

# 1 Association of spectroscopically determined leaf nutrition 2 related traits and breeding selection in *Sassafras tzumu*

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## 7 **Abstract:**

8 **Background:** The nutrition related to traits is an influential role in tree growth, tree production  
9 and nutrient cycling. Therefore, the influence of genetic parameters on leaf nutrition traits  
10 ought to take account of optimal tree breeding selection. However, the measurement methods  
11 are seriously affected by the progress of breeding selection program. In this study, we tested  
12 the ability of spectroscopy to quantify the specific leaf nutrition traits including Anthocyanins  
13 (ANTH), flavonoids (FLAV) and Nitrogen balance index (NBI), and estimated the genetic  
14 variation of these leaf traits based on the spectroscopic predicted data. Live fresh leaves of  
15 *Sassafras tzumu* were selected for spectral collection, after which concentrations of ANTH,  
16 FLAV and NBI were analyzed by standard analytical methods. Partial least squares regression  
17 (PLSR), five spectra pre-processing methods, and four variable selection algorithms were  
18 conducted for the optimal prediction model selection. Each trait model was simulated 200 times  
19 for error estimation.

20 **Results:** The stander normal variation (SNV) to the ANTH model and 1<sup>st</sup> derivatives to the  
21 FLAV and NBI models, combined with significant Multivariate Correlation (sMC) algorithm  
22 variable selection are finally regarded as the best performance model. The ANTH model  
23 produced the highest accuracy of prediction with a mean  $R^2$  of 0.72 and mean RMSE of 0.10 %,  
24 followed by FLAV and NBI model (mean  $R^2$  =0.58, mean RMSE = 0.11 % and mean  $R^2$  =0.44,

25 mean RMSE = 0.04 %). High heritability was found of ANTH FLAV and NBI with  $h^2$  of 0.78,  
26 0.58 and 0.61 respectively. It shows that it is benefitting and possible of breeding selection for  
27 the improvement of leaf nutrition traits.

28 **Conclusions:** Spectroscopy can successfully characterize the leaf nutrition traits in living tree  
29 leaves and the ability to simultaneous multiple plant traits provides a promising and high-  
30 throughput tool for the quick analysis of large size samples and serves for genetic breeding  
31 program.

32 **Keyword:** spectroscopy; Anthocyanins (ANTH); flavonoids (FLAV); Nitrogen balance index  
33 (NBI), breeding selection

## 34 Background

35 Nitrogen (N) is one of the most essential nutrients in plant growth, which is needed to improve  
36 grain yield and quality (Cánovas *et al.*, 2018). While excessive N fertilizer application brings  
37 severe environment problems, its importance for plant productivity still cannot be  
38 underestimated. The precise N application in the plant has been an important demand for a long  
39 time (Srinivasan, 2006). The nutrition state in plant should be precisely measured at all stage  
40 to set up a guide for precise fertilization to avoid N deposition (Payne *et al.*, 2017). N is the  
41 most common limiting factor for the individual, natural and artificial ecosystems growth of the  
42 plant. Plant requires N to maintain plant metabolism for growth mainly through external and  
43 internal sources, including Soil organic matter, fertilizers, atmospheric deposition and stored  
44 N by plant themselves (Millard, 1996). Plants, such as boreal species, store N seasonally  
45 through the process of internal cycling and it is a major source of N supplement for tree growth  
46 especially when the external availability of N is limited (Nambiar and Fife, 1991; Millard and  
47 Proe, 1993). Trees store N in the pattern of proteins mainly in their perennial wood and bark  
48 tissues in summer and winter. In addition, other parts of foliage trees, like roots and leaves,  
49 also store N which provides nutrition for young roots and needles development. Tree N

50 remobilisation often occurs during the growth season. The stored N mainly determines the  
51 amount of N remobilised and plays an important role for the tree seasonal growth. The  
52 dynamics and mobilization of N stored in trees have been widely studied (Cyr *et al.*, 1990;  
53 Malagoli *et al.*, 2005). The variation of plant species, genotype, soil and environment leads to  
54 the diversity of leaf nitrogen content (Sinclair and Horie, 1989; Famula *et al.*, 2019). It is  
55 reported that the chlorophyll content has a strong positive correlation with N content which is  
56 an estimative index for N status in leaf (Wood *et al.*, 1993). A portable chlorophyll meter,  
57 which collects the leaf light interaction that related to greenness and relative chlorophyll  
58 content, is developed for the estimation of N status (Moreau *et al.*, 2004; Hardin *et al.*, 2012).  
59 In addition to chlorophyll content, flavonoids (FLAV), one of the main polyphenol components,  
60 which have antioxidant activity, are confirmed as biological activity and potential health  
61 benefit and also applied to the estimation of N status (Tremblay *et al.*, 2012). Evidence shows  
62 that the rise of N fertilization will lead to flavonoid content decreasing and chlorophyll content  
63 increasing (Padilla *et al.*, 2014). Another N status index, N balance index (NBI), which is the  
64 ratio of chlorophyll to flavonoid, is verified that it has a better and more reliable correlation  
65 with leaf N concentration than chlorophyll content alone (Tremblay *et al.*, 2012).  
66 Anthocyanins (ANTH) are a group of water soluble flavonoid pigments that occur in all plant  
67 tissues. Anthocyanins are mostly related to a wide range of plant colour but often appear as red  
68 (Croft and Chen, 2017). In addition, unfavourable conditions will transiently have an impact  
69 on anthocyanins accumulation in both juvenile and senescent observable plant leaves (Garriga  
70 *et al.*, 2014; Naing *et al.*, 2017; Trojak and Skowron, 2017). Thus, Anthocyanins are taken as  
71 an indicator of plant leaf senescence and stresses (Paul *et al.*, 2017; Liu *et al.*, 2019).  
72 However, the dearth of research on plant growth, the variation of N storage and remobilization  
73 driving are mainly ascribed to the high consuming methods and the labour to measure the N  
74 concentration and index properties (NBI, chlorophyll content, ANTH, and FLAV), such as

75 Atomic absorption spectrometry (Borges and Holcombe, 2017; Hu *et al.*, 2019),  
76 chromatography (Rivero-Villar *et al.*, 2018) and so on. These analytical methods will limit the  
77 breeding selection of tree growth with a large number of samples.

78 Alternatively, Near-infrared spectroscopy (NIRS) is a rapid, high-throughput technique that  
79 has been used for chemical components analysis in many fields. NIRS is a promising and  
80 reliable method that can be used for the assessment of a large number of samples (Forina *et al.*,  
81 2015; Ramirez *et al.*, 2015; Guillemain *et al.*, 2017; Malegori *et al.*, 2017; Li *et al.*, 2018a). It  
82 basically relies on the spectra variation of absorption because of the vibration, stretching and  
83 bending of molecular bonds. Special bonds, including C–H, N–H and O–H bonds (Bokobza,  
84 2002), will interact with the specific wavelengths in the NIR spectroscopy. A stable and  
85 uniform illumination source of NIR spectra with collected samples will provide a better  
86 platform for the organic chemicals (Siesler *et al.*, 2008). To obtain a better predicting result,  
87 the multivariate methods such as partial least squares regression (PLSR) (Wold *et al.*, 2001)  
88 will be used by pairing the NIR spectra and the independent chemical measurements together  
89 to calibrate a high accurate prediction model. PLSR holds the advantages of producing reliable  
90 coefficients, reducing the bias and estimated error, and consuming fewer PLSR components,  
91 all of which make it one of the most popular methods for chemometric analyses (Bolster *et al.*,  
92 1996; Asner *et al.*, 2011). The satisfied model will then be applied to unknown samples by  
93 their spectra data for independent chemical prediction. Our recent research shows that leaf  
94 chlorophyll content and colour parameters are predictable on fresh leaf samples with field near  
95 infrared spectrophotometry (Li *et al.*, 2019). The total FLAV and ANTH concentration also  
96 have been predicted by a general calibration model in *Ginkgo biloba* leaf and four Indonesian  
97 herbal plant species, including *Syzigium oleana*, *Piper betle*, *Jasminum* and *Graptophyllum*  
98 *pictum* with NIR reflectance spectroscopy. NIR also serves as an reliable and promising tool

99 for tree breeding selection programs during its robust prediction. And with robust calibration  
100 and skill, it is able to screen massive samples (Gebreselassie *et al.*, 2017; Li *et al.*, 2019).

