

1 Canopy spectral reflectance detects oak wilt at the 2 landscape scale using phylogenetic discrimination

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Author contribution statement

J.C.B. Conceived of and managed the project. G.S., C.L., A.S., J.J., R.M. and J.C.B conceived the experimental design and data analysis. C.L., A.S., and J.J. collected ground data. Z.W., H.G., P.T., and J.G. collected and processed airborne data. G.S. analyzed the data. G.S., J.C.B., and J.J., wrote the manuscript with contributions from C.L., A.S., R.M., H.G., P.T., and J.G. J.C.B, J.J., and R.M. obtained funding for this project.

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29 **Abstract**

30 The oak wilt disease caused by the invasive fungal pathogen *Bretziella fagacearum* is one of the greatest
31 threats to oak-dominated forests across the Eastern United States. Accurate detection and monitoring
32 over large areas are necessary for management activities to effectively mitigate and prevent the spread
33 of oak wilt. Canopy spectral reflectance contains both phylogenetic and physiological information across
34 the visible near-infrared (VNIR) and short-wave infrared (SWIR) ranges that can be used to identify
35 diseased red oaks. We develop partial least square discriminant analysis (PLS-DA) models using airborne
36 hyperspectral reflectance to detect canopies at early stages of disease development and assess the
37 importance of VNIR, SWIR, phylogeny, and physiology for oak wilt detection. We achieve high accuracy
38 through a three-step phylogenetic process in which we first distinguish oaks from other species (90%
39 accuracy), then red oaks from white oaks (*Quercus macrocarpa*) (93% accuracy), and, lastly, infected from
40 non-infected trees (80% accuracy). Including SWIR wavelengths increased model accuracy by ca. 20%
41 relative to models based on VIS-NIR wavelengths alone; using a phylogenetic approach also increased
42 model accuracy by ca. 20% over a single-step classification. SWIR wavelengths include spectral
43 information important in differentiating red oaks from other species and in distinguishing diseased red
44 oaks from healthy red oaks. We determined the most important wavelengths to identify oak species, red
45 oaks, and diseased red oaks. We also demonstrated that several multispectral indices associated with
46 physiological decline can detect differences between healthy and diseased trees. The wavelengths in
47 these indices also tended to be among the most important wavelengths for disease detection within PLS-
48 DA models, indicating a convergence of the methods. Indices were most significant for detecting oak wilt
49 during late August, especially those associated with canopy photosynthetic activity and water status. Our
50 study suggests that coupling phylogenetics, physiology, and canopy spectral reflectance provides an
51 interdisciplinary and comprehensive approach that enables detection of forest diseases at large scales

52 even at early disease stages. These results have potential for direct application by forest managers for
53 early detection to initiate actions to mitigate the disease and prevent pathogen spread.

54 **Keywords:** Oak wilt, photosynthetic decline, spectral reflectance, disease response, water content,
55 remote sensing, physiology.

56 **1. Introduction**

57 Invasive tree pathogens are a major threat to forest diversity and function (Evans et al., 2010; Hulcr
58 and Dunn, 2011). The damage caused by invasive species can have negative consequences for ecosystem
59 processes and services, including air and water quality maintenance, nutrient and carbon cycling, wood
60 and food provision, and climate regulation (Cavender-Bares et al., 2019; Díaz et al., 2019; Waller et al.,
61 2020). In North American forests, invasive pathogens and pests that infect trees have had devastating
62 impacts over the last century due to multiple factors, including global trade and climate change (Bergot
63 et al., 2004; Liebhold et al., 1995; Sturrock et al., 2011), leading to the loss or potential loss of multiple
64 foundational canopy species such as American chestnut (*Castanea dentata*), elm and ash species (*Ulmus*
65 and *Fraxinus* spp.), and eastern hemlock (*Tsuga canadensis*).

66 The oak genus (*Quercus*) is under threat from multiple pathogens and is of critical management
67 interest due to its dominance in temperate forests of the Eastern US (Johnson et al., 2019). Oaks rank
68 among the most diverse and important tree lineages in the United States, with 91 oak species comprising
69 nearly 30% of biomass in US temperate forests (Cavender-Bares, 2019). Among the pathogens affecting
70 oaks, oak wilt caused by the fungus *Bretziella fagacearum* (de Beer et al., 2017) is considered one of the
71 most destructive threat to oaks (Appel, 1995; Haight et al., 2011; Wilson and Lindsey, 2005). The oak wilt
72 fungus is spread below-ground from diseased trees to neighboring oaks through networks of grafted
73 roots, thus forming centers (i.e., pockets or foci) of diseased oaks. The pathogen is also transmitted above-

74 ground by nitidulid beetles (family *Nitidulidae*) and oak bark beetles (*Pityophthorus spp*) (Gibbs and French
75 1980). Multiple species of nitidulid beetles are attracted to spore-producing fungal mats that form on
76 branches and main stems of recently wilted red oaks (Gibbs and French, 1980; Juzwik et al., 2011; Juzwik
77 and French, 1983). On a land parcel to larger scale, oak wilt can be most effectively controlled when newly
78 established centers are detected and appropriately treated (Juzwik et al., 2011; Koch et al., 2010). This
79 prevents spread or minimizes disease intensification within a stand or the surrounding landscape. Surveys
80 of large, forested areas to identify suspect diseased trees are time-intensive and require expert training.
81 Such surveys are needed for landscape level oak wilt management efforts. Current operational
82 surveillance of forest landscapes in the Upper Midwest USA utilize aerial surveys conducted with fixed
83 wing aircraft, helicopters, and UAVs (Juzwik, 2009). Other airborne imaging spectrometry offers potential
84 for early and accurate detection of oak wilt at landscape scales.

85 Canopy spectral reflectance can potentially be used to detect the physiological decline resulting from
86 oak wilt fungus infection, and thus provide forest managers with a powerful tool. Airborne spectral
87 reflectance and indices derived from reflectance spectra have successfully been used to detect other
88 diseases and insect damage, such as Rapid Ohia Death, Emerald Ash Borer, bark beetles, and olive decline
89 due to *Xylella fastidiosa* (Asner et al., 2018; Lausch et al., 2013; Pontius et al., 2008, 2005; Zarco-Tejada et
90 al., 2018). To date, spectral indices for oak wilt detection have only been developed for oak seedlings
91 (Fallon et al., 2020). Oaks respond to oak wilt infection by forming balloon-like structures called tyloses
92 that occlude vessels within the xylem (Juzwik and Appel, 2016; Yadeta and Thomma, Bart, 2013). Vessel
93 occlusion potentially blocks or slows the spread of the pathogen but also reduces water transport and
94 limits canopy physiological performance by reducing transpiration and photosynthesis and potentially
95 causing photoinhibition (Fallon et al., 2020; Juzwik and Appel, 2016; Struckmeyer et al., 1954). In red oak
96 species, the fungus is rapidly spread internally in the transpiration stream through large diameter
97 springwood vessels before tylose formation limits the pathogen's spread. However, the tyloses formed

98 contribute to the development of wilt symptoms. Blockage of vascular conduits by tyloses and metabolites
99 produced by the fungus can lead to declines in transpiration and canopy water content as water supply
100 to the canopy is significantly impaired. Changes in photosynthetic activity, foliar pigment pool sizes, and
101 water status can be detected from canopy spectra (Hanavan et al., 2015; Pontius et al., 2005; Serbin et
102 al., 2015). Fallon et al. (2020) identified several spectral wavelengths predictive of oak wilt in greenhouse
103 seedlings that were related to leaf photosynthesis and water status. However, spectral properties of
104 seedlings grown and measured under greenhouse conditions may differ significantly from adult trees
105 grown under natural conditions due to growing conditions (e.g., sun, shade, humidity, and selective
106 filtering of solar radiation by glasshouse materials), ontogeny, canopy position, degree of canopy
107 emergence and other factors (Cavender-Bares et al., 2020; Fernandes et al., 2020; Ollinger, 2011). Hence,
108 it is important to explicitly test the extent to which we can detect oak wilt in natural populations of adult
109 trees using spectral reflectance. Identification of wavelengths associated with physiological function may
110 enable detection of trees with incipient oak wilt that would otherwise remain undetected until oak wilt
111 damage is more extensive.

