 101 recent research now focuses on quantifying the extent and ecological implications of 102 intraspecific trait variation (Bolnick et al., 2011; Violle et al., 2012; Siefert et al., 2015; 103 Anderegg et al., 2018; Westerband et al., 2021). Given the role that phenotypic plasticity and 104 inheritable genetic variation play in governing plant ecophysiology and morphology, plant

species can exhibit a high degree of intraspecific variation across a range of traits (Siefert et al.,

2015) and trait dimensions (Isaac et al., 2017; Anderegg et al., 2018). Quantifying intraspecific trait variation is especially critical in agroecosystems such as vineyards, where a relatively small number of plant species or varieties drive rates of ecosystem functioning on account of high abundances (Martin & Isaac, 2015; Milla et al., 2015). Indeed, considerable interest and efforts have been dedicated to quantifying the causes and consequences of intraspecific variation in the traits that are directly responsible for crop growth, survival, and reproduction.

Efforts to comprehensively assess intraspecific trait variation in a given species, especially crops, are often limited at the data collection phase of scientific enquiry (Cadle-Davidson et al., 2019). Traditionally, trait data are collected or derived from a combination of field and laboratory measurements, most of which can be laborious and time-consuming. This is especially true for "hard" traits (sensu Diaz et al., 2004) that are part of the LES such as A_{max} and R_{d} which are generated through point sampling of gas exchange using portable infrared gas analyzers. Furthermore, in wine grapes specifically, V_{cmax} and J_{max} are key parameters in photosynthetic acclimation to increased and extreme temperatures (e.g., Greer & Weedon, 2012). However, these traits that contribute to the physiological basis of crop responses to environmental change rely on the execution and analysis of time-consuming photosynthetic CO_2 response curves $(A-C_i)$ (reviewed by Saathoff & Welles, 2021). These methodological limitations often preclude trait collection across large numbers of vines, motivating the search for techniques capable of supporting high-throughput phenotyping in grapes and other crops (Cadle-Davidson et al., 2019).

Reflectance spectroscopy has emerged as a central component of high-throughput phenotype assessments and related collection of physiological, chemical, and morphological trait data (Fahlgren et al., 2015). While multi- and hyperspectral sensors form a key component of remotely-sensed spectral diversity assessments at ecosystem scales (Asner et al., 2015; Singh et al., 2015; Asner et al., 2016; Chadwick et al., 2020), field-based reflectance spectroscopy offers an opportunity to rapidly amass species- or variety-scale data on leaf physiological, chemical, and morphological traits including those forming the LES (Serbin et al., 2012; Serbin et al., 2014; Kothari et al., 2023). Specifically, using Partial Least Square Regression (PLSR) models (Burnett et al., 2021a), studies have reported strong predictive relationships between reflectance spectra and LES traits including A_{max} , leaf N, LMA, and related physiological parameters

including V_{cmax} and J_{max} (Serbin et al., 2014; Dechant et al., 2017; Doughty et al., 2017; Lamour et al., 2021).

Spectroscopy coupled with PLSR models has been successful in estimating plant traits, particularly when using multi-species datasets that present a wide range of trait values and spectral profiles (Serbin et al., 2014; Ely et al., 2019; Lamour et al., 2021). More recently, studies have begun employing these techniques to quantify and predict finer-scale intraspecific trait variation (Vasseur et al., 2022), including trait variation across individuals or genotypes of the same crop species (Heckmann et al., 2017; Yendrek et al., 2017; Silva-Perez et al., 2018; Meacham-Hensold et al., 2019; Fu et al., 2020; Burnett et al., 2021b). Analyses on intraspecific trait variation—where trait values and spectra are more constrained—are less common vs. studies analyzing trait values and spectral signatures from a number of species differing in lifehistory strategies (Serbin et al., 2014; Lamour et al., 2021) or agronomic profiles (Ely et al., 2019). Furthermore, studies using reflectance spectroscopy to detect intraspecific trait variation in crops, commonly screen plants from a range of managed environmental conditions, which further contributes a wider range of trait values (Yendrek et al., 2017). While these results are promising, there remains uncertainty regarding whether or not these techniques are able to differentiate LES traits across individuals or genotypes of the same species, in agroecosystems where environmental conditions are more homogeneous.

