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# An Industry Survey of the Composition and Variability of Soybean Meal Across US Soybean Processing Plants

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## Summary

Soybean meal is the primary protein source used in swine diets; however, updated, large-scale surveys describing its current composition and variability across US soybean processing plants are limited. This survey captured approximately half of the US soy processing plants (29 unique plants including two extruded-expelled plants), ensuring a representative range in crush capacity and geographical location. Samples were collected at two timepoints within the same crop year (from October 2024 to January 2025 and from June to August 2025). At each timepoint, five samples were collected over the course of one month to provide a thorough representation of the soybean meal composition at that facility. Therefore, 271 soybean meal samples in total were received for analysis. Samples were analyzed in duplicate for proximate analysis, neutral detergent fiber, oligosaccharides, fatty acid profile, amino acid profile, protein dispersibility index (PDI), protein solubility in potassium hydroxide (KOH), trypsin inhibitor units, urease activity, mineral analysis, bulk density, and flowability at the University of Missouri (Columbia, MO) or the Kansas State University Swine Laboratory (Manhattan, KS), depending on the assay. Overall, soybean meal composition was noticeably consistent between seasonal sampling periods; however, processing method largely affected the composition of the soybean meal. As expected, solvent-extracted soybean meal had higher crude protein (47 vs. 42%), lower ether extract (1.9 vs. 9.5%), and lower trypsin inhibitor units (4.6 vs. 14.7 TIU/mg) compared with extruded-expelled soybean meal. Furthermore, measurable variation was observed, both between and within processing plants, particularly in ether extract, calcium, trypsin inhibitor units, KOH, PDI, and particle size. For solvent extraction plants, ether extract ranged from 0.73 to 5.22%, calcium ranged from 0.18 to 0.82%, trypsin inhibitor units ranged from 0.61 to 9.58 TIU/mg, KOH ranged from 74.82 to 93.65%, PDI ranged from 8.60 to 48.37%, and particle size ranged from 546 to 1,508 μm. Other analyses, notably crude protein, amino acids, and fatty acids showed less variability, both between and within processing plants. For samples collected from solvent extraction plants, the average crude protein was 46.9 ± 0.97% with lysine averaging 3.07 ± 0.12%. These findings provide an updated

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industry benchmark describing the current composition and variability of US soybean meal to support precision diet formulation, quality assessment, and informed collaboration between soybean processors and animal nutritionists.

## Introduction

Soybean meal (SBM) continues to be a primary protein source used in animal diets since its rapid integration starting in the late 1930s. However, much of the analytical information generated is either outdated with the current advancements in soybean processing technology, on a smaller scale with surveys capturing only a fraction of the industry, or missing key analytical components. Advances in soybean genetics, expansion of crush capacity, improvements in oil extraction efficiency, and variability in processing conditions across facilities may influence soybean meal nutrient composition and consistency. Furthermore, key analytical components such as amino acid profile, fiber, oligosaccharides, mineral concentrations, and trypsin inhibitor units are not always evaluated across a broad range of commercial soy processing plants.

With continued increases in soybean crushing facilities expected in the coming years, it is critical that soybean processors and animal nutritionists have an updated, comprehensive view of soybean meal composition. A large-scale industry survey evaluating soybean meal composition, quality, and consistency provides valuable benchmarking information reflective of current US soybean processing practices. Therefore, the objective of this study was to conduct a comprehensive industry survey to characterize the chemical and physical composition and variation of soybean meal collected from US soybean processing plants across multiple sampling timepoints.

## Procedures

A total of 271 soybean meal samples from 29 soybean processing plants across 16 different companies were used in the industry survey. The individual plants surveyed constitute approximately 40% of total US soybean meal production, while the 16 companies represent 90% of the total US soybean meal production. The majority of the soy processing plants sampled were solvent extracted, while two plants were mechanically extruded-expelled. Soybean meal samples were collected at two different timepoints within the same crop year: from October 2024 to January 2025 and from June to August 2025. At each timepoint, five samples were collected over the course of one month to provide a thorough view of the soybean meal composition at that facility. Two plants within the survey only provided samples represented at timepoint 1 and one plant only provided samples represented at timepoint 2. Three plants had either three or four samples represented at timepoint 2, as samples were not received by the deadlines set for the analysis.

Plants received pre-labeled sampling bags (Whirl-Pak, Nasco, Fort Atkinson, WI) at each timepoint of collection. Upon receipt of the sampling packages, an employee from the soybean processing plant collected samples across five separate days throughout a month for both timepoints. Information regarding the date of collection, employee name and contact information, and whether an oil refinery was located adjacent to the plant was recorded. Optional information could be provided regarding the addition of by-products and/or flow agents to the soybean meal, along with the specific by-products added. Once collected, the samples were shipped to Kansas State University to be prepared for analysis. All samples were stored at room temperature until analyses were performed.

