# Characterizing Soybean Meal Value Variation across the United States: A Swine Case Study

Spyridon Mourtzinis,\* Barton S. Borg, Seth L. Naeve, John Osthus, and Shawn P. Conley

### ABSTRACT

Soybean [Glycine max (L.) Merr.] is the most important oilseed crop in the United States; however, the quality characteristics of the soybean meal (SBM) produced from soybean grown in various regions can vary significantly, often leading to region-specific commodity price differentials. Currently, a fast, cost-effective, and accurate estimation method of SBM value does not exist. Our objectives were to (i) develop a model using existing data that precisely estimates SBM value targeted for swine nutrition, (ii) quantify the swine-specific SBM value variability within and among states and (iii) evaluate the predictive effectiveness of the model for estimating SBM value. The compositional characteristics of 8282 soybean samples from 2013 to 2016 in 29 states were determined. Assuming constant energy content, considering meal protein content and the concentrations of four essential amino acids (AA) (lysine [Lys], methionine [Met], tryptophan [Tryp], and isoleucine [Iso]) from these samples, a model that precisely estimates swine-specific SBM value was developed. Within each state, US\$17 to \$66 t<sup>-1</sup> SBM value range was estimated. A model based on combined and maturity group-specific analysis showed that using a simple base-line seed content of  $>350 \text{ g kg}^{-1}$ for protein and >190 g kg<sup>-1</sup> for oil to identify high-quality cultivars can be misleading and that the proposed model can estimate swine-specific SBM value more precisely, both locally and regionally. This method can also be used for other, economic important animal diets (e.g., poultry) which could help U.S. soybean producers choose high-yielding cultivars that are more likely to produce seed with increased ration-specific SBM value.

#### Core Ideas

- A model that precisely estimates soybean meal value targeted for swine nutrition was developed.
- A large soybean meal value range was observed among and within each state.
- Minimum protein and oil content as the only soybean meal value criteria can be misleading.

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Copyright © 2018 by the American Society of Agronomy 5585 Guilford Road, Madison, WI 53711 USA All rights reserved States, grown mainly as a protein and oil source for animal and human consumption. In the United States, soybean production increased by 60% from 1996 to 2016 as a result of a 30% increase in planted area, continual adoption by soybean producers of higher-yielding cultivars, and improved crop management practices (Specht et al., 2014; USDA-NASS, 2017). Despite the substantial historic seed yield increases, U.S. soybean producers constantly explore opportunities to optimize cultivar selection and crop management to increase soybean seed yield and thereby maximize net profit.

Upon seed delivery, elevators do not typically analyze soybean seed for quality; however, end-user processors do. The quality characteristics of SBM can ultimately affect the local soybean per tonne price offered to soybean producers after soybean processors begin to receive and valuate the new crop soybean seed. Soybean meal is commonly used as feed source for non-ruminant species due to its high protein concentration, excellent AA profile and adequate supply (Kim et al., 1999; Cromwell, 2000). However, substantial variation in SBM composition has been observed among meals produced in different countries or areas within a country (Karr-Lilienthal et al., 2004; van Kempen et al., 2006; Ravindran et al., 2014; García-Rebollar et al., 2016; Lagos and Stein, 2017). Soybean seed harvested in the northern U.S. Corn Belt states is consistently lower in protein compared to that in southern and southeastern United States (Rotundo et al., 2016). Hurburgh et al. (1990) found significant spatial and inter-annual variability for soybean seed protein in that seed produced in northern United States contained 15 to  $20\,\mathrm{g\,kg^{-1}}$ less protein and 2 to 5 g kg<sup>-1</sup> more oil than seed produced in the southern and southeastern United States. The location of U.S. production thus appears to have a great influence on seed as a result of cultivar selection and weather and therefore by extension to meal composition as well.

