

Rapid Measurement of Corn Amino Acids using Near Infrared Whole Grain Analyzers

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***ISU Extension Iowa Grain Quality Initiative
Michael Fields Agricultural Institute
ISU Extension Value Added Agriculture Program***

Objective

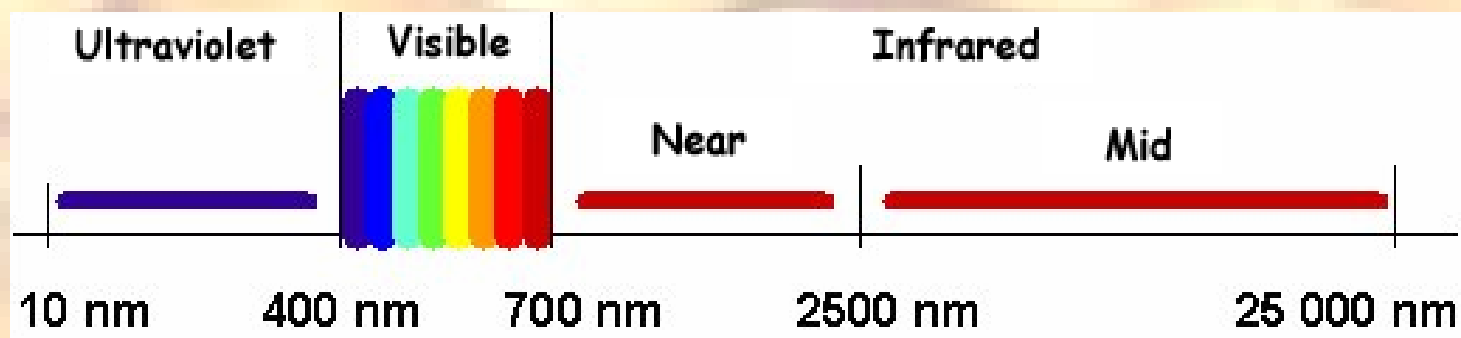
Develop rapid method to measure important amino acids in corn for poultry and livestock rations using near-infrared spectroscopy (NIRS) whole grain analyzers



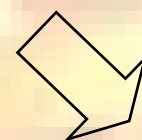
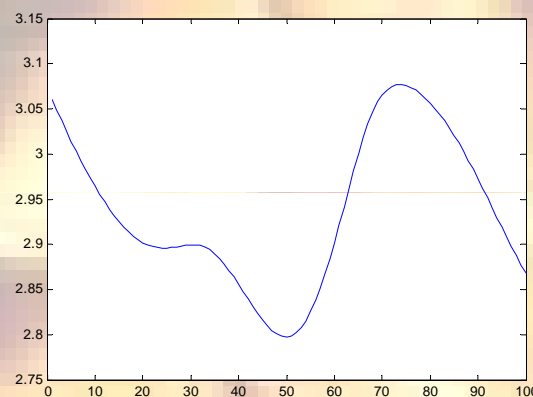
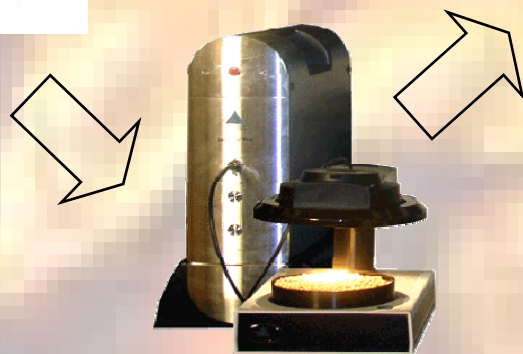
Why?

- Current lab methods are costly and time consuming
- Corn breeding programs and feed ration balancing will be facilitated with rapid measurement systems

NIRS measures light energy absorption

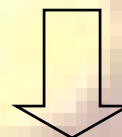


How NIRS analyzers work...



Prediction model

$$\hat{Y} = b_0 + b_1x_1 + b_2x_2 + \dots + b_kx_k$$



Protein content: **14 g.kg⁻¹**

Can't we do this already?

- Calibration attempts to measure selected amino acids in grain usually ***predict total protein*** and only ***calculate a typical amino acid level*** based on the protein level.
- Accurate measurement of amino acids may rely primarily on the characteristics of samples used for calibration.



Good samples are the key to success!

The corn samples available from breeding programs coordinated by Michael Fields Agricultural Institute ***represent unique ratios of selected amino acids*** (methionine, lysine, cysteine) to total protein; thus the analyzer can “learn” this new relationship and provide a more accurate measurement.



What did we do?

- We used breeder samples with relatively high level levels of selected amino acids from harvest years 2006 (106 samples) and 2007 (406 samples)
 - Lysine 0.26-0.53
 - **Methionine 0.14-0.39**
 - Cysteine 0.14-0.37

What else did we do?