### *Chemical analysis*

Soybean meal samples were received and analyzed for bulk density (Method C29-07; ASTM, 2007), angle of repose (120-125; Prof. Anim. Sci., 2006), particle size (Method S319.4; ANSI/ASAE, 2008), and urease activity (Method Ba 9-58; AOCS, 2017) at the Kansas State University Swine Laboratory (Manhattan, KS). Soybean meal samples were then ground and analyzed in duplicate at the University of Missouri Agricultural Experiment Station Chemical Laboratory (Columbia, MO). Proximate composition was determined including dry matter (Method 934.01; AOAC, 2006), crude protein (Method 990.03; AOAC, 2006), ether extract (Method 920.39; AOAC, 1998), crude fiber (Method 978.10, AOAC, 2006), and ash (Method 942.05; AOAC, 2005), as well as neutral detergent fiber (ANKOM Technology, 2017). Complete amino acid profile excluding tryptophan (Method 982.30 E (a, b, c); AOAC, 2006), tryptophan by alkaline hydrolysis (Method 988.15, AOAC, 2006), fatty acid profile using capillary gas-liquid chromatography (Method 996.06; AOAC, 2001), mineral analysis by inductively coupled plasma optical emission spectroscopy (Method 985.01 A, B, and D; AOAC), soybean meal oligosaccharides including sucrose, raffinose, stachyose, and verbascose (153:539; J. Chromatogr., 1978), protein dispersibility index (Method 46-24; AACC, 2006), and potassium hydroxide (KOH) protein solubility (69:2918–2924; J. Anim. Sci., 1991) were also analyzed in duplicate. Each soybean meal sample was submitted for analysis of trypsin inhibitor units in triplicate at the Agricultural Research Service, US Department of Agriculture (Columbia, MO), using procedures outlined by Kim and Krishnan (2023).[3] All results are reported on an as-is basis.

### *Statistical analysis*

Descriptive statistics were used to show the simple means and standard deviation of each analytical criterion within soybean meal type and timepoint of sample collection. Additionally, the range was included, which represented the minimum and maximum values for each analytical criterion within the soybean meal type and timepoint of sample collection. The range was based on an individual analysis and does not represent the values of a sample analyzed in duplicate.

## Results and Discussion

For both solvent-extracted and extruded-expelled sources, proximate composition and amino acid profiles were consistent with expected reference values[4], indicating minimal seasonal influence on nutrient composition.

As expected, processing method affected the composition and physical characteristics of the soybean meal (Tables 1 to 7). Extruded-expelled soybean meal contained numerically greater dry matter, ether extract (Figure 1), and neutral detergent fiber (Figure 2), but had lower crude protein compared with solvent-extracted soybean meal. Notably, extruded-expelled samples exhibited substantially greater trypsin inhibitor units ranging from 7.84 to 20.68 TIU/mg compared with solvent-extracted soybean meal, which ranged from 0.61 to 9.58 TIU/mg (Figure 3), consistent with the lack of toasting following the mechanical oil extraction. Extruded-expelled soybean meal also had

[3] Kim, S., and H. B. Krishnan. 2023. A fast and cost-effective procedure for reliable measurement of trypsin inhibitor activity in soy and soy products. Methods Enzymol. 680:195–213. doi:10.1016/bs.mie.2022.08.016.

[4] NRC. 2012. Nutrient Requirements of Swine, 11th ed. Natl. Acad. Press, Washington, DC.

increased values for angle of repose and lower values for bulk density and particle size (Figure 4), indicative of poorer flowability compared with solvent-extracted soybean meal. These physical differences are likely driven by greater residual oil content and mechanical processing of extruded-expelled soybean meal, which influences handling, storage, and feed manufacturing characteristics. Fatty acid profiles were similar between solvent-extracted and extruded-expelled soybean meal across both sampling timepoints, with polyunsaturated fatty acids comprising approximately 60% of total lipid. This profile closely reflects that of soybean oil, indicating minimal alteration of lipid composition during processing. Although minor differences in saturated and monounsaturated fatty acid proportions were observed, these were small relative to differences in ether extract concentration, reinforcing that processing method primarily affects residual oil content rather than fatty acid composition. Protein quality indicators were similar between extruded-expelled and solvent-extracted soybean meal, with protein solubility in potassium hydroxide (KOH) averaging 86.4 and 86.5% and protein dispersibility (PDI) averaging 16.9 and 21.1%, respectively, indicating no evidence of excessive heat damage.

When evaluating solvent-extracted soybean meal, which represented the majority of samples collected, notably crude protein, amino acids, and fatty acids showed less variability both between and within processing plants. For example, the average crude protein was 46.9 ± 0.97% with lysine averaging 3.07 ± 0.12%, methionine averaging 0.65 ± 0.03%, and threonine averaging 1.86 ± 0.10%. This trend remained consistent for essential and non-essential amino acids (Table 2). Ether extract averaged 1.86% and 1.96% across sampling timepoints; however, a wide range of 0.73% to 5.22% was observed when evaluating all individual samples analyzed. Although ether extract values remained relatively consistent within individual plants, variability between processing plants likely reflects differences in oil extraction efficiency, processing conditions, and additions of soybean byproducts such as soybean gums and soapstocks. Despite variability in ether extract, fatty acid profile remained consistent and closely reflected that of soybean oil. Trypsin inhibitor units in solvent-extracted soybean meal ranged from 0.61 to 9.58 TIU/mg. This range in trypsin inhibitor units results from both variation between processing plants, as well as within processing plants, with one plant producing samples ranging from 1.98 to 9.58 TIU/mg, specifically from timepoint 2. Although heat processing is designed to inactivate trypsin inhibitor, these results indicate measurable differences in processing conditions. Protein quality indicators such as PDI and KOH further support differences in heat processing. A wide range for PDI and KOH was observed from 8.60 to 48.37% and 74.82 to 93.65%, respectively. A range of 15 to 30% for PDI and 73 to 86% for KOH is commonly considered indicative of adequately processed soybean meal.[5] Values below these suggested ranges indicate less soluble protein due to excessive heat exposure and values greater than the suggested ranges indicate potential underprocessing. Calcium concentrations averaged 0.39 ± 0.13% across sampling timepoints; however, a wide range of 0.18 to 0.82% was observed when evaluating all individual samples. Evaluation by processing plant indicated that calcium variability occurred both within and between processing plants, as some plants exhibited relatively consistent calcium concentration compared with others which showed sizable within-plant variation (Figure 5). Additionally, differences in average calcium concentration between processing plants were evident, which could be partially driven by the inclusion of limestone as a flow agent in soybean meal, with allowable inclusion

