

1 Near Infrared Hyperspectral Imaging of *Fusarium*- Damaged Oats (*Avena sativa* L.)

2 Selamawit Tekle^{1,2}, Ingrid Måge³, Vegard H. Segtnan³, Åsmund Bjørnstad¹

3 ABSTRACT

4 The feasibility of hyperspectral imaging (HSI) to detect deoxynivalenol (DON) content
5 and *Fusarium* damage in single oat kernels was investigated. Hyperspectral images of oat kernels
6 from a *Fusarium*-inoculated nursery were used after visual classification as asymptomatic, mildly
7 damaged, and severely damaged. Uninoculated kernels were included as controls. The average
8 spectrum from each kernel was paired with the reference DON value for the same kernel and a
9 calibration model was fitted by partial least squares regression (PLSR). To correct for the skewed
10 distribution of DON values and avoid nonlinearities in the model, the DON values were
11 transformed as $DON^* = [\log(DON)]^3$. The model was optimized by cross-validation, and its
12 prediction performance was validated by predicting DON^* values for a separate set of validation
13 kernels. The PLSR model and linear discriminant analysis (LDA) classification were further used
14 on single-pixel spectra to investigate the spatial distribution of infection in the kernels. There were
15 clear differences between the kernel classes. The first component separated the
16 uninoculated/asymptomatic from the severely damaged kernels. Infected kernels showed higher
17 intensities at 1920, 2070 and 2140 nm, while non-infected kernels were dominated by signals at
18 1420, 1620 and 1850 nm. The DON^* value of the validation kernels were estimated using their
19 average spectrum, and the correlation (R) between predicted and measured DON^* was 0.8. Our

¹ Department of Plant Sciences, Norwegian University of Life Sciences, P. O. Box 5003, 1432 Ås, Norway

² Corresponding email: selag@nmbu.no

³ Nofima AS, Osloveien 1, NO-1430 Ås, Norway

20 results show that HSI has great potential in detecting *Fusarium* damage and predicting DON in
21 oats but it needs more work to develop a model for routine application.

22 **Abbreviations**

23 DON: Deoxynivalenol, FHB: Fusarium Head Blight, HSI: Hyperspectral Imaging, LDA: Linear
24 Discriminant Analysis, NIR: Near Infrared, PCA: Principal Component Analysis, PLSR: Partial
25 Least Squares Regression, VIS: Visible.

INTRODUCTION

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Fusarium head blight (FHB) is one of the important diseases of cereals worldwide. The disease causes substantial yield and quality losses every year (Parry et al., 1995, McMullen et al., 1997). It results in light-weighted shriveled kernels with pink to brownish discoloration (McMullen et al., 1997). *Fusarium* spp. produce a wide array of toxins (Bottalico & Perrone, 2002) which are involved in isolate aggressiveness and species pathogenicity (Langevin et al., 2004). These toxins raise food and feed safety issues and impair animal production as they cause feed refusal, vomiting, and reduced weight gain in farm animals. They are also associated with various acute and chronic ailments in animals and humans (Bergsjø et al., 1993, D’Mello et al., 1999). Deoxynivalenol (DON) and its derivatives, mainly produced by *F. graminearum* and *F. culmorum*, are the most commonly encountered *Fusarium*-toxins in Europe (Bottalico & Perrone, 2002) and in Norwegian small grain cereals (Bernhoft et al., 2013). Among the small grain cereals produced in Norway, oats (*Avena sativa* L.) are the most frequently and highly DON-contaminated cereal species (Bernhoft et al., 2013).

Fusarium infection has a significant impact on grain quality. *Fusarium graminearum* infection in barley (*Hordeum vulgare* L.) results in significant reduction in germination and kernel plumpness (Schwarz et al., 2001). In wheat (*Triticum aestivum* L.), infection results in poor baking performance and flour color, reduced loaf volume, and weak dough properties (Dexter et al., 1996, Nightingale et al., 1999, Wang et al., 2005). Infection destroys starch granules, storage proteins, and cell walls (Bechtel et al., 1985, Wang et al., 2005). Wheat kernels infected with *F. culmorum* display damaged starch granules, complete or partial lack of the protein matrix and complete disappearance of the starchy endosperm under severe infection (Jackowiak et al., 2005).

23 Significant degradation of the endosperm protein and lower content of storage proteins in *F.*
24 *avenaceum* and *F. graminearum*- infected wheat are also reported (Nightingale et al., 1999).

25 The level of fungal secondary metabolites in grains (such as DON) is very low compared
26 to the major seed constituents. Conventional NIR spectroscopy is not very sensitive to such minor
27 constituents (Gowen et al., 2007). Therefore, efforts to calibrate DON contamination in bulk
28 samples using NIR spectroscopy must rely on major effects of the disease on grain constituents
29 that are correlated with DON (Siuda et al., 2008, Tekle et al., 2013). Hyperspectral imaging (HSI)
30 is a powerful non-destructive tool to detect contaminants in food and feed (Gowen et al., 2007,
31 Feng & Sun, 2012). It has higher sensitivity to minor seed constituents than conventional NIR
32 spectroscopy (Gowen et al., 2007) due to the local enhancement of constituent signals. It combines
33 conventional imaging and spectroscopy to provide a three-way data matrix known as a hypercube
34 made of two spatial (x, y) and one wavelength (z) dimensions. It is made of hundreds of single
35 channel, grayscale images, each representing a single band of spectral wavelength (Gowen et al.,
36 2007). This combination of spatial and spectral information enables building ‘chemical maps’ that
37 show distribution of grain components in individual kernels (Feng & Sun, 2012, Williams et al.,
38 2010). Powerful and efficient data processing methods, however, are required to extract useful
39 information from such hyperspectral data (Feng & Sun, 2012).