Region-specific agricultural management, in-season weather conditions, and their interactions greatly affect soybean seed yield and composition (Mourtzinis et al., 2017), which in turn can affect SBM composition. An important region-specific

Abbreviations: AA, amino acid; SBM, soybean meal; Lys, lysine; Met, methionine; Tryp, tryptophan; Iso, isoleucine; Cys, cysteine; Thr, threonine; Val, valine

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management practice is producer selection of maturity group cultivars with photoperiod adaptation to their region. In a recent study seven maturity group zones were identified based on using soybean yield as the criteria for local adaptation (Mourtzinis and Conley, 2017). Planting date is a key management practice, with early planting typically resulting in higher yield than late planting and can also affect seed composition (Mourtzinis et al., 2017). For example, in Minnesota and Wisconsin, the combination of a maturity group 2 with early planting (late April-early May) resulted in the highest yield, oil, and oleic acid potential; however, late planting (late June) led to a reduction in seed yield but resulted in the highest seed protein and essential AA content (Mourtzinis et al., 2017). The AA profile also varies among seeds with different protein content. Soybean with lower crude protein content have a higher proportion of the five critical essential AAs of Lys, cysteine (Cys), Met, threonine (Thr), and Tryp per unit of protein (Thakur and Hurburgh, 2007; Medic et al., 2014; Garvin and Naeve, 2016). The relative proportion of these AAs, present in the seed protein is also dependent on the selected cultivar and planting date (Mourtzinis et al., 2017).

Many underlying weather and environmental factors have been suggested to explain this variation, including in-season temperature variance (Thomas et al., 2003; Wilson, 2004; Yaklich and Vinyard, 2004). The effect of temperature on seed composition is especially pronounced during seed fill (Kane et al., 1997), and particularly so from R5 to R8 (Mourtzinis et al., 2017). Wolf et al. (1982) reported increased protein, oil and oleic acid content, and decreased linolenic and linoleic acids as the temperature during seed fill was increased. Naeve and Huerd (2008) found that oil concentrations increased by 6.6 g kg<sup>-1</sup> °C<sup>-1</sup> during seed fill in Minnesota, but protein was not affected. Additionally, Specht et al. (2001) observed that irrigation significantly altered soybean seed protein and oil content. Obviously, compositional differences, as shaped by environmental and management factors, ultimately affect seed and meal composition and AA balance. The resultant SBM value will thus vary and can potentially affect the per bushel price offered locally, regionally, and nationally each year.

By knowing which cultivars produce higher yields and higher quality SBM, U.S. producers can better compete in the world soybean market by responding to intrinsic or explicit pricing premiums/discounts offered by soybean seed purchasers. Most animal nutritionists use ration formulation software that compares many feed ingredients simultaneously to generate a ration to optimize animal weight gain relative to feed cost. Due to the aforementioned genetic × environment effect on soybean seed composition, the need to identify cultivars that produce meal with desirable composition, but with no concurrent reduction in yield is essential. However, doing so requires analysis of a large number of samples each year in each locality but such estimation would be costly and time consuming. We argue that a fast, precise, and cost-effective method of estimation would be valuable for producers, nutritionists, local elevators, and regional soybean processors. Therefore, using SBM for swine nutrition as a case-study, our objectives in this study were to (i) develop a model that precisely estimates SBM value specific for optimizing swine nutrition based on synthetic or hypothetical SBM derived from soybean quality parameters, (ii) quantify the swine-feeding-specific SBM value variability within and among

all soybean-producing states, and (iii) evaluate the predictive effectiveness of the model for estimating SBM value.

## MATERIALS AND METHODS

# Data Description and Compositional Analysis

Data collection and compositional analysis were described by Rotundo et al. (2016). Briefly, from 2013 to 2016, a total of 8282 soybean samples were collected from U.S. soybean producers who indicated the zip code of the town closest to the farm where the soybean crops were grown. Based on the zip code information, each sample was then assigned to a state. The developed database included data from 29 states (Iowa, Kansas, Minnesota, Missouri, Nebraska, North Dakota, South Dakota, Illinois, Indiana, Michigan, Ohio, Wisconsin, Delaware, Maryland, New Jersey, New York, Pennsylvania, Virginia, Arkansas, Kentucky, Louisiana, Mississippi, Oklahoma, Tennessee, Texas, Alabama, Georgia, North Carolina, and South Carolina).

