Evaluating Soybean Genotypes for SDS Resistance Using Canopy Spectral Reflectance

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Introduction

Sudden Death Syndrome (SDS) has become a leading cause for yield reduction in soybean (Koeing and Wrath, 2010). A primary control of the disease is varietal resistance. Screening currently requires extensive visual evaluation. Using canopy reflectance to characterize SDS resistance might improve efficiency and accuracy of selection.

Objectives

1) Determine if spectral reflectance can be used to evaluate SDS resistance in soybean genotypes. 2) Determine which reflectance wavebands best characterize SDS resistance.

Materials and Methods

Experimental Design

- NAM10 (IA3013 X LD00-3309) population of 140 progeny, parents and checks (a total of 160 genotypes) were planted in Manhattan, KS (MAN) in 2015 and in Manhattan and Rossville, KS (ROS) in 2016.
- Entries planted in 2-row plots, 3.7m long, and spaced 76cm apart, in a randomized complete block design with four replications, irrigation was applied to increase SDS severity.
- SDS foliar symptoms was visually rated at the R6 growth stage (Figure 1 A & B). Using a two part evaluation scale for disease incidence and severity which is used to create the disease index (DX) (Schmidt, 2007).

Reflectance Measurements

- Spectral reflectance measured using two Ocean Optics USB2000+ , on near cloud-free days within 2 hours of solar noon for wavelengths 350 to 1027 nm (Figure 1C).
- Data was collected and processed using CDAP-2© software.
- Reflectance collected weekly during reproduction phases of development.

Analysis of Variance

- Data analyzed using the MIXED procedure in SAS.
- Genotype and environment treated as fixed, bloc treated as random.

Data Reduction

- Reflectance 10 nm band regions were created to reduce dimensionality.
- Mixed procedure used for each waveband to identify days when reflectance values were significant among genotypes.
- Spectral reflectance for significant wavebands from each plot were averaged across days for a season average.
- SAS Correlation was used to characterize relationship between reflectance and DX.

Model Building

- Spectral band regions subjected to stepwise selection in PROC REG to predict DX.

Figure 1. A) SDS foliar symptoms. B) Premature death in susceptible check . C) Spectral equipment during use.

Results

- Significant differences were detected among genotypes for DX at each location.
- DX severity differed across environments, and the relative performance of the genotypes for DX differed across environments (Tables 1 and 2).
- An average of five spectral readings were collected for each environment during reproductive growth. Significant differences in reflectance among entries were detected on two readings in each environment between the R5 and R6 growth stages.
- On the significant days, most of the wavelengths differed among genotypes.
- Correlations between genotype mean for DX and reflectance were the largest between 505-645 nm at 15 MAN, 475-705 at 16 MAN and 525-705 nm at 16 ROS (Figure 2).
- Models developed using wavebands correlated with DX, explained up to 40% of the variation among genotypes in DX at 15 MAN and 16 ROS (Figure 3).
- Selecting the bottom 25% of genotypes based on predicted DX, identified 11 of the 16 most susceptible lines at 16 ROS, and 12 of the 16 most susceptible at 15 MAN and 2 out of the 16 most susceptible at 16 MAN.

Table 1. ANOVA for DX and sample waveband.

Source	DF	DX	w525
Environment (ENV)	2	<.01	0.5
Genotype (G)	159	<.01	<.01
ENV*G	317	<.01	<.01

Table 2. Means of DX by environment and range across genotypes.

Environment	DX $\bar{X}$ Score	DX Range Score
15 MAN	8.5 a†	0.0 - 57.7
16 MAN	12.1 b	0.5 - 68.1
16 ROS	15.4 b	0.8 - 68.8

†Means followed by same letter are not significantly different at p≤.05.