101 The robustness and reliability of model accuracy are largely determined by the spectra quality  
102 and feature selection. The massive overtones, combinations vibrations information and noise  
103 of the raw NIR spectra (Yang *et al.*, 2018) will result in overlapping and difficulty to directly  
104 distinguish the target plant properties (Inagaki *et al.*, 2018). Spectra pre-processing methods,  
105 can efficiently reduce the overlapping and noise influence, such as stander normal variation  
106 (SNV), 1<sup>st</sup> and 2<sup>nd</sup> derivatives and so on (Jin *et al.*, 2017; Park *et al.*, 2018). To yield a robust  
107 and reliable model and avoid the influence of irrelevant variables and noise, it is essential to  
108 carry out variable selection methods to pick the most relevant variables responding to the target  
109 properties instead of the full length of spectra (Fernández *et al.*, 2019; Liang *et al.*, 2020).

110 Nowadays, the joint analyses of chemometric statistics and variable selection algorithms is on  
111 a rise to eliminate the irrelevant variables and improve the model accuracy (Caliari *et al.*, 2017;  
112 Mancini *et al.*, 2018). The most common methods of variable selection are Genetic algorithm  
113 (Ga) (Zhao and Cao, 2016), Regularized elimination procedure (Rep) algorithm (Mehmood *et*  
114 *al.*, 2012), Iterative predictor weighting (Ipw) (Forina *et al.*, 1999) and significant Multivariate  
115 Correlation (sMC) algorithm (Tran *et al.*, 2014). However, the comparison of variable selection  
116 algorithms along with PLSR for prediction of multiple leaf nutrition traits is less studied.

117 *Sassafras tzumu* is a deciduous tree species that has colourful leaves in autumn. Zhejiang  
118 province in China is vigorously promoting the cultivation of colourful species and makes the  
119 *S. tzumu* become a famous tree species which has been widely planted in Zhejiang province to  
120 develop the urban and mountain landscape (Jiang aiping *et al.*, 2016).

121 Our latest study addresses that the leaf colour and chlorophyll are under genetic control (Li *et*  
122 *al.*, 2019). However, the relationship between inheritance and variation of leaf nutrition traits  
123 (NBI, ANTH and FLAV) in *S. tzumu* is less discovered.

124 Therefore, the aims of this research are to 1) test the capacity of reflectance spectroscopy to  
125 characterize the NBI, ANTH and FLAV with PLSR model; 2) find out the most optimal pre-  
126 processing method for these three leaf traits. 3) identify the most important wavelength that  
127 related to NBI, ANTH and FLAV by four variable selection methods, including significant  
128 multivariate correlation (sMC), regularized variable elimination procedure (Rep), iterative  
129 predictor weighting (Ipw), and Genetic algorithm (Ga) variable selection; 4) estimate genetic  
130 parameters and correlations of NBI, ANTH and FLAV in *S. tsumu*.

## 131 **Methods and materials**

### 132 **Materials**

133 50 half-sib families of *S. tsumu* were selected for our study from 6 different regions. Trees were  
134 planted in a randomised complete block by a 2 m × 3 m spacing Changle Forest Farm Nursery  
135 (30°27' N, 119°48' E), Hangzhou, Zhejiang, China in 2016 with 5 replications and 6 individual  
136 trees.

### 137 **NIR spectra collection**

138 Samples spectra data was collected through 5-6 leaves from each tree in October 2018. The  
139 NIR spectra data was taken from the upside surface of the leaves for three times with a handheld  
140 fibre optic contact prob from a field-based spectrometer (LF-2500, Spectral evolution, USA).  
141 Each spectrum took averagely 32 scans with a range of 1100 to 2500 nm by a 6 nm resolution.  
142 All spectra were obtained from the leaves of 1500 trees and 500 trees leaves were placed in a  
143 marked paper bag and transferred to the refrigerator immediately for chemical measurement.

### 144 **Leaf FLAV measurement**

145 Each leaf was ground into powder and being mixed with methanol for 24hrs. 0.5 ml (1mg/mL)  
146 extract of each sample was taken to mixed with methanol (1.5 ml), 10% aluminium chloride

147 (0.1 ml), 1 M potassium acetate (0.1 ml) and distilled water (2.8 ml). The mixture was being  
148 placed under room temperature for 30 mins and then measured at 415 nm for the absorbance  
149 by UV–Visible spectrophotometer (UV-1280, Shimadzu, Japan). The flavonoid content of the  
150 sample was accessed by the value of absorbance density (Eom *et al.*, 2007).

### 151 **Pigment extraction and NBI estimation**

152  
153 A weighed circular piece cutting from each leaf was place into a mortar by a pestle ground  
154 with 100% methanol until the colour changed into white. The extract was being centrifuged for  
155 6 mins by 14,000 rpm at 4 °C and subsequently assayed by a UV–Visible spectrophotometer  
156 (UV-1280, Shimadzu, Japan). It conducted the equation and specific absorption in the  
157 wavelength which was reported by Wellburn (1994). The solution was mixed with 3 ml  
158 acidified methanol (1 % HCl) at 4 °C with moderate shaking for 12 hrs and then being  
159 centrifuged for 10 mins at 14,000 rpm. The extraction was then placed into the  
160 spectrophotometer, and it took the absorption at 530 and 657 nm wavelengths to determine the  
161 ANTH concentration (Strack and Wray, 1989). The NBI index was figured as the ratio of  
162 chlorophyll to flavonoid content.

### 163 **Model calibration and validation**

164 The original five different types of pre-processing spectra (SNV, 1<sup>st</sup>, 2<sup>nd</sup> derivatives, SNV+1<sup>st</sup>  
165 derivatives, SNV+ 2<sup>nd</sup> derivatives) combined with PLSR (Wold *et al.*, 2001) algorithm were  
166 compared in our study. The Savitzky-Golay smoothing (Press and Teukolsky, 1990) with a  
167 window size of 15 data points was applied in both 1<sup>st</sup> and 2<sup>nd</sup> derivatives spectra. PLSR models  
168 were generated with leave-one-out cross-validation for the prediction of ANTH, NBI, and  
169 FLAV content. Data were randomly split 200 times into calibration (80%) for model building  
170 and validation (20%) for model test respectively. Therefore, the PLSR model has been  
171 conducted 200 times for the evaluation of model performance. Each model combined with four  
172 variable selections (sMC, Ipw, Rep and Ga) was conducted to find out the most important

173 spectral variables. The coefficient of determination ( $R^2$ ) and root-mean-square error (RMSE)  
 174 in each model derived from both calibration (Cal) and validation (Val) were applied for the  
 175 evaluation model performance.

