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Chemical and Nutritional Characteristics of United States Soybeans and Soybean Meals

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Two experiments were conducted to determine U.S. soybean meal (SBM) variation. In experiment 1, SBM from 55 U.S. processors was evaluated. Significant ($P < 0.05$) but numerically small differences were detected in dry matter (DM) and organic matter (OM) concentrations. Crude protein (CP) concentrations (51.6−54.6%) were higher ($P < 0.05$) in SBM produced in the southern U.S. Lipid and total dietary fiber concentrations also differed ($P < 0.05$). The protein dispersibility index was affected ($P < 0.05$) by the source of SBM. In experiment 2, soybeans and resultant SBMs were obtained from 10 U.S. processing plants. Soybean DM, OM, and CP concentrations differed ($P < 0.05$). Soybean meal varied ($P < 0.05$) in CP (48.2−56.2%), acid-hydrolyzed fat (3.3−9.2%), total dietary fiber (17.0−20.7%), and lysine concentrations. Soybean meal carbohydrate composition was also affected by processing conditions. These results indicate a significant variation in chemical and nutritional characteristics of U.S. SBM from different sources.

KEYWORDS: Soybean; soybean meal processing; nutrition

INTRODUCTION

Accurate information on SBM composition and availability of nutrients is important if a precise animal feed formulation is to be achieved. Soybean variety, growing conditions, and processing conditions (*1*) all may influence composition of the resultant SBM. The nutritive value of SBM is determined not only by quantity and availability of amino acids but also by the processing conditions used in its preparation (*2*).

Solvent extraction is the most common procedure in the U.S. for separation of oil (fat) from the remainder of the soybean. This procedure has an extraction efficiency of 99% and is capable of handling large volumes of soybeans (*3*). Another means of processing soybeans is mechanical oil expression, which supplies a niche market. Although this process appears to have the potential to produce SBM free of any chemical residues, it has an oil extraction efficiency of less than 70% (*3*). The mechanical oil extraction rate must be improved if this process is to be economically viable on a large scale in the U.S. soybean industry.

Variation in processing conditions, such as temperature and time, is common among processors in the SBM production industry to optimize processing efficiency and end product quality. Unfortunately, though, failure to process soybeans properly can result in decreased nutrient availability to the animal. Two experiments were designed with the objective of determining the variation in chemical composition and nutritive value of SBM produced in the U.S. The processing plants surveyed in these projects used common soybean processing technologies and were representative of the industry.

It was not the goal of either of these experiments to determine the effect of soybean genotype or environmental growing conditions on the nutritive values of the resultant SBM. It is acknowledged that both of these factors can influence the nutritive value of SBM, but it is impossible to control for these factors in an experiment such as this or in practical SBM procurement. Furthermore, because soybean genotypes typically perform optimally under a particular set of environmental conditions, it would be impractical to test a particular soybean genotype across widely varying environmental zones, as was the objective here.

MATERIALS AND METHODS

Sample Collection. Experiment 1 was designed to quantify the variability of SBM produced in the U.S. Fifty-five soybean processing plants distributed among soybean maturity zones 1−7 (**Figure 1**) were used. Each plant was visited at approximately 2 week intervals over a 4 week period for a total of three samples from each plant. Samples from individual plants were not pooled but rather analyzed individually to provide replication within each plant. During each visit, approximately 2 kg of SBM was collected for analysis. All samples were collected while the plants were running normally, and no processing information was collected.

To evaluate the effect of processing conditions on chemical and nutritional characteristics, both soybean and resultant SBM samples

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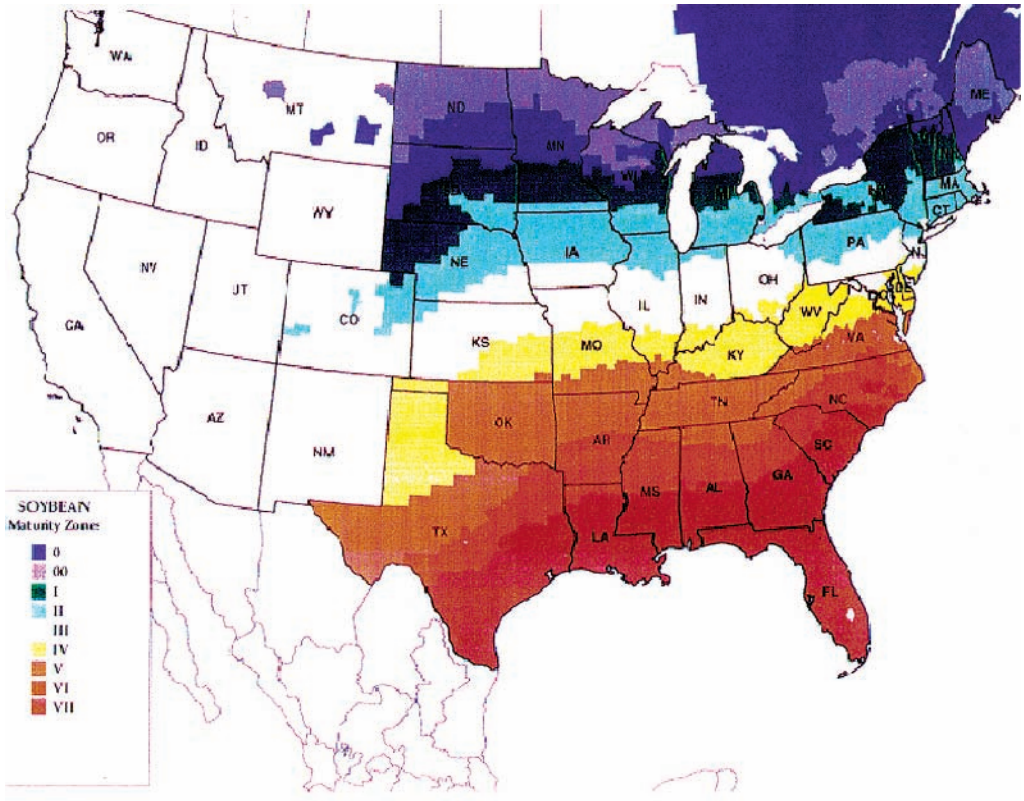