40 Hyperspectral imaging has previously been used to classify kernels and kernel regions
41 based on fungal damage and/ or DON contamination (Gowen et al., 2007, Polder et al., 2005,
42 Williams et al., 2010). The technique has been adapted for detection of maize kernels and regions
43 within each kernel that were infected by *F. verticillioides* (Williams et al., 2010). Others have
44 used HSI to detect *Fusarium* damage in wheat (Delwiche et al., 2011, Shahin & Symons, 2011,
45 Shahin & Symons, 2012). Visible-NIR HSI classified wheat kernels into sound and *Fusarium*-

68 (well filled kernels with no visible discoloration or mycelium). Clean seeds of the same cultivar
69 from an uninoculated nursery were used as control. The kernels were assigned randomly to the
70 calibration set ($n= 4$ categories x 31 kernels) or the validation set ($n= 4$ categories x 14 kernels)
71 and for scanning microscopy ($n= 4$ categories x 10 kernels).

72 **Hyperspectral imaging**

73 Hyperspectral images were acquired using SWIR hyperspectral camera (Specim, Spectral
74 Imaging Inc, Oulu, Finland) with a Mercury Cadmium Telluride (HgCdTe) detector. SpectralDAQ
75 (Specim, Spectral Imaging Inc, Oulu, Finland) was used for image acquisition software. The
76 images were obtained in the 1000-2500 nm wavelength range distributed in 256 channels. The
77 images had a spatial resolution of 200 μ m. Image acquisition was set at 5 mm/s scanning speed,
78 5ms exposure time and a frame rate of 25HZ. The ventral and dorsal surfaces of 31 kernels
79 representing the calibration set of each kernel category were scanned following the sample
80 presentation shown in Figure 1A. The same was done on 14 kernels from each kernel category
81 representing the validation set following the sample presentation shown in Figure 1B.
82 Hyperspectral images of kernels comprising seven uninoculated, seven asymptomatic, seven
83 mildly damaged and ten severely damaged kernels were taken following the sample presentation
84 shown in Figure 5A. Kernels were directly placed on the black sample holder and a 99% reflecting
85 white reference bar was included in each image.

86 *Figure 1 comes here.*

87 **Analysis of hyperspectral images**

88 All data analysis was done in MATLAB (Release 2013b, The MathWorks, Inc., Natick,
89 Massachusetts), using the Image Processing Toolbox, Statistics toolbox and in-house routines for

90 Principal Component Analysis (PCA) and Partial Least Squares Regression (PLSR). The analysis
91 of the images followed these steps:

92 1. Transformation of raw signal into percent reflectance

93 Every image contains a white and black reference, as shown in Figure 1. The reflectance spectrum
94 R_{rc} in row r and column c was calculated as

$$95 \quad R_{rc} = \frac{I_{raw,rc} - I_{black,c}}{I_{white,c} - I_{black,c}},$$

96 where $I_{raw,rc}$ is the raw signal of row r and column c , and $I_{black,c}$ and $I_{white,c}$ were the average black
97 and white references of column c . By doing the calculations column wise, variations due to line
98 scanning were accounted for.

99 2. Remove background

100 In order to separate kernels from background, a threshold rule based on differences in reflectance
101 spectra was used. The threshold was set by visual inspection of the spectra.

102 3. Preprocess spectra

103 Reflectance spectra were transformed to absorbance, and normalized by standard normal variate
104 (SNV) to remove scattering effects.

105 4. Multivariate data analysis based on average spectra for each kernel

106 The average spectrum from each kernel was paired with the reference DON value, and a calibration
107 model based on 248 images ((4 ventral + 4 dorsal images) x 31 kernels representing each kernel

108 category) was fitted by PLS regression. The DON values were transformed as $DON^* =$
109 $[\log(DON)]^3$ prior to analysis in order to obtain a more even distribution and avoid curvature in
110 the prediction model. The model was optimized by full cross-validation, and the prediction
111 performance was validated by predicting DON^* values of 112 separate validation kernels ((4
112 ventral + 4 dorsal images) x 14 kernels representing each kernel category).

113 A linear discriminant analysis (LDA) classification model was built using the latent variables from
114 the PLS model. Only uninoculated and severely damaged kernels were used to define the
115 classification rule, in order to get a clear separation between infected and non-infected samples.

116 5. Application of pixel-level multivariate models

117 The PLSR model and LDA classification were used on single-pixel spectra to investigate the
118 spatial distribution of *Fusarium* infection within the kernels.

119 **Microscopy and DON analysis**

120 Cross-sections and surfaces of hulled and dehulled kernels representing each kernel
121 category were further studied under the scanning electron microscope, SEM (ZEISS EVO 50-EP
122 Environmental Scanning Electron Microscope, Carl Zeiss AG, Germany) at the Imaging Centre of
123 the Norwegian University of Life Sciences. Ten kernels representing each kernel category were
124 used. Samples were dissected in the middle and near the embryo to study the effect of infection on
125 the grain ultra structure. The samples were mounted on aluminum stubs with conductive carbon
126 adhesive tabs and double coated with gold-palladium (SC7640 Auto/ manual high resolution
127 sputter coater) before examination under the SEM operating at an accelerating voltage of 25 kV.