## 176 **Statistical analysis**

177 The estimation of genetic parameters were measured by A multivariate restricted maximum  
 178 likelihood (REML) linear mixed model, details can be found in (Li *et al.*, 2018a). The narrow  
 179 sense heritability ( $h^2$ ) of trait  $i$  and genetic correlations ( $r_{gij}$ ) and phenotypic correlation ( $r_{pij}$ )  
 180 between trait  $i$  and trait  $j$  were calculated as:

$$181 \quad h_i^2 = \frac{2.5\sigma_{f_i}^2}{\sigma_{f_i}^2 + \sigma_{e_i}^2}$$

$$182 \quad r_{gij} = \frac{\sigma_{fifj}}{\sqrt{\sigma_{f_i}^2 + \sigma_{f_j}^2}}$$

$$183 \quad r_{pij} = \frac{\sigma_{fifj} + \sigma_{eiej}}{\sqrt{(\sigma_{f_i}^2 + \sigma_{e_i}^2)(\sigma_{f_j}^2 + \sigma_{e_j}^2)}}$$

184 where  $\sigma_{f_i}^2$  is the estimated family variance for trait  $i$ , and  $\sigma_{f_j}^2$  is the estimated family variance  
 185 for trait  $j$ ,  $\sigma_{e_i}^2$  and  $\sigma_{e_j}^2$  are the residual variances for trait  $i$  and  $j$ , and  $\sigma_{fifj}$  and  $\sigma_{eiej}$  are the  
 186 family and residual covariances between traits  $i$  and trait  $j$ . The realized genetic gain ( $\Delta G_R$ )  
 187 was calculated by the difference between the mean breeding values of selected top ratio leaf  
 188 traits and the total mean of the leaf traits.

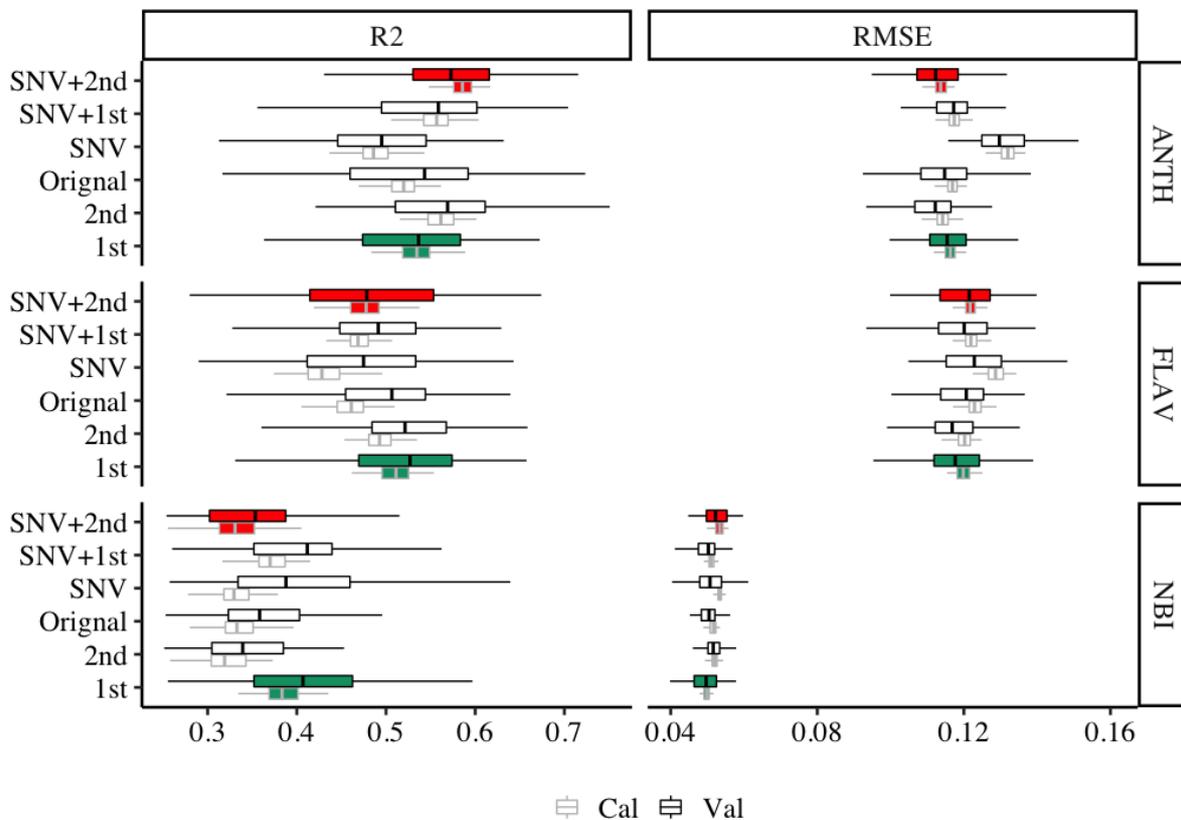
189 R software (version 3.1.2) (R Core Team, 2017) was taken for all of the data analysis. The *pls*  
 190 package (Mevik *et al.*, 2015) in R was carried out for PLSR model building, the *plsVarSel*  
 191 (Mehmood *et al.*, 2012) for variables selection, the *prospectr* package (Stevens and Ramirez–  
 192 Lopez, 2014) for NIR spectra manipulation, the *lme4* package (Bates *et al.*, 2015) for  
 193 estimation of genetic parameters, and the *ggplot2* package (Wickham, 2016) for visualization  
 194 plot.

## 195 Results

### 196 Model performance

197 Three leaf traits ANTH, FLAV and NBI constructed the NIR spectral PLSR model. The results  
198 are shown in Figure 1. ANTH model has the highest accuracy, followed by FLAV and NBI  
199 model. The average of  $R^2$  and RMSE for these three models in calibration sets (Cal) is 0.54  
200 (range: 0.43-0.63), 0.47 (range: 0.35-0.58) and 0.36 (range: 0.26-0.45), in validation sets (Val)  
201 is 0.54 (range: 0.28-0.75), 0.47 (range: 0.28-0.69) and 0.38 (range: 0.25-0.64) respectively. As  
202 for all spectral pre-processing models, SNV+2<sup>nd</sup> derivative prediction model is found to be the  
203 highest well-performing for predicting ANTH concentration than the other pre-processing  
204 methods, with a mean  $R^2_{Cal}$  and  $RMSE_{Cal}$  of 0.59 (range: 0.55-0.63), 0.11% (range: 0.11-  
205 0.12%), a mean  $R^2_{Val}$  and  $RMSE_{Val}$  of 0.57 (range: 0.38-0.72), 0.11% (range: 0.09-0.13%),  
206 followed by 2<sup>nd</sup>, SNV+1<sup>st</sup>, 1<sup>st</sup>, original with the mean of  $R^2$  in the calibration sets (Cal) is 0.56  
207 (range: 0.42-0.75), 0.56 (range: 0.51-0.60), 0.53 (range: 0.48-0.59), 0.52 (range: 0.47-0.56),  
208 and RMSE 0.11% (range: 0.11-0.12%), ), 0.11% (range: 0.11-0.12%), 0.11% (range: 0.11-  
209 0.12%), 0.12% (range: 0.11-0.12), and in the validation sets (Val) is 0.57 (range: 0.42-0.75),  
210 0.54 (range:0.30-0.70), 0.53 (range: 0.36-0.67), 0.52 (range: 0.32-0.72), and RMSE 0.11%  
211 (range: 0.09-0.13%), 0.12% (range: 0.10-0.14%), 0.12% (range: 0.10-0.14%), 0.11% (range:  
212 0.09-0.14%) respectively. SNV shows the worst effect with the mean of  $R^2$  and RMSE for  
213 calibration sets (Cal) and validation sets (Val) 0.49 (range: 0.44-0.54), 0.49 (range: 0.28-0.63),  
214 and 0.13% (range: 0.13-0.14%), 0.13% (range: 0.12-0.16%) respectively. However, 1<sup>st</sup> yields  
215 the best PLSR model in the prediction of FLAV and NBI than the other pre-processing model,  
216 with high mean  $R^2_{CV}$ ,  $R^2_v$  of 0.51 (range: 0.46-0.58), 0.52 (range: 0.29-0.68), and low mean of  
217  $RMSE_{CV}$ ,  $RMSE_v$  of 0.12% (range: 0.11-0.13%), 0.12 (range: 0.10-0.12%) in FLAV model  
218 and high mean  $R^2_{CV}$ ,  $R^2_v$  of 0.39 (range: 0.33-0.45), 0.41 (range: 0.26-0.60), and low mean of  
219  $RMSE_{CV}$ ,  $RMSE_v$  of 0.05% (range: 0.05-0.05%), 0.05 (range: 0.04-0.06%) in NBI model