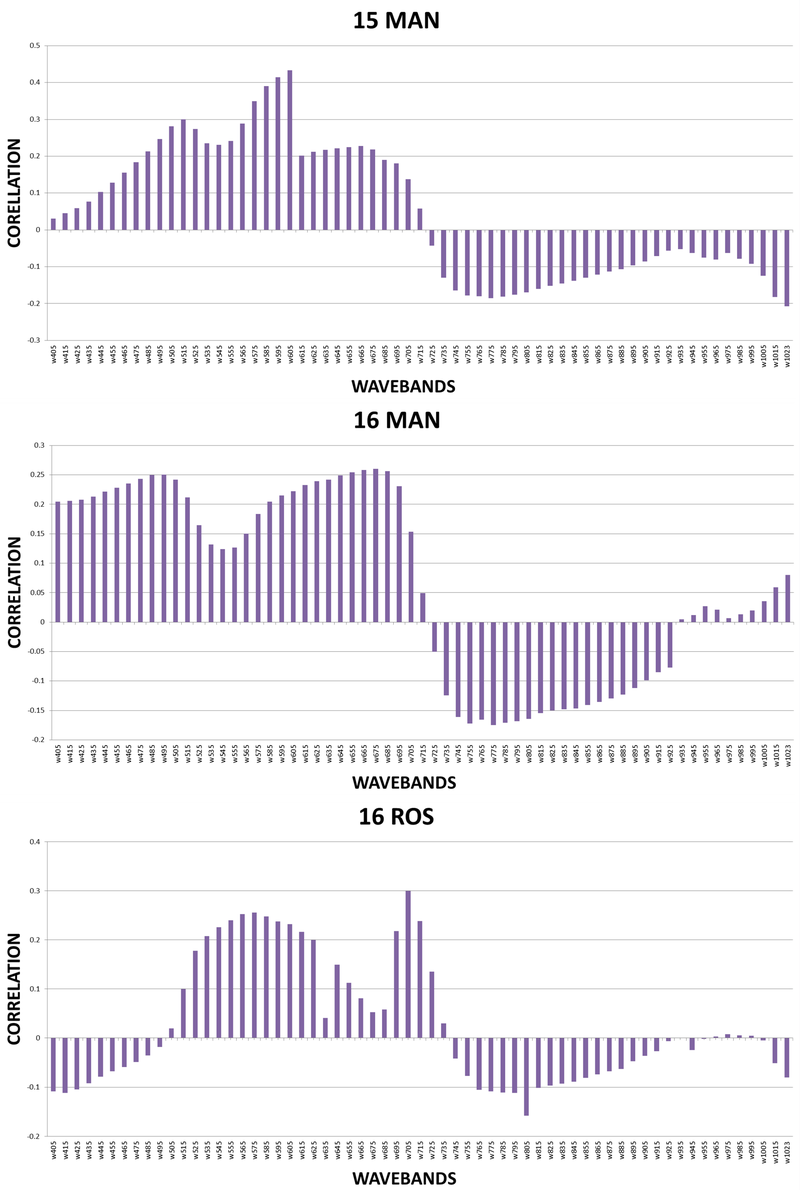

Figure 2. Correlations between DX and waveband reflectance for season average based on significant days, by location. At α of .05, pr ≤-.15 and pr ≥ .15. At α of 0.01, pr ≤-.2 and pr ≥ .2, n=160)

Table 3. Stepwise regression for DX estimation of genotype mean, by environment.

Loc.	Variable (nm)	Variable R^2	Model R^2	Model
AT 15	w535	0.1142	0.41***	DX=1.054 - 25.85 (w535) + 24.2 (W565) + 1.7(w605)
	w565	0.1619		
	w605	0.1287		
TO 15	w525	0.171	0.43***	DX= 13.04 - 51.2(w525)+55.5(w575) -10.2(w645)
	w575	0.1557		
	w645	0.03		
AT 15	w675	0.0678	0.067***	DX= 4.705+.10*(w675)

*** Significance at <.001.

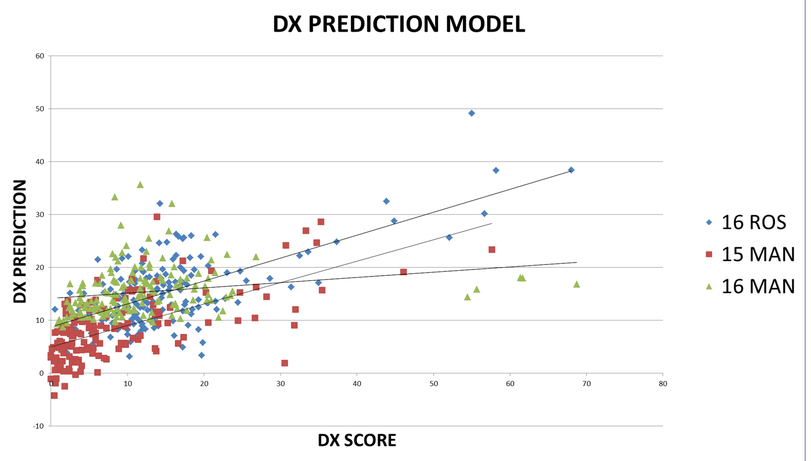

Figure 4. DX prediction model for 15 MAN, 16 MAN, 16 ROS, based on stepwise regression.

Conclusions

- Spectral bands between 505-705 nm provided the most useful in predicting SDS severity.
- Late season readings tended to have more significant days and were used to create season averages.
- Models predicted SDS susceptible entries better than they did more SDS resistant entries.
- Canopy reflectance measurements were informative in predicting SDS severity in soybeans, but additional work is needed to increase throughput of scanning ability, increase differentiation among genotypes, and improve consistency across environments to more effectively use this tool in breeding.

References

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