In grape and wine science spectroscopy has long been an important method for rapidly assessing berry composition and quality (Gishen et al., 2005). There also exists a small number of studies applying reflectance spectroscopy to quantifying leaf trait variation in wine grapes (e.g., De Bei et al., 2011; Diago et al., 2013). Though to our knowledge, studies evaluating whether or not this high-throughput technique is capable of quantifying the variation in leaf traits that exists among wine grape varieties, are absent from the literature. Our study therefore aims to contribute to the literature on high-throughput assessments of intraspecific trait variation, by evaluating the potential of reflectance spectroscopy to predict LES trait variations across multiple wine *V. vinifera* varieties. In this study we specifically ask: can reflectance spectroscopy reliably and rapidly estimate leaf functional traits in six of the world's most widely cultivated wine grape varieties?

Materials and Methods

168 Study site

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169 We collected LES and related trait and spectral reflectance data for six of the most 170 common wine grape varieties—Cabernet Franc, Cabernet Sauvignon, Merlot, Pinot Noir, 171 Sauvignon Blanc, and Viognier—at the Niagara College Teaching Vineyard, Niagara-on-the-172 Lake, Ontario, Canada (43.1522° N, 79.1652° W). The site is an operational vineyard is situated 173 in Canada's largest wine-producing province (Hewer & Gough, 2020), characterized as non-174 irrigated, with imperfectly drained silty clays overlaying clay loam, till mixed with poorly 175 drained lacustrine heavy clay, and uniformly tilled and sprayed (Macklin et al., 2022; Martin et 176 al., 2022). All trait and reflectance data were collected during the fruit setting stage (at our site, 177 from June 6-17, 2022) between 6:00-12:00. For each variety, we sampled 30 vines evenly 178 distributed across three planting rows, which were roughly 10 meters apart from each other 179 within one row, totalling n=180 individual vines. One leaf on each vine was selected from the 180 uppermost segment of the individual for data collection, with all leaves being fully exposed, 181 newly developed, fully expanded, and free of any damage (Perez-Harguindeguy et al., 2016). 182 183 Functional trait data collection 184 Trait data in our study included A_{max} , V_{cmax} , and J_{max} , leaf N concentrations, and LMA. 185 First, V_{cmax} , J_{max} , and A_{max} data were collected in the field using a LI-6800 Portable 186 Photosynthesis System (Licor Bioscience, Lincoln, Nebraska, USA). We first performed an $A-C_i$ 187 curve on each leaf using the Dynamic Assimilation Technique (DAT) (Saathoff & Welles, 2021; Gregory et al., 2023; McClain & Sharkey, 2023) in order to estimate rates of $V_{\rm cmax}$ and $J_{\rm max}$. For 188 each curve, CO₂ assimilation rates on a per leaf area basis (A_{area}; µmol CO₂ m⁻² s⁻¹) were logged 189 190 every four seconds across continuously ramping CO₂ concentrations, with a ramp rate of 100 μmol mol⁻¹ min⁻¹ (consistent with recommendations by Stinziano et al., 2019; McClain & 191 Sharkey, 2023) beginning at 5 μ mol mol⁻¹ CO₂ and concluding at 1700 μ mol mol⁻¹ CO₂. 192 193 Otherwise, conditions in the leaf chamber were set to a photosynthetic photon flux density (PPDF) of 1500 µmol m⁻² s⁻¹ of photosynthetically active radiation (PAR; 400-700 nm), 50% 194 195 relative humidity, leaf vapour pressure deficits of 1.7 KPa, and leaf temperatures of 25°C.

Furthermore, CO₂ and H₂O sensors were readjusted using the range match function after every

five leaf measurements, and each DAT $A-C_i$ curve required approximately 10 minutes, including

a 60-120 second acclimation period (Saathoff & Welles, 2021). Following the completion of each A- C_i curve, we then allowed leaves to acclimate to ambient conditions for ~10 minutes. Then, we collected steady-state $A_{\rm max}$ values for each leaf at the same environmental conditions as mentioned above with a constant CO_2 concentration at 420 ppm which matched current ambient levels. We logged steady-state gas $A_{\rm max}$ values after leaves were allowed to stabilize for 5-10 minutes.