150 The microscopic study showed that the uninoculated and the asymptomatic kernels to be
151 plump and free of any fungal mycelia. The severely damaged kernels were shriveled and heavily
152 colonized with *F. graminearum*. Dense mycelial growth on the hulls and on the caryopsis of the
153 severely damaged kernels was frequently observed. Denser mycelia were observed near the crease
154 of the severely damaged kernels (Figures. 2 and 3). The cross-sections of the uninoculated kernels
155 revealed a well-formed aleurone layer and intact endosperm, while the severely damaged kernels
156 had collapsed and highly colonized aleurone layer with partially digested endosperm structure
157 (Figures 3 and 4). Damage to the seed coat and the aleurone layers were also observed in the mildly
158 damaged kernels, but the inner endosperm structure was intact. Similar effects of infection were
159 observed in wheat (Bechtel et al., 1985, Jackowiak et al., 2005). Hyphae of *F. culmorum* were
160 most prevalent in the layers of the seed coat tissues but were much less prevalent in the endosperm
161 tissues of damaged wheat kernels (Jackowiak et al., 2005). Another study reported the pericarp
162 and the aleurone layer to be the most affected tissues in *F. graminearum* infected wheat (Bechtel
163 et al., 1985).

164 *Figure 2, 3 and 4 come here*

165 **Hyperspectral image analysis**

166 The level and the range of DON contamination in ground bulk samples do not correspond
167 to that of individual kernels. In this study, the bulk DON content of the sample used was 6.8 ppm
168 while the DON level of the individual kernels ranged from non-detectable levels to 386.5 ppm
169 (Table 1). In a previous study, we investigated the potential of conventional VIS-NIR spectroscopy
170 to estimate DON content of *Fusarium*-inoculated oat genotypes. Spectra were taken and DON
171 level was analyzed from bulk ground samples. One hundred sixty six samples with DON value
172 ranging from 0.05 ppm to 28.1 ppm were used. It was possible to develop a calibration model

173 which can be used for rough screening of the genotypes (Tekle et al., 2013). However, we
174 hypothesized that a better calibration model for DON and *Fusarium* damage could be developed
175 if the wider variation in DON among individual kernels and the higher sensitivity of HSI were
176 utilized.

177 The average kernel size across all images was 554 pixels, ranging from 345 to 567 pixels.
178 The correlation between the number of pixels and the measured kernel weight was 0.72, showing
179 that the pixel size is fairly representative for the actual size of the kernels. The PLSR model, using
180 the average spectra and the DON* values as x and y variables, respectively, was optimized by full
181 cross-validation, and a 5-component model was selected. The model had a R² of 0.75 and 0.71 for
182 calibration and cross-validation, respectively. The model was able to describe the majority of the
183 DON* variation, although the prediction was not very good. The first PLS component was the
184 most dominant, describing 32.9% of the DON* variation and 70.5% of the spectral variation. The
185 second PLS component described additional 8.2% of the DON* variation and 14.2% of the spectral
186 variation. The PLS score plot of component 1 versus component 2 in Figure 5A shows that there
187 is a systematic pattern due to kernel category. These first two components separate uninoculated
188 and asymptomatic kernels from severely damaged kernels. The mildly damaged kernels are
189 overlapping with the severely damaged and the asymptomatic kernels. This can be explained by
190 the large variation in DON value of the mildly damaged kernels (Table 1).

191 The line in Figure 5A is the LDA discrimination line that separates uninoculated kernels
192 from severely damaged kernels. This line is used to discriminate between non-infected and
193 infected pixels in the validation images. The loadings for the first component are shown in Figure
194 5B. The main peaks representing positive changes associated with increased infection are seen at
195 1925 nm, 2070 nm and 2140 nm, while negative changes at 1400 nm, 1626 nm and 1850 nm

196 corresponded to non-infection. In a previous study, peaks centered at 1432 and 1924 nm classified
197 DON-contaminated samples into high-DON and low-DON classes. These peaks were attributed
198 to O-H bands of water (Tekle et al., 2013). In comparison, absorbance peaks for *F. verticillioides*-
199 infected maize kernels were observed at 1960 nm and 2100 nm and at 1450 nm 2300 nm and 2350
200 nm for non-infected kernels (Williams et al., 2010).

201 *Figure 5 comes here*

202 Figure 6 shows the image analysis performed on the mixed calibration set kernels. The
203 mixed calibration set kernels were comprised of seven uninoculated, seven asymptomatic, seven
204 mildly damaged and ten severely damaged kernels arranged randomly as shown in Figure 6A. The
205 reflectance image of a selected channel of these kernels is shown in Figure 6B. The background
206 noise was removed by using the mask shown in Figure 6C. *Fusarium*-damaged/ DON
207 contaminated regions (depicted by red pixels) and healthy/ DON free regions (depicted by green
208 pixels) of each kernel were predicted using PLSR and LDA (Figure 6D). The severely damaged
209 kernels were dominated by red pixels while the uninoculated and asymptomatic kernels were
210 dominated by green pixels showing that HSI can successfully detect level of *Fusarium*-damage.
211 This observation is clearly shown by the differences in the mean percentage of damaged pixels in
212 the calibration images of each kernel category (Table 2).

213 *Figure 6 comes here.*

214 Figure 7 shows the PLS-LDA classification model used for classification of individual
215 pixels in the eight validation images. There was a clear difference between classes, as indicated by
216 the extent of red and green pixels and by the differences among the mean percentage of damaged
217 pixels in the validation images of each kernel category. (Figure 7 and Table 2). Hyperspectral

218 imaging detected *Fusarium* damage and DON level more precisely than visual examination.
219 Kernels with very high DON but categorized as mildly damaged were dominated by infected
220 regions. On the other hand, kernels with very low DON but categorized as severely damaged were
221 dominated by healthy regions after image analysis (Figure 7).