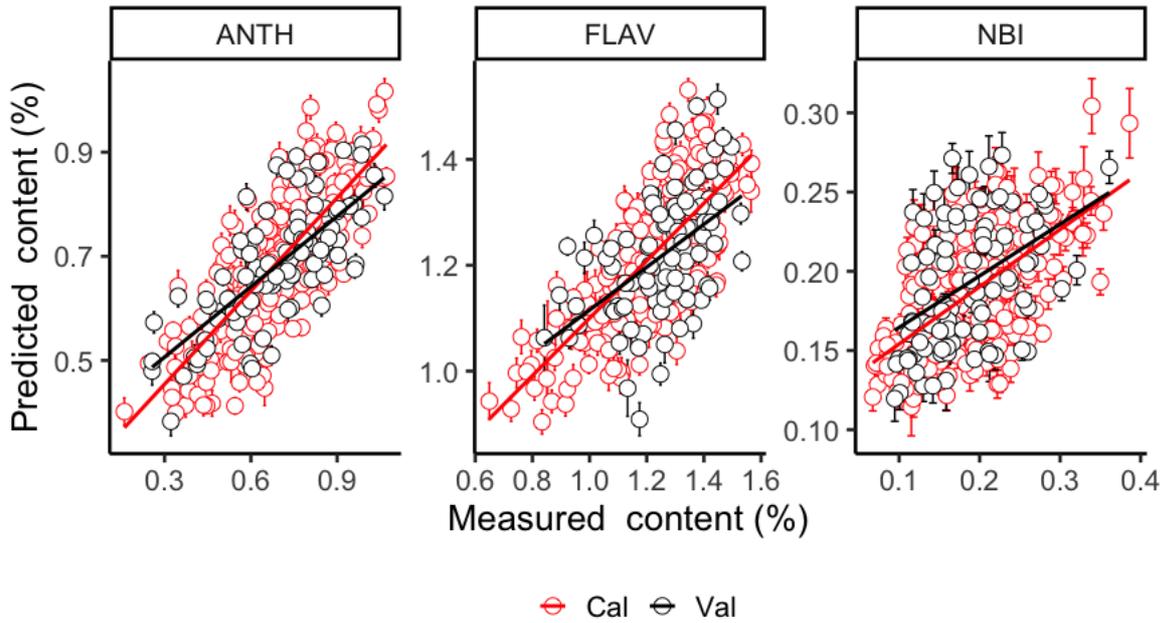
220 respectively. The effect of SNV shows a poor prediction in the FLAV and NBI as well. The  
 221 mean of  $R^2_v$  is 0.40 (range: 0.26-0.64) and 0.47 (range: 0.29-0.64) respectively.



222  
 223 Figure 1 Distribution (95% confidence intervals) of calibration and validation statistics from 200 simulations of models  
 224 predicting ANTH, FLAV and NBI with full length NIR spectra. Each model permutation included 80% of the data for internal  
 225 calibration and the remaining 20% for validation.  $R^2$ : coefficient of determination of cross-validation; RMSE: root-mean-  
 226 square error of cross-validation; The black vertical line in each box represents median value, the red colour box represents the  
 227 SNV+ 2<sup>nd</sup> model. the green colour box represents the 1<sup>st</sup> model.

228 The relationship between the predicted and measured content of Cal and Val datasets by ANTH  
 229 model with SNV+ 2<sup>nd</sup> derivative spectra, FLAV and NBI model with 1<sup>st</sup> derivative spectra was  
 230 plotted in Figure 2. The error bar represents the prediction error of 200 times per sample. It  
 231 shows that due to the high accuracy of the ANTH and FLAV models, the predicted values are  
 232 more correlated with the measured values, while the relationship between predicted and  
 233 measured values of NBI model is relatively poor. Although the prediction accuracy of each  
 234 model is different, the prediction error of the Cal and Val data sets is still little.

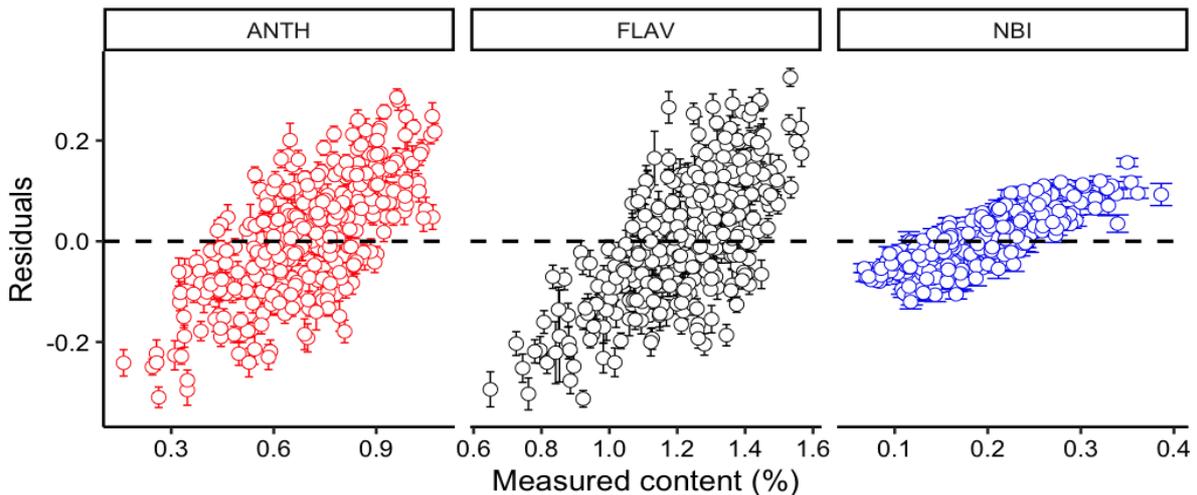
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236

237 Figure 2 Measured and predicted ANTH, FLAV and NBI contents with full length of NIR spectra. Error bars for predicted  
 238 values represent the standard deviations obtained from the 200 simulated models.

239 The residual of the best processing spectra model for each leaf trait shows that all of these three  
 240 models tend to be underpredicted when the measurement value is small. With the rise of the  
 241 measurement value, the prediction value has the tendency of overprediction. The residual value  
 242 of ANTH, FLAV and NBI model is between an acceptable range from -0.3 to 0.3.