Figure 1. Map of U.S. soybean maturity zones (unknown origin).

were obtained from 10 soybean processing plants located throughout the major U.S. soybean growing regions in experiment 2. Each plant was visited three times: fall, l998; winter, l998/1999; and spring, 1999. Samples collected at each of the visits were analyzed separately. Processing plants involved in this study were numerically identified as 1−10, but their locations and owners remained confidential. Limited processing information was collected from each plant at the time of SBM manufacturing.

Laboratory Analyses. Prior to laboratory analyses, SBM samples were ground in a Wiley Mill model Y through a 2 mm screen (protein solubility and urease activity (UA) assays required a 0.5 mm grind) and stored at room temperature. Soybean samples were ground with dry ice (to avoid fat loss) and stored frozen at −20 °C. All samples were analyzed for DM, OM, CP (*4*), amino acid composition (*5*, *6*; experiment 2 only), acid-hydrolyzed fat (*7*), and TDF (*8*). NDF (*9*) rather than TDF was determined on soybean samples due to the high levels of fat in the soybean samples interfering with the TDF assay. In addition, because crude fat is the typical expression of oil content in the soybean processing industry, this analysis (*4*) was performed on all SBM samples collected in experiment 2. Indicators of nutritional value of the SBM that were determined on these samples included protein solubility in KOH (*10*), PDI (*11*), and UA (*12*).

Experiment 2 soybean and SBM carbohydrate content were characterized by analysis of TNC (*13*), oligosaccharides and sucrose (*14*), uronic acids (*15*), and free monosaccharides (*14*; with the modification that the eluent used was water with postcolumn addition of 300 mmol of NaOH). If the variability between duplicates of a sample was greater than 5%, the assay was repeated, with the exception of acid-hydrolyzed fat, crude fat, protein solubility in KOH, and NDF analyses, where a variability of 10% or less was accepted.

Statistical Analyses. Statistical comparisons among maturity zones in experiment 1 were made using the General Linear Models Procedure of SAS (*16*). Sources of variation in the model included maturity zone, plant within zone, and collection time. Statistical analysis for experiment 2 was conducted using the General Linear Models Procedure of SAS (*16*). The effect of processing plant was analyzed using a completely randomized design. Processing plant and collection time were the sources of variation included in the model.

RESULTS

Experiment 1. Six of the 55 plants supplied only one or two samples. The distribution of soybean processing plants within the U.S. soybean maturity zones is provided in **Table 1**. SBM samples were collected from only three processing plants in maturity zone 7, the extreme southern U.S., while samples were collected from 22 processing plants in maturity zone 3, the midwestern region. This distribution is somewhat indicative of the distribution of SBM production in the U.S.

Although statistical differences ($P < 0.05$) existed in DM and OM concentrations of SBM produced in the various maturity zones, these differences were numerically small and of questionable biological significance (**Table 1**). SBM CP concentration was lower ($P < 0.05$) in samples collected from maturity zones 1 and 2 as compared to those collected from any other zone (**Table 1**). SBM processed in maturity zone 6 had numerically the highest concentration of CP.

Acid-hydrolyzed fat concentrations did not follow a consistent pattern (range of 3.7−4.8%), although values among maturity zones differed ($P < 0.05$). SBM produced in maturity zone 6 had a higher ($P < 0.05$) acid-hydrolyzed fat concentration than SBM produced in any other zone. Similarly, the SBM TDF concentration (range of 18.2−20.5%) differed ($P < 0.05$) among maturity zones but did not follow a consistent pattern (**Table 1**).

The nutritional value of SBM samples was assessed using protein solubility, UA, and PDI assays. Protein solubility (range of 76.8−82.6%) and UA (range of 0.01−0.03 pH units) values did not differ ($P > 0.05$) among SBM samples collected from the seven maturity zones. PDI values differed ($P < 0.05$) among maturity zones, with SBM collected from maturity zone 2 having the highest numerical value and those collected from maturity zone 7 having the lowest (**Table 1**).

Table 1. Chemical Composition and Nutritive Value Characteristics of SBMs Produced at 55 Processing Plants in the U.S. (Experiment 1)[a]

	maturity zone							
item	1	2	3	4	5	6	7	SEM
no. of plants	4	10	22	7	4	5	3	
DM (%)	89.8^{ab}	90.2^{a}	89.6^{b}	89.8^{ab}	89.6^{b}	88.9^{c}	89.1^{c}	0.15
				% of DM				
OM	92.8^{a}	92.6^{b}	92.4^{c}	92.4^{c}	92.9^{a}	91.8^{d}	91.9^{d}	0.07
CP	51.6^{d}	52.8^{c}	53.5^{b}	53.6^{b}	53.6^{ab}	54.6^{a}	54.0^{ab}	0.26
acid-hydrolyzed fat	4.0^{bc}	3.7^{c}	3.8^{c}	3.9^{bc}	4.2^{b}	4.8^{a}	4.1^{bc}	0.11
TDF	20.5^{a}	19.2^{b}	18.9^{b}	19.3^{ab}	19.0^{b}	18.2^{b}	19.7^{ab}	0.39
protein solubility (% of CP)	77.9	79.2	79.2	77.2	78.7	76.8	82.6	1.41
UA (pH units)	0.02	0.03	0.03	0.03	0.01	0.03	0.02	0.01
PDI	25.8^{bc}	30.6^{a}	27.6^{bc}	29.6^{ab}	28.2^{abc}	26.3^{bc}	24.3^{c}	1.19

[a] a,b,c,d: Means in rows with different letters differ ($P < 0.05$).