[5] USSEC. 2021. Comparing soybean meal processing conditions. US Soybean Export Council.

rates up to 0.5% (NOPA, 2025).[6] Neutral detergent fiber (NDF) concentrations were relatively consistent with average values of 6.61 and 8.00% across sampling timepoints; however, a wide range of 4.41 to 13.19% was observed when evaluating all individual samples (Table 1). This was a result of within-plant variability, which is likely driven by differences in incoming soybean quality and the processing plants' ability to consistently remove hulls during processing. Inconsistencies in aspiration prior to soy oil extraction likely contributed to the observed within-plant variability, as NDF concentration in soybean meal is closely related with residual hull content.

Overall, seasonal variation in soybean meal quality and composition was minimal; however, measurable between- and within-plant variability was observed for key criteria for diet formulation including ether extract, calcium, trypsin inhibitor units, and particle size. These findings indicate notable differences in processing procedures and potentially incoming soybean quality. This data set provides an updated benchmark describing the current composition and variability of US soybean meal to support precision diet formulation and quality assessments.

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*Brand names appearing in this publication are for product identification purposes only. No endorsement is intended, nor is criticism implied of similar products not mentioned. People using such products assume responsibility for their use in accordance with current label directions of the manufacturer.*

[6] NOPA. 2025. Soybean meal trading rules. Natl. Oilseed Process. Assoc., Washington, DC.

**Table 1.** Soybean meal proximate composition by processing type and sampling timepoint (as-is basis)[1]

| | Solvent extracted | | | | Extruded-expelled | | | |
|---|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 | |
| Item[2] | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean | Range |
| Samples, n | 130 | | 121 | | 10 | | 10 | |
| Dry matter, % | 89.57 ± 0.77 | 86.82 - 92.02 | 88.72 ± 0.57 | 87.02 - 90.39 | 95.66 ± 0.63 | 93.89 - 96.38 | 93.01 ± 2.15 | 90.30 - 95.37 |
| Crude protein, % | 47.22 ± 0.98 | 45.05 - 51.03 | 46.61 ± 0.84 | 44.16 - 49.41 | 43.02 ± 1.66 | 39.60 - 45.34 | 41.72 ± 2.99 | 36.36 - 46.22 |
| Ether extract, % | 1.86 ± 0.62 | 0.73 - 3.85 | 1.96 ± 0.62 | 1.07 - 5.22 | 9.52 ± 1.10 | 8.23 - 11.39 | 9.53 ± 0.71 | 8.38 - 10.60 |
| Crude fiber, % | 3.42 ± 0.38 | 2.65 - 4.31 | 3.44 ± 0.42 | 2.47 - 4.67 | 5.80 ± 0.24 | 5.52 - 6.50 | 5.62 ± 0.27 | 5.03 - 6.09 |
| Ash, % | 6.40 ± 0.30 | 5.74 - 7.13 | 6.19 ± 0.33 | 5.63 - 7.41 | 6.03 ± 0.23 | 5.69 - 6.34 | 5.52 ± 0.20 | 5.09 - 5.89 |
| NDF, % | 6.61 ± 0.84 | 4.41 - 8.93 | 8.00 ± 1.41 | 5.26 - 13.19 | 9.91 ± 1.40 | 8.40 - 13.20 | 9.49 ± 0.87 | 8.08 - 11.55 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] All samples were analyzed in duplicate at University of Missouri (Columbia, MO) besides TIU. TIU was analyzed in triplicate at USDA-ARS (Columbia, MO).

[3] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal type and timepoint of sample collection.

[4] The range is the minimum and maximum value for each individual analytical criterion within soybean meal type and timepoint of sample collection.

NDF = neutral detergent fiber.