Immediately following gas exchange measurements, we used an HR1024i full spectrum portal field spectroradiometer (Spectra Vista Corporation, Poughkeepsie NY, USA) to collect reflectance spectra for each leaf. This instrument is a full-range spectroradiometer (350-2500 nm) with a spectral resolution of \leq 3.5 nm (350-1000 nm), \leq 9.5 nm (1000-1800 nm), and \leq 6.5 nm (1800-2500 nm), outfitted with an LC-RP Pro leaf clip that includes a calibrated internal light source. Reflectance spectra were collected at the same location on the adaxial side of each leaf from which A-C_i and steady state gas exchange were performed, with integration times set to two seconds, and reference spectra taken on a white Spectralon standard prior to each measurement.

Once physiological and reflectance data were acquired, we collected and transported individual leaves to the University of Toronto Scarborough for quantification of LMA and leaf N concentrations. First, we removed all petioles, and the fresh area of all leaves was quantified using an LI-3100C leaf area meter (Licor Bioscience, Lincoln, Nebraska, USA), and then dried for 48 hours to constant mass. Dried leaves were then weighed and LMA was calculated as mass/area. Finally, dried leaves were ground to a fine and homogeneous powder using a MM400 Retsch ball mill (Retsch Ltd., Hann, Germany), and a LECO CN 628 elemental analyzer (LECO Instruments, Ontario, Canada) was used to determine leaf N concentrations on ~0.1 grams of powdered tissue.

Data analysis

We used R statistical software v. 4.2.0 (R Foundations for Statistical Computing, Vienna, Austria) for all data analysis. First, we fit the Farquhar, von Caemmerer and Berry (FvCB) model to each individual A- C_i curve, using the 'fitaci' function in the 'plantecophys' R package (Duursma, 2015), in order to estimate rates of $V_{\rm cmax}$ and $J_{\rm max}$, along with their standard errors. These FvCB models were fit using non-linear least square regression (Duursma, 2015), such that $V_{\rm cmax}$ and $J_{\rm max}$ were corrected to 25°C, and $V_{\rm cmax}$ and $J_{\rm max}$ are considered apparent as mesophyll

conductance was assumed to be infinite. These data were merged with other traits, and the distribution of each individual trait was assessed using the 'fitdist' function in the 'fitdistrplus' R package (Delignette-Muller & Dutang, 2015). Traits were determined to be either normally or log-normally distributed (as per the highest log-likelihood value) and transformed data was employed in further analyses in accordance with these results. We then performed an analysis of variance (ANOVA) to test for significant trait differences across varieties.

We then followed the methods described by Burnett et al. (2021a) to evaluate how reflectance spectra predicted trait values across our dataset, using a PLSR modelling approach. All PLSR models included reflectance spectral data from the 500-2400 nm wavelength range and aimed to predict either non-transformed or log-transformed trait data, as informed by our distribution fitting procedure. For each PLSR model, the spectra-trait dataset was split into a calibration dataset (which included 80% of all data points) and a validation dataset (comprised of the remaining 20% of data). Since we were explicitly interested in testing the ability of reflectance spectra to quantity variation in leaf traits across grapes broadly, and the ability to differentiate varieties, we performed and analyzed two data splits. First, datasets were split into calibration vs. validation according to variety identity, such that both the validation and calibration datasets had approximately equal proportions of trait and spectra data from all varieties. Second, we used a completely randomized data split, whereby the proportion of data across varieties was allowed to vary randomly.

Using the calibration datasets, we then used the 'find_optimal_components' function in the 'spectratrait' R package (Lamour & Serbin, 2023) to determine the optimal number of components used in the final PLSR model, based on the minimization of the prediction residual sum of squares (PRESS) statistic. For each trait, a PLSR model was fitted from the calibration dataset using the leave-one-out cross-validation (LOO) procedure, specified with the 'plsr' function in the 'plsr' R package (Liland et al., 2022). Model performance was then assessed with the validation datasets as an external validation, in which the predicted values and the observed values in the validation dataset were compared. For the final models, we used the validation coefficient of determination (r^2), root mean squared error of prediction (RMSE), and percent root mean squared error of prediction (%RMSE) as metrics to illustrate model fits.