112 Oak lineages vary in susceptibility to oak wilt. Consequently, identification of oak subgenus is crucial
113 to disease detection and prevention of spread. White oaks (*Quercus* subgenus *Quercus*), such as *Q. alba*
114 and *Q. macrocarpa*, have narrower vessels (Cavender-Bares and Holbrook, 2001) and may produce tyloses
115 efficiently (Cochard and Tyree, 1990) and in a more targeted manner in response to fungal infection (cf.
116 Yadeta and Thomma, Bart, 2013). This slows the spread or compartmentalizes (cf. Shigo, 1984) the
117 pathogen in infected white oak species (Jacobi and MacDonald, 1980; Koch et al., 2010; Schoenweiss,
118 1959). Thus, symptoms of oak wilt in white oaks appear as scattered wilt or as dieback in the crown that
119 develops over several to many years. In contrast, red oaks (*Quercus* subgenus *Lobatae*), such as *Q.*
120 *ellipsoidalis* and *Q. rubra*, have larger diameter springwood vessels and tend to delay tylose formation in
121 response to fungal infection, limiting their effectiveness in halting the spread of the fungus through the

122 vascular system (Juzwik and Appel, 2016; Struckmeyer et al., 1954; Yadeta and Thomma, Bart, 2013). Thus,
123 crown wilt symptoms in red oaks progress rapidly and lead to tree death within the same season or early
124 in the subsequent growing season. The comparatively rapid mortality of red oaks, the common
125 occurrence of intra-specific root grafts, and their common production of spore mats on recently wilted
126 trees contribute to the importance of the red oak lineage in driving disease epidemics in the landscape
127 (Menges and Loucks, 1984). Distinguishing red oaks from white oaks and other species across the
128 landscape is therefore a critical step towards large-scale management of oak wilt. Leaf level and canopy-
129 level modeling approaches using spectroscopic data have previously been successful in distinguishing
130 these lineages in experimental systems and manipulated forest communities (Cavender-Bares et al., 2016;
131 Fallon et al., 2020; Williams et al., 2020). We thus anticipate that it is possible to detect red oaks across
132 the landscape remotely by mapping lineage identities from classification algorithms using airborne
133 spectroscopic imagery. Here, we outline a stepwise phylogenetic approach to remote sensing of oak wilt
134 that entails: 1) identifying trees belonging to the oak genus, 2) identifying oaks belonging to the red oak
135 subgenus, and 3) identifying red oaks infected with oak wilt.

136 The goal of this study is to identify the optimal spectral range for early detection of oak wilt in red oak
137 species (*Q. ellipsoidalis* and *Q. rubra*) across landscapes. We compare both full-range (visible, near-
138 infrared, shortwave infrared, VSWIR, 400-2500 nm) and VNIR (visible, near-infrared, 400-1000 nm)
139 imaging spectroscopy for accuracy of oak wilt detection. While the VNIR is sensitive to photosynthetic
140 activity and pigments (Curran et al., 1995; Gamon and Surfus, 1999; Ustin et al., 2009), use of the SWIR
141 provides structural and phenotypic information (Townsend et al., 2013) that is strongly coupled with
142 phylogenetic information (Meireles et al., 2020a) including mesophyll integrity, chemical composition,
143 and canopy water content (Jacquemoud and Ustin, 2001; Ramirez et al., 2015; Romero et al., 2012; Sims
144 and Gamon, 2003). A second objective is to test the efficacy of spectral vegetation indices known to be
145 sensitive to physiological decline and disease response for their ability to differentiate healthy and

146 diseased trees (Pontius, 2014; Pontius 2020) (Table S1). Spectral indices can increase flexibility in the
147 detection approach because they use only a handful of wavelengths and can be easily calculated across
148 platforms as long as the same wavelengths are present (Pontius, 2014). Spectroscopic models that require
149 hundreds of wavelengths can have limited applicability across platforms when sensor measurement
150 characteristics vary (Castaldi et al., 2018; Crucil et al., 2019; Nouri et al., 2017).

151 Here, we develop statistical models for oak wilt detection at the landscape scale using airborne
152 spectroscopic imagery collected by two airborne systems (AISA Eagle and AVIRIS-NG) (Gholizadeh et al.,
153 2019; Hamlin et al., 2010) covering different ranges of wavelengths (VNIR and VSWIR, respectively). We
154 coupled on-ground tree identification and status surveys with airborne imaging spectroscopy data to
155 assess the capacity of airborne spectroscopy to detect oak wilt during early stages of disease development
156 in a temperate, mixed hardwood forest that included adult red oak populations. In doing so, we tested
157 the following hypotheses:

- 158 i) Canopy reflectance from airborne spectroscopic imagery can accurately detect oak wilt
159 infected trees in a natural forest landscape;
- 160 ii) Detection accuracy increases by first distinguishing trees in the oak genus and red oak
161 subgenus from other species based on spectral features specific to their phylogenetic lineage;
- 162 iii) Spectral reflectance models including both VNIR and SWIR wavelengths exhibit increased
163 accuracy relative to models including only VNIR wavelengths due to additional spectral
164 information related to phylogenetic identity and plant structure; and
- 165 iv) Spectral indices including wavelengths associated with photosynthetic activity, pigment
166 content, and canopy water status--associated with early symptom development in diseased
167 red oaks--differentiate early diseased red oaks from healthy red oaks.

168

169 **2. Methods**

170 2.1 Study area

171 The study area was the University of Minnesota Cedar Creek Ecosystem Science Reserve (CCESR)
172 (N 45°40'21", W 93°19'94"). Located in central Minnesota at approx. 280 m above sea level, CCESR has a
173 continental climate with cold winters (January mean -10 °C), hot summers (July mean 22.2 °C), and a mean
174 annual precipitation of 660 mm, spread fairly evenly throughout the year. The vegetation is comprised of
175 a mosaic of uplands dominated by oak savanna, prairie, mixed hardwood forest, and abandoned
176 agricultural fields, with lowlands comprised of ash and cedar swamps, acid bogs, marshes, and sedge
177 meadows. The presence of oak wilt fungus has been documented in central Minnesota since the 1940's
178 where it has led to widespread mortality in forests not treated for the disease. The diversity of tree species
179 and the presence of many active oak wilt centers make CCESR well suited to assess the capacity of airborne
180 spectroscopy to detect oak wilt in red oaks during its early stages of disease development.

181 2.2 Airborne data collection and tree survey

182 We collected two airborne imaging spectroscopy datasets across the whole study area on two
183 dates in 2016. The first dataset was collected on 07/22/2016 between 9:08 am and 10:24 am local time
184 using "CHAMP" (the CALMIT Hyperspectral Airborne Monitoring Platform), the University of Nebraska –
185 Lincoln's (UNL) aircraft operated by UNL's Center for Advanced Land Management Information
186 Technologies (CALMIT) and equipped with a pushbroom imaging spectrometer (AISA Eagle, Specim, Oulu,
187 Finland). Data were collected at an average flight altitude of 1150 m above ground level in the northwest-
188 southeast direction, yielding a spatial resolution of 0.75 m. The AISA Eagle comprises 488 spectral
189 channels covering 400-982 nm with a spectral resolution of 1.25 nm and a field of view of 37.7° under
190 nadir viewing conditions. To increase the signal-to-noise-ratio of the data, spectral on-chip binning was
191 applied. The final product had 63 bands at ca. 9 nm intervals. The AISA Eagle images were geometrically

192 corrected using aircraft GPS and IMU data in Specim's CaliGeoPRO software. Radiance data were
193 converted to reflectance using the empirical line correction (Conel et al., 1987) on reflectance
194 measurements collected from three calibration tarps (white, grey and black, with approx. 5%, 10%, and
195 40% reflectance, respectively; Odyssey, Ennis Fabrics, Edmonton, Alberta, Canada) with a portable
196 spectroradiometer (SVC HR-1024i, Spectra Vista Corporation, Poughkeepsie, NY, USA; 350 – 2500 nm)
197 simultaneous to the overflights. SVC reflectance data were resampled to match the wavelength of
198 airborne data and then used in the empirical line correction approach. The second dataset was collected
199 using the Airborne Visible/Infrared Imaging Spectrometer - Next Generation (AVIRIS-NG) by the National
200 Aeronautics and Space Administration (NASA) on 08/22/2016 starting at 03:43 PM local time at an average
201 flight altitude of 1210 m above ground level in the near West-East direction, yielding a spatial resolution
202 of 0.9 m. AVIRIS-NG comprises 432 spectral channels covering 380-2510 nm with a spectral resolution of
203 5 nm and a field of view of 36° under nadir viewing conditions. We measured the three calibration tarps
204 with our portable spectroradiometer (SVC HR-1024i, Spectra Vista Corporation, Poughkeepsie, NY, USA;
205 350 – 2500 nm) during the overflights for empirical line correction. Images were delivered by the NASA
206 Jet Propulsion Laboratory (JPL) orthorectified and preprocessed to apparent surface reflectance
207 (Thompson et al., 2015).