**Table 2.** Soybean meal amino acid profile by processing type and sampling timepoint (as-is basis)[1,2]

| | Solvent extracted | | | | Extruded-expelled | | |
|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 |
| Amino acid, % | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean |
| Samples, n | 130 | | 121 | | 10 | | 10 |
| Essential | | | | | | | |
| Arginine | 3.41 ± 0.10 | 3.16 - 3.79 | 3.41 ± 0.19 | 3.05 - 4.09 | 3.13 ± 0.16 | 2.84 - 3.42 | 3.05 ± 0.22 |
| Histidine | 1.24 ± 0.03 | 1.15 - 1.36 | 1.25 ± 0.05 | 1.16 - 1.43 | 1.13 ± 0.05 | 1.05 - 1.23 | 1.13 ± 0.07 |
| Isoleucine | 2.27 ± 0.07 | 2.09 - 2.57 | 2.31 ± 0.13 | 2.06 - 2.74 | 2.07 ± 0.10 | 1.88 - 2.25 | 2.04 ± 0.10 |
| Leucine | 3.65 ± 0.09 | 3.40 - 4.04 | 3.68 ± 0.19 | 3.40 - 4.31 | 3.32 ± 0.14 | 3.09 - 3.59 | 3.26 ± 0.17 |
| Lysine | 3.05 ± 0.07 | 2.87 - 3.33 | 3.09 ± 0.15 | 2.85 - 3.60 | 2.82 ± 0.12 | 2.58 - 3.05 | 2.79 ± 0.18 |
| Methionine | 0.65 ± 0.02 | 0.60 - 0.71 | 0.66 ± 0.04 | 0.61 - 0.81 | 0.60 ± 0.02 | 0.56 - 0.62 | 0.59 ± 0.02 |
| Phenylalanine | 2.45 ± 0.07 | 2.27 - 2.73 | 2.48 ± 0.14 | 2.29 - 2.95 | 2.23 ± 0.10 | 2.05 - 2.41 | 2.19 ± 0.11 |
| Threonine | 1.84 ± 0.04 | 1.72 - 1.98 | 1.88 ± 0.14 | 1.73 - 2.38 | 1.70 ± 0.06 | 1.59 - 1.79 | 1.68 ± 0.11 |
| Tryptophan | 0.62 ± 0.03 | 0.38 - 0.70 | 0.64 ± 0.04 | 0.50 - 0.72 | 0.55 ± 0.04 | 0.50 - 0.64 | 0.56 ± 0.04 |
| Valine | 2.35 ± 0.07 | 2.16 - 2.65 | 2.37 ± 0.11 | 2.10 - 2.74 | 2.16 ± 0.11 | 1.95 - 2.36 | 2.12 ± 0.14 |
| Non-essential | | | | | | | |
| Alanine | 2.05 ± 0.05 | 1.91 - 2.25 | 2.07 ± 0.10 | 1.92 - 2.39 | 1.88 ± 0.08 | 1.76 - 2.02 | 1.85 ± 0.11 |
| Aspartic acid | 5.27 ± 0.13 | 4.95 - 5.85 | 5.40 ± 0.31 | 4.98 - 6.50 | 4.84 ± 0.20 | 4.48 - 5.18 | 4.82 ± 0.31 |
| Cysteine | 0.69 ± 0.03 | 0.62 - 0.76 | 0.72 ± 0.06 | 0.62 - 0.92 | 0.67 ± 0.03 | 0.58 - 0.72 | 0.67 ± 0.02 |
| Glutamic acid | 8.74 ± 0.23 | 8.18 - 9.76 | 8.88 ± 0.59 | 8.15 - 11.03 | 7.89 ± 0.36 | 7.28 - 8.54 | 7.80 ± 0.51 |
| Glycine | 2.00 ± 0.05 | 1.87 - 2.19 | 2.01 ± 0.10 | 1.86 - 2.37 | 1.88 ± 0.08 | 1.73 - 2.01 | 1.84 ± 0.13 |
| Hydroxylysine | 0.08 ± 0.02 | 0.00 - 0.14 | 0.06 ± 0.01 | 0.03 - 0.14 | 0.09 ± 0.01 | 0.07 - 0.10 | 0.06 ± 0.01 |
| Hydroxyproline | 0.07 ± 0.03 | 0.00 - 0.19 | 0.06 ± 0.02 | 0.03 - 0.18 | 0.10 ± 0.02 | 0.06 - 0.13 | 0.10 ± 0.02 |
| Ornithine | 0.03 ± 0.01 | 0.00 - 0.15 | 0.03 ± 0.01 | 0.00 - 0.12 | 0.03 ± 0.00 | 0.03 - 0.04 | 0.03 ± 0.01 |
| Proline | 2.56 ± 0.12 | 2.27 - 3.05 | 2.43 ± 0.12 | 2.19 - 2.71 | 2.31 ± 0.10 | 2.17 - 2.57 | 2.18 ± 0.17 |
| Serine | 2.08 ± 0.08 | 1.90 - 2.51 | 2.14 ± 0.20 | 1.91 - 3.06 | 1.94 ± 0.06 | 1.85 - 2.04 | 1.89 ± 0.13 |
| Taurine | 0.15 ± 0.02 | 0.05 - 0.18 | 0.13 ± 0.02 | 0.08 - 0.16 | 0.17 ± 0.01 | 0.15 - 0.19 | 0.14 ± 0.02 |
| Tyrosine | 1.77 ± 0.06 | 1.54 - 1.93 | 1.71 ± 0.12 | 1.42 - 2.09 | 1.65 ± 0.06 | 1.54 - 1.76 | 1.52 ± 0.08 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] All samples were analyzed in duplicate at University of Missouri (Columbia, MO).

[3] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[4] The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection. Values represent an individual analysis for each sample submitted in duplicate.