Table 2. Processing Methods Used at 10 U.S. Soybean Processing Plants (Experiment 2)

plant no.	dehulling[a]	expander (%)[b]	solvent extractor[c]	desolventize/ toast/dry/cool
1	hot	0	shallow	DTDC[d]
2	hot	0	shallow	DTDC
3	conventional	50	deep	DT/DC[e]
4	hot	25	shallow	DTDC
5	conventional	30	deep	DTDC
6	conventional	0	deep	DT/DC
7	conventional	0	deep	DT/DC
8	hot	0	shallow	DT/DC
9	hot	40	deep	DTDC
10	none[f]	0	extrude/expel	none

[a] Conventional dehulling involves drying soybeans to approximately 12% moisture, tempering for up to 3 days, cracking, and aspirating the hulls off. The meats are cooked to approximately 60 °C before flaking. Hot dehulling involves heating soybeans to approximately 88 °C for a short period of time followed by cracking, aspirating, and flaking. [b] Expander is a process used to improve the efficiency of oil removal in extraction by breaking the oil cells by means of an extruder with the addition of steam. Numbers presented represent the percent of the meal passing through the expander. [c] Shallow extractors have a bed depth of approximately 0.9 m whereas deep extractor bed depths can be up to 2.7–3.0 m. [d] DTDC is desolventizing, toasting, drying, and cooling operations stacked in a single vessel. The purposes of these processes are as follows: desolventizing, removal of residual solvent from the crude oil; toasting, inactivation of enzymes and destruction of antinutritional factors; drying, reduction of the moisture content to approximately 12–13%; and cooling, reduction of the temperature of the SBM to approximately ambient temperature. [e] DT/DC, these processes occur in separate dual vessels. [f] None, nonsolvent (mechanical) extraction.

Table 3. Summary of Operating Conditions at 10 U.S. Soybean Processing Plants (Experiment 2)

plant no.	soybean source[a]	cycle time (h)[b]	expander[c]	dome temp (°C)[d]	toast temp (°C)[e]
1	local	2.2	no	74	105
2	local	2.0	no	74	104
3	NC/midwest [f]	2.0	yes	80	109
4	local	2.3	yes	73	105
5	local	3.0	yes	74	107
6	local	1.6	no	71	108
7	local	2.3	no	87	110
8	local	2.4	no	73	108
9	local	unknown	yes	71	104
10	no information available				

[a] Local soybeans generally originate within 60 miles of the processing plant. [b] Cycle time is the time required for preparation, extraction, and DTDC. [c] Expander is the process used to improve the efficiency of oil removal in extraction by breaking the oil cells by means of an extruder with the addition of steam. [d] Dome temperature is the temperature in the dome of the DTDC compartment. [e] Toast temperature is the temperature in the toasting section of the DTDC compartment. [f] Samples were collected from both North Carolina and the Midwest.

Experiment 2. Table 2 provides general processing methods used at each of the SBM manufacturing plants. Plants 1−9 were solvent extraction facilities, while plant 10 was a mechanical extraction facility. Processing information collected from each plant at the time of sampling included as follows: source of soybean (i.e., local or rail), cycle time (total time for preparation, extraction, desolventization, toasting, drying, and cooling (DTDC)), expander usage (percentage of production flow passing through an expander), and temperatures in the dome and toast sections of the DTDC unit (**Table 3**).

Soybean Composition and Nutritive Value Characteristics. DM concentrations (range of 87.8−91.3%) of soybean samples from the 10 U.S. processing plants differed statistically ($P < 0.05$) but were numerically similar (**Table 4**). Although soybean OM concentrations among the 10 plants differed statistically ($P < 0.05$), they were numerically similar (range of 94.3−94.7%; **Table 4**).

Soybean CP concentrations ranged from 40.1 to 42.2% (**Table 4**). Differences ($P < 0.05$) in CP concentration among samples from different plants existed, with soybeans from plant 10 having the lowest and soybeans from plant 4 the highest CP concentrations. However, individual amino acid concentrations, in addition to TEAA, TNEAA, and TAA concentrations in soybean samples among processing plants, were not different ($P > 0.05$; **Table 5**).

There were numerically large but statistically insignificant ($P > 0.05$) differences in acid-hydrolyzed fat concentrations among soybeans collected from the processing plants (**Table 4**). Soybeans from plant 10 had the lowest fat concentration (17.4%) while that from plant 1 was the highest (20.1%). The NDF concentration of soybean samples ranged from 11.1 to 13.0% in samples from plants 9 and 3, respectively (**Table 4**), but statistical differences ($P > 0.05$) were not detected among plants.