208 About one year after collecting airborne data, between June-August of 2017, we tagged 456 adult
209 trees of 12 species with apparently healthy crowns in woodland and savanna areas (see Table S2 for
210 species and sample sizes) including 47 *Quercus ellipsoidalis* E.J. Hill (red oak subgenus, particularly
211 vulnerable to oak wilt). In addition, we tagged 41 adult *Q. ellipsoidalis* trees with foliar symptoms
212 characteristic of oak wilt (i.e., bronzing and wilting leaves in sections of the canopy) (Fig. S1). Current
213 season crown wilt in 2017 suggested that incipient or initial crown wilt was present during mid to late
214 August 2016 when airborne spectral data were collected. Finally, we georeferenced the canopy center of

215 each tagged tree using a high-precision Trimble Pro6H GPS (Trimble, Sunnyvale, CA, USA) during the leaf-
216 off stage the following winter 2017-2018.

217 2.3 Canopy spectra extraction

218 We built a 1m-radius circular buffer around each canopy center using ArcGIS (version 10.6.1, ESRI,
219 2011) to sample several representative fully sunlit canopy pixels per individual tree (Table S2), which were
220 then linked to the respective species and oak wilt status (i.e., healthy, diseased). Spectral data processing
221 employed the package *spectrolab* (Meireles et al. 2018) in R (version 3.6.0, R Development Core Team,
222 2020). First, we resampled the extracted spectral data to 410-980 nm for AISA Eagle and 410-2400 nm for
223 AVIRIS-NG (both at 5 nm resolution to match wavelengths across sensors within the VNIR range) to
224 remove noisy wavelengths at the range ends of the sensors and reduce the number of bands in the
225 analyses. For AVIRIS-NG data only, we removed atmospheric water absorption bands between 1335-1430
226 nm and 1770-1965 nm and corrected artifacts at the sensor overlap region around 950 nm. Finally, for
227 both datasets we unit vector-normalized reflectance values to reduce illumination differences among
228 spectra (i.e., standardize differences in amplitude) (Feilhauer et al., 2010) while preserving differences in
229 the shape of spectra that are important for species classification (Meireles et al., 2020b). After processing
230 spectra, we calculated 21 spectral indices commonly used in the literature related to plant photosynthetic
231 activity (e.g., RDVI, SIPI, SIF), water status (e.g., WBI, NDWI), and photoprotective stress (e.g., PRI, CRI700,
232 NPQI) (see Table S1 for full index list). In cases where an index required a wavelength that was not a
233 multiple of 5 and therefore missing in our spectra, we approximated the reflectance value of that
234 wavelength based on the reflectance of the neighboring wavelengths either by using the nearest
235 wavelength if the difference was ≤ 1 nm or otherwise by interpolation between the two nearest wavelengths.
236 We assessed whether vector normalization affected the capacity of spectral indexes to detect oak wilt
237 infected trees and found no major differences in spectral index performance (Appendix S1).

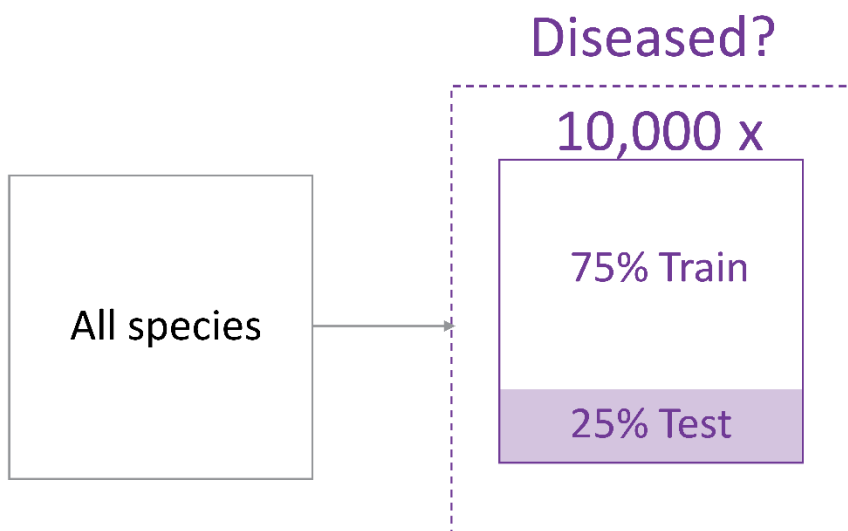
238 2.4 Statistical analyses

239 All statistical analyses were performed in R (version 3.6, R Development Core Team, 2020). To
240 assess the capacity of canopy spectral reflectance to distinguish healthy trees from those infected with
241 oak wilt, we performed partial least square discriminant analyses (PLS-DAs) (Barker and Rayens, 2003)
242 using AISA Eagle (410-980 nm), AVIRIS-NG VNIR (410-980 nm), AVIRIS-NG SWIR (985-2400 nm) and AVIRIS-
243 NG VSWIR (410-2400 nm). Performing PLS-DAs for each spectral range allowed us to assess the
244 importance of each range of wavelengths for accurate detection. We treated each pixel as an observation
245 because oak wilt disease does not manifest uniformly across the canopy of a tree, especially during early
246 stages of infection. At early stages, the fungus may have infected only a fraction of the vessels within the
247 tree trunk. Thus, curtailing the water supply to a few branches that become symptomatic while others
248 remain asymptomatic. Treating pixels -rather than the whole tree- as observations is critical for early
249 detection because early infected trees may display a small number of symptomatic pixels. Thus, averaging
250 pixels across a canopy composed of mostly healthy pixels may hide the signal from the infected pixels and
251 lead to high false negative classification rates. In all PLS-DAs, we used ANOVA to compare models with
252 different numbers of components and to identify the minimal number of components that maximized
253 Kappa, a model performance statistic that quantifies model performance compared to random
254 classification (Cohen, 1960). PLS-DAs were then run with the optimal number of components and the
255 “Bayes” option to account for differences in prior probability distributions among classes (Brereton and
256 Lloyd, 2014). The optimal number of components varied by model and are reported in the results section.

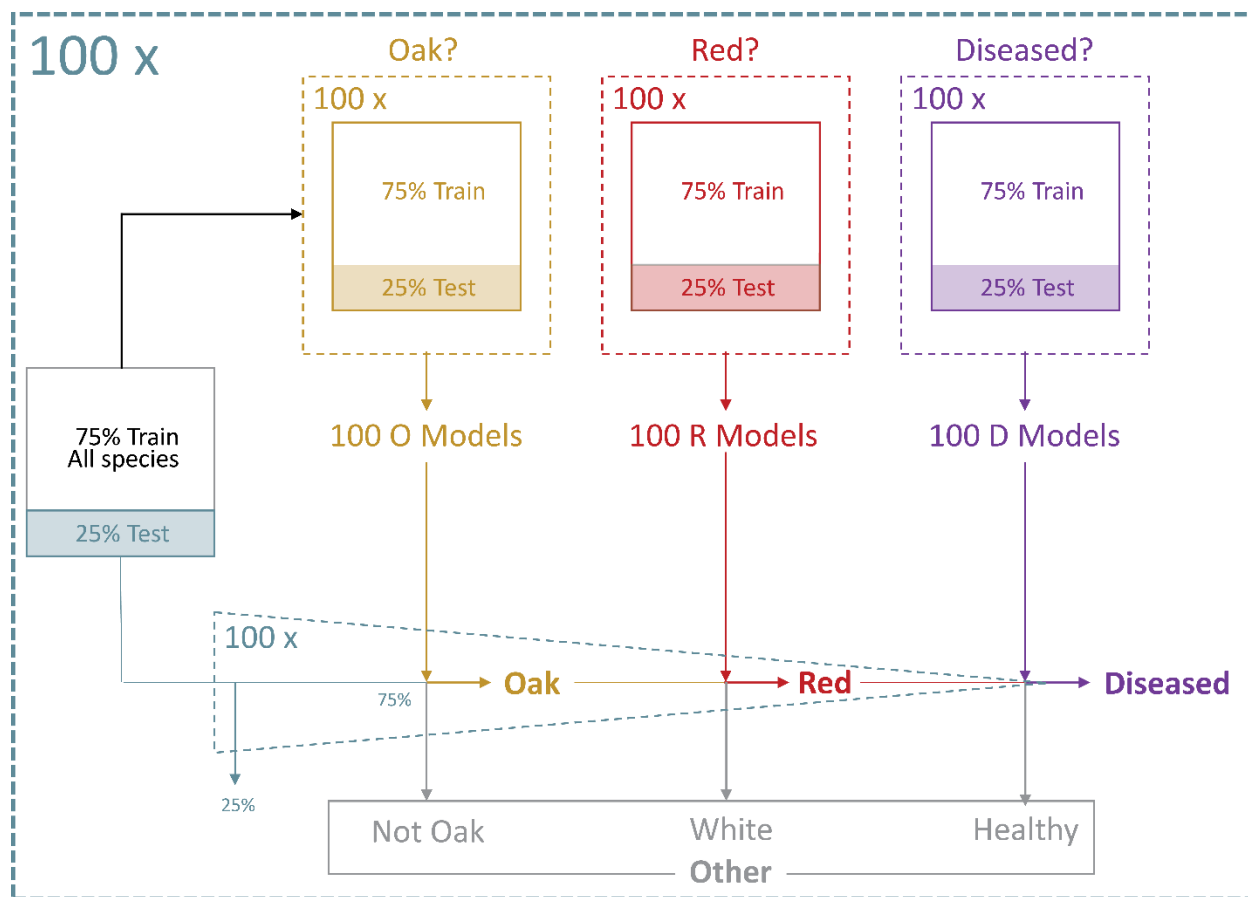
257 We tested the extent to which distinguishing red oaks from other species before oak wilt status
258 classification improved the predictive performance of our models by evaluating two approaches for oak
259 wilt detection: a modelling pipeline that did not consider species identities (“direct” approach) and one
260 that differentiated red oaks from other species first (“phylogenetic” approach) (Fig. 1). Both approaches
261 were applied to each sensor type and spectral range. In the direct approach, we ignored species identities