**Table 3.** Soybean meal fatty acid profile by processing type and sampling timepoint (as-is basis)[1,2]

| | Solvent extracted | | | | Extruded-expelled | | | |
|---|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 | |
| Item | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean | Range |
| Samples, n | 130 | | 121 | | 10 | | 10 | |
| SFA, %[5] | | | | | | | | |
| C14:0 | 0.12 ± 0.07 | 0.07 - 0.43 | 0.09 ± 0.02 | 0.07 - 0.22 | 0.08 ± 0.01 | 0.07 - 0.12 | 0.08 ± 0.00 | 0.07 - 0.09 |
| C15:0 | 0.06 ± 0.03 | 0.00 - 0.17 | 0.05 ± 0.01 | 0.00 - 0.08 | 0.03 ± 0.01 | 0.02 - 0.04 | 0.03 ± 0.00 | 0.02 - 0.03 |
| C16:0 | 15.33 ± 1.26 | 8.44 - 18.08 | 15.79 ± 0.80 | 12.86 - 18.14 | 11.48 ± 0.16 | 11.30 - 11.95 | 11.54 ± 0.46 | 10.89 - 12.44 |
| C17:0 | 0.18 ± 0.08 | 0.05 - 0.64 | 0.15 ± 0.01 | 0.10 - 0.19 | 0.11 ± 0.02 | 0.02 - 0.14 | 0.12 ± 0.01 | 0.11 - 0.13 |
| C18:0 | 4.41 ± 0.31 | 3.53 - 5.19 | 4.33 ± 0.24 | 3.62 - 4.90 | 4.66 ± 0.44 | 4.25 - 5.57 | 4.67 ± 0.39 | 4.22 - 5.30 |
| C20:0 | 0.24 ± 0.03 | 0.18 - 0.35 | 0.23 ± 0.03 | 0.16 - 0.40 | 0.33 ± 0.03 | 0.30 - 0.39 | 0.33 ± 0.03 | 0.26 - 0.39 |
| C22:0 | 0.43 ± 0.08 | 0.27 - 0.84 | 0.39 ± 0.04 | 0.15 - 0.70 | 0.38 ± 0.03 | 0.35 - 0.44 | 0.35 ± 0.03 | 0.26 - 0.39 |
| C24:0 | 0.28 ± 0.04 | 0.13 - 0.46 | 0.23 ± 0.05 | 0.00 - 0.35 | 0.17 ± 0.02 | 0.15 - 0.22 | 0.16 ± 0.02 | 0.12 - 0.19 |
| Total SFA | 21.25 ± 1.40 | 13.84 - 26.04 | 21.39 ± 0.81 | 18.62 - 23.56 | 17.34 ± 0.54 | 16.76 - 18.43 | 17.37 ± 0.33 | 16.78 - 17.92 |
| MUFA, %[5] | | | | | | | | |
| C16:1 | 0.39 ± 0.30 | 0.08 - 1.36 | 0.10 ± 0.02 | 0.07 - 0.24 | 0.17 ± 0.07 | 0.09 - 0.26 | 0.09 ± 0.01 | 0.08 - 0.10 |
| C17:1 | 0.04 ± 0.10 | 0.00 - 0.86 | 0.04 ± 0.02 | 0.00 - 0.10 | 0.03 ± 0.02 | 0.01 - 0.06 | 0.05 ± 0.00 | 0.05 - 0.06 |
| C18:1[6] | 13.89 ± 6.76 | 9.70 - 60.60 | 12.34 ± 1.65 | 10.29 - 21.24 | 18.79 ± 0.54 | 18.17 - 20.08 | 18.83 ± 0.58 | 18.22 - 20.00 |
| C20:1 | 0.13 ± 0.05 | 0.07 - 0.30 | 0.10 ± 0.02 | 0.05 - 0.26 | 0.17 ± 0.01 | 0.15 - 0.17 | 0.15 ± 0.04 | 0.02 - 0.17 |
| C24:1 | 0.07 ± 0.13 | 0.00 - 0.69 | 0.03 ± 0.04 | 0.00 - 0.15 | 0.03 ± 0.03 | 0.02 - 0.15 | 0.02 ± 0.01 | 0.00 - 0.04 |
| Total MUFA | 16.01 ± 6.87 | 11.39 - 63.24 | 14.05 ± 1.68 | 11.84 - 23.09 | 20.72 ± 0.57 | 20.05 - 21.97 | 20.62 ± 0.62 | 19.93 - 21.79 |
| PUFA, %[5] | | | | | | | | |
| C18:2[6] | 51.77 ± 5.53 | 17.05 - 56.92 | 53.39 ± 1.26 | 45.49 - 56.24 | 53.19 ± 0.91 | 51.57 - 54.17 | 53.28 ± 0.65 | 52.26 - 54.30 |
| C18:3[6] | 7.95 ± 1.04 | 3.80 - 11.21 | 8.06 ± 0.71 | 6.55 - 10.33 | 7.60 ± 0.27 | 7.07 - 7.91 | 7.54 ± 0.29 | 6.98 - 7.95 |
| C20:5 | 0.07 ± 0.09 | 0.00 - 0.42 | 0.01 ± 0.03 | 0.00 - 0.13 | 0.01 ± 0.02 | 0.00 - 0.08 | 0.00 | 0.00 - 0.00 |
| Total PUFA | 60.13 ± 6.00 | 20.89 - 65.34 | 61.50 ± 1.44 | 52.46 - 64.68 | 60.94 ± 1.04 | 59.27 - 62.17 | 60.89 ± 0.92 | 59.31 - 62.29 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] All samples were analyzed in duplicate at University of Missouri (Columbia, MO).

[3] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[4] The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[5] Presented as a percentage of extracted lipid.

[6] Concentration includes isomers.

MUFA = monounsaturated fatty acids; PUFA = polyunsaturated fatty acids; SFA = saturated fatty acids.