The protein solubility of soybeans ranged from a low of 70.7% in samples from plant 6 to a high of 83.8% in samples from plant 10 (**Table 4**; $P > 0.05$). The UA index was lowest (1.93 pH units) in soybean samples from plant 8 and highest (2.22 pH units) in those from plant 10, although this difference was not significant ($P > 0.05$; **Table 4**). Similarly, the PDI values (range of 81.4−86.3) among soybean samples were numerically but not statistically different ($P > 0.05$; **Table 4**).

Concentrations of TNCs, free monosaccharides, sucrose, oligosaccharides, and uronic acids of soybean samples are presented in **Table 6**. The concentration of TNC (12.3−16.0%) was similar among soybean samples ($P > 0.05$), but the

Table 4. Chemical Composition and Nutritive Value Characteristics of Soybeans Collected at 10 U.S. Processing Plants (Experiment 2)[a]

	plant no.										
item	1	2	3	4	5	6	7	8	9	10	SEM
DM (%)	89.1^{bcd}	87.8^{d}	90.0^{abc}	88.9^{cd}	89.5^{bc}	91.3^{a}	90.6^{ab}	89.5^{bc}	90.1^{abc}	89.3^{bcd}	0.49
					% of DM						
OM	94.6^{bcd}	94.7^{cd}	94.4^{ab}	94.5^{bcd}	94.7^{cd}	94.5^{bcd}	94.4^{ab}	94.4^{abc}	94.7^{d}	94.3^{a}	0.08
CP	42.0^{a}	41.5^{ab}	41.1^{bc}	42.2^{a}	40.6^{bc}	41.4^{ab}	40.8^{bc}	41.5^{ab}	40.7^{bc}	40.1^{c}	0.34
acid-hydrolyzed fat	20.1	18.3	19.4	18.5	18.3	17.8	17.7	19.3	19.3	17.4	1.05
NDF	12.1	11.4	13.0	12.0	11.2	12.2	12.1	11.6	11.1	11.3	0.58
protein solubility (% of CP)	78.8	75.0	71.5	77.4	73.8	70.7	75.8	77.3	78.0	83.8	3.75
UA (pH units)	2.07	2.01	1.98	2.15	2.08	1.98	2.01	1.93	2.12	2.22	0.07
PDI	85.1	82.8	84.3	84.0	83.7	81.4^{a}	83.4	81.7	85.2	86.3	1.71

[a] a,b,c,d: Least squares means in a column with different letters are different ($P < 0.05$).

Table 5. Amino Acid Concentrations (% of DM) of Soybeans Collected at 10 U.S. Processing Plants (Experiment 2)

	plant no.										
item	1	2	3	4	5	6	7	8	9	10	SEM
					essential amino acids						
arginine	3.1	3.0	2.9	2.9	2.7	2.9	2.8	3.0	3.0	2.8	0.08
histidine	1.1	1.1	1.1	1.1	1.0	1.1	1.1	1.1	1.1	1.0	0.03
isoleucine	2.0	1.9	1.9	1.9	1.8	1.9	1.8	1.9	1.9	1.9	0.04
leucine	3.3	3.3	3.2	3.2	3.1	3.1	3.1	3.2	3.2	3.1	0.07
lysine	2.7	2.7	2.6	2.6	2.5	2.6	2.5	2.7	2.6	2.5	0.06
methionine	0.6	0.5	0.5	0.6	0.5	0.5	0.5	0.6	0.5	0.5	0.03
phenylalanine	2.1	2.1	2.1	2.1	2.0	2.0	2.0	2.1	2.1	2.0	0.05
threonine	1.7	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	0.04
valine	2.1	2.0	2.0	2.0	1.9	2.0	2.0	2.0	2.0	2.0	0.04
					nonessential amino acids						
alanine	1.8	1.8	1.8	1.8	1.7	1.8	1.7	1.8	1.8	1.7	0.04
aspartate	4.9	4.8	4.7	4.8	4.5	4.7	4.6	4.9	4.8	4.6	0.10
cystine	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.4	0.03
glutamate	8.0	7.7	7.6	7.7	7.3	7.6	7.4	7.8	7.7	7.4	0.16
glycine	1.8	1.8	1.8	1.8	1.7	1.8	1.7	1.8	1.7	1.7	0.03
proline	2.4	2.2	2.4	2.4	2.3	2.4	2.3	2.5	2.4	2.2	0.07
serine	2.2	2.1	2.2	2.2	2.1	2.1	2.0	2.2	2.2	2.1	0.05
tyrosine	1.3	1.3	1.2	1.2	1.1	1.2	1.2	1.3	1.3	1.2	0.05
TEAA	**18.6**	**18.3**	**17.8**	**18.0**	**17.1**	**17.7**	**17.4**	**18.2**	**18.1**	**17.9**	**0.35**
TNEAA	**22.9**	**22.4**	**22.1**	**23.4**	**21.2**	**22.0**	**21.4**	**22.6**	**22.4**	**22.2**	**0.41**
TAA	**41.5**	**40.7**	**39.9**	**40.3**	**38.3**	**39.7**	**38.7**	**40.8**	**40.4**	**40.1**	**0.75**