Soybean seed samples were analyzed for protein  $(g kg^{-1})$  and oil  $(g kg^{-1})$ , for seven essential AAs  $(g kg^{-1})$  which were Lys, Cys, Meth, Thr, Tryp, Iso, and valine (Val), and for moisture content  $(g kg^{-1})$ . The analyses were conducted via near-infrared spectroscopy technology using a Perten DA7250 diode array instrument (Perten Instruments, Springfield, IL) equipped with calibration equations developed by the University of Minnesota in cooperation with Perten Instruments. Protein, oil, and AA data were adjusted to the standard of 13 g kg<sup>-1</sup> seed moisture base for use in the subsequent analyses.

The modeled SBM for all 8282 soybean samples was created using the United Soybean Board Estimated Processed Value calculator (Brumm and Hurburgh, 1990). This calculator simulates the process of soybean processing (i.e., soy oil extraction, hull removal etc.), with the output being a nutrient matrix for SBM that is very representative of common SBM, but based on the nutrient content of the single sample of soybean inputted in the calculator. In this formulation exercise, only AA values varied from sample to sample. It was assumed that oil content, and hull removal/addition was similar across each simulated soybean meal (Brumm and Hurburgh, 1990). Additionally, SBM energy content was assumed to be constant in all calculations. Furthermore, to estimate AA concentration in SBM, it was assumed that each AA's concentration, as percent of protein content, remains constant after processing. Thus, the concentration in the meal was based on the change of protein content from whole soybean seed to meal.

## Model to Estimate Soybean Meal Value

The current major challenge in the soybean commodity sector is the lack of a single variable that best describes SBM quality. Although it is widely accepted that the greater the protein content the greater the value of the meal, it is not clear as to how oil content and the relative proportions of the seven essential AAs (Lys, Cys, Meth, Thr, Tryp, Iso, and Val) affect SBM value. To overcome this problem, we used principal component analysis (PCA), which is a multivariate dimension reduction technique, to combine the information of all the sample-specific constituents (protein, oil, AA) of the synthetic/hypothetical SBM into one variable (Y\_pca). Eight principal components were used to capture about 98% of constituent variability, with the Y\_pca value calculated by fitting each principal component equation Table 1. Pearson correlations of Y\_pca (combined information of all the variety-specific constituents using principal component analysis) and all measured soybean meal constituents from 8282 samples across years and locations.

											Sum of	Sum of
											seven amino	, five amino
Constituent	Y_pca	Protein	Oil	Lysine	Cysteine	Methionine	Threonine	Tryptophan	Isoleucine	Valine	acids†	acids‡
Y_pca	Ι	0.8533***	0.212 <b>9</b> ***	0.4652***	° 0.6433***	0.5899***	0.4889***	0.5281***	0.7495***	0.6959***	0.8810***	0.8246***
Protein		I	–0.0971***	°0.3966***	°0.5129***	0.4533***	0.4513***	0.1982***	0.7967***	0.8006****	0. <b>7992</b> ***	0.6314***
Oil			Ι	0.0709***	° 0.0017***	-0.0520***	-0.1281***	0.3845***	0.0646***	-0.0657***	0.0504***	0.0859***
Lysine				I	0.1531***	0.1025***	0.4569***	0.1745***	0.4491***	0.2719***	0.6943***	0.8227***
Cysteine					I	0.7023***	0.1246***	0.3060***	0.4665***	0.5377***	0.6050***	0.5572***
Methionine						I	-0.0775***	0.4282***	0.4259***	0.6617***	0.5889***	0.4915***
Threonine							I	-0.1615***	0.4635***	0.1321***	0.5032***	0.5753***
Tryptophan								I	0.3368***	0.3466***	0.4586***	0.4553***
Isoleucine									I	0.7509***	0.8662***	0.6868***
Valine										I	0.7842***	0.5362***
Sum of 7 AAs	5										I	0.9328***
Sum of 5 AAs	5											I
*** Significant	correla	ations at alr	$h_{2} = 0.001$									

\*\*\* Significant correlations at alpha = 0.001.

† Sum of lysine, cysteine, methionine, threonine, tryptophan, isoleucine, and valine.

‡ Sum of lysine, cysteine, methionine, threonine, and tryptophan.

Table 2. Nutrient specifications of the common diet, which is representative of a pig at about 60 kg body weight.