**Table 4.** Soybean meal mineral analysis by processing type and sampling timepoint (as-is basis)[1,2]

| | Solvent extracted | | | | Extruded-expelled | | | |
|---|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 | |
| Item | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean | Range |
| Samples, n | 130 | | 121 | | 10 | | 10 | |
| Macrominerals, % | | | | | | | | |
| Ca | 0.39 ± 0.13 | 0.21 - 0.75 | 0.39 ± 0.14 | 0.18 - 0.82 | 0.28 ± 0.02 | 0.25 - 0.31 | 0.27 ± 0.04 | 0.21 - 0.33 |
| K | 2.22 ± 0.14 | 1.37 - 2.50 | 2.30 ± 0.12 | 1.87 – 2.60 | 2.10 ± 0.10 | 1.88 - 2.24 | 2.09 ± 0.14 | 1.86 - 2.33 |
| Mg | 0.25 ± 0.01 | 0.22 - 0.30 | 0.27 ± 0.02 | 0.21 - 0.33 | 0.24 ± 0.01 | 0.22 - 0.26 | 0.24 ± 0.02 | 0.22 - 0.28 |
| Na | < 0.02 | < 0.02 | < 0.02 | < 0.02 | < 0.02 | < 0.02 | < 0.02 | < 0.02 |
| P | 0.63 ± 0.04 | 0.54 - 0.73 | 0.66 ± 0.04 | 0.53 – 0.77 | 0.57 ± 0.02 | 0.53 - 0.60 | 0.54 ± 0.06 | 0.44 - 0.64 |
| Microminerals, mg/kg | | | | | | | | |
| Cu | 14.20 ± 1.44 | 10.50 - 22.90 | 11.94 ± 1.59 | 9.01 - 18.60 | 12.54 ± 1.31 | 10.60 - 15.20 | 11.18 ± 2.70 | 8.22 - 17.80 |
| Fe | 103.69 ± 21.20 | 70.00 - 196.00 | 95.11 ± 23.39 | 61.20 - 219.20 | 119.05 ± 15.64 | 85.00 - 152.00 | 91.06 ± 7.62 | 77.40 - 104.00 |
| Mn | 34.72 ± 4.73 | 23.90 - 48.20 | 34.29 ± 5.04 | 23.10 – 45.40 | 32.73 ± 6.35 | 24.00 - 44.10 | 29.35 ± 5.58 | 22.30 - 39.20 |
| Zn | 58.01 ± 6.07 | 45.70 - 76.70 | 47.64 ± 4.53 | 35.50 – 65.20 | 54.29 ± 6.54 | 43.00 - 62.90 | 45.05 ± 3.97 | 38.00 - 50.80 |

[1]Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2]All samples were analyzed in duplicate at University of Missouri (Columbia, MO).

[3]Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[4]The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection. Values represent an individual analysis for each sample submitted in duplicate.

**Table 5.** Soybean meal sugars analysis by processing type and sampling timepoint (as-is basis)[1,2]

| | Solvent extracted | | | Extruded-expelled | | |
|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2[3] | Timepoint 1 | Timepoint 2 | |
| Item, % | Mean[4] | Range[5] | Range | Range | Mean | Range |
| Samples, n | 130 | | 25 | 10 | 4 | |
| Sucrose | 6.47 ± 0.81 | 3.88 - 8.70 | 5.98 - 7.97 | 5.12 - 8.06 | 5.80 ± 0.53 | 5.34 - 6.26 |
| Stachyose | 5.27 ± 0.71 | 3.96 - 8.56 | 3.00 - 7.44 | 4.26 - 6.67 | 4.52 ± 1.07 | 3.59 - 5.45 |
| Raffinose | 1.03 ± 0.16 | 0.65 - 1.81 | 0.88 - 1.70 | 0.36 - 1.51 | 1.20 ± 0.22 | 1.01 - 1.39 |
| Verbascose | 0.17 ± 0.05 | 0.05 - 0.32 | 0.05 - 0.26 | 0.06 - 0.30 | 0.13 ± 0.08 | 0.06 - 0.19 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] All samples were analyzed in duplicate University of Missouri Agricultural Experiment Station Chemical Laboratory.

[3] One sample per plant was analyzed in timepoint 2.

[4] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[5] The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection. Values represent an individual analysis for each sample submitted in duplicate.

**Table 6.** Soybean meal quality characteristics by processing type and sampling timepoint (as-is basis)[1]

| | Solvent extracted | | | | Extruded-expelled | | | |
|---|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 | |
| Item[2] | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean | Range |
| Samples, n | 130 | | 121 | | 10 | | 10 | |
| TIU/mg | 4.34 ± 0.45 | 0.61 - 7.97 | 4.86 ± 0.43 | 1.98 - 9.58 | 14.91 ± 1.35 | 7.84 - 20.68 | 14.57 ± 1.55 | 9.61 - 19.90 |
| UA, Δ pH[5] | 0.22 ± 0.28 | 0.03 - 1.23 | 0.29 ± 0.49 | 0.03 - 2.20 | 0.86 ± 0.84 | 0.12 - 1.70 | 1.02 ± 0.63 | 0.45 - 1.56 |
| PDI, % | 25.28 ± 6.89 | 14.05 - 48.37 | 16.43 ± 3.86 | 8.60 - 28.44 | 18.76 ± 6.83 | 9.11 - 27.29 | 15.10 ± 3.05 | 9.37 - 20.40 |
| KOH, %[5] | 87.50 ± 2.75 | 82.53 - 93.65 | 85.53 ± 4.33 | 74.82 - 92.76 | 84.50 ± 2.96 | 80.63 - 87.34 | 88.25 ± 1.12 | 86.63 - 89.05 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] Samples were analyzed in duplicate at University of Missouri (Columbia, MO), TIU was analyzed in triplicate at USDA-ARS (Columbia, MO), and UA was analyzed at the Kansas State University Swine Laboratory (Manhattan, KS).

[3] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[4] The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection. Values represent an individual analysis for each sample submitted in duplicate.

[5] One sample per plant was analyzed for UA and KOH. Solvent extracted timepoint 1, n = 26; solvent extracted timepoint 2, n = 25; extruded expelled, n = 2.