Table 6. Carbohydrate Composition of Soybeans Collected at 10 U.S. Processing Plants (Experiment 2)[a]

	plant no.										
item	1	2	3	4	5	6	7	8	9	10	SEM
total nonstructural carbohydrate (% of DM)	14.7	15.0	14.5	12.3	16.0	14.5	14.7	14.0	14.3	13.9	0.92
total sugars (% of DM)[b]	13.7^{abc}	13.7^{abc}	13.4^{bc}	11.7^{d}	14.4^{a}	13.8^{ab}	13.5^{abc}	13.5^{abc}	14.2^{ab}	12.8^{c}	0.34
					mg/g DM						
galactose	3.7^{a}	3.1^{ab}	1.2^{bc}	2.9^{ab}	3.0^{ab}	0.8^{c}	0.7^{c}	1.4^{bc}	3.6^{a}	4.0^{a}	0.65
glucose	3.1	2.2	3.0	4.7	2.8	1.2	1.5	2.7	3.7	3.1	1.31
fructose	3.0	2.0	2.9	4.7	2.6	1.1	1.2	2.6	3.5	3.0	1.33
sucrose	48.1^{abc}	52.3^{ab}	45.8^{bc}	30.9^{d}	56.6^{a}	52.3^{ab}	50.0^{abc}	48.3^{abc}	53.1^{ab}	42.0^{c}	3.35
raffinose	6.2	5.0	6.3	7.4	6.0	6.3	6.5	5.7	6.2	5.9	0.77
stachyose	38.4^{ab}	36.9^{abc}	38.9^{ab}	30.8^{d}	39.1^{ab}	41.3^{a}	40.1^{ab}	39.2^{ab}	36.4^{bc}	34.3^{cd}	1.46
verbascose	1.6^{abc}	1.4^{bcd}	1.6^{bcd}	2.0^{a}	1.2^{d}	1.8^{ab}	1.6^{abcd}	1.7^{ab}	1.3^{cd}	1.5^{bcd}	0.14
uronic acid	33.1	33.6	34.2	33.8	33.2	32.9	33.7	33.9	34.3	34.2	0.82

[a] a,b,c,d: Means in a row with different letters differ ($P < 0.05$). [b] Total sugars = sum of the concentrations of the sugars analyzed.

concentration of total sugars analyzed (11.7−14.4%) differed ($P < 0.05$), with plant 4 having the lowest and plant 5 having the highest total sugar concentration. Although the concentrations of free glucose and fructose did not differ among soybean processing plants, the free galactose concentration ranged from a low of 0.7 mg/g in soybeans from plant 7 to a high of 4.0 mg/g in soybeans from plant 10 ($P < 0.05$; **Table 6**). Both sucrose and stachyose were present in high concentrations (30.9−56.6 and 30.8−41.3 mg/g, respectively) and differed among soybean samples. Soybeans from plant 4 had a particularly low concentration of sucrose (30.9 mg/g) as compared with soybeans collected at the other processing plants. Soybean raffinose concentrations varied little among plants (range of 5.0−7.4 mg/g). Differences in verbascose concentration of soybean samples were small but statistically significant ($P < 0.05$) and ranged from 1.2 mg/g in samples from plant 5 to 2.0

Table 7. Composition of SBMs Collected at 10 U.S. Soybean Processing Plants (Experiment 2)[a]

	plant no.										
item	1	2	3	4	5	6	7	8	9	10	SEM
DM (%)	89.0	88.9	88.3	88.9	88.2	89.4	90.2	88.2	88.3	90.2	0.64
					% of DM						
OM	92.1	92.5	92.2	92.0	93.2	92.2	91.6	92.8	93.1	93.4	0.40
CP	55.3^{ab}	55.1^{ab}	54.8^{ab}	54.9^{ab}	54.0^{b}	55.0^{ab}	53.5^{b}	56.2^{a}	55.1^{ab}	48.2^{c}	0.70
crude fat	0.9^{d}	1.4^{bcd}	1.3^{cd}	2.3^{b}	1.1^{d}	1.5^{bcd}	1.1^{d}	2.3^{bc}	0.8^{d}	7.0^{a}	0.38
acid-hydrolyzed fat	3.6^{cd}	4.1^{bc}	3.5^{cd}	4.5^{b}	3.9^{bcd}	3.9^{bcd}	3.8^{bcd}	4.4^{bc}	3.3^{d}	9.2^{a}	0.27
TDF	17.3^{a}	17.3^{a}	18.5^{a}	18.6^{a}	18.5^{a}	17.0^{a}	18.5^{a}	17.0^{a}	17.7^{a}	20.7^{b}	0.66
protein solubility (% of CP)	82.5^{ab}	80.8^{ab}	78.0^{ab}	79.1^{b}	84.6^{a}	82.9^{ab}	80.7^{ab}	83.0^{ab}	78.3^{b}	65.4^{c}	1.76
UA (pH units)	0.10	0.04	0.04	0.04	0.07	0.08	0.04	0.03	0.03	0.05	0.02
PDI	33.8^{a}	34.0^{a}	24.3^{bc}	24.2^{bc}	30.8^{a}	33.3^{a}	30.7^{a}	33.9^{a}	21.6^{c}	7.1^{d}	1.58

[a] a,b,c: Least squares means in a row with different letters are different ($P < 0.05$).