		-	
Nutrient	Unit	Minimum	Maximum
Metabolizable energy	Kcal kg <sup>-1</sup>	3222	_
Calcium	%	0.60	0.71
Available P	%	0.35	_
SID Lysine†	%	0.85	_
SID Methionine + Cysteine	% of SID lysine	0.57	_
SID Isoleucine	% of SID lysine	0.55	_
SID Threonine	% of SID lysine	0.63	_
SID Tryptophan	% of SID lysine	0.18	-
SID Valine	% of SID lysine	0.65	-
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† Standardized Ileal digestibility.

and summing the results. We hypothesized that the greater the Y\_pca value, the greater the SBM value. Indeed, Y\_pca was strongly and positively correlated (i.e., >0.70) with protein, Iso, Val, sum of 5, and sum of 7 essential AAs in SBM (Table 1). Correlations of Y\_pca with the rest of the seed constituents were moderate, except for oil content which was very low.

The 8282 samples were then ranked in descending Y\_pca value. A subset (n = 145) was specifically selected and used in Dalex least cost formulation program (Dalex Livestock Solutions, LLC) to determine the least cost mix of ration ingredients based on the specifications in Tables 2, 3, and 4. A diet specification, representative of a typical mid-finishing swine diet, was common to all comparisons, as were the prices for other ingredients needed in that diet formulation. The output used for further statistical modeling in this project was total value per metric tonne of the common diet (\$ tonne<sup>-1</sup>). This swine-diet-specific SBM value then became a common descriptor for relative comparisons of the 8282 soybean samples. The 145 selected samples included 40 seed samples with the highest Y\_pca and 40 seed samples with the lowest Y\_pca values. These 80 samples served as constraining boundaries for model calibration. In addition, 30 other seed samples were randomly selected from the (8282-80 =) 8202 remaining samples. The remaining 35 samples (145–110) were used for an independent validation test of the model.

To develop a model that precisely estimates SBM value ( tonne<sup>-1</sup>), multiple linear regression was applied to 110 out of the

Table 3. Ingredient specifications of the common diet. Prices used are representative of prices in the market in 1 Nov. 2016.

Cum of

Ingredient	Price	Minimum	Maximum
	\$ t <sup>-1</sup>	kg t <sup>-1</sup>	kg t <sup>−l</sup>
Corn	115.00	_	-
Soybean meal	315.00	_	-
Calcium carbonate	50.56	_	-
Mono-calcium phosphate	570.00	_	-
Salt	88.80	3.6	3.6
Vitamin and trace mineral	2000.00	2.3	2.3
L-Threonine	1869.00	_	1.4
L-Lysine	1586.00	_	4.1
L-Tryptophan	7984.00	_	0.9
DL-Methionine	4000.00	_	1.4
L-Valine	6530.00	_	0.9

Table 4. Description of key formulation nutrients of soybean meal.
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Nutrient	Unit	Value				
Protein	%	Varied by sample				
Total of individual amino acid	%	Varied by sample				
Metabolizable energy	Kcal kg <sup>–l</sup>	3333				
Standardized ileal digestibility coefficients of amino acids						
Lysine	%	90				
Methionine	%	91				
Cysteine	%	87				
Threonine	%	87				
Tryptophan	%	90				
Isoleucine	%	89				
Valine	%	88				

145 samples for model calibration. Protein, oil, Lys, Cys, Meth, Thre, Tryp, Iso, and Val meal concentrations were used as independent variables. The simplest model, in which all independent variables were significant (P < 0.05) was selected. Statistical criteria such as coefficient of determination ( $R^2$ ), adjusted  $R^2$ , mean square error (MSE), root mean square error (RMSE), and coefficient of variation (CV), were used for the final selection decision as described by Mourtzinis et al. (2013).

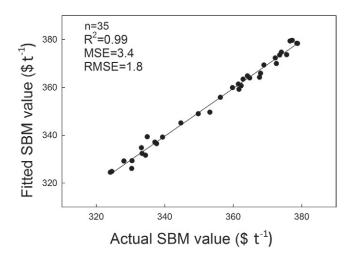


Fig. 1. Comparison of soybean meal (SBM) value ( $t^{-1}$ ) as was estimated by ration software (actual) and from the developed model (Eq. [I]) (fitted). Note: n, number of samples;  $R^2$ , coefficient of determination; MSE, mean square error; RMSE, root mean square error.