222 *Figure 7 comes here.*

223 *Table 2 comes here.*

224 The DON* value for the 112 validation set kernels ((4 dorsal + 4 ventral images) x 14
225 kernels representing each kernel category) were predicted in two alternative ways: 1) using the
226 average spectrum of the kernels as x-variables and the PLSR model, and 2) classifying every pixel
227 using the PLS-LDA model, and calculating the ratio of damaged pixels in each grain. . The
228 correlation (R) between predicted and measured DON* values were 0.81 and 0.79 respectively
229 (Figure 8). The difference between the two prediction methods is not statistically significant,
230 showing that they are equivalent. Both methods indicate a valid model showing a good potential
231 of HSI in detecting *Fusarium* damage and predicting DON in oats.

232 *Figure 8 comes here.*

233 **CONCLUSIONS**

234 Hyperspectral images of individual oat kernels with different levels of *Fusarium* damage
235 and DON content were analysed. Hyperspectral imaging successfully detected *Fusarium* damage
236 of kernels with better accuracy than visual inspection. Detection of *Fusarium* damage with HSI
237 gave a better indication of DON content of kernels than visual assessment of damage. Regions
238 within single kernels were further classified as *Fusarium*-damaged and healthy regions. A PLSR

239 model was developed using the transformed DON* values as y-variables and the average spectra
240 of each kernel as x-variables. The model was proved to be valid and stable by detecting DON*
241 values of a set of separate validation kernels. The results reported in this paper indicate that HSI
242 can successfully be implemented to detect *Fusarium* damage and DON contamination in single
243 oat kernels. Thus, highly damaged and contaminated kernels can be detected and removed to
244 significantly lower toxin contamination and improve grain quality of seed lots. Kernels used in
245 this paper are of a single oat genotype originating from a single experimental year. Testing the
246 feasibility of HSI to detect *Fusarium* damage and DON contamination in several genotypes across
247 experimental years would be an important step towards the routine application of the method for
248 screening purposes.

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257 **LITERATURE CITED**

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321

322 Table 1: Mean (\pm standard deviation), minimum and maximum kernel weight (g) and
 323 deoxynivalenol content (ppm) of calibration ($n=31$) and validation ($n=14$) set samples of
 324 asymptomatic (A), mildly damaged (MD), severely damaged (SD) and uninoculated (U) kernels.
 325 'nd' stands for non-detectable level of DON (< 5 ng/ sample).

		Calibration set		Validation set	
		Kernel weight (g)	DON (ppm)	Kernel weight (g)	DON (ppm)
Mean	A	0.054 ± 0.005	1.93 ± 4.49	0.056 ± 0.005	4.99 ± 7.83
	MD	0.048 ± 0.008	25.31 ± 53.94	0.046 ± 0.010	56.82 ± 107.43
	SD	0.036 ± 0.009	136.34 ± 123.04	0.032 ± 0.008	117.61 ± 107.25
	U	0.050 ± 0.013	0.09 ± 0.05	0.045 ± 0.008	0.01 ± 0.05
Minimum	A	0.045	nd	0.051	0.18
	MD	0.034	nd	0.029	nd
	SD	0.019	0.48	0.018	0.52
	U	0.033	nd	0.034	nd
Maximum	A	0.062	20.50	0.064	21.91
	MD	0.061	267.37	0.061	355.32
	SD	0.056	386.51	0.048	340.10
	U	0.062	0.66	0.058	0.18

326

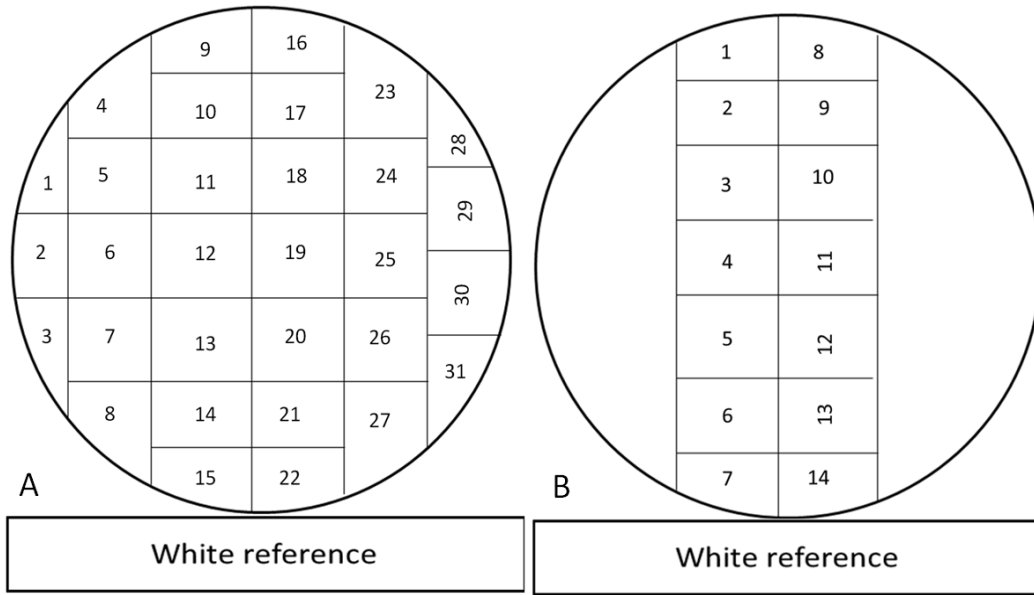
327

328 Table 2 Mean (\pm standard deviation) percentage of damaged pixels in uninoculated, asymptomatic,
329 mildly damaged and severely damaged kernels of the calibration ($n= 248$) and validation ($n=112$)
330 images. Ventral and dorsal images were pooled for each kernel category.