Table 8. Amino Acid Concentrations (% of DM) of SBMs Collected at 10 U.S. Soybean Processing Plants (Experiment 2)[a]

	plant no.										
item	1	2	3	4	5	6	7	8	9	10	SEM
					essential amino acids						
arginine	4.7	4.0	4.0	3.9	3.9	3.9	3.8	4.1	3.9	3.4	0.20
histidine	1.7	1.5	1.4	1.5	1.4	1.5	1.4	1.5	1.4	1.3	0.07
isoleucine	2.8	2.5	2.4	2.6	2.4	2.5	2.4	2.5	2.4	2.2	0.12
leucine	4.9	4.3	4.3	4.4	4.3	4.3	4.1	4.4	4.2	3.9	0.20
lysine	4.1^{a}	3.5^{b}	3.5^{b}	3.6^{ab}	3.5^{b}	3.5^{ab}	3.4^{bc}	3.7^{ab}	3.4^{bc}	2.9^{c}	0.18
methionine	0.7	0.9	0.7	0.6	0.7	0.8	0.7	0.8	0.7	0.7	0.06
phenylalanine	3.3^{a}	2.8^{bc}	2.8^{bc}	2.9^{b}	2.8^{bc}	2.8^{bc}	2.7^{bc}	2.9^{b}	2.8^{bc}	2.5^{c}	0.13
threonine	2.6	2.2	2.2	2.2	2.1	2.2	2.2	2.3	2.2	2.0	0.12
valine	3.0	2.6	2.6	2.7	2.6	2.6	2.5	2.7	2.6	2.3	0.13
					nonessential amino acids						
alanine	2.8	2.4	2.4	2.4	3.8	2.4	2.4	2.5	2.4	2.2	0.12
aspartate	6.9	6.4	6.3	6.5	6.1	6.4	6.2	6.6	6.3	5.7	0.21
cystine	0.7	0.7	0.7	0.6	0.6	0.7	0.6	0.7	0.6	0.6	0.05
glutamate	11.5	10.3	10.2	10.4	9.9	10.2	9.8	10.7	10.1	9.1	0.40
glycine	2.7	2.3	2.3	2.3	2.3	2.3	2.3	2.4	2.3	2.2	0.11
proline	3.7	3.1	3.0	3.0	3.0	3.1	3.1	3.3	3.2	2.9	0.14
serine	3.3	2.9	2.9	2.9	2.8	2.9	2.8	3.0	2.9	2.7	0.14
tyrosine	1.9	1.7	1.7	1.8	1.6	1.6	1.7	1.8	1.6	1.6	0.10
TEAA	**27.6**	**24.3**	**23.9**	**24.4**	**23.7**	**24.0**	**23.2**	**25.0**	**23.5**	**21.1**	**1.12**
TNEAA	**33.4**	**29.9**	**29.4**	**29.9**	**29.8**	**29.6**	**28.8**	**31.0**	**29.3**	**26.9**	**1.14**
TAA	**61.0**	**54.2**	**53.3**	**54.3**	**52.5**	**53.6**	**52.1**	**56.0**	**52.9**	**48.6**	**2.25**

[a] a,b,c: Means in a row with different letters differ ($P < 0.05$).

mg/g in samples from plant 4. Uronic acids concentrations (range of 32.9−34.3 mg/g) did not differ ($P > 0.05$) among samples.

SBM Composition and Nutritive Value Characteristics. Similar to results for soybean samples, the DM and OM of SBM varied little (88.2−90.2 and 91.6−93.4%, respectively) and did not differ significantly among plants ($P > 0.05$; **Table 7**).

SBM CP concentrations ranged from 53.5 to 56.2% ($P < 0.05$; **Table 7**) with the exception of the samples from plant 10 that had the lowest CP ($P < 0.05$) concentration (48.2%). Lysine (range of 2.9−4.1%) and phenylalanine (range of 2.5−3.3%) concentrations varied ($P < 0.05$) among SBM samples (**Table 8**). In both cases, the concentrations of these amino acids were lowest in samples from plant 10 and highest in samples from plant 1. TEAA, TNEAA, and TAA concentrations did not differ significantly ($P > 0.05$; **Table 8**) among SBM samples, although they followed the same trends as observed with individual amino acids.

SBM crude fat concentration in samples from plants 1 to 9 was low (range of 0.8−2.3%; **Table 7**) and differed among plants ($P < 0.05$). The crude fat concentration of samples from plant 10 was exceptionally high, 7.0%, and differed from samples obtained from the other plants ($P < 0.05$). Acid-hydrolyzed fat concentrations from plants 1 to 9 were higher (range of 3.3−4.5%) than crude fat values and differed among plants ($P < 0.05$; **Table 7**). Again, the acid-hydrolyzed fat concentration of samples from plant 10 was exceptionally high, 9.2%, and differed from samples obtained from the other plants ($P < 0.05$). Although TDF concentrations of SBM from these plants were fairly consistent (range of 17.0−20.7%), they did differ among plants ($P < 0.05$; **Table 7**).

The protein solubility of SBM ranged from a low of 65.4% in SBM from plant 10 to a high of 84.6% in samples from plant 5 and differed among plants ($P < 0.05$; **Table 7**). The protein solubility of SBM from plant 10 was lower ($P < 0.05$) than that of samples from all other plants. The UA index was low for all SBM samples and ranged from 0.03 for SBM from plants 8 and 9 to a high of 0.10 in plant 1 samples ($P > 0.05$; **Table 7**). The SBM PDI ranged from 7.1 in samples from plant 10 to 33.9 in SBM from plant 8 (**Table 7**). The PDI of SBM from plants 1 to 9 ranged from 21.6 to 34.0, with plant 9 being numerically lowest and plant 2 being numerically highest. Again, plant 10 was much lower (7.1) and differed ($P < 0.05$) from all other samples. The PDI values of SBM from plants 3, 4, and 9 also were lower ($P < 0.05$) than the remaining plants.