To further evaluate the model performance, we used the model coefficients and variable influences on projection (VIP) values to explore the effect of different areas of the spectra on

predicting the trait variable. Following this, we performed a jackknife permutation analysis to assess model uncertainty, using the jackknife argument of the 'plsr' function in the 'plsr' R package (Liland et al., 2022). The resulting jackknife coefficients were then compared to that of the full model. And finally, using the full model and jackknife permutation outputs, the mean, and 95% confidence and prediction intervals were calculated for each predicted trait value from the validation dataset.

Results

Reflectance spectroscopy for predicting within-variety leaf traits

Leaf traits measured here all varied significantly as a function of variety identity (p<0.001 in all cases). Specifically, across the entire dataset, physiological traits were most variable, with A_{max} ranging from 3.8-29.0 μ mol CO₂ m⁻² s⁻¹ (CV=34.8), V_{cmax} from 28.9-131.7 μ mol m⁻² s⁻¹ (CV=27.5), and J_{max} from 60.3-253.1 μ mol m⁻² s⁻¹ (CV=25.8). In comparison, LMA and leaf N also varied significantly across varieties, though these traits were less variable with LMA ranging from 52.8-101.8 g m⁻² (CV=12.8) and leaf N from 2.04-4.39% (CV=13.7). All reflectance spectra presented generally the same shape, with a few Cab. Franc individuals situated closer to the lower range, Merlot and Pinot Noir closer to the upper range, and others in and around the 95% confidence interval (Figure 1).

When calibration vs. validation data were evenly split across varieties (i.e., 80% of each variety allocated to each dataset), reflectance spectra and PLSR models explained between 18-64% of the variation in wine grape traits (Table 1, Figure 2). Specifically, physiological traits including A_{max} , J_{max} , and V_{cmax} were predicted by 4-5 spectral components which cumulatively explained 18%, 44%, and 30% of the variation in these traits, respectively. In these cases, model %RMSE values ranged from 21.6% in A_{max} models, 24.1% in V_{cmax} models, and 18.9% in J_{max} models. Comparatively, reflectance spectra and PLSR models expressed stronger predictive ability towards log-LMA and leaf N, with models (r^2) explaining 64% (%RMSE=14.3) and 62% (%RMSE=15.2%) of the variation, respectively (Table 1, Figure 2).

The predictive power of PLSR models was sensitive to the configuration of calibration and validation datasets, though general trends were nuanced. When calibration and validation datasets were comprised of varieties in random proportions, physiological traits were better predicted than in datasets where variety proportions were equal. Specifically, in randomized data

splits, A_{max} model r^2 =0.29, V_{cmax} r^2 =0.58, and J_{max} r^2 =0.55, all of which were higher vs. the same models in variety-weighted data splits. Alternatively, PLSR models for log-LMA and leaf N had lower predictive power when calibration and validation datasets were randomly created, with r^2 values of 0.53 and 0.5, respectively (Table 1, Figure 2). In all cases, the number of spectral components retained in the final PLSR models also differed depending on the nature of calibration and validation dataset construction.

The impact of the data splitting method is also observed in the model regression coefficient trends, which reflect the contribution of certain wavelengths to trait prediction. For physiological traits, the shapes of regression coefficient trends are similar within the same splitting method, but distinctly different between splitting methods (Figure 3). Here we ignore the random split model of A_{max} from this comparison, due to its limited number of model components. On the other hand, splitting data randomly or proportionally across varieties did not influence the regression coefficient distributions of log-LMA or leaf N (Figure 3). VIP scores of the models suggest similar wavelength regions of importance for model prediction across different traits, regardless of data splitting methods (Figure 4).

Discussion

Our findings contribute to the growing literature that reflectance spectroscopy is well-equipped to detect trait variation within and among plant species (Serbin et al., 2014; Ely et al., 2019; Serbin et al., 2019; Burnett et al., 2021b; Lamour et al., 2021; Vasseur et al., 2022; Kothari et al., 2023). A considerable proportion of earlier work in this area focused on quantifying the interspecific trait variation that exists among plants of different functional types, that differ widely their evolutionary histories and trait diversity (e.g., Serbin et al., 2014; Kothari et al., 2023). To this end, previous studies have indicated that reflectance spectroscopy is better equipped to explain trait variation, in situations where trait values within calibration and validation datasets vary more widely (Lamour et al., 2021). This tendency positions these techniques for rapid trait estimation in natural ecosystems (Asner et al., 2016), with many such studies reporting a high predictive ability of PLSR models in quantifying interspecific trait variation. Though a recent renewed focus on the importance of intraspecific trait variation in driving ecosystem functioning (Siefert et al., 2015; Westerband et al., 2021), along with

applications of these techniques in agroecology, necessitates quantifying and disentangling the drivers of finer-scale trait variation that generally exists within species (Martin & Isaac, 2015).