The final model (Eq. [1]) included protein, Lys, Meth, Tryp, and Iso as the five independent variables. That model provided a good fit to data of the 110 cultivar samples in view of the calibration  $R^2$  and adjusted  $R^2 = 0.991$ , RMSE = 1.76, and CV = 0.5.

Value (\$) of SBM tonne<sup>-1</sup> =  $72.16361 + 1.65587 \times$ Protein + 27.24420 × Lys + 57.25507 × Meth + 84.56061 × Tryp + 21.80598 × Iso [1]

Units of independent variables were presented as percent on a dry basis (db). The five variables in this model exhibited small variance inflation factors (VIF < 5), which suggest that there was no multicollinearity among them (Montgomery et al., 2006), although that is usually a problem in explanatory, but not in predictive, models we argue here in this case.

## **RESULTS AND DISCUSSION**

### **Model Performance**

The predictive reliability of the model was evaluated using the 35 samples (Fig. 1) that were not included in the model calibration process. Actual vs. fitted values were closely correlated with  $R^2 = 0.99$  and MSE and RMSE reaching 3.4 and 1.8, respectively. These validation results suggested that the calibrated model can precisely estimate SBM value of seed soybean produced by cultivars grown in any year and in any locality in the United States based on fixed ingredient prices, thereby precluding the need to go to the expense and time of completing the process of a least cost formula for each soybean sample. It should be noted that the three AAs that we did not include in the model (Cys, Thr, and Val) are still important for swine diet value. The only reason for their exclusion from the final model (Eq. [1]) is that the model adequately captured most of swinebased SBM value variability in the 8282 samples without them.

To examine the relationship between soybean seed yield and hypothetical SBM value, we used compositional and seed yield data from an independent data set (from Mourtzinis et al., 2017). Results show that there is no strong relationship between seed yield and protein content but there is a strong relationship between protein and SBM value (Fig. 2A). Additionally, there is no relationship between soybean seed yield and SBM value (Fig. 2B), which shows that cultivar selection for increased SBM value among the highest-yielding cultivars can maximize a farmer's profit.

Farmers typically select cultivars among those that seed companies promote and advertise as the highest yielding. Application of our simple model (Eq. [1]), allows any producer, elevator, or processor to estimate the value based on fixed ingredient prices of swine-based SBM for any specific soybean seed sample. Additionally, cultivars can be compared for their hypothetical SBM values, which can aid the producer when selecting cultivars to plant in a given year and elevators and processors to offer a premium or discount based on the estimated SBM value. This same technique, based on fixed ingredient prices, can be applied by plant breeders during the selection phase of cultivar breeding and release programs.

#### **Estimating Soybean Meal Value Variability**

The location where a soybean cultivar is grown is known to affect the quality of the seed which impacts SBM quality (Karr-Lilienthal et al., 2004; van Kempen et al., 2006; García-Rebollar et al., 2016; Lagos and Stein, 2017), and therefore can affect its value. Indeed, mapping the SBM values ( $\$ t^{-1}$ ), as estimated by applying our model (Eq. [1]), revealed substantial monetary differences among the 29 states (Fig. 3). On average, soybean seed harvested in northern states produced SBM values up to  $\$15 t^{-1}$  lower than in southern states. Assuming AA digestibility is consistent across regions, our model confirms that southern U.S. producers harvest do as has been documented in the prior literature.

Another important finding is the large SBM value range within each state, which was attributed to genetic, management, and environmental differences (Fig. 3). Within each state, the minimal range was \$17 in Georgia vs. a maximal range of \$66 in Indiana. The wider value range associated with the northern and mid-western states could possibly be due to the larger number of samples tested there compared with southern states or due to weather differences (e.g., consistently drier conditions in a few states compared to others). Another reason could be the result of years of genetic improvement of cultivars targeted for the Corn Belt, due to its importance as an agricultural region. For example, breeding-mediated improvement in maturity groups 2, 3, and 4 cultivars for increased yield is invariably the overarching goal which has resulted over time in lower seed protein content (Rincker et al., 2014).