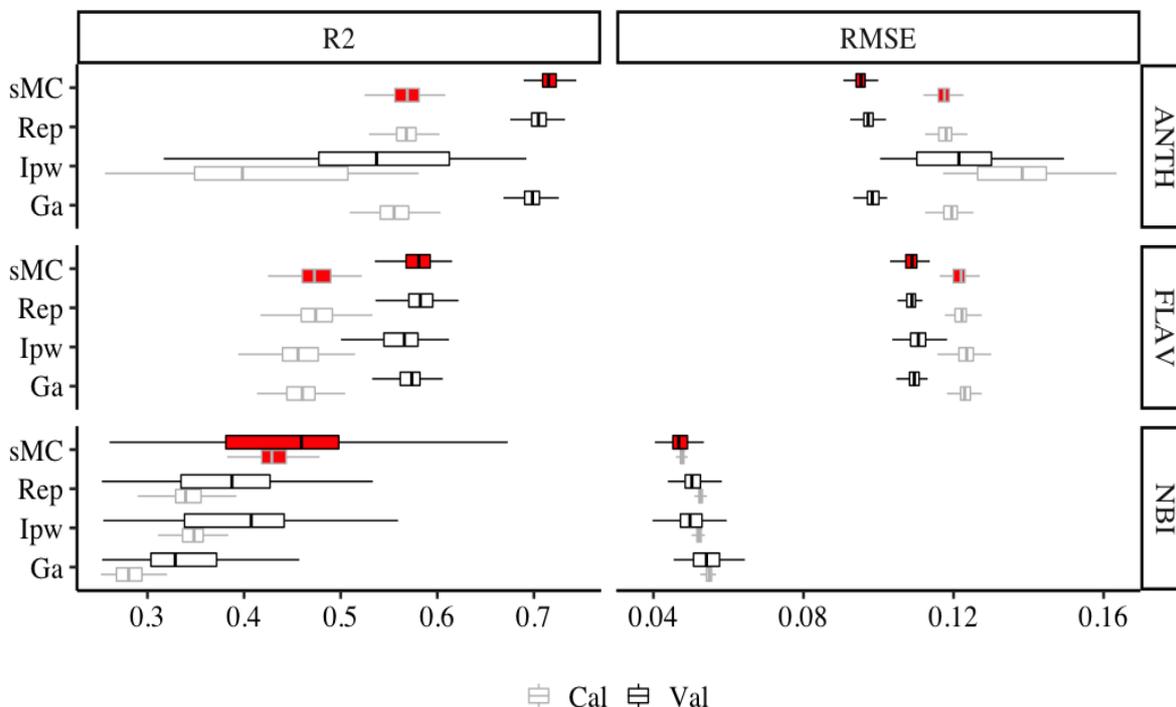


243

244 Figure 3 Residuals plotted against measured ANTH, FLAV and NBI with full length of spectra. Error bars for predicted values  
 245 represent the standard deviations obtained from the 200 simulated models.

246 **Variable selection and model optimization**

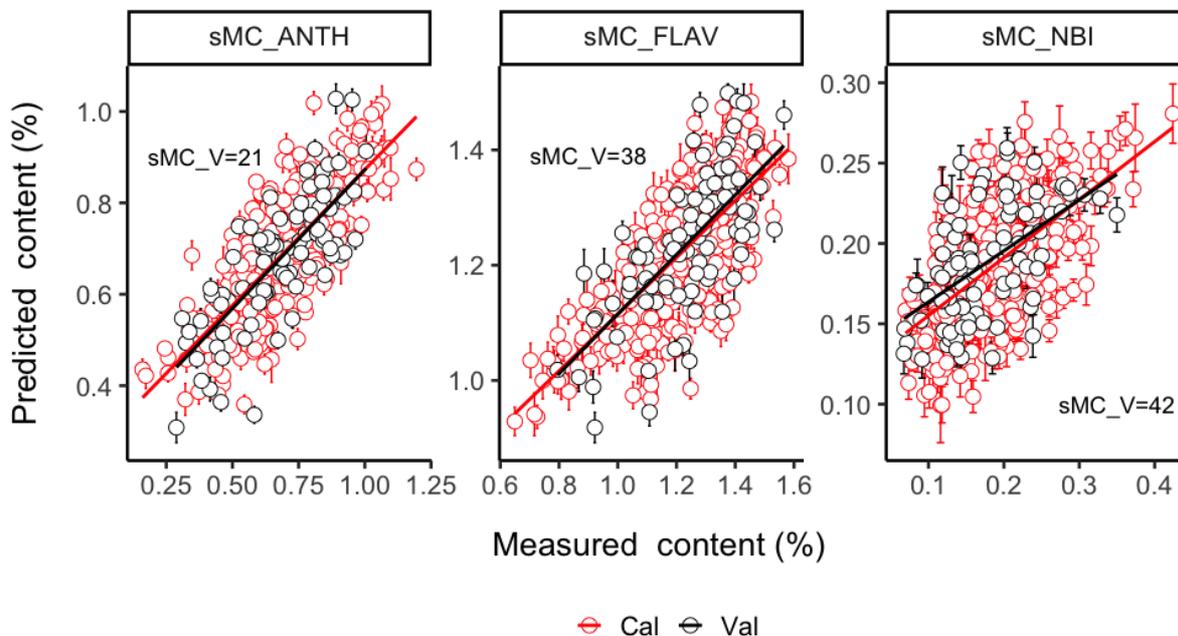
247 Four types of variable selection methods were compared to test the performance of ANTH,  
 248 FLAV, and NBI PLSR models (Figure 4). The prediction accuracy of ANTH, FLAV, and NBI  
 249 PLSR models was enhanced much better than the full-length spectra models by these four  
 250 different variable selection methods. ANTH model still holds the highest  $R^2$  and RMSE value  
 251 in both Cal and Val data, followed by the FLAV and NBI model. The highest prediction model  
 252 for ANTH, FLAV and NBI was found through sMC-selected NIR spectra variables with the  
 253 mean  $R^2_{Val}$  of 0.72 (ranged: 0.69 to 0.75), 0.58 (ranged from: 0.54 to 0.62), 0.44 (ranged from:  
 254 0.26 to 0.67), and of the mean  $RMSE_{Val}$  of 0.10 % (range: 0.09-0.10 %), 0.11 % (range: 0.10-  
 255 0.12 %), 0.04 % (range: 0.04-0.05 %) respectively. The sMC\_PLSR models reached a more  
 256 stable prediction with less than 16% of full length of spectra on each leaf trait (Figure 5), and  
 257 having a similar residual range to the model with full spectral information (Figure 6).  
 258



259  
 260 Figure 4 Distribution (95% confidence intervals) of calibration and validation statistics from 200 simulations for models  
 261 predicting ANTH, FLAV and NBI contents using sMC, Rep, Ipw and Ga variable selection. Each model permutation included

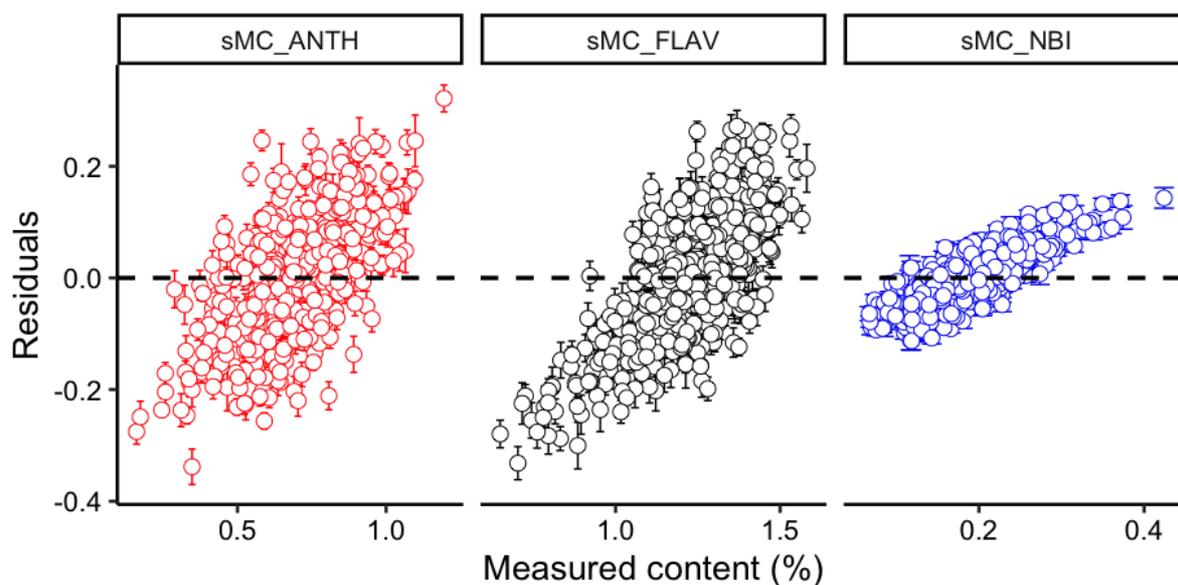
262 80% of the data for calibration and the remaining 20% for validation.  $R^2$ : coefficient of determination of cross-validation;  
 263 RMSE: root-mean-square error of cross-validation; The black vertical line in each box represents median value, the red colour  
 264 box represents the sMC model.

