Methods and Acknowledgements: Crop Year 2018*

- 1. Reported values are based on soybean samples provided to USB by USDA-NASS from their Objective Yield Survey for crop year 2018.
- 2. The smallest geographical unit for which values are reported are multi-county Federal Information Processing Standard (FIPS) districts.
- 3. The USDA-NASS survey is a random sample of soybeans from 11 major soybean producing states. To be included in this report, a FIPS district had to have results from a minimum of three soybean samples. The number of observations per district is included in the expanded Excel tables for certain web pages that can be accessed by clicking on embedded links.
- 4. For more information regarding USDA-NASS's Objective Yield survey, please utilize the following link to their web site: <u>https://www.nass.usda.gov/Surveys/Guide_to_NASS_Surveys/Objective_Yield/index.php</u>
- 5. Soybean samples were analyzed using Near Infrared (NIR) spectrometry at the USDA's National Center for Agricultural Utilization Research (NCAUR), Peoria, IL. Whole soybean samples received from USDA-NASS were first ground using a FOSS Knifetec grinder and then scanned on a FOSS XDS NIR Instrument.
- 6. NIR spectra from the FOSS XDS NIR Instrument were predicted using ISIPredict Software version 1.10.2.4842.

Calibrations provided by FOSS North America, were used to predict soybean composition from the NIR spectra. NIR Prediction Model Filename, Equation type and adjustments employed are presented in the following table.

				Adjustments		
Constituent	Unit	Prediction Model Filename	Equation Type	Bias Applied to Reported NIR Results*	Slope Adjustment	
Protein	%	GSBDPR3.ANP	ANN	0.00	None	
Oil	%	GSBDFA3.ANP	ANN	0.00	None	
Lysine	%	feedingre_lysineai_20140415.eqa	PLS	-0.18	None	
Threonine	%	feedingre_threonineai_20140415.eqa	PLS	-0.20	None	
Methionine	%	feedingre_methininieai_20140415.eqa	PLS	-0.07	None	
Cysteine	%	feedingre_cysteineai_20140415.eqa	PLS	-0.07	None	
Tryptophan	%	feedingre_tryptophanai_20140415.eqa	PLS	-0.03	None	
Arginine	%	feedingre_arginineai_20140415.eqa	PLS	0.00	None	
Leucine	%	feedingre_leucineai_20140415.eqa	PLS	-0.16	None	
Isoleucine	%	feedingre_isoleucineai_20140415.eqa	PLS	0.00	None	
Valine	%	feedingre_valineai_20140415.eqa	PLS	0.00	None	

* Reported on a dry matter basis. Where the calibrations reported results on an As Is basis, such as for amino acids, results were calculated to a DM basis prior to reporting.

To allow for a comparison between wet-chemistry and NIR results for crude protein and 9 amino acids, 41 soybean samples were utilized. Samples were analyzed at the University of Missouri ESCL lab for Amino Acids and Crude Protein using wet-chemistry methods. A second sub-set of 22 samples were analyzed for oil by Eurofins. These samples are not included in the NIR calibrations utilized to predict compositional values for the overall sample set.

Wet-chemistry results were compared to their respective NIR predictions and used to calculate NIR Accuracy. Accuracy was calculated by determining the standard deviation of the difference, corrected for bias, between wet-chemistry results and respective NIR predictions.

The lower the value for Accuracy and its Ratio to Set Average, the better the level of NIR performance. Higher values for Accuracy identify constituents that have less reliable NIR predictions and that should be the focus of efforts toward further improvement.

Constituent	Number of Observations	Accuracy*	Accuracy as a Coefficient of Variation (Accuracy/Set Average), %
Protein	41	0.68	1.8%
Oil	22	0.59	2.6%
Lysine	41	0.067	2.6%
Threonine	41	0.048	3.2%
Methionine	41	0.028	5.4%
Cysteine	41	0.048	8.3%
Tryptophan	41	0.037	8.9%
Arginine	41	0.088	3.1%
Leucine	41	0.071	2.4%
Isoleucine	41	0.047	2.5%
Valine	41	0.069	3.5%

* Reported on a dry matter basis. Where the calibrations reported results on an As Is basis, such as for amino acids, results were calculated to a DM basis prior to reporting.

As should be the case whenever analytical results are being utilized, the reliability of analytical methods should be a consideration in the subsequent use of results. While analytical performance is not typically reported, it is reported here to allow for a more informed use of the results presented and hopefully lead to efforts resulting in further improvements.

 Estimates of soybean <u>product</u> yields per bushel, soybean meal compositional characteristics and commodity product Processed Value (EPV) were calculated using reported soybean composition values and models. Prices and selected assumptions used in these models are summarized below.

Prices used for Estimated Processor								
Value (EPV) Calculation								
	<u>Unit</u>	<u>\$/Unit</u>						
Soybean Oil	\$/lb.	\$	0.29					
Soybean Meal, Hi Pro	\$/ton	\$	325.00					
Soybean Mill Run (Hulls)	\$/ton	\$	120.00					

- Prices intended to be reflective of mid-June 2019.
- The same set of prices and base assumptions were used in calculating EPV's for all districts.
- For no-hull meal with a theoretical protein level greater than 48%, hulls were included to reduce protein to 48% to the extent that the estimated Crude Fiber level did not exceed 3.5%
- Low Meal Protein (<48.0% CP) Penalty Applied if Applicable

8. Models and Their Use

To foster dialogue and better understanding, compositional results from the analysis of samples have also been used in models to gain perspective on applied implications. In viewing and considering these results, please bear the following statements in mind:

- Models are mathematical equations that <u>estimate</u> outcomes based on a given set of data and assumptions. When trying to better understand complex systems, models can be helpful.
- The use of information from models must be tempered with the understanding that the outputs from models are <u>estimates</u>, which are dependent upon the set of assumptions utilized.
 - However, when critically viewed, such information can be useful in the development of valuable insights toward the identification of issues that merit further exploration.
- Disclaimer:

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Information for Items Presented in Data Maps:

Federal Information Processing Standard (FIPS) Districts

FIPS districts are multi-county territories within each state. Each district is identified by a numeric code which is a combination of the respective state and district codes. As an example, district 1710 is District 10 in Illinois which has a

state code of 17. For a FIPS district to be reported, results from at least three samples from within it were required.

Amino Acids as a Percent of Crude Protein:

The percentage of total crude protein represented by a given amino acid. This is a consideration in assessing protein quality.

*Disclaimer:

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