Notably, state-to-state mean differences in SBM value and the wide SBM value range within each state, highlight the importance of local soybean producer cultivar selection. The authors fully recognize the North-to-South and East-to-West variation in cultivar seed composition; however, these results show the potential of individual producers to maximize their profit by identifying high-yielding cultivars, among those advertised by seed companies, which perform better locally, in terms of SBM value, than others in the same locality. Furthermore, seed companies could potentially utilize this simple model based on fixed ingredient prices to select, evaluate, and promote cultivars with superior seed quality characteristics. Regardless for both domestic and export markets, increasing the SBM value of the seed or meal product is a desired goal.

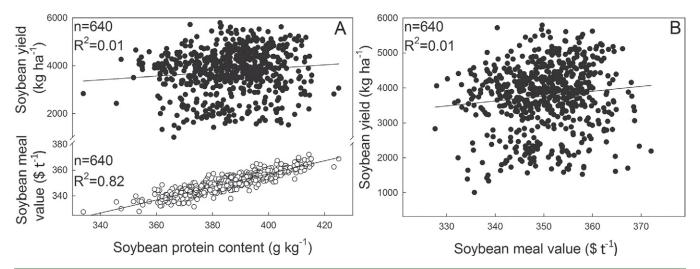


Fig. 2. Relationship of soybean seed yield (kg ha<sup>-1</sup>) and protein content (g kg<sup>-1</sup>) (upper line-black circles) and soybean meal (SBM) value ( $t^{-1}$ ) as was estimated by Eq. [I] and protein content (g kg<sup>-1</sup>) (bottom line-white circles) (A). Relationship of soybean seed yield (kg ha<sup>-1</sup>) and soybean meal (SBM) value ( $t^{-1}$ ) as was estimated by Eq. [I] (B). Note: n, number of samples;  $R^2$ , coefficient of determination.

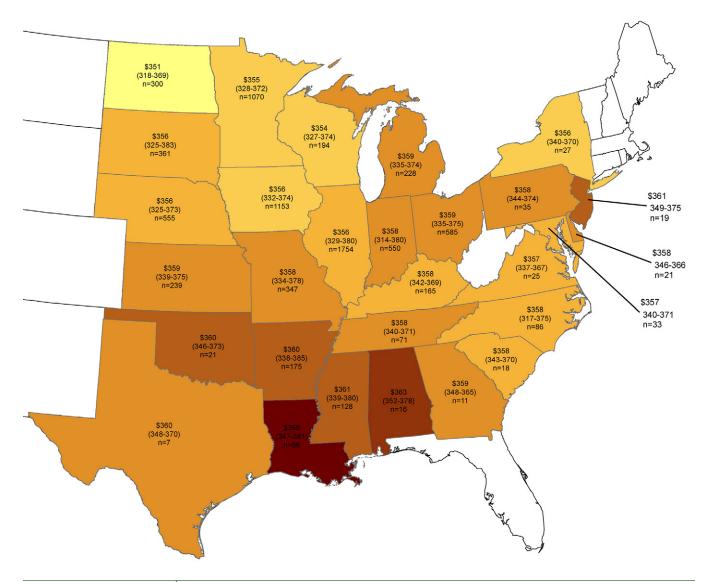


Fig. 3. Soybean meal value ( $t^{-1}$ ) means for soybean seed harvested in 2013 to 2016 in 29 states. The gradation of yellow-to-brown color denotes the mean state-specific soybean meal value. The values (t) within every state show the mean and the range (minimum-maximum) of soybean meal value due to the samples tested. Note: n, number of samples tested within every state.