265



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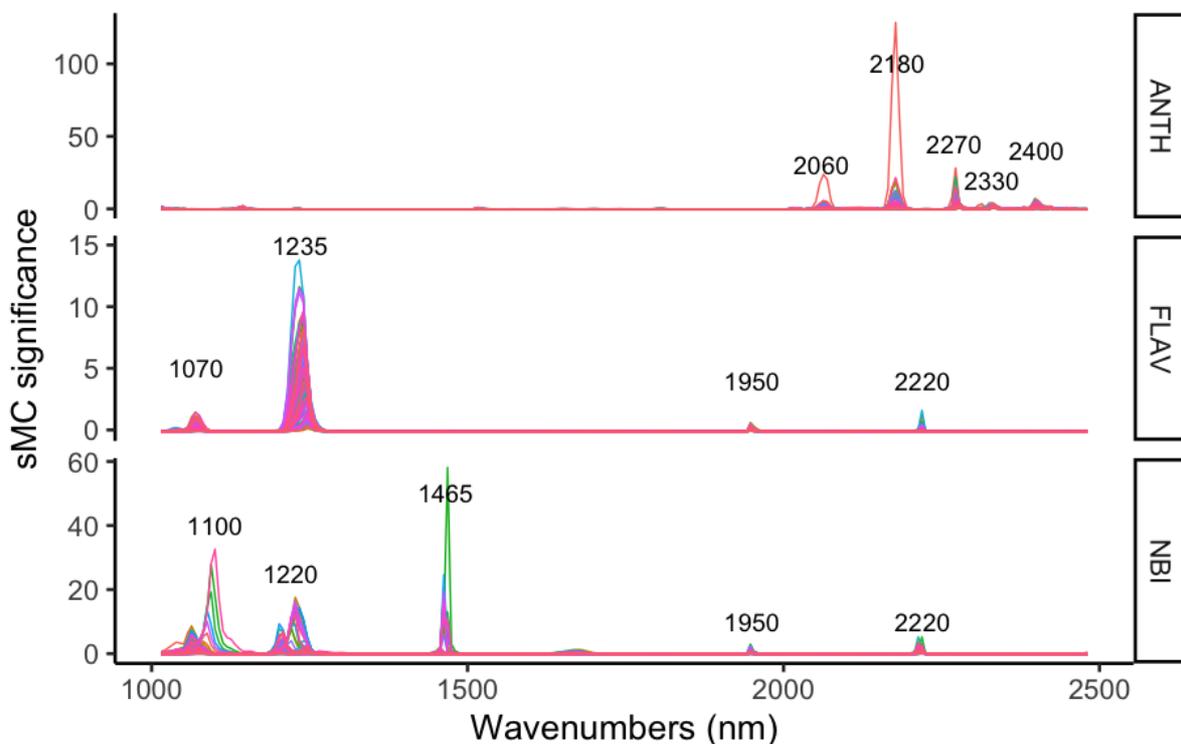
267 Figure 5 Measured and predicted ANTH, FLAV and NBI contents with sMC selected NIR spectra. Error bars for predicted  
 268 values represent the standard deviations obtained from the 200 simulated models. sMC\_V: the total selected number of  
 269 variables.



270

271 Figure 6 Residuals plotted against measured ANTH, FLAV and NBI with sMC selected spectra. Error bars for predicted values  
 272 represent the standard deviations obtained from the 200 simulated models.

273 Figure 7 displays the important variable information area selected by sMC variable selection  
 274 method in the ANTH, FLAV and NBI model which conducted 200 times on each model. Even  
 275 the predicted model of three leaf traits was being run 200 times, sMC variable selection brought  
 276 out stability for the selected important variable areas with a few relative spectral region in  
 277 prediction models. The variables at 2060, 2180, 2270, 2330 and 2440nm are considered as  
 278 the vital roles in the construction of ANTH prediction model. As for FLAV, 1070, 1235,  
 279 1950 and 2220 nm are more important areas. Spectroscopic variables at 1100, 1220, 1465,  
 280 1950 and 2220 nm make a critical difference in the NBI predictive model.



281  
 282 Figure 7 Spectra influence in ANTH, FLAV and NBI models that randomly being conducted 200 times; each line means one  
 283 time of modelling with sMC variable selection.

284 **Heritability, genetic and phenotypic correlation among traits**

285 Table 1 shows the correlation (genetic and phenotypic) and heritability of three traits. Leaf  
 286 ANTH produces the highest heritability of 0.78, followed by FLAV and NBI with  $h^2$  of 0.58  
 287 and 0.61 respectively. There has no significant genetic and phenotypic correlation between

288 ANTH, FLAV and NBI. FLAV was found to have the highest positive genetic correlation with  
 289 ANTH of a value of 0.36.

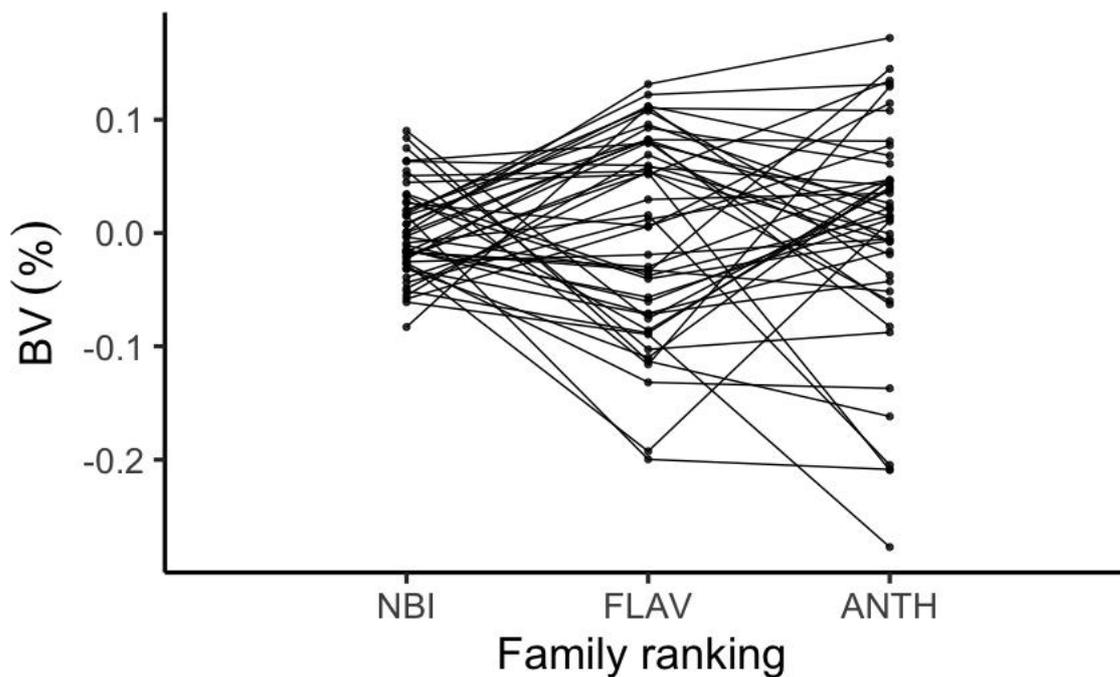
290 Table 1 The heritability, genetic (above diagonal) and phenotypic correlation (below diagonal) between ANTH, FLAV and  
 291 NBI traits with standard error between parentheses.