262 and split the data within each class (“diseased” and “other”) into 75:25 randomly sampled subsets for
263 model training and testing, respectively (Brereton and Lloyd, 2014; Fallon et al., 2020). We used the *caret*
264 and *p/s* packages in R (Kuhn 2008, Mevik et al. 2018) to assess model performance (accuracy, sensitivity,
265 specificity, kappa) and obtain model-predicted values for each class (Congalton, 2001; Fassnacht et al.,
266 2006). The random sampling, model training, model testing, performance assessment loop was iterated
267 10,000 times to generate 10,000 different training and test subsets, classification models, and
268 corresponding performance estimates. We assessed overall performance of the direct approach by
269 calculating the average and standard deviation of the performance outputs across all iterations.

Direct Approach



Phylogenetic Approach



270

271 **Figure 1:** Workflow of the direct and phylogenetic modeling approaches used to classify diseased red oaks.
272 In the phylogenetic approach, data were randomly split into 75% and 25% for model training and testing,
273 respectively. The training set was used iteratively to train three sets of 100 models for distinguishing oaks
274 from other species, red oaks from white oaks, and diseased red oaks from healthy red oaks. The trained
275 models were coupled to filter out any observations that do not belong to the red oak group before running
276 the disease detection step. This filtering process was tested using the initial 25% withheld test data. The
277 whole process was iterated 100 times using different subsets of data to generate uncertainty around the
278 performance estimates of the model. All classification results presented in the text utilize the 25%
279 withheld data sets. See Table S3 for sample sizes within each step.

280

281 In the phylogenetic approach, we chained three distinctive PLS-DA types to solve the oak wilt
282 classification problem sequentially through the steps illustrated in Fig. 1. First, we split our data into 75:25
283 randomly sampled subsets and left the 25% aside to test the overall performance of the phylogenetic
284 approach at the end of the process (see below). Second, we used the 75% to train three types of PLS-DAs
285 specifically aimed to distinguish 1) oaks from other species, 2) red oaks from white oaks, and 3) diseased
286 red oaks from healthy red oaks. Accordingly, each model type had a different data structure: data from
287 all species for PLS-DAs that distinguished oaks from other species, data belonging to the red and white
288 oak group only for PLS-DAs that distinguished red from white oaks, and data including only putative red
289 for PLS-DAs that distinguished diseased from healthy red oaks. All three PLS-DA types were performed
290 following the same iterative approach described above by randomly sampling a subset of the 75% of the
291 data for training, testing against the unused data of the subset (a 25% of the 75%), and assessing predictive
292 performance of each PLS-DA. The purpose of these iterations was not to average model coefficients but
293 rather to test how well PLS-DA types perform on average by generating confidence intervals for model
294 performance estimates. We assessed performance of each PLS-DA type by calculating the average and

295 standard deviation of the performance estimates across all iterations. We ran a total of 100 iterations for
296 each PLS-DA type, thus obtaining 100 separate models of each type capable of distinguishing either oaks
297 from other species, red oaks from white oaks, or diseased red oaks from healthy red oaks.

298 Finally, as an independent validation, we sequentially applied the 100 models of each PLS-DA type
299 to the 25% of data originally set aside through another 100 iterations. During each iteration, the 25%
300 subset containing all species was first split into 75:25 randomly sampled subsets (stratified by class, i.e.,
301 taxonomic grouping or health status) and only the 75% of the data were used with the aim of generating
302 variation among iterations. In the first step of the phylogenetic pipeline, the selected data—which
303 included all species —were classified as either oak or “other species” using the oak discrimination model.
304 Then, the data classified as oak were classified as either “red” or “white oak” using the red oak
305 discrimination model. Lastly, the data classified as red oak were classified as either “diseased” or “healthy
306 red oak” using the disease discrimination model. Data classified as “other species”, “white oak”, or
307 “healthy red oak” were later reclassified as “other” and their predicted classes were compared to their
308 true identities to evaluate predictive performance. The full phylogenetic approach was iterated 100 times
309 to ensure that the initial 75% split reflected all the existing variability within the dataset. Hence, we report
310 performance across a total of 10,000 (100x100) models of each type (Fig. 1, see Table S3 for sample sizes
311 and performance). We assessed overall performance of the phylogenetic approach by calculating the
312 average and standard deviation of the multistep classification performance outputs across all iterations.
313 Additionally, we performed direct PLS-DAs to classify the 12 dominant species present in our study area
314 to identify those potentially causing misclassification of red oaks.

315 To determine which combination of wavelengths was most useful for early detection of oak wilt,
316 we extracted wavelength importance factors from PLS-DAs corresponding to AISA Eagle and AVIRIS-NG
317 VSWIR and for both direct and phylogenetic approaches using the `varImp()` function in *caret* (Kuhn, 2008).
318 We focused on these four PLS-DAs because they included the full range of wavelengths covered by each

319 sensor with and without considering species identity. For simplicity, we limited our selection to the top
320 20 wavelengths with the highest average importance across all iterations within each model.

321 To assess whether reflectance indices associated with physiology could distinguish healthy red
322 oaks from those infected with oak wilt, we used ANOVA to perform pairwise comparisons between
323 healthy and diseased red oaks across all spectral reflectance indices and for both AISA Eagle and AVIRIS-
324 NG. Finally, we compared the effect sizes of these pairwise comparisons using Cohen's *d* statistic (Cohen,
325 1988) to assess differences in the detectability of oak wilt between late July and late August.