Table 9. Carbohydrate Composition of SBMs Collected at 10 U.S. Soybean Processing Plants (Experiment 2)[a]

item	plant no. 1	2	3	4	5	6	7	8	9	10	SEM
total nonstructural carbohydrate (% of DM)	19.4^{bcde}	19.8^{abcde}	20.7^{ab}	18.3^{e}	20.6^{abc}	20.1^{abcd}	20.5^{abc}	19.0^{cde}	21.2^{a}	18.8^{de}	0.57
total sugars (% of DM)[b]	17.7^{a}	17.0^{a}	17.0^{a}	13.6^{b}	17.9^{a}	16.9^{a}	17.5^{a}	16.9^{a}	17.5^{a}	14.4^{b}	0.43
					mg/g DM						
sucrose	69.4^{ab}	72.2^{ab}	68.5^{b}	42.4^{c}	77.2^{a}	68.0^{b}	69.8^{ab}	69.3^{ab}	73.4^{ab}	48.2^{c}	2.92
raffinose	13.3^{ab}	11.5^{cd}	10.8^{de}	13.4^{a}	12.7^{abc}	10.2^{de}	10.2^{e}	9.8^{e}	14.3^{a}	11.8^{cd}	0.54
stachyose	57.2^{a}	49.3^{de}	51.6^{bcd}	41.5^{f}	50.6^{cde}	52.2^{bcd}	54.3^{ab}	53.0^{bc}	47.4^{e}	41.0^{f}	1.24
verbascose	2.3^{bc}	2.0^{cd}	2.2^{bc}	2.9^{a}	1.6^{e}	2.3^{b}	2.3^{b}	2.4^{b}	1.9^{de}	2.0^{bcd}	0.10
uronic acids	34.7^{b}	34.8^{b}	36.6^{b}	35.8^{b}	36.5^{b}	36.3^{b}	38.0^{b}	34.8^{b}	37.9^{b}	41.5^{a}	1.15

[a] a,b,c,d,e,f: Means in a row with different letters differ ($P < 0.05$). [b] Total sugars = sum of the concentrations of the sugars analyzed.

The TNC concentration of the SBM samples differed ($P < 0.05$), ranging from 18.3 to 21.2% (**Table 9**), with plant 4 being numerically lowest and plant 9 being numerically highest. The total sugars concentration ranged from 13.6 to 17.9% with plants 4 and 10 having lower values ($P < 0.05$) as compared to all other plants (**Table 9**). Free galactose, glucose, and fructose were not detected in any SBM sample (data not shown). Sucrose concentrations for plants 1−3 and 5−9 were different ($P < 0.05$) among samples, ranging from 68.0 to 77.2 mg/g (**Table 9**). Plants 4 and 10 had significantly ($P < 0.05$) lower concentrations of sucrose (42.4 and 48.2%, respectively). Concentrations of the galactooligosaccharides, raffinose, stachyose, and verbascose also differed ($P < 0.05$) among SBM samples. Raffinose concentrations ranged from a low of 9.8 (plant 8) to 14.3 (plant 10). SBM stachyose concentrations ranged from a low of 41.0 (plant 10) to a high of 57.2 (plant 1). Concentrations of verbascose were much smaller and ranged from 1.6 (plant 5) to 2.4 (plant 8). The uronic acids concentration in SBM from plant 10 (41.5 mg/g) was higher ($P < 0.05$) than for samples from any other plant (34.7−38.0 mg/g).

DISCUSSION

The experimental objective of determining the variation in chemical characteristics and nutritive value of SBM was achieved by evaluation of both soybeans and SBM produced throughout the U.S. As stated previously, the objective was not to determine the effects of genotype or environmental growing condition on SBM quality; therefore, the results reported here may in fact partially be due to these sources of variation as well. The low variability in soybean DM and OM concentrations (**Table 4**) in the samples collected in experiment 2 suggests either uniformity among U.S. soybean genetic varieties or uniform drying prior to receipt of soybeans at the processing plant. Similarly, a narrow range in DM and OM concentrations in SBM samples (**Tables 3** and **7**) implies a high degree of consistency in the resultant SBM.

Differences in soybean CP concentrations possibly are due to genotypic variations and (or) environmental conditions under which the soybeans were grown. Hurburgh et al. (*17*) found that during 1986, 1987, and 1988 U.S. soybeans showed consistent state and regional differences in protein and oil content. Soybeans from the northern and western soybean-growing states contained 1.5−2% less protein and 0.2−0.5% more oil than soybeans from southern states. This supports the observation in experiment 1 that CP concentrations of SBM samples collected from the southern U.S. maturity zones were higher than those collected from the northern maturity zones. Soybean processing also can influence CP concentration. Results of experiment 2 indicate a wide variation in CP concentrations (48.2−56.2%) in SBM from the 10 processing plants sampled.

SBM amino acid concentrations were higher than for soybeans, as expected. Although no significant differences in individual or TAA concentrations were detected in soybeans collected from the various processing plants in experiment 2, differences were detected in the meals. Differences in individual amino acid concentrations probably are due to differences in susceptibility to heat treatment or time of processing. If processing conditions in a particular plant involved use of higher temperatures, it is possible that a portion of certain amino acids could be destroyed. Chang et al. (*18*) reported that the lysine concentration was 3.10, 3.12, 3.01, and 2.87% in underprocessed, normal, overprocessed, and ruminal escape SBM, respectively. Furthermore, they reported a statistically insignificant downward trend in ileal apparent digestibility of lysine with increases in heat treatment. Marty and Chavez (*19*) also found a reduction in apparent and true ileal lysine digestibilities by pigs fed roasted full fat soybeans. Clandinin et al. (*20*) demonstrated that overheated SBM severely depressed feeding value for chicks. In this case, lysine was determined to be the most limiting amino acid in the diet.