In this regard, our results show the strong predictive power of PLSR models to capture between 50-64% of the within-species trait variation in wine grapes, for key LES and related traits including $V_{\rm cmax}$, $J_{\rm max}$, log-LMA, and leaf N (Table 1, Figure 2). Previous studies that examined within-species trait variation using PLSR approaches have yielded broadly similar results. For example, Meacham-Hensold et al. (2019) reported PLSR models that explained 60%, 59%, and 83% of the variation in $V_{\rm cmax}$, $J_{\rm max}$, and leaf N, respectively, across six tobacco (*Nicotiana tabacum*) genotypes, though when three additional genotypes and larger sample sizes were included in analyses, these PLSR model r^2 values increased to 0.61 for $V_{\rm cmax}$, and 0.62 for $J_{\rm max}$ in the validation dataset. Similarly, Fu et al. (Fu et al., 2020) modelled photosynthetic traits of six tobacco genotypes using PLSR methods, and reported similar r^2 values (0.60 and 0.56) for $V_{\rm cmax}$ and $J_{\rm max}$, respectively.

Other single-species studies that applied reflectance spectroscopy and PLSR models to predict leaf traits across experimental treatments or environmental gradients have also presented similar results. For example, Yendrek et al. (2017) found reflectance spectra were strong predictors of leaf N (r^2 = 0.92-0.96) and $V_{\rm cmax}$ (r^2 =0.56-0.65) of maize ($Zea\ mays$) genotypes grown across gradients of ozone and soil N availability. Finally, in an analysis that screened over 200 genotypes of wheat ($Triticum\ aestivum$, $T.\ turgidum$, and triticale germplasm) from six sets of experiments, Silva-Perez et al. (2018) included detected high predictive power of PLSR models, with r^2 values ranging from 0.70-0.89 for leaf N, LMA, $V_{\rm cmax}$, and $J_{\rm max}$. Though in this same experiment, consistent with our results, CO₂ assimilation rates were relatively poorly captured by PLSR models: in our analysis, the r^2 for models for $A_{\rm max}$ were 0.18-0.29, vs. r^2 values of 0.49 in Silva-Perez et al. (2018).

In addition to model diagnostics alone, in our analysis PLSR models generally support the same inferences surrounding the comparative trait biology of wine grape varieties (relative to observed trait data). Specifically, our previous analysis of LES trait variation—with trait data observed in the field using traditional gas exchange and analytical chemistry techniques—found that white grape varieties Sauvignon Blanc and Viognier occupy the "resource-acquiring" end of an intraspecific LES in wine grapes (characterized by high rates of A_{max} , V_{cmax} , J_{max} , leaf N, and low LMA), while red varieties (Cabernet Franc, Cabernet Sauvignon, Merlot) define the

"resource-conserving" end of the wine grape LES (characterized by low A_{max} , V_{cmax} , J_{max} , leaf N, and high LMA). Our PLSR models support this same general trend (Figure 1), with white varieties expressing predictions that indicate resource-acquiring trait values.

Quantifying functional trait variation across the wide diversity of wine grapes is challenging, with estimates suggesting there exist anywhere between 6,000-10,000 varieties *Vitis vinifera* subsp. *vinifera* worldwide. In turn, ~1,100 of these varieties are cultivated solely for wine production, though recent data suggests the genetic diversity being planted on vineyards is narrowing considerably, with ~12 "international varieties" now comprising up to 70-80% of vineyards in prominent wine-growing nations (Wolkovich et al., 2018). Reflectance spectroscopy therefore representing one potential avenue for quantifying this wide phenotypic diversity, and in turn, meeting a pressing need for high-throughput techniques able to quantify the traits that underpin wine grape responses to environmental change (Cadle-Davidson et al., 2019).