326 **3. Results**

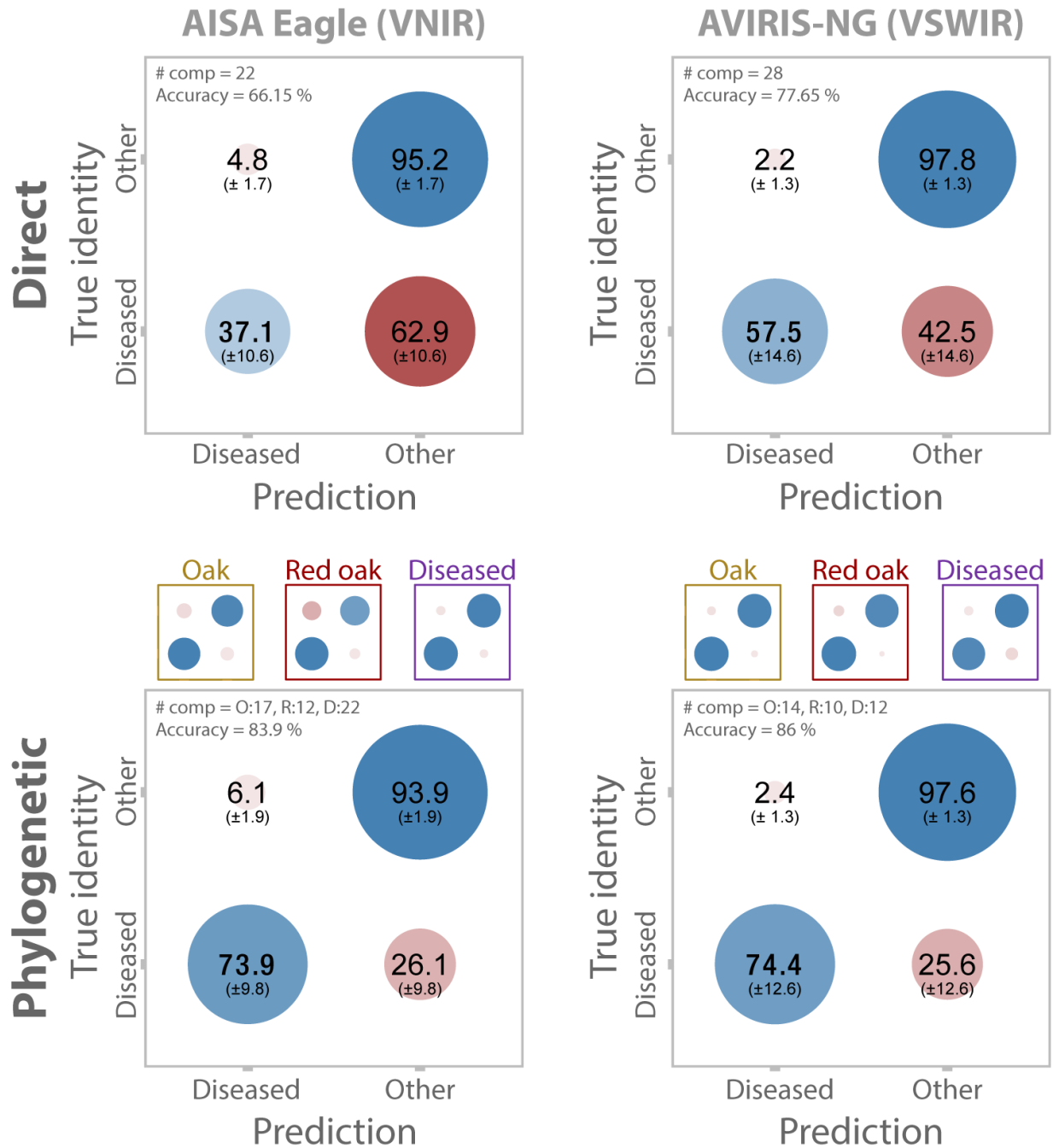
327 All classification accuracy results are reported for the sets of 25% of samples withheld from the PLS-DA
328 modeling steps, with the standard deviation calculated across the 10,000 iterations performed. All
329 classification results are reported in Table S3.

330 3.1 Tree species classification accuracy was high

331 The tree species classification PLS-DA demonstrated that it is possible to accurately identify most
332 of our 12 study species from spectral reflectance (AISA Eagle: 73.0% ($\pm 1.7\%$) correctly identified, AVIRIS-
333 NG VSWIR: 89.0% ($\pm 1.3\%$), Appendix S2). Models correctly classified and differentiated white oaks (*Q.*
334 *macrocarpa*) (AISA Eagle: 71.6% ($\pm 4.3\%$), AVIRIS-NG VSWIR: 87.3% ($\pm 2.2\%$)) and red oaks (*Q. ellipsoidalis*
335 and *Q. rubra*) (AISA Eagle: 57.6% ($\pm 4.0\%$), AVIRIS-NG VSWIR: 80.4% ($\pm 2.4\%$)). However, models classifying
336 the oak genus as a whole had higher accuracies (82.1% ($\pm 5.9\%$) and 94.0% ($\pm 5.0\%$) for AISA Eagle and
337 AVIRIS-NG VSWIR, respectively, Appendix S3) than individual species models, similar to results from leaf
338 level spectra (Cavender-Bares et al., 2016).

339 3.2 Spectral reflectance models detected diseased red oaks the season prior to full crown wilt

340 Spectral reflectance models did not accurately distinguish diseased red oaks from other trees
341 unless red oaks were first distinguished from other species (Table S3). In the direct approach, overall
342 model accuracy was significantly better than expected by chance (AISA Eagle: 66.2% ($\pm 6.2\%$), components
343 (k) = 22; AVIRIS-NG VSWIR: 77.7% ($\pm 8.0\%$), k = 28, Fig. 2), but only healthy trees (true negatives) were
344 correctly classified with high accuracy (AISA Eagle: 95.2% ($\pm 1.7\%$), AVIRIS-NG VSWIR: 97.8% ($\pm 1.3\%$),
345 indicating high model specificity). Diseased red oaks were misclassified (false negatives) in more than
346 62.9% ($\pm 10.6\%$) and 42.5% ($\pm 14.6\%$) of the AISA Eagle and AVIRIS-NG VSWIR cases, respectively, indicating
347 low model sensitivity (Fig. 2). As a result, isolating oaks and then red oaks through a stepwise phylogenetic
348 PLS-DA model prior to disease detection reduced misclassification errors and improved the overall
349 performance of both AISA Eagle and AVIRIS-NG VSWIR models (AISA Eagle: 83.9% ($\pm 5.9\%$), k = oaks: 17,
350 red oaks: 12, diseased red oaks: 22; AVIRIS-NG VSWIR: 86% ($\pm 6.95\%$), k = oaks: 14, red oaks: 10, diseased
351 red oaks: 12; Appendix S3-5, Table S3). The increase in performance was mostly due to a major increase
352 in correct classification (true positives) of diseased red oaks (AISA Eagle: 73.9% ($\pm 9.8\%$), AVIRIS-NG VSWIR:
353 74.4% ($\pm 12.6\%$)) (Fig. 2, Appendix S5) resulting in increased model sensitivity compared to the direct PLS-
354 DA approach.



355

356 **Figure 2:** A stepwise phylogenetic classification approach enhanced early detection of oak wilt in red oaks.

357 Models that included both VNIR and SWIR wavelengths (AVIRIS-NG VSWIR) showed better prediction

358 capacity than models including VNIR only. Blue and red circles represent correct and incorrect

359 classifications, respectively. The size and color intensity of the circle represent the average percentage of

360 classifications into each group based on the 25% of data withheld from 10,000 model-fitting iterations,

361 one standard deviation is shown in parentheses. Grey boxes describe the overall predictive performance
362 for a given approach and dataset. Red and blue circles in colored inset boxes above each phylogenetic
363 model describe the performance of the steps within the phylogenetic model at discriminating oaks (gold),
364 red oaks (red), and diseased red oaks (purple), respectively. The number of components used for each
365 model or model step (O = oaks, R = red oaks, D = diseased) is given at the top left corner of the plot. See
366 Appendices S3, S4, and S5 and Table S3 for detailed performance of the phylogenetic steps).

367

368 All steps within the phylogenetic PLS-DA model showed high performance (Table S3). The oak
369 detection step showed high accuracy (AISA Eagle: 84% ($\pm 1.5\%$), $k = 17$; AVIRIS-NG VSWIR: 96% ($\pm 0.3\%$), k
370 = 14) and only misclassified oaks as other species in 17.9% ($\pm 5.9\%$) and 6% ($\pm 5\%$) of the AISA Eagle and
371 AVIRIS-NG VSWIR cases, respectively (Appendix S3). Similarly, the red oak detection step showed high
372 accuracy (AISA Eagle: 85% ($\pm 2.1\%$), $k = 12$; AVIRIS-NG VSWIR: 96% ($\pm 0.6\%$), $k = 10$) and only misclassified
373 red oaks as white oaks in 8.9% ($\pm 3.8\%$) and 2% ($\pm 3\%$) of the AISA Eagle and AVIRIS-NG VSWIR cases,
374 respectively (Appendix S4). Finally, the diseased red oak detection step also showed high accuracy (AISA
375 Eagle: 94% ($\pm 1.8\%$), $k = 22$; AVIRIS-NG VSWIR: 91% ($\pm 1.1\%$), $k = 12$) and misclassified diseased red oaks as
376 healthy red oaks in only 5.5% ($\pm 1.8\%$) and 12.3% ($\pm 3.5\%$) of the AISA Eagle and AVIRIS-NG VSWIR cases,
377 respectively (Appendix S5). We note, however, that the complexity of the model in this last step was
378 nearly twice as high in AISA Eagle ($k = 22$) than in AVIRIS-NG VSWIR models ($k = 12$).