	Uninoculated	Asymptomatic	Mildly Damaged	Severely Damaged
Calibration set	21.5 \pm 5.4	28.1 \pm 8.0	39.8 \pm 12.9	62.8 \pm 16.4
Validation set	26.5 \pm 7.4	29.3 \pm 7.1	46.9 \pm 18.4	73.3 \pm 16.3

331

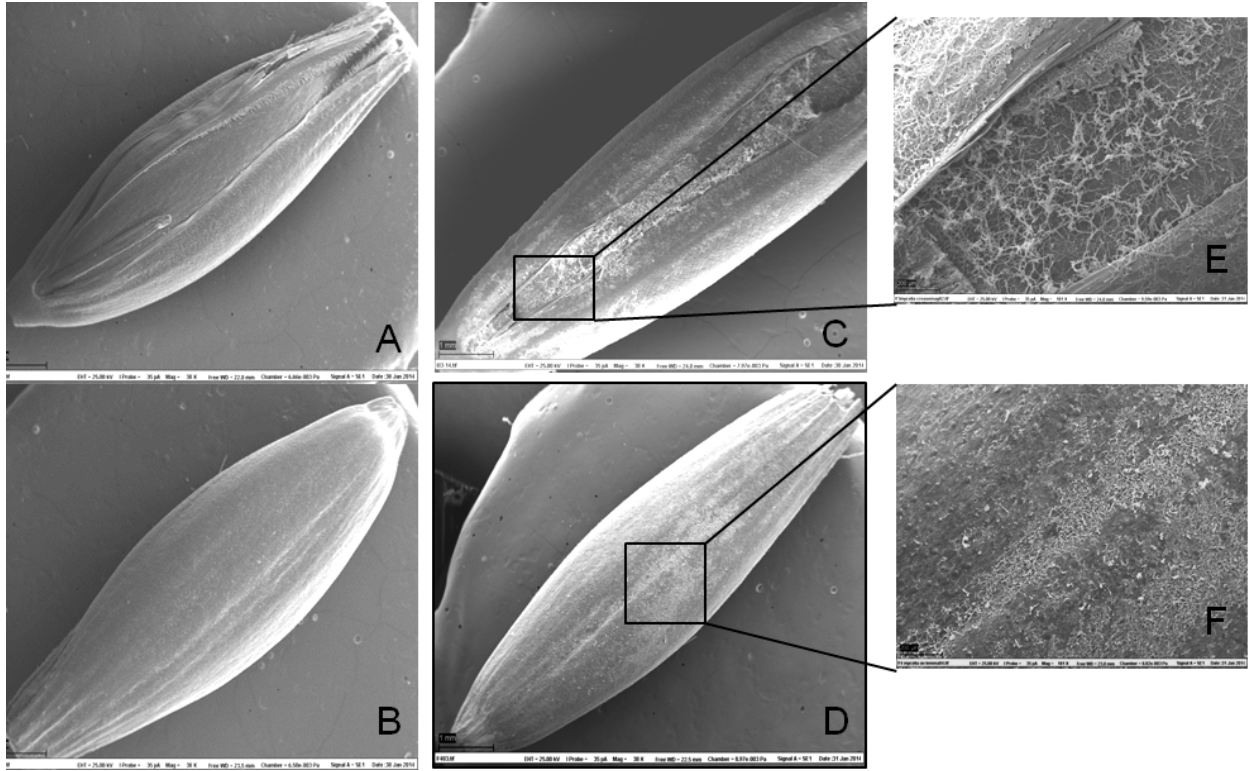
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334 Figure 1: Presentation of kernels for hyperspectral imaging. Ventral and dorsal surfaces of 31 test
 335 set kernels (A) and the 14 validation set kernels (B) from each kernel category were scanned.
 336 Numbers in the cells represent kernel numbers. Kernels were scanned with their basal portions
 337 towards the white reference. Kernels 28, 29, and 30 in the calibration set and kernels 11, 12 and
 338 13 in the validation set were rotated 90° to serve as signposts.