To this end, our analysis contributes evidence that reflectance spectroscopy and PLSR modelling approaches can be used to 1) directly predict intraspecific trait variation with a relatively high degree of accuracy in wine grapes, and 2) differentiate intraspecific variation in life-history strategies in across grape varieties. Though our analysis here is based on a small subset of the 1,000s of wine grape varieties that exist globally (Wolkovich et al., 2018), expanding this work to include a greater number of wine grape genotypes and traits such as those associated with drought tolerance (De Bei et al., 2011; Silva-Perez et al., 2018), presents a viable opportunity to more rapidly screen trait expression in one of the world's most economically important crops.

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383 **Author Contributions** 384 B.C. and A.R.M. planned and designed the research; A.R.M., B.C., and R.O.M. 385 performed field and lab analyses; B.C. performed statistical analyses; B.C. and A.R.M. wrote the 386 draft manuscript; R.O.M., G.R., and K.C. edited the manuscript; K.C, G.R., and A.R.M. secured 387 funding related to this research. 388 389 **Data Availability Statement** 390 Functional trait data employed in this analysis are available through the TRY Functional 391 Trait Database. Furthermore, raw spectral reflectance data, PLSR models, and functional trait 392 datasets are also available upon request to the corresponding author. 393 394 **Conflict of Interest Statement** 395 The authors declare no conflicts of interest. 396 397 References 398 Anderegg LD, Berner LT, Badgley G, Sethi ML, Law BE, HilleRisLambers J. (2018). Within-399 species patterns challenge our understanding of the leaf economics spectrum. Ecology 400 Letters **21**(5): 734-744. 401 Asner GP, Knapp DE, Anderson CB, Martin RE, Vaughn N. (2016). Large-scale climatic and 402 geophysical controls on the leaf economics spectrum. Proceedings of the National 403 Academy of Sciences 113(28): E4043-E4051. 404 Asner GP, Martin RE, Anderson CB, Knapp DE. (2015). Quantifying forest canopy traits: 405 Imaging spectroscopy versus field survey. Remote Sensing of Environment 158: 15-27. Bernardo S, Dinis L-T, Machado N, Moutinho-Pereira J. (2018). Grapevine abiotic stress 406 407 assessment and search for sustainable adaptation strategies in Mediterranean-like 408 climates. A review. Agronomy for Sustainable Development 38(6): 66. 409 Blonder B, Violle C, Bentley LP, Enquist BJ. (2011). Venation networks and the origin of the 410 leaf economics spectrum. Ecology Letters 14(2): 91-100. 411 Bolnick DI, Amarasekare P, Araújo MS, Bürger R, Levine JM, Novak M, Rudolf VH, Schreiber 412 SJ, Urban MC, Vasseur DA. (2011). Why intraspecific trait variation matters in 413 community ecology. Trends in Ecology & Evolution 26(4): 183-192. 414 Burnett AC, Anderson J, Davidson KJ, Ely KS, Lamour J, Li Q, Morrison BD, Yang D, Rogers 415 A, Serbin SP. (2021a). A best-practice guide to predicting plant traits from leaf-level 416 hyperspectral data using partial least squares regression. Journal of Experimental Botany 417 **72**(18): 6175-6189.

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Tables and Figures

Table 1. Partial least squares regression model fits evaluating the ability of reflectance spectra to explain variation in leaf traits measured on six wine grape varieties. Presented here are results from two different modelling approaches which divide our total sample into calibration (80% of our data) vs. validation (20% of our data) datasets. In the results associated with the "Variety" approach, calibration and validation data both included approximately the same proportions of observations from all varieties, while the "Random" approach made this division randomly. Here, $n_{\rm obs}$ refers to the total observations in our dataset for a given trait, which entails a corresponding sample size in the validation dataset ($n_{\rm val}$). For each model, we present the number of components derived from reflectance spectra that were included in the final predictive model ($n_{\rm comp}$), along with the root mean square error (RSME), r^2 value, and %RMSE for the final predictive model. All models were based on Trait acronyms as follows: light saturated photosynthetic rate ($A_{\rm max}$), maximum velocity of Ribulose 1,5-bisphosphate (RuBP) carboxylation ($V_{\rm cmax}$), maximum rate of electron transport ($J_{\rm max}$), leaf mass per area (LMA), leaf nitrogen (N) concentration.