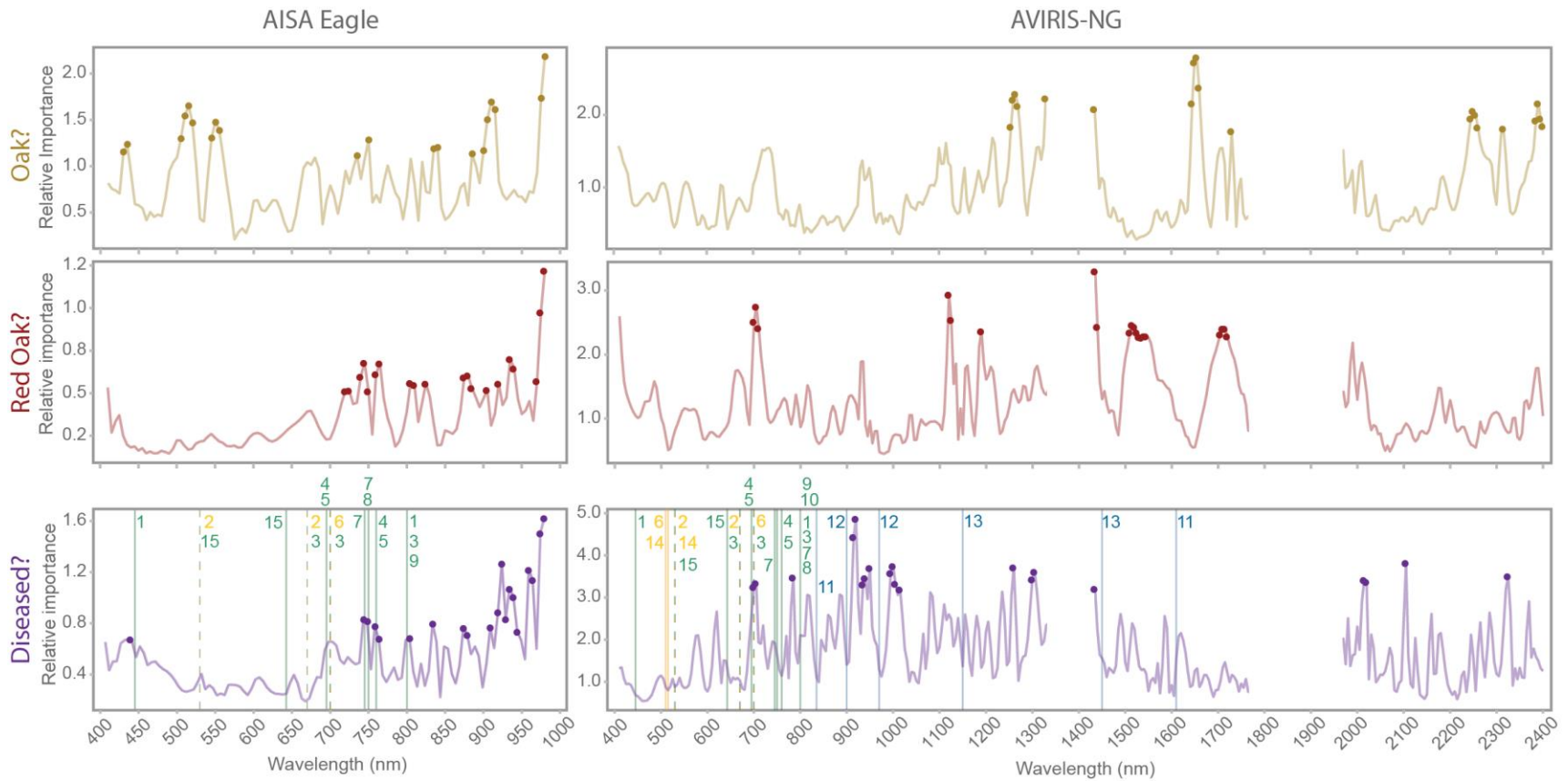
379 3.3 VNIR and SWIR ranges are both important in detecting oak wilt

380 AVIRIS-NG SWIR models showed slightly higher classification accuracy (true positive rate) of
381 diseased trees than AVIRIS-NG VNIR models in both direct (AVIRIS-NG SWIR: 44.9% ($\pm 14.9\%$), AVIRIS-NG
382 VNIR: 31.4% ($\pm 13.7\%$)) and phylogenetic approaches (AVIRIS-NG SWIR: 64.3% ($\pm 14.1\%$), AVIRIS-NG VNIR:
383 57.9% ($\pm 14.3\%$)) (Fig. S2). When both AVIRIS-NG VNIR and SWIR were used together, models

384 outperformed those using either VNIR or SWIR only. This was the case under both direct (AVIRIS-NG
385 VSWIR: 57.5% (± 14.6)) and phylogenetic approaches (AVIRIS-NG VSWIR: 74.4% (± 12.6)).

386 When differentiating oaks from other species using AISA Eagle models, important wavelengths
387 were clustered within the 440-550 nm, 725-750 nm, and the 850-980 nm regions of the VNIR range (Fig.
388 3). However, in AVIRIS-NG models that included both VNIR and SWIR, the importance of these regions
389 was outweighed by regions 1200-1450 nm, 1600-1750 nm, and 2200-2400 nm within the SWIR range.
390 When differentiating red oaks from white oaks using AISA Eagle models, we found important wavelengths
391 clustered within the 700-760 nm, 780-820 nm, and 860-980 nm regions. However, in AVIRIS-NG VSWIR
392 models, the importance of VNIR regions was strongly outweighed by regions within the SWIR range except
393 for several wavelengths at the red-edge. Within the SWIR, the important wavelengths were clustered
394 within 1100-1200 nm and 1490-1550 nm in addition to two spikes at 1450 nm and 1700 nm. When
395 differentiating healthy red oaks from diseased red oaks using AISA Eagle models, important wavelengths
396 appeared at 440 nm and across the 750-980 nm region of the VNIR range. AVIRIS-NG VSWIR models also
397 identified important wavelengths within the 700-1000 nm range but also identified important
398 wavelengths within the SWIR range such as wavelengths 1250, 1300, 1440, 2010, 2100, and 2320 nm.
399 Most importantly, the twenty most important wavelengths for detection of oaks, red oaks, and diseased
400 red oaks did not overlap in the AVIRIS-NG VSWIR models (Fig. 3). This was not the case for AISA Eagle
401 models where several of the most important wavelengths were the same in sequential classification steps.
402 Both AISA Eagle and AVIRIS-NG VSWIR models shared important wavelengths for oak wilt detection
403 around 800 nm and across the 910-980 nm range.

404



405

406 **Figure 3:** The twenty most important wavelengths—based on variable importance in projection (VIP)—differed among steps discriminating oaks
 407 (gold) from other species, red oaks (red) from white oaks, and diseased red oaks (purple) from healthy red oaks, and among models using either
 408 VNIR range (AISA Eagle) or both VNIR and SWIR ranges (AVIRIS-NG VSWIR). Vertical lines with numbers indicate wavelengths used in spectral
 409 indices associated with photosynthetic capacity (green), photoprotective pigment content (yellow), and water status (blue) that showed