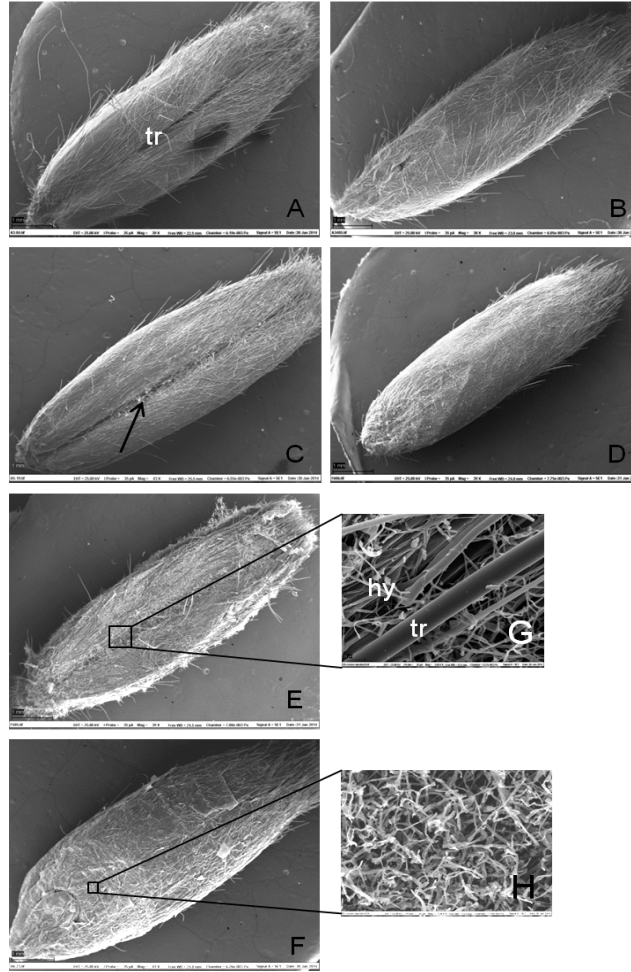
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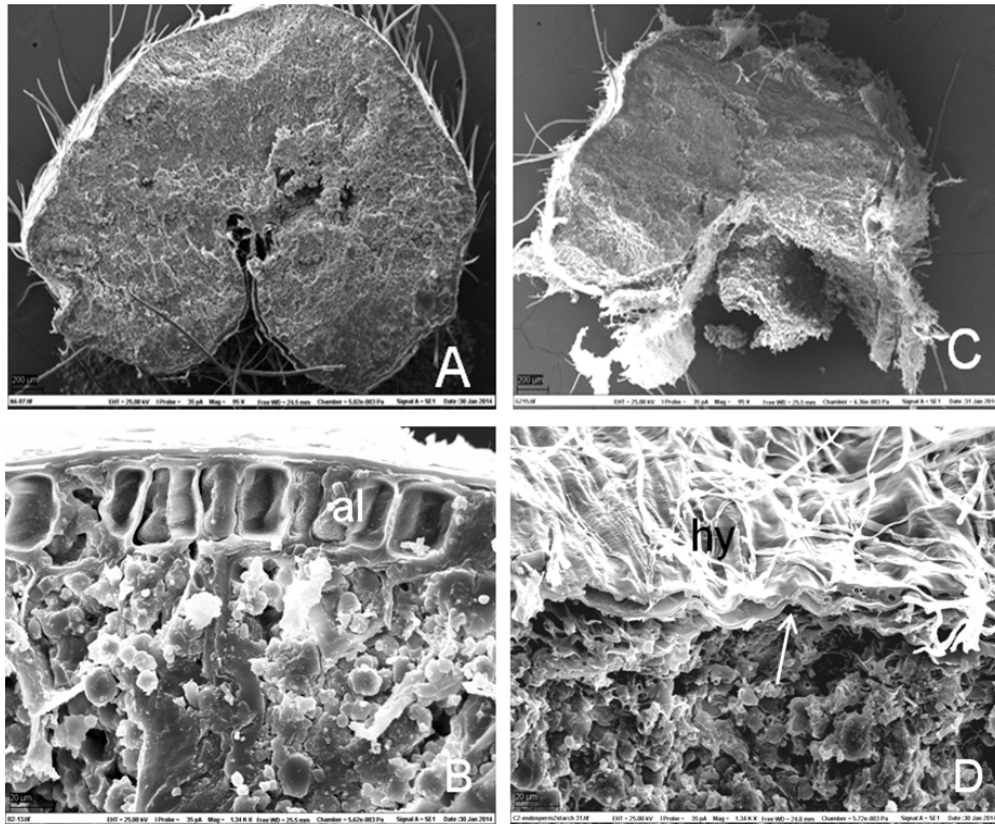
341 Figure 2: Scanning electron micrographs of ventral and dorsal surfaces of hulled kernels of healthy
 342 (A and B, magnification = 38 x) and *Fusarium*-damaged (C and D, magnification= 38x) kernels
 343 of the oat cv. Bessin. Higher magnification reveals profuse growth of *F. graminearum* mycelia in
 344 the crease on the palea (E, magnification= 181x) and on the lemma (F, magnification= 181x).

345



346

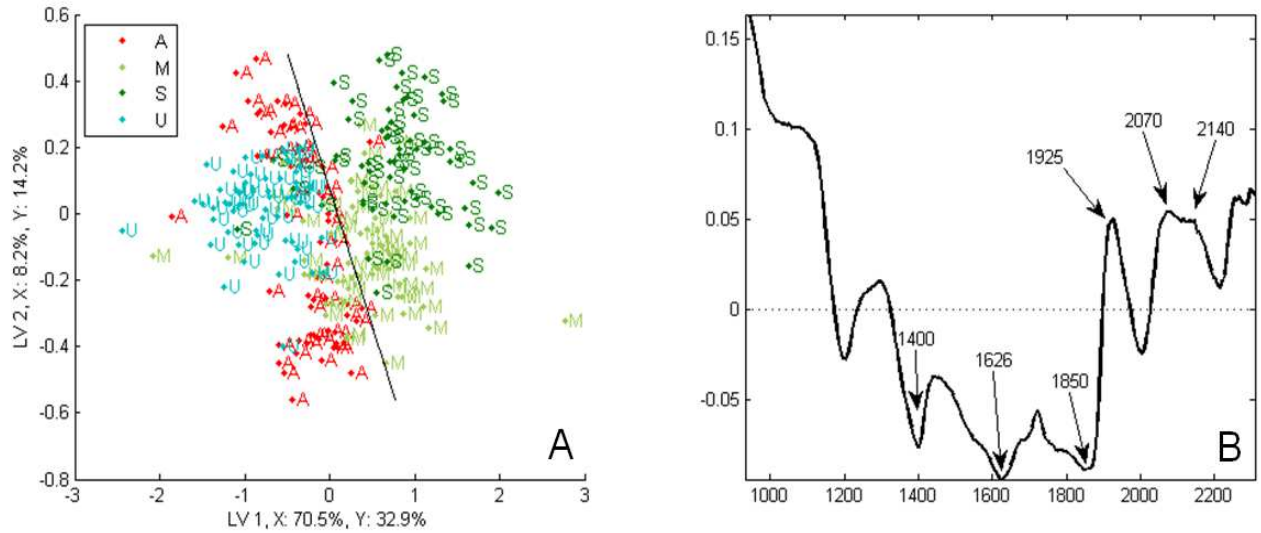
347 Figure 3: Scanning electron micrographs of ventral and dorsal surfaces of dehulled kernels of the
 348 oat cv. Bessin. A and B show well-formed mycelium on ventral (A, magnification= 39x) and
 349 dorsal (B, magnification= 38x) surfaces of healthy kernels, with the trichomes (tr). C and D show
 350 ventral (C, magnification= 43x) and dorsal (D, magnification= 39x) surfaces of mildly damaged
 351 kernels, arrow indicates mycelia of *Fusarium graminearum*. E and F are micrographs of ventral
 352 (E, magnification= 39x) and dorsal (F, magnification= 41x) surfaces of severely damaged kernels.
 353 G and H are higher magnifications of fungal growth on the ventral (G, magnification= 1.6kx, hy=
 354 hyphae, and tr= trichome) and dorsal surfaces (H, magnification= 1.46kx).