Typically, the soybean processing industry utilizes crude fat analysis to determine the oil content of SBM. Unfortunately, this analysis does not quantify all forms of lipids such as phospholipids and sphingolipids. The acid-hydrolyzed fat technique quantifies all forms of lipid. For this reason, fat content of SBM was analyzed in experiment 2 using both techniques. Significant differences in both crude fat and acid-hydrolyzed fat concentrations of SBM samples were detected. SBM samples from plant 10 in experiment 2 contained more lipid ($P < 0.05$) than SBM from any other plant as determined by both crude fat and acid-hydrolyzed fat analyses. Plant 10 was a mechanical extraction facility, rather than a solvent extraction plant, so this result is expected. Processing conditions, addition of soapstock to the SBM, and geographic source of soybean all can account for variability in oil concentration of SBM.

Fiber content of soybeans was quantified using the NDF analysis, while fiber content of SBM was quantified using the TDF analysis. Although the latter analysis is preferred because it measures both soluble and insoluble fiber, interference of the TDF assay by soybean oil precluded its use with soybean samples. Soybean fiber concentrations did not vary greatly among processing plants. Soybean NDF values ranged from 11.1 to 13%. These values are similar to those previously reported for heat-processed soybean seed (*21*), raw chick peas, and kidney beans (*22*).

The protein solubilities in KOH, PDI, and UA were used as indicators of nutritional quality of SBM. Protein solubility is one method of assessing overprocessing or excess heating of SBM (*23*). Growth of chicks fed autoclaved SBM decreased when protein solubility decreased from 74 to 65% (*10*). The critical protein solubility value for maintenance of optimal growth is approximately 60−70% (*10*, *24*). In both of our experiments, all SBM protein solubility values were above 70%, except for SBM from plant 10 in experiment 2 (65%). These data imply that SBM produced in plant 10 would potentially result in suboptimal growth of nonruminant animals.

Soybeans contain urease, the enzyme that converts urea to ammonia. Destruction of the urease enzyme in soybeans by heating is correlated with destruction of trypsin inhibitors (*23*). Soybean UA has, therefore, been used as an indicator of the degree of soybean processing. UA of SBM has been reported to range from 0.19 pH units for underprocessed SBM to 0.01 and 0.02 pH units for overprocessed and ruminal escape SBM, respectively (*18*). Veltmann et al. (*25*) characterized four commercially heated SBM and reported UA values of 0.19, 0.11, 0.06, and 0.03 pH units for subnormal, normal, over, and rumen escape heat treatments, respectively. McNaughton et al. (*26*) showed that SBM with UA values of 0.02 pH units resulted in improved chick growth and feed efficiency when compared with chicks fed meals with UA values of 0.19 pH units. In contast, Waldroup et al. (*27*) found that soy flakes with urease in excess of 0.2 pH units were acceptable for use in diets for broiler chickens. Additionally, Hansen et al. (*28*) concluded that pigs would be expected to perform similarly on SBM with urease activities ranging from 0.19 to 0.10. In the present study, UA values for SBM from experiment 1 ranged from 0.01 to 0.03 pH units, while samples from experiment 2 ranged from 0.03 to 0.10 pH units. According to data of Veltmann et al. (*25*) and Chang et al. (*18*), most plants in our studies were overprocessing SB.

PDI is used to characterize protein quality of processed soybeans (*29*). Chang et al. (*18*) found PDI values for underprocessed, normal processed, overprocessed, and ruminal escape SBM to be 54.0, 63.7, 40.6, and 7.3%, respectively. The PDI values determined on SBM in experiment 1 ranged from 24.3 to 30.6 (**Table 1**). In experiment 2, PDI values ranged from 7.1 in SBM from plant 10 to 33.9 for samples from processing plant 8 (**Table 7**). According to the data of Chang et al. (*18*), all plants were overprocessing SBM.

As demonstrated in experiment 2, soybean galactooligosaccharides (raffinose, stachyose, and verbascose) were not eliminated by processing. In poultry, removal of the majority of the oligosaccharides from SBM with ethanol increased the true ME value by 20% (*30*). Similar results have been demonstrated in poultry fed genetically modified low oligosaccharide SBM (*31*). However, in dogs, conventional SBM is used as efficiently as low oligosaccharide SBM (*32*). In our experiment, processing conditions significantly affected the concentrations of raffinose, stachyose, and verbascose in SBM (**Table 9**). Because of the potential positive effects of minimizing these compounds in poultry diets, further investigation in this area is warranted.

Our results demonstrate that the processing of soybeans introduces compositional variability that may impact the nutritive value of SBM. Soybean processing plant conditions should be defined and adjusted so as to optimize the nutritional value of the resultant SBM. However, as postulated by Qin et al. (*33*), optimal processing conditions may be dependent on the composition and characteristics of the soybean. Therefore, optimal processing procedures for one batch of soybeans may not necessarily be optimal for another batch. To maintain and enhance a stable market share for SBM in the U.S. and internationally, quality characteristics of soybeans entering and SBM leaving the processing plant must be accurately and consistently monitored throughout the year.

ABBREVIATIONS USED

SBM, soybean meal; DM, dry matter; OM, organic matter; CP, crude protein; TDF, total dietary fiber; KOH, potassium hydroxide; PDI, protein dispersibility index; UA, urease assay; NDF, neutral detergent fiber; TNC, total nonstructural carbohydrates; TEAA, total essential amino acids; TNEAA, total nonessential amino acids; TAA, total amino acids.

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