Traits	ANTH	FLAV	NBI	$h^2$
ANTH		0.36 (0.01)	0.11 (0.02)	0.78 (0.10)
FLAV	0.16 (0.03)		0.09 (0.01)	0.58 (0.11)
NBI	0.09 (0.01)	0.12 (0.01)		0.61 (0.08)

292

293 **Family selection**

294



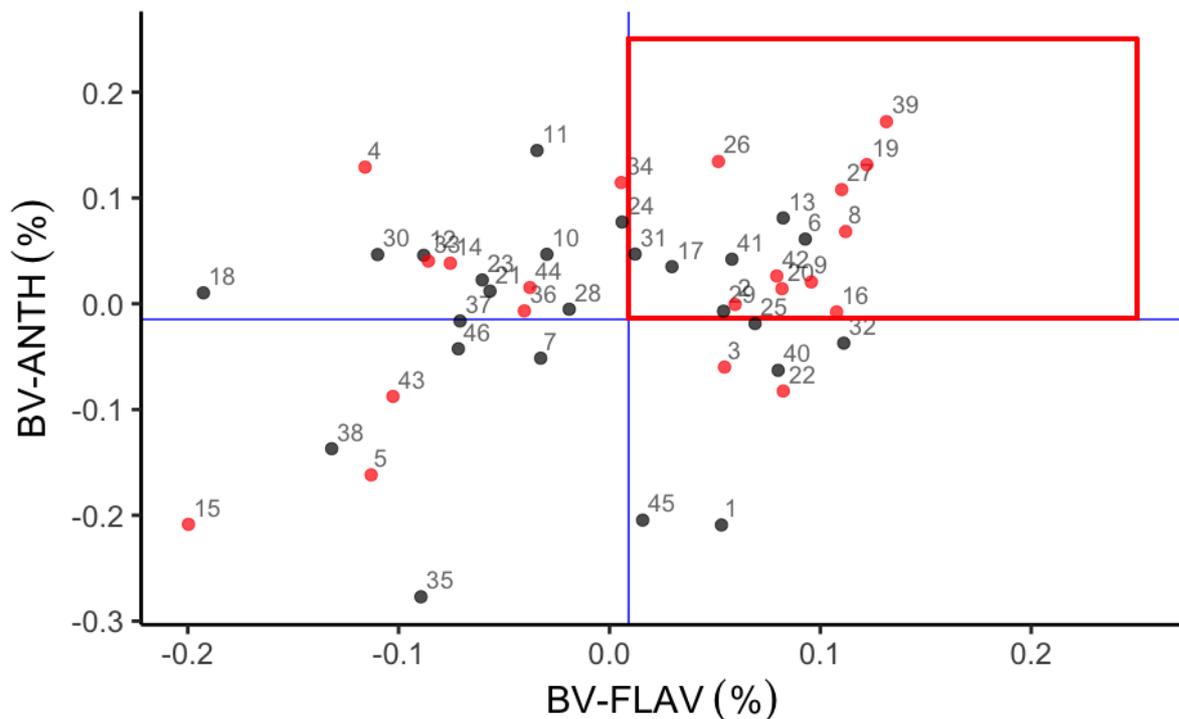
295

296 Figure 8 Family ranking for ANTH, FLAV and NBI content in *Sassafras tzumu* at age 2. Family values are expressed as  
 297 deviation from each trait mean. BV: Breeding values.

298

299 The best models of ANTH, FLAV and NBI were applied to predict the remaining 1000 trees  
 300 spectra. In total ,1500 trees of 50 families were selected for breeding analysis. Figure 8 shows

301 the distribution of three leaf traits in the ranking of breeding value from 50 families. The  
 302 ranking of three leaf traits in different families is inconsistent as well as a part of families  
 303 consistently displaying in the breeding value, which explains that it is feasible to make a family  
 304 selection of ANTH, FLAV and NBI at the same time through genetic selections.



305  
 306 Figure 9 Relationship between ANTH, FLAV and NBI content breeding values of *Sassafras tzumu* families at age 2. BV-  
 307 ANTH: breeding value of ANTH; BV-FLAV: breeding value of FLAV; the blue solid line: the mean value of each trait  
 308 breeding value; red square: the region that most interesting.

309 Figure 9 demonstrates the breeding value distribution of 50 families of three leaf traits. The  
 310 blue solid lines represent the average of ANTH and FLAV respectively. The families with a  
 311 higher NBI breeding value than its mean are shown in red, and below the mean is in black. 16  
 312 families have high FLAV and ANTH breeding value. 10 families with a high breeding value  
 313 will be selected If NBI breeding values are required to be above mean. These families can be  
 314 further taken as genetic family materials for second-generation breeding.

## 315 Discussion

316 The health of tree growth is dictated by main factors, such as soil, nutrients, environment,  
317 genetic and so on. N is a key role of nutrient which highly influences the tree growth.

318 The internal N cycling in trees (Swarts, 2016) is a hot topic in numerous study (Millard and  
319 Neilsen, 1989; García-Sánchez *et al.*, 2017; Li and Coleman, 2019). However, the  
320 measurement of N concentration limits the access to the further study. In this study, the filed-  
321 base reflectance spectroscopy is proved to be a reliable and accurate method to characterize the  
322 plant nutrition properties in fresh leaves. The SNV + 2<sup>nd</sup> derivative spectra for ANTH, and 1<sup>st</sup>  
323 derivative spectra for FLAV and NBI have been identified to increase the model accuracy when  
324 calibrating the PLSR prediction models. Incorporate with spectra variable selection, the model  
325 accuracy is significantly improved with less variables for the prediction of leaf nutrition traits.

326 Our model offered a promising and reliable result for predicting the FLAV content in fresh leaf  
327 ( $R^2_{\text{Val}}=0.58$ ,  $\text{RMSE}_{\text{Val}} = 0.11\%$ ), which was lower than the result reported for *fresh Ginkgo*  
328 *biloba* leaf in different colors ( $R^2_{\text{CV}} = 0.82$  and  $\text{RMSE} = 2.62\%$ ). The variability lessened by  
329 small range of NBI value lead to an inefficient prediction. (Blanco and Villarroya, 2002).

330 Conversely, our result of the prediction of ANTH content illustrates a higher accuracy then the  
331 other two leaf traits, with a mean  $R^2_{\text{Val}}$  of 0.72 (range: 0.69-0.75) and a mean of  $\text{RMSE}_{\text{Val}} =$   
332 0.09 % (range: 0.09-0.10 %). Similar result was discovered in wine grapes by NIR  
333 hyperspectral imaging and PLSR model, which gave  $R^2$  of 0.84 and  $\text{RMSEP}$  of 0.013% for  
334 estimating ANTH content.