355

356 Figure 4: Scanning electron micrographs of cross sections of healthy (A, magnification= 95x; and
 357 B, magnification= 1.34 kx) and *Fusarium*-damaged (C, magnification= 95x; and D,
 358 magnification= 1,34 kx) kernels of the oat cv. Bessin. A well formed aleurone layer (al) and
 359 endosperm with small and large starch granules in the protein matrix of the healthy kernel is
 360 displayed in B. Hyphae (hy) of *Fusarium graminearum* and collapsed aleurone layer and damaged
 361 endosperm are shown in D.

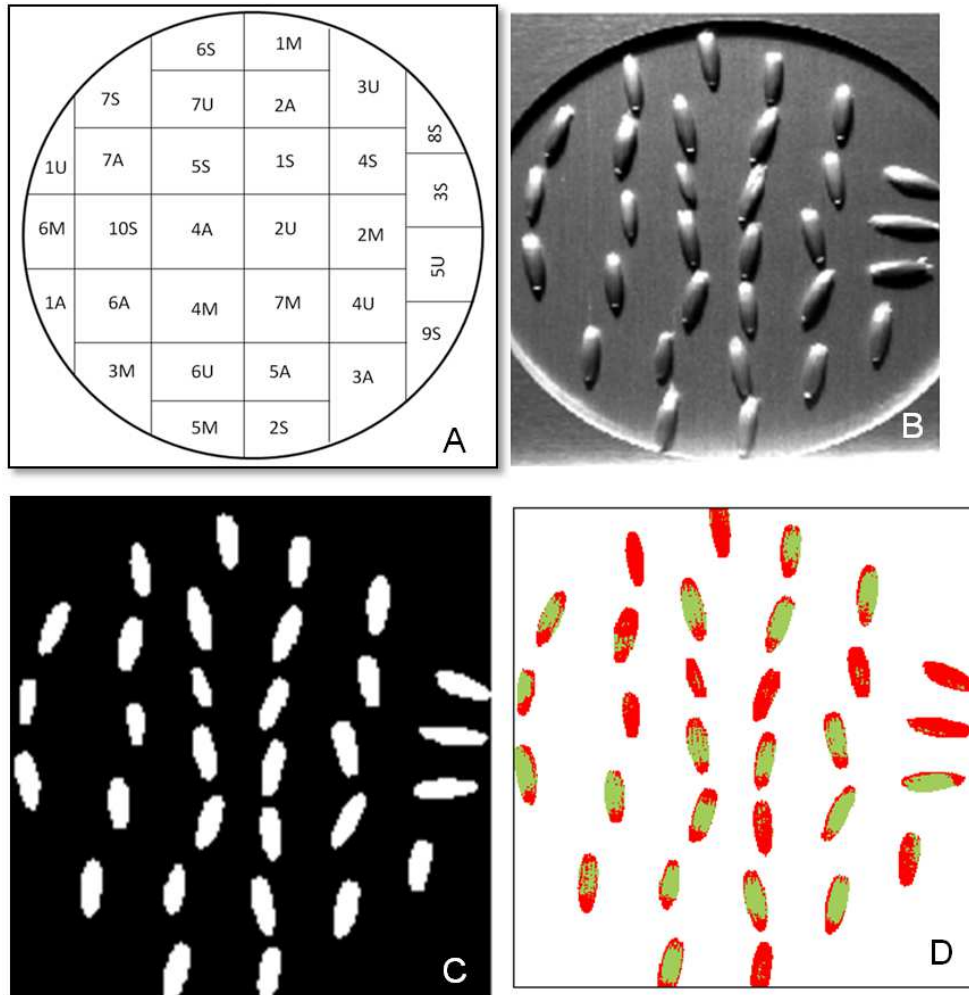
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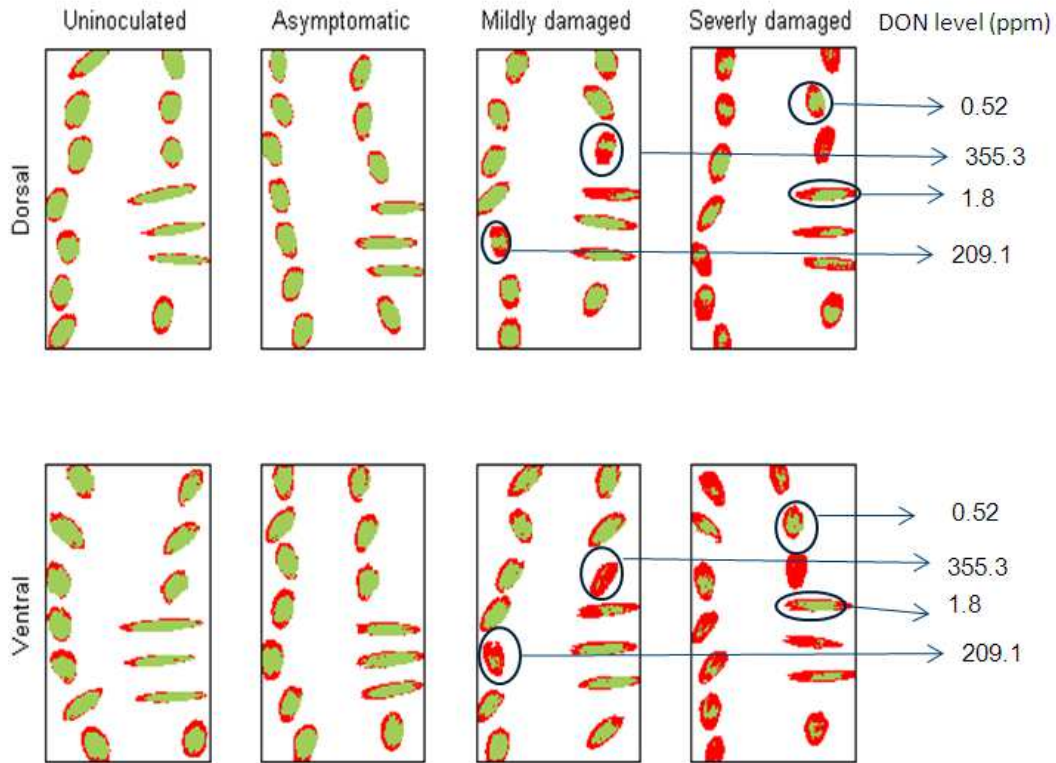
364 Figure 5: Partial least squares (PLS) regression on the calibration set kernels with the average
 365 spectra of kernels as X variables and $\text{DON}^* = [\log(\text{DON})]^3$ values as Y variables. (A) PLS scores
 366 of calibration set kernels on component 1 versus component 2, with separation line from linear
 367 discriminant analysis. A- asymptomatic, M- mildly damaged, S- severely damaged and U-
 368 uninoculated kernels. (B) PLS loading weights from the first component. Wavelengths of interest
 369 are marked by arrows.