Data split	Trait	$n_{ m obs}$	$n_{ m val}$	$n_{\rm comp}$	RMSE	r^2	%RMSE
Variety	A_{\max}	178	36	4	3.9	0.18	21.63
	$V_{ m cmax}$	177	36	5	14.62	0.3	24.1
	$J_{ m max}$	177	36	4	24.22	0.44	18.88
	log-LMA	178	36	10	0.08	0.64	14.27
	Leaf N	176	36	9	0.25	0.62	15.16
Random	A_{\max}	178	36	1	4.42	0.29	19.25
	$V_{ m cmax}$	177	36	9	14.47	0.58	15.6
	$J_{ m max}$	177	36	8	28.35	0.55	15.6
	log-LMA	178	36	13	0.08	0.53	16.44
	Leaf N	176	36	11	0.33	0.5	15.92

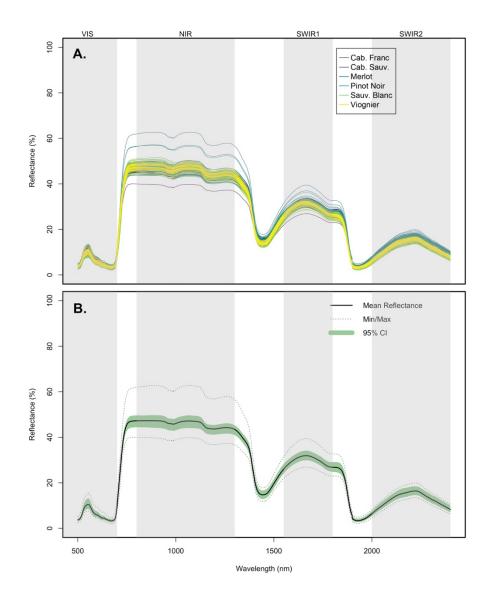


Figure 1. Reflectance spectra of 179 wine grape leaves plotted A) individually with six wine grape varieties specified, and B) all together with mean, range, and 95% confidence interval estimates. All spectral data were trimmed to the 500-2400 nm range where the PLSR models were built from. The grey shaded areas indicate different spectral regions: Visible Spectrum (VIS), Near Infrared (NIR), Short Wave Infrared 1 (SWIR1), and Short Wave Infrared 2 (SWIR2).

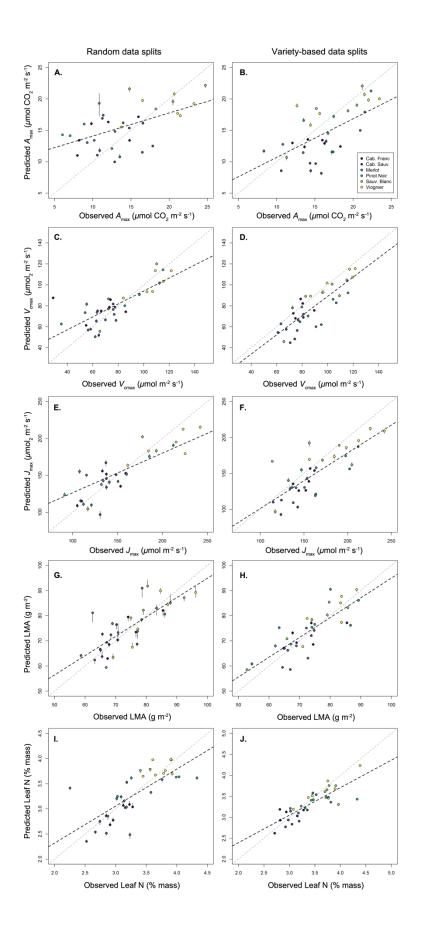


Figure 2. Results of partial least squares regression (PLSR) models predicting leaf physiological, chemical, and morphological traits in six wine grape varieties. Shown here are the data points used to validate the models (n=36 in all cases) fitted to a set of calibration data points (n=140-142; see Table 1). Calibration and validation datasets were selected on the basis of a fully randomized data split (left panels), and a data split where all six varieties were equally represented in the calibration datasets (right panels). Dashed black lines represent linear model fits between observed vs. expected trait values, while the dotted gray lines represent a 1:1 relationship.