$^{KOH}$ = protein solubility in 0.2% potassium hydroxide; PDI = protein dispersibility index; TIU = trypsin inhibitor units; UA = urease activity.

**Table 7.** Soybean meal physical characteristics by processing type and sampling timepoint (as-is basis)[1,2]

| | Solvent extracted | | | | Extruded-expelled | | |
|---|---|---|---|---|---|---|---|
| | Timepoint 1 | | Timepoint 2 | | Timepoint 1 | | Timepoint 2 |
| Item | Mean[3] | Range[4] | Mean | Range | Mean | Range | Mean |
| Samples, n | 130 | | 121 | | 10 | | 10 |
| Bulk density, g/cm$^3$ | 0.64 ± 0.02 | 0.59 - 0.71 | 0.62 ± 0.03 | 0.57 - 0.75 | 0.56 ± 0.04 | 0.51 - 0.60 | 0.58 ± 0.02 |
| Angle of repose, ° | 40.04 ± 1.51 | 36.67 - 42.86 | 41.20 ± 1.14 | 38.50 - 44.06 | 46.03 ± 0.53 | 45.17 - 46.69 | 43.70 ± 0.51 |
| Particle size, µm | 925 ± 189 | 614 - 1,508 | 864 ± 154 | 546 - 1,336 | 551 ± 222 | 335 - 832 | 798 ± 112 |

[1] Five samples from each plant were collected at two timepoints within the survey: Timepoint 1 from October 2024 to January 2025 and Timepoint 2 from June to August 2025.

[2] Samples were analyzed at the Kansas State University Swine Laboratory.

[3] Means represent the average value ± standard deviation for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

[4] The range is the minimum and maximum value for each individual analytical criterion within soybean meal processing type and timepoint of sample collection.

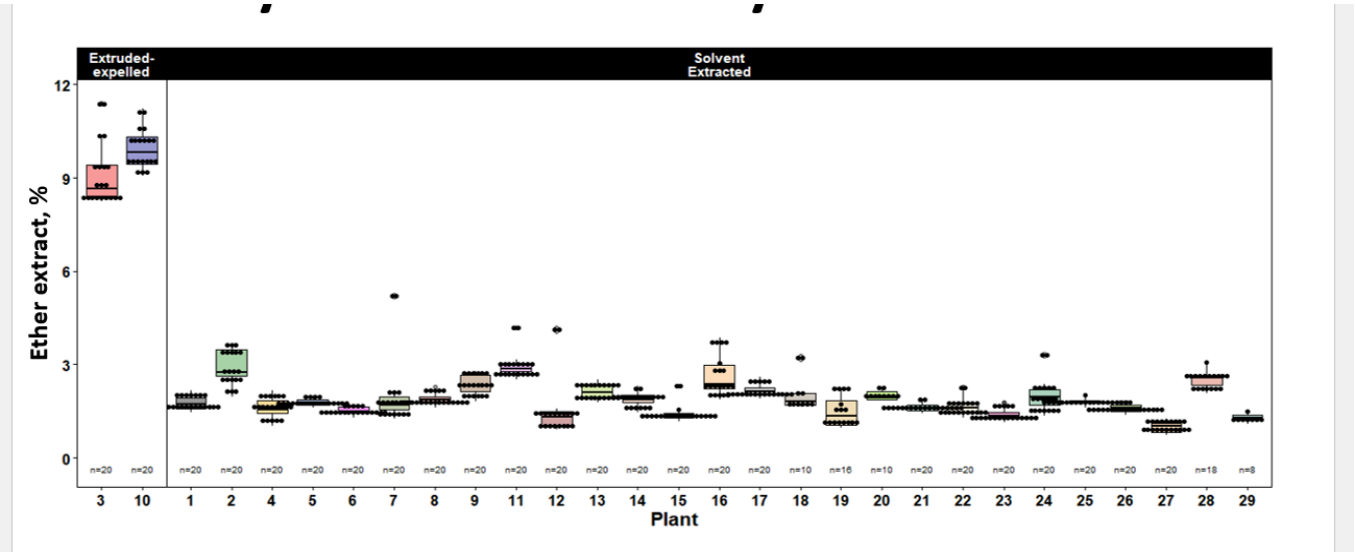



**Figure 1**. Ether extract of soybean meal samples by soybean processing type and plant (as-is basis). Individual boxplots are presented for each soybean processing plant where each data point represents a sample analyzed in singlet. The line within the boxplot represents the median, the lower and upper bounds represent the 25th and 75th percentiles, respectively, the lower and upper whiskers represent the minimum and maximum data points within 1.5 times the interquartile range, and individual data points outside the whiskers represent points exceeding 1.5 times the interquartile ranges.