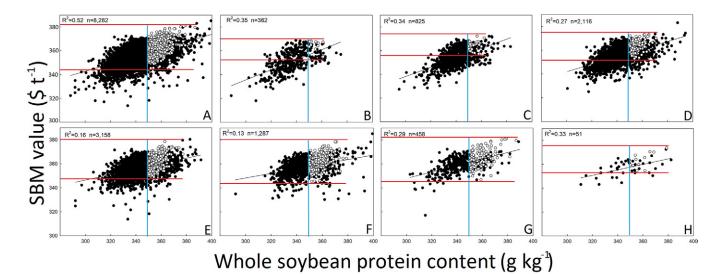


Fig. 4. Relationship of soybean seed protein content (g kg<sup>-1</sup>) and soybean meal (SBM) value ( $t^{-1}$ ) as was estimated by the developed model (Eq. [I]) for: (A) all 8282 samples collected during 2013 to 2016 for cultivar maturity groups in 29 states, (B) only maturity groups 0, (C) maturity groups 1, (D) maturity groups 2, (E) maturity groups 3, (F) maturity groups 4, (G) maturity groups 5, and (H) maturity groups 6. White circles denote the cultivars with a protein content >350 g kg<sup>-1</sup> (35%) and an oil content >190 g kg<sup>-1</sup> (19%) in each graph panel, whereas black circles denote cultivars that do meet either the protein or the oil criterion (or both). The red horizontal and blue vertical lines demark the limiting maximum and minimum SBM values that correspond to the aforementioned protein and oil content criteria. Note:  $R^2$ , coefficient of determination, and n, sample number in chart.

### Evaluating the Predictive Effectiveness of the Model for Estimating Soybean Meal Value

Seed yield potential is the foremost criterion in which soybean breeders have selected cultivars for advancement. Only after this criterion is met are other traits such as compositional quality considered. Until recently the quest for increased seed quality has been primarily focused on seed protein and oil content as cut-off criteria for choosing which of the high-yielding breeding lines have seed protein contents closer to the desired levels. Soybean producer organizations have promoted the use of a cut-off value for protein seed content >350 g kg<sup>-1</sup> (35%) and for oil content >190 g kg<sup>-1</sup> (19%) (13% moisture basis) when possible, based on the perception that doing so would potentially increase SBM value. However, by focusing only on protein and oil content minimum criteria, other important compositional information is not simultaneously considered, such as the AA concentration and digestibility of individual AA, which could affect the animal feeding ration based SBM value in unpredictable ways. Here, we have shown that the model (Eq. [1]) we developed based on 4-yr, 29-state set of 8282 samples, was a reliable predictor of SBM value for evaluating SBM-specific for a desired swine ration.

When using whole soybean protein content as explanatory variable, about 50% of SBM value variability was captured (Fig. 4A). When using protein and oil content limits (protein seed content >350 g kg<sup>-1</sup> [35%], and oil content >190 g kg<sup>-1</sup> [19%]) as the only SBM value indicator for "high-quality" cultivars (white circles), the red-line-delineated SBM value range was \$43 t<sup>-1</sup> (Fig. 4A). The high-quality samples accounted for <14% of all samples. In short maturity groups ( $\leq 2$ ), the high-quality samples did not exceed 8% of total whereas, for longer maturity groups ( $\geq 3$ ) the proportion reached 40%. Seed samples produced by cultivars that did not meet the high-quality criteria (black circles) were also within the same value range and some exhibited an even greater value. The same response was observed

when repeating the analysis by disaggregating the 8282 samples into maturity group based subsample sets (Fig. 4B–H). Thus, one can infer from this graphical presentation that with only protein/oil content serving as a high-quality criteria important compositional information is not considered.

These results suggest that using minimum protein and oil content as the only criteria for SBM value indicator, a large proportion in value variability remains unexplained. Adding other seed quality constituents, such as essential AAs that also contribute to SBM value, as we do in our model (Eq. [1]), will better target high SBM value cultivars, compared to just targeting cultivars meeting just a simple standard of protein and oil content >350 and 190 g kg<sup>-1</sup>, respectively. This is also clearly evident in the maturity group-specific graphs (Fig. 4B–H). Therefore, including the AA profile along with protein content profile provides a more reliable estimate of SBM value, particularly when modeling SBM for soybean meal destined to be used in animal feeding rations.

### CONCLUSIONS

The work presented here has important implications for soybean cultivar selection and breeding efforts across the United States. Using swine diet as a case-study, we showed that when assuming constant SBM energy content, by considering meal protein content and the concentrations of four essential AAs (Lys, Meth, Tryp, and Iso), a precise estimate of SBM value can be obtained. A simple model based on fixed ingredient prices was presented that allows soybean producers, elevators, and processors to estimate the relative cultivar-specific SBM value for swine nutrition. This method can also be replicated for other, economic important, diets (e.g., poultry) and help US soybean producers to select appropriate cultivars, among those promoted by seed companies as the highest yielding, for production of greater SBM quality. Future models should value differentiation by estimating SBM energy values and layer that value alongside amino acid value differences. Ultimately, the United States as a whole could improve its position in the world soybean market due to the increased seed quality characteristics.

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