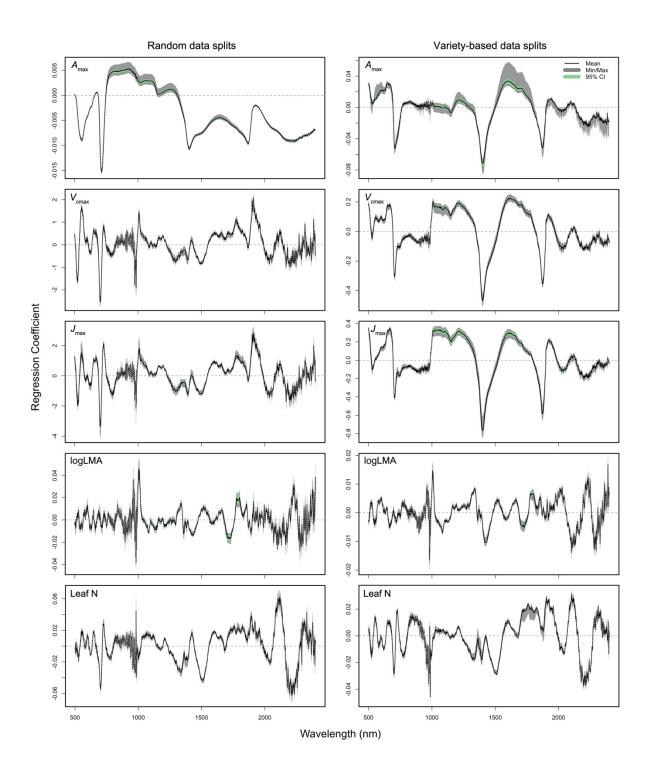
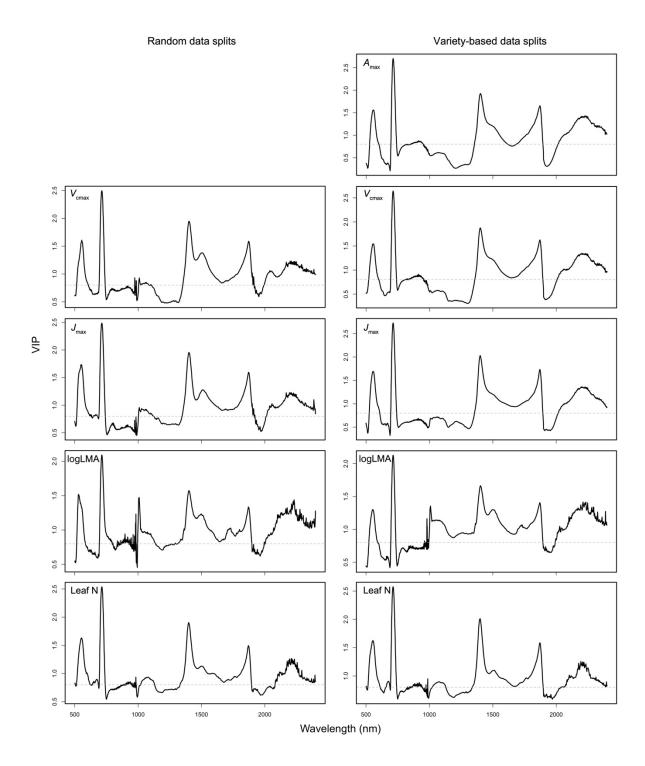


Figure 3. Jackknife regression coefficients of the PLSR models of A_{max} , V_{cmax} , J_{max} , log-LMA, and leaf N, based on the calibration data. The dashed horizontal line in each panel indicates where the coefficient is zero. The black curve represents the mean, the grey area represents the range, and the green area represents the 95% confidence interval.



- Figure 4. Variable influences on projection (VIP) scores of the final PLSR models of A_{max} ,
- $V_{\rm cmax}$, $J_{\rm max}$, log-LMA, and leaf N. The dashed horizontal line in each panel indicates where the
- VIP score is 0.8. The A_{max} model using random data split method had one component and
- therefore did not generate valid VIP scores.