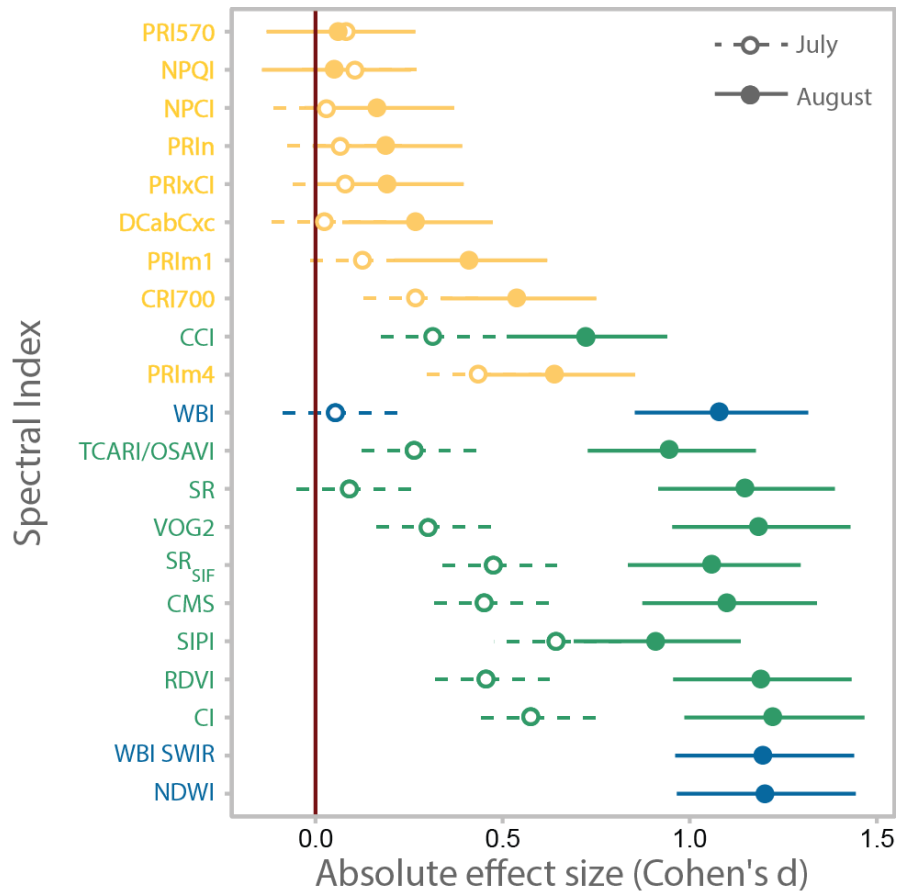
410 significant differences between healthy and oak wilt-infected trees. Numbers indicate spectral indices
411 SIPI (1), PRIM4 (2), TCARI/OSAVI (3), CMS (4), SR_{SIF} (5), CRI700 (6), VOG2 (7), CI (8), RDVI (9), SR (10),
412 NDWI (11), WBI (12), WBI-SWIR (13), PRI_m1 (14), CCI (15).

413

414 3.4 Declines in photosynthetic capacity and water status signal oak wilt

415 Overall, spectral indices calculated from the AVIRIS-NG dataset collected during late August
416 showed more pronounced differences between healthy and diseased red oaks than those calculated from
417 the AISA Eagle dataset collected in late July (Fig. 4). Spectral indices associated with canopy
418 photosynthetic capacity showed significant differences between healthy and diseased red oaks for both
419 sensors and time periods. Within the AISA Eagle dataset, all indices associated with photosynthetic
420 capacity except Normalized Pigment Chlorophyll Index (NPCI) and Simple Ratio (SR) were significantly
421 different between healthy and diseased red oaks (Table S4). Within the AVIRIS-NG dataset, all indices
422 associated with photosynthetic capacity except NPCI were significantly different between healthy and
423 diseased red oaks. In addition, the differences between healthy and diseased red oaks were markedly
424 greater for AVIRIS-NG data relative to the AISA Eagle data. Most spectral indices associated with
425 photoprotective stress showed no significant differences between healthy and diseased red oaks. Those
426 that did—Photochemical Reflectance Index (PRI_m4), Carotenoid Reflectance Index (CRI700), and (only in
427 AVIRIS-NG) PRI_m1—share wavelengths with indices of photosynthetic capacity, such as the SR and
428 Transformed Chlorophyl Absorption in Reflectance Index/Optimized Soil-Adjusted Vegetation Index
429 (TCARI/OSAVI) indices. Indices associated with canopy water status also showed significant differences
430 between healthy and diseased red oaks, but only within the AVIRIS-NG dataset. The effect sizes of the
431 differences were comparable to those of indices associated with photosynthetic capacity. Within the AISA
432 Eagle dataset, Water Band Index (WBI)—the only spectral index associated with canopy water content

433 that could be calculated using the VNIR range—did not show significant differences between healthy and
 434 diseased red oaks.



435
 436 **Figure 4:** Spectral indices associated with photosynthetic (green) and water status (blue) differentiated
 437 early diseased red oaks from healthy red oaks. Each point represents the magnitude of the difference
 438 between healthy and diseased trees—shown by the absolute value of the Cohen’s d—for a given index
 439 and time of data collection (July or August). Effect size can be understood as the amount of overlap
 440 between the distributions of two groups. For an effect size of 0, the mean of group 2 falls within the
 441 50th percentile of group 1, and the distributions overlap completely, meaning there is no difference
 442 between them. For an effect size of 0.8, the mean of group 2 falls within the 79th percentile of group 1;
 443 thus, an average sample from group 2 would have a higher value than 79% of all samples from group 1
 444 (Sullivan and Feinn, 2012). The Indices associated with photoprotective pigments (yellow) fail to do so

445 unless they also include wavelengths associated with photosynthetic capacity. Differences between
446 healthy and diseased trees were more pronounced when indices were calculated from AVIRIS-NG
447 spectral data collected in late August. Lines represent 95% confidence intervals. Effect sizes are
448 significantly different from zero when their confidence intervals do not overlap with the red zero line.

449

450 **4. Discussion**

451 The negative impacts of oak wilt and its rate of spread across North American ecosystems calls for
452 early detection tools that accurately identify trees affected by oak wilt at landscape scales (Haight et al.,
453 2011; Hulcr and Dunn, 2011; Juzwik et al., 2011). We show that PLS-DA models developed from airborne
454 spectroscopic imagery can accurately detect oak wilt-infected red oaks at early stages of disease
455 development. We demonstrate an approach to identify oak wilt-infected red oaks, which takes advantage
456 of the physiological and phylogenetic information embedded in their reflectance spectra (Cavender-Bares
457 et al., 2016; Meireles et al., 2020a). By first differentiating oaks from non-oaks, and then identifying red
458 oaks—which are highly susceptible to rapid disease development—classification models based on spectral
459 reflectance data can be used to distinguish oak-wilt affected and healthy red oaks with high accuracy. We
460 also found that spectral indices associated with plant photosynthesis and water status can confirm
461 infection and are potentially sensitive to disease progression through physiological decline. Spectral
462 indices also provide a mechanistic basis for understanding and tracking the physiological changes that
463 allow classification models to detect oak wilt.

464 *4.1 Including short wave infrared reflectance improves model accuracy*

465 Including SWIR wavelengths in spectral reflectance models increases oak wilt detection accuracy.
466 We observed higher oak wilt detectability in direct AVIRIS-NG SWIR and VSWIR than direct AISA Eagle

467 VNIR models. Direct PLS-DAs using AVIRIS-NG VNIR showed similar performance to that of AISA Eagle VNIR
468 models (Fig. S2). We can therefore attribute the greater performance of direct AVIRIS-NG VSWIR models
469 to the addition of SWIR wavelengths. Direct AISA Eagle models rely on many of the same wavelengths to
470 distinguish red oaks from other species and to distinguish diseased and healthy red oaks (Fig. 3). As such,
471 they often misclassify diseased red oaks as other species (Fig. 2, Appendix S3 & S4). However, even direct
472 models show much higher accuracy when both VNIR and SWIR ranges are included (AVIRIS-NG VSWIR).
473 The additional information-rich SWIR wavelengths allow models to use different wavelength regions to
474 distinguish oaks from other species, red oaks from white oaks, and diseased red oaks from healthy red
475 oaks (Fig. S2). Consequently, the critical wavelengths to identify oaks, red oaks, and diseased red oaks
476 overlap less, which reduces the chances of confusion among classes (Fig. 3). Most likely, including SWIR
477 reflectance provides temporally stable spectral features containing phylogenetic information associated
478 with plant structural traits (Cavender-Bares et al., 2020; Meireles et al., 2020a) that serve to reduce
479 misclassification of diseased red oaks as other species. Indeed, we find that the SWIR range was more
480 important than the VNIR range in correctly identifying oak species and red oaks (Fig. 3). In particular, the
481 20 and 17 most important wavelengths for identifying oaks and red oaks, respectively, fell within the SWIR
482 range. The SWIR was also important for distinguishing diseased from healthy red oaks. Among the most
483 important SWIR wavelengths were those associated to plant water content and leaf chemistry such as
484 protein, sugars, lignin, and cellulose content (Asner et al., 2018; Fourty et al., 1996). Based on our results,
485 the SWIR range appears to contain disease-specific and phylogenetic information highly relevant to
486 detecting symptoms of oak wilt and to identifying its hosts. Hence, similar to previous work combining
487 VNIR reflectance with SIF or thermal data (Zarco-Tejada et al., 2018, 2016), when SWIR wavelengths are
488 combined with VNIR in oak wilt detection models, detection rates are maximized.