370



371

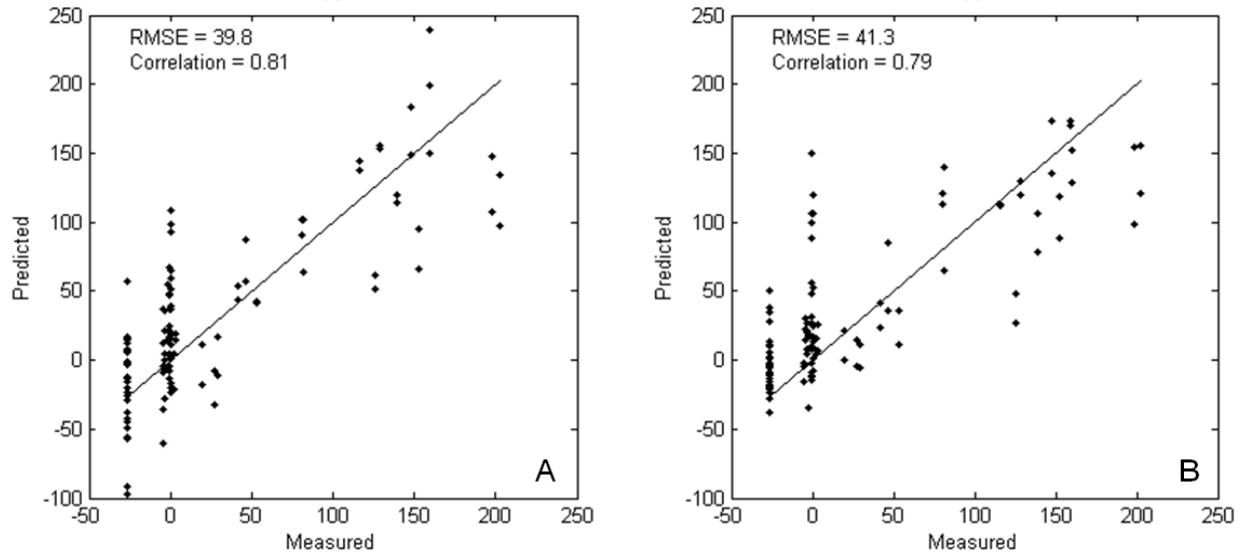
372 Figure 6: Image analysis of calibration set kernels comprising seven uninoculated, seven
 373 asymptomatic, seven mildly damaged and ten severely damaged kernels. (A) Sample presentation
 374 for scanning. Numbers represent the kernel number in the original calibration set and letters
 375 represent kernel category. A- asymptomatic, M- mildly damaged, S- severely damaged and U-
 376 uninoculated kernels. (B) Reflectance spectra of one selected channel. (C) Mask used to remove
 377 background from images. (D) Image showing infection in grains. Red pixels represent DON-
 378 contaminated/ *Fusarium*-damaged areas and green pixels represent DON-free/ healthy areas.



379

380 Figure 7: Classification of pixels in validation images. *Fusarium*-damaged/ DON-contaminated
 381 areas are depicted in red while healthy/ DON-free areas are depicted in green. DON values of
 382 kernels of interest (kernels with relatively high DON level in the mildly damaged category and
 383 kernels with low DON level in the severely damaged category) are shown.

384



385

386 Figure 8: Measured versus predicted $\text{DON}^* = [\log(\text{DON})]^3$ values of validation kernels using the
387 partial least squares (PLS) regression model developed (A) and the PLS- linear discriminant
388 analysis model (B).

389