335 A robust statistical methodology for model calibration which was first conducted by Couture  
336 *et al.* (2016) was carried out to predict plant leaf secondary metabolites with reflectance  
337 spectroscopy. It was being run 200 randomized simulations for calibrating the models to  
338 provide an estimation of the model uncertainty and overall stability (Figures 1-7). It is similar  
339 to our previous study which takes use of filed spectroscopy to predict the leaf colour and

340 chlorophyll content (Li *et al.*, 2019). Random sampling (Quentin *et al.*, 2017) and Kennard-  
341 Stone sampling algorithm (Li *et al.*, 2018b) in other studies, which sample only once for model  
342 calibration, may cause instability for model prediction. Thus, we highly recommend to use this  
343 methodology for model calibration and validation on NIR analysis.

344 The NIR spectra involves not only the favourable information but noise and irreverent  
345 information which will encumbrance the model accuracy of prediction. Therefore, variable  
346 selection is regarded as an efficient way to find out the most important wavelengths which  
347 contributes the minimum error for model calibration and helps to reduce the model processing  
348 time For spectral models. Variables in the spectrum play a key role in the predictive accuracy  
349 of the model. The spectral information is extensive along with the relevant and irrelevant  
350 information, both of which will overlap to interfere the model construction of the useful  
351 information and the PLSR model with a specific trait (Workman Jr and Weyer, 2012). Thus, it  
352 is vital to screen important variables for spectral information. In this study, four variable  
353 selection methods were compared to pick the best variable selection method. It shows that the  
354 sMC-PLSR model efficiently identified the key wavelengths and enables us to select a small  
355 set of variables to yield a promising and robust calibrated model for the prediction of ANTH,  
356 FLAV and NBI. Our results support the research announced by Li and Altaner (2018), who  
357 successfully took the sMC variable selection method to improve the accuracy of an NIR  
358 calibration model to predict concentrations in extracts of heartwood of *Eucalyptus bosistoana*  
359 trees, and Li *et al.* (2019) who found that sMC selection algorithm held the advantage of finding  
360 the most relevant variables for the prediction of leaf chlorophyll content and colour parameters.  
361 Some studies also states that significance multivariate correlation (sMC) (Tran *et al.*, 2014) is  
362 a positive algorithm to remove confounding effects from NIR calibrations (Wijewardane *et al.*,  
363 2016).

364 Several important variables which are related to the ANTH, FLAV, and NBI have been selected  
365 similarly in each model, including the range at 2060, 2180, 2270, 2330 and 2440 nm for  
366 ANTH, 1070, 1235, 1950, 2220 nm for FLAV, and 1100, 1220, 1465, 1950, 2220 nm for NBI  
367 respectively. As reported by Ramirez *et al.* (2015), the regions around 2060, 2180, 2270, 2330  
368 and 2440 nm are mostly associated with O–H and C–H stretching vibrations as well as the  
369 starch and sugar (Decruyenaere *et al.*, 2012). However, in our study, these regions have been  
370 ignored. The regions around 1070, 1100, 1220, 1235 nm are mainly assigned to the 1<sup>st</sup>  
371 overtones of C–H combination bands and 1<sup>st</sup> and 2<sup>nd</sup> overtones of O–H and N–H stretching  
372 vibrations, while the bands around 1465 nm are mostly related to the 1<sup>st</sup> overtones of O–H  
373 stretching vibration, both of which are associated with starch and protein (Curran, 1989;  
374 Kokaly, 2001; De Bei *et al.*, 2017). In NIR spectra, water has a wide absorbance region which  
375 is a major influence on the other chemical information because of spectra overlap. In our study,  
376 the band around 1950 nm related to the water has less contribution to the FLAV and NBI model  
377 but no influence on the ANTH model. It probably influences the accuracy of model for the  
378 prediction of FLAV and NBI. Correlational study was found by Min *et al.* (2006), who stressed  
379 that the regions of 1910 and 1938 nm highly related to water might have a strong impact on  
380 the N concentration prediction.

381 Trees N internal cycling is considered as one of the major ecology factors for tree growth and  
382 is an augment for the tree uptake of soil N (Millard, 1989). In addition, it also helps to  
383 understand numerous aspects of plant ecology, for instance, to evaluate the effect of the N  
384 storage and remobilization in different part tissues of trees in relation to current demands for  
385 growth (Schneider *et al.*, 1996), to find out the role of N on growth stress, the relationship with  
386 N deposition in forest (Gundersen, 1991; Gundersen *et al.*, 1998) and the relationship with  
387 dynamics of carbon recourse in trees (Villar-Salvador *et al.*, 2015; Han and Kabeya, 2017).  
388 Our fast and accurate measurement of N index, including ANTH, FLAV and NBI traits of trees

389 with NIR spectroscopy provides an advanced way for the study of N internal cycling and allows  
390 to quickly measure large number of samples.

391 In this study, we continue to use the coefficients of 1/2.5 for the calculation of heritability of  
392 ANTH, FLAV and NBI traits based on our previous study to avoid the assembling of half-  
393 siblings and inbreeding effects. (Li *et al.*, 2019). The moderate heritability of ANTH, FLAV  
394 and NBI was found, with the value of  $h^2$  ranging from 0.61 to 0.78. The leaf ANTH heritability  
395 of 0.78 in our study is similar to the result found by Yihu *et al.* (2009) who figured out the  
396 anthocyanin content heritability ranging from 0.79 to 0.91 in leaves of chili pepper higher than  
397 0.29 reported in the leaf of Aspen (*Populus tremula* L.) (Robinson *et al.*, 2012). For FLAV, a  
398 significant high rang of heritability from 0.94 to 0.99 was reported in the leave of Ginkgo Trees  
399 (Zhang *et al.*, 2017) which was much higher than our study ( $h^2= 0.58$ ). It indicates that genetic  
400 control capacity is different between species even the same traits. Our study proves there is  
401 also a potential for the selection for NBI traits in breeding programs while with less study on  
402 the estimation of NBI heritability.

403 The consistence of families ranking of ANTH, FLAV and NBI indicates that the selection for  
404 a good leaf nutrition tree is workable, and the selection of qualified nutrition plant is supposed  
405 to involve multiple traits, which will afford a stable inheritance.

## 406 Conclusion

407 In conclusion, NIR spectroscopy is potentially taken to estimate the nutrition related traits by  
408 fresh leaf. Our reasonable high accuracy of ANTH and FLAV prediction and moderate  
409 accuracy of NBI prediction provide an alternative way for the N index traits and open a door  
410 to the efficient analysis of the internal N cycling in trees. The pre-processing method and  
411 variable selection much influence the performance of model prediction. Our study found that  
412 by using of 1<sup>st</sup> and SNV+ 2<sup>nd</sup> derivative spectra processing method and sMC variable selection  
413 algorithm, the PLSR models have been highly improved. In addition, the repeated spectral

414 statistical methodology that we applied provided an efficient way to deal with variation in  
415 calibration data and generate information on the response of plant nutrition traits with NIR  
416 spectra. NIR model serves as an efficient tool for the estimation of genetic parameters and  
417 breeding selection in high throughput way to improve the leaf traits quality.

## 418 **Declarations**

### 419 **Ethics approval and consent to participate**

420 Not applicable.

### 421 **Consent for publication**

422 Not applicable.

### 423 **Availability of data and material**

424 Not applicable.

### 425 **Competing interests**

426 The authors declare that there is no conflict of interest.

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### 431 **Authors' contributions**

432 Yanjie Li designed the study, conducted the experiment, analysed the data and wrote the  
433 manuscript. Wenjian Liu and Zifeng Tan conducted lab experiments, Jun Liu and Jingmin  
434 Jiang supervised the experiments at all stages and reviewed the manuscript. All authors have  
435 read and approved the final manuscript.

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