489 *4.2 A multi-step phylogenetic approach increases accuracy*

490 Partitioning the classification process into simple binary steps within a phylogenetic framework
491 reduces potential misclassification and increases model accuracy. We used a hierarchical classification
492 approach (Allen and Walsh, 1996; Townsend et al., 2009; Wolter et al., 1995) aimed towards distinguishing
493 the more susceptible red oaks from white oaks and other species that are less susceptible to oak wilt.
494 During the first step, phylogenetic models distinguish between oaks and other species because the
495 reflectance spectrum shows phylogenetic conservatism among the oaks (Cavender-Bares et al., 2016;
496 Cavender-Bares, 2019), including those infected by oak wilt. The model is not required to distinguish
497 between healthy and diseased conspecifics in this first step, thus simplifying the task. Reducing the
498 number of potential classes becomes increasingly important as the individuals become more
499 phylogenetically related—and hence more phenotypically similar—which makes correct classification
500 more challenging (Meireles et al., 2020b). Removing non-oak species significantly reduces variation in
501 phylogenetically conserved regions of the spectra, allowing the model to be trained on spectral
502 differences that distinguish white and red oaks and subsequently on the spectral variation that
503 distinguishes diseased and healthy red oaks. Because of these filtering steps, the disease detection
504 algorithm is highly accurate (>90%; Fig. 2, appendix S5) and significantly more accurate than a single-step,
505 direct approach. While the phylogenetic approach gains complexity in terms of number of steps, each
506 binary classification step is simple and requires few independent components. Although each step
507 generates classification errors that propagate through the modeling pipeline, these errors are captured
508 by the overall performance metrics, indicating that the increase in accuracy gained through the
509 phylogenetic filtering outweighs the propagated errors. Interestingly, implementing a stepwise
510 phylogenetic approach boosted model performance to a greater extent in AISA Eagle and AVIRIS-NG VNIR
511 than in AVIRIS-NG VSWIR models. This suggests that the main contribution of the phylogenetic approach
512 is the same as that of adding SWIR range. The phylogenetic approach increases accuracy by reducing the
513 number of classes to compare while inclusion of the SWIR range increases accuracy by increasing the

514 number of informative wavelengths. Reduced boosts from using the stepwise phylogenetic approach in
515 the performance in AVIRIS-NG VSWIR relative to VNIR models may be a consequence of including SWIR
516 and increasing informative wavelengths beyond what is available within the VNIR, avoiding
517 misclassification (see previous section, Fig. 3). Reduced boosts in AVIRIS-NG VNIR relative to AISA Eagle
518 VNIR models could be due to differences in sampling date or to sensor type and/or data quality (e.g.,
519 associated with spectral binning and/or signal-to-noise).

520 Our results highlight that species classification is critical for increasing model accuracy for a simple
521 reason: if the disease is host-specific, modeling can be more tractable by detecting potential hosts first.
522 Future studies should test whether phylogenetic models with simple binary classification steps such as
523 the one used here make disease detection models generic enough to be applicable across different sites
524 and years.

525 *4.3 Targeted spectral indices help understand physiological changes associated with oak wilt disease*

526 Diseased red oaks were more easily differentiated from healthy red oaks by spectral reflectance
527 indices associated with photosynthetic activity (Carter and Knapp, 2001; Vogelmann et al., 1993; Zarco-
528 Tejada et al., 2002) and water status (Ceccato et al., 2001; Serrano et al., 2000; Ullah et al., 2014) than by
529 photoprotective pigment content indices. Indices based on photoprotective pigment content could not
530 differentiate diseased trees from asymptomatic trees unless they included wavelengths also associated
531 with photosynthetic activity (Figs. 3 & 4). These results suggest that oak wilt infection in adult trees in
532 natural ecosystems triggers declines in photosynthetic rate, stomatal conductance, and water content
533 just as in greenhouse seedlings (Fallon et al., 2020). All indices showed greater sensitivity in late August
534 relative to late July suggesting that oak wilt symptoms had progressed. Moreover, our results also uncover
535 an important temporal pattern in physiological decline: photosynthesis declines first, and dehydration
536 follows. By July, indices of photosynthetic activity showed greater sensitivity to oak wilt than indices of

537 water status (Fig. 4). At early stages, both tylose production (in response to infection) and plugging of
538 vessels by metabolites of the fungus are likely to have contributed to diminished water transport. In turn,
539 reduced transpiration and stomatal closure induced by reduced water supply is expected to have caused
540 photosynthetic decline (Fallon et al., 2020). However, trees may not yet have experienced enough
541 vascular occlusion to cause canopy dehydration. By August, water status indices showed greater overall
542 sensitivity to oak wilt than photosynthetic activity indices (Fig. 4). Although different sensors were used
543 at each time point, the normalized indices should be comparable across sensor types. The results are
544 consistent with experimental work indicating that photosynthesis is the first physiological process to
545 decline as stomata shut down (Fallon et al., 2020) followed by water content as vessel occlusion develops
546 and the fungus damages cell walls and membranes (e.g., through pathogen-produced toxins) leading to
547 dehydration and tissue death (Oliva et al., 2014). Pairing photosynthetic activity and water status indices
548 can provide powerful tools to delineate oak wilt centers across areas of the landscape dominated by red
549 oaks. Pockets of affected trees may show a center-outward radial gradient with dry dead trees at the
550 center, dehydrated and photosynthetically impaired trees in the middle, and trees with slightly lower
551 photosynthetic capacity than expected around the edge of the pocket (i.e., early disease development
552 phase) (Figs. 5, S3, & S4). Hence, paired indices could provide information about the stage of disease
553 development, thus allowing managers to better assess risk of spread and adjust the magnitude of their
554 interventions accordingly (Pontius and Hallett, 2014).

555



556

557 **Figure 5.** A typical oak wilt pocket observed through true color and a combination of spectral indices
558 using the 2016 AVIRIS-NG data. A tree killed by oak wilt during 2015 (orange circle) can be observed at
559 the center of the oak wilt pocket in true color (red as 640 nm, green as 550 nm, and blue as 470 nm).
560 Three diseased trees (blue circles) stand next to it that cannot be detected with true color images. Both
561 dead and diseased trees are surrounded by an outer ring of healthy trees. Diseased trees become
562 apparent through spectral indices associated with photosynthetic function and water status -such as the
563 Carter-Miller Stress index (CMS), Chlorophyll Index red edge (CI), and Water Band Index in the SWIR
564 range (WBI SWIR)- placed on the red (R), green (G), and blue (B) channels.

565

566 **5. Conclusions**

567 Protecting ecosystems from the threats of invasive species resulting from globalization and a
568 changing climate is one of the most pressing challenges of our times (Díaz et al., 2019; Liebhold et al.,
569 1995; Waller et al., 2020). Early detection greatly enhances the ability of managers to prevent the

570 enormous ecological and economical damage caused by invasive species (Juzwik, 2000; Poland et al.,
571 2021). Airborne spectroscopic imagery enables landscape-level detection of diseases caused by invasive
572 pathogens, like oak wilt, at their earliest stages due to the phylogenetic and physiological information
573 embedded in spectral reflectance. SWIR wavelengths increased model accuracy by enabling detection of
574 disease-specific hosts, a critical step in identifying forested areas vulnerable to infection. Additionally,
575 inference of the physiological basis of oak wilt symptom development using spectral indices associated
576 with known spectral features points to the potential to delineate oak wilt centers using remote sensing
577 products that monitor canopy photosynthetic capacity and water status. Importantly, in our study
578 landscape detection was made possible by coupling airborne spectroscopic imagery with traditional
579 knowledge from taxonomic and disease experts and high precision ground GPS reference data. While
580 landscape detection of oak wilt will facilitate the task of detecting infected trees, there is still much work
581 to do. Future studies should assess whether PLS-DA models will be general enough to detect oak wilt
582 across years and sites and whether the physiological basis of oak wilt symptom development will be
583 sufficient to make accurate inferences about the presence of new oak wilt infections. Further investigation
584 of the physiological changes that accompany disease progression may also provide the link to scale
585 spectral detection to regional scales via spaceborne platforms. The work done here points to the benefit
586 of research that might lead to an “optimal” remote sensing system (airborne or satellite) for detecting
587 invasive diseases. We hope that our research motivates such work.

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602

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