- Scanned samples in two whole seed transmission analyzers - Bruins OmegAnalyzer G and Foss Infratec™ 1241 Grain Analyzer
- Used CAMO Unscrambler v.9.7 software

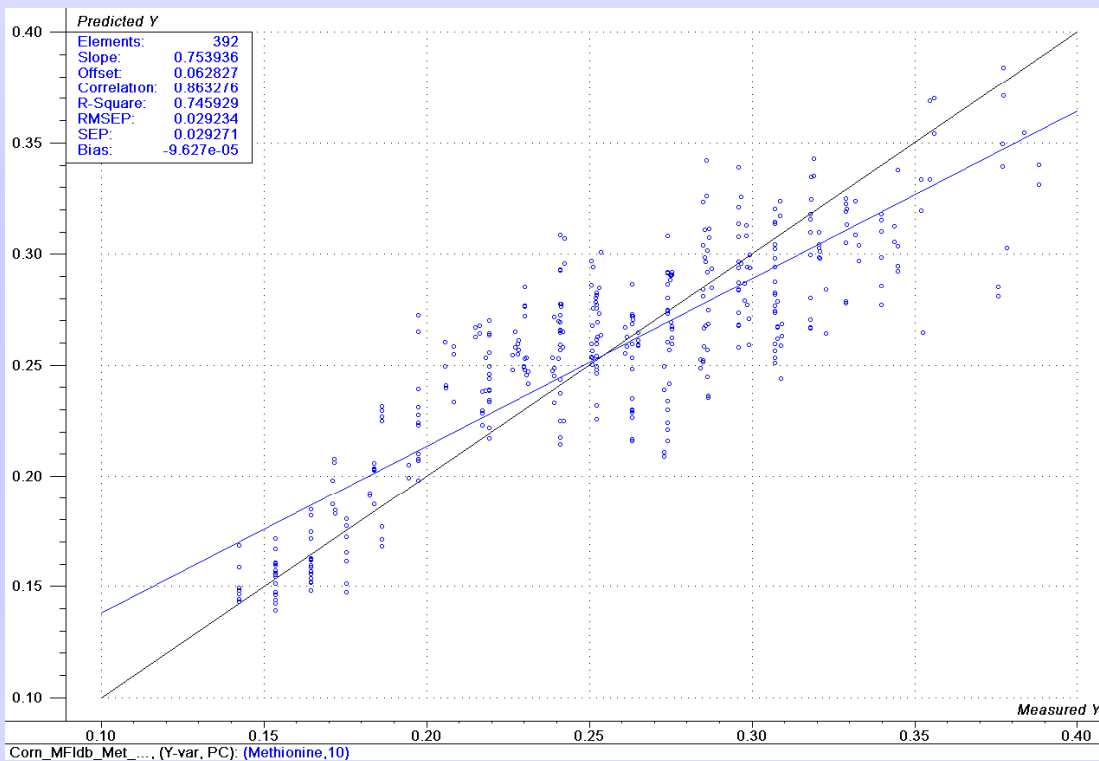


Methionine

$$R^2 = 0.75$$

**Standard Error of Cross
Validation (SECV) = 0.029**

Range: 0.14 – 0.39

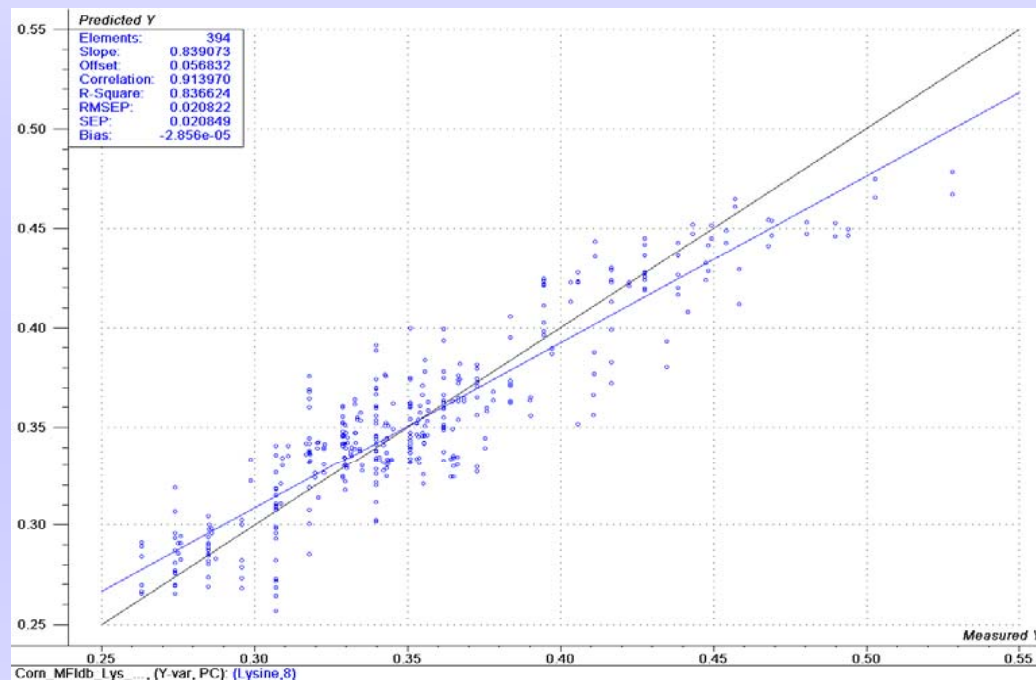


Lysine

$$R^2 = 0.84$$

**Standard Error of Cross
Validation (SECV) = 0.021**

Range: 0.26 – 0.53

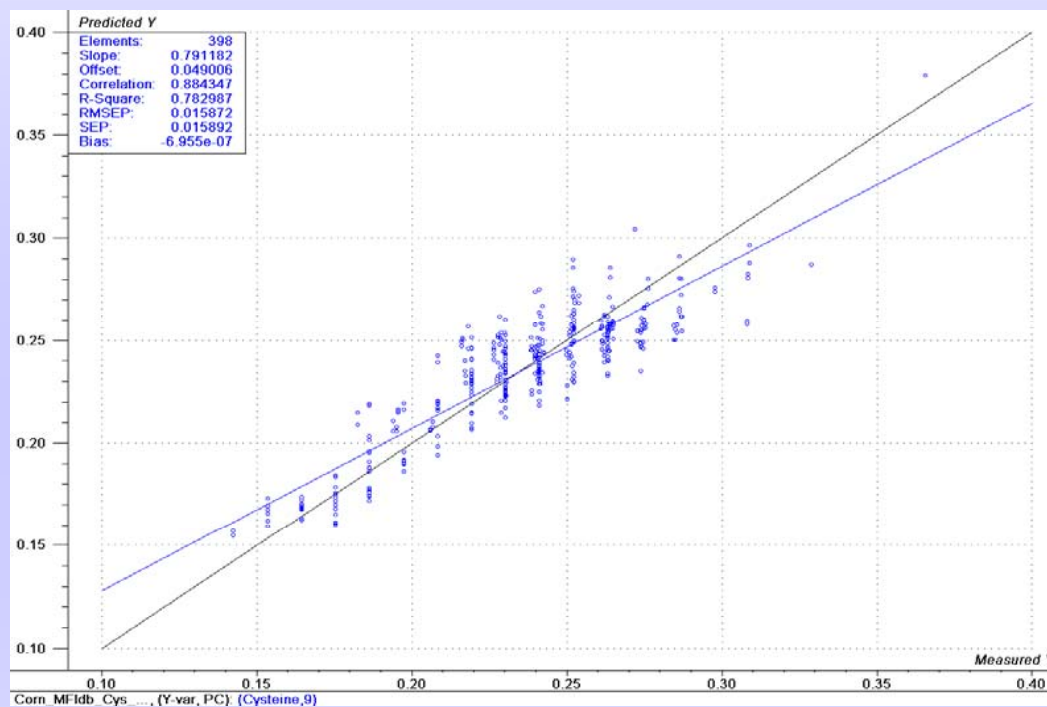


Cysteine

$$R^2 = 0.78$$

**Standard Error of Cross
Validation (SECV) = 0.016**

Range: 0.14 – 0.37



Spectral correlations with amino acids vs. total protein

| <i>R² Determination with</i> | | | | |
|---|-----------|---------|----------|---------|
| | Range | Omega | Infratec | Total |
| | (%db) | Spectra | Spectra | Protein |
| MET | 0.14-0.39 | 0.746 | 0.730 | 0.542 |
| LYS | 0.26-0.53 | 0.837 | 0.842 | 0.390 |
| CYS | 0.14-0.37 | 0.783 | 0.787 | 0.797 |

Kovalenko et al. 2006 proposed using R² or RPD (Relative Predictive Determinant) to test whether values are calculated values or true predicted values.

What do the results mean?

- **Methionine** and **lysine** can be measured by NIRS with sufficient accuracy for genetic screening.
- Measurement of **cysteine** reflected protein measurement, therefore we cannot conclude that we are able to measure cysteine independently.
- Additional carefully selected calibration samples from future harvests will likely enhance accuracy and serve as a validation set.

Thanks! to our sponsor and
colleagues



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