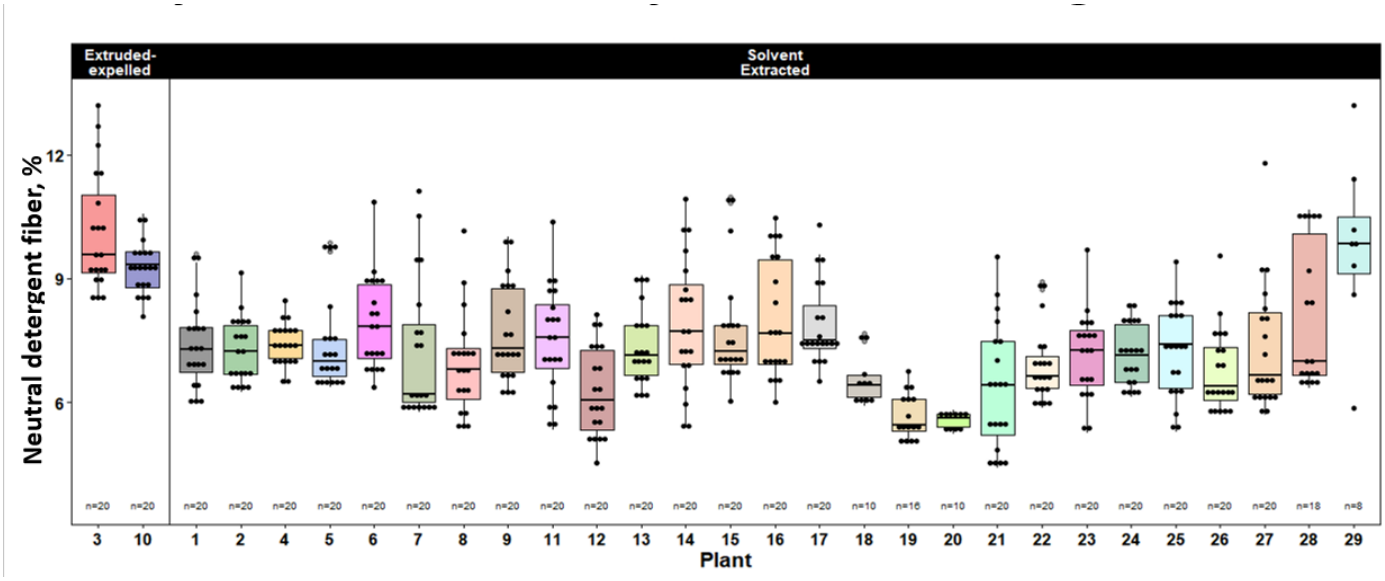



**Figure 2.** Neutral detergent fiber of soybean meal samples by soybean processing type and plant (as-is basis). Individual boxplots are presented for each soybean processing plant where each data point represents a sample analyzed in singlet. The line within the boxplot represents the median, the lower and upper bounds represent the 25th and 75th percentiles, respectively, the lower and upper whiskers represent the minimum and maximum data points within 1.5 times the interquartile range, and individual data points outside the whiskers represent points exceeding 1.5 times the interquartile ranges.

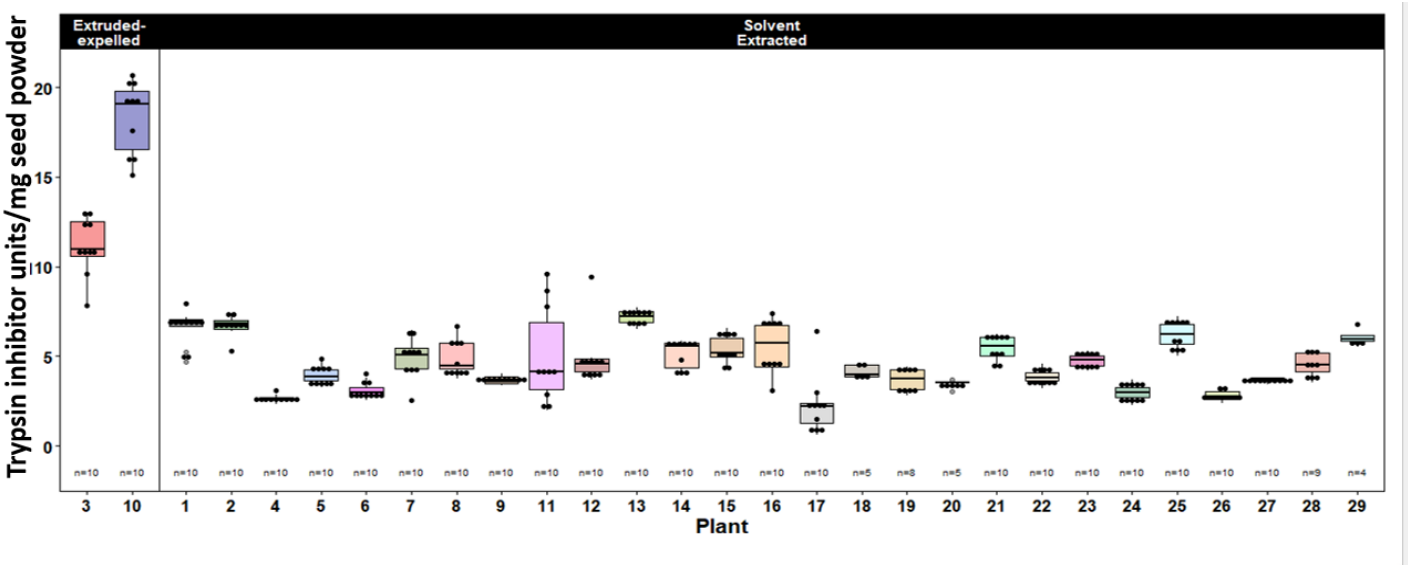



**Figure 3**. Trypsin inhibitor units of soybean meal samples by soybean processing type and plant (as-is basis). Individual boxplots are presented for each soybean processing plant where each data point represents a sample analyzed in singlet. The line within the boxplot represents the median, the lower and upper bounds represent the 25th and 75th percentiles, respectively, the lower and upper whiskers represent the minimum and maximum data points within 1.5 times the interquartile range, and individual data points outside the whiskers represent points exceeding 1.5 times the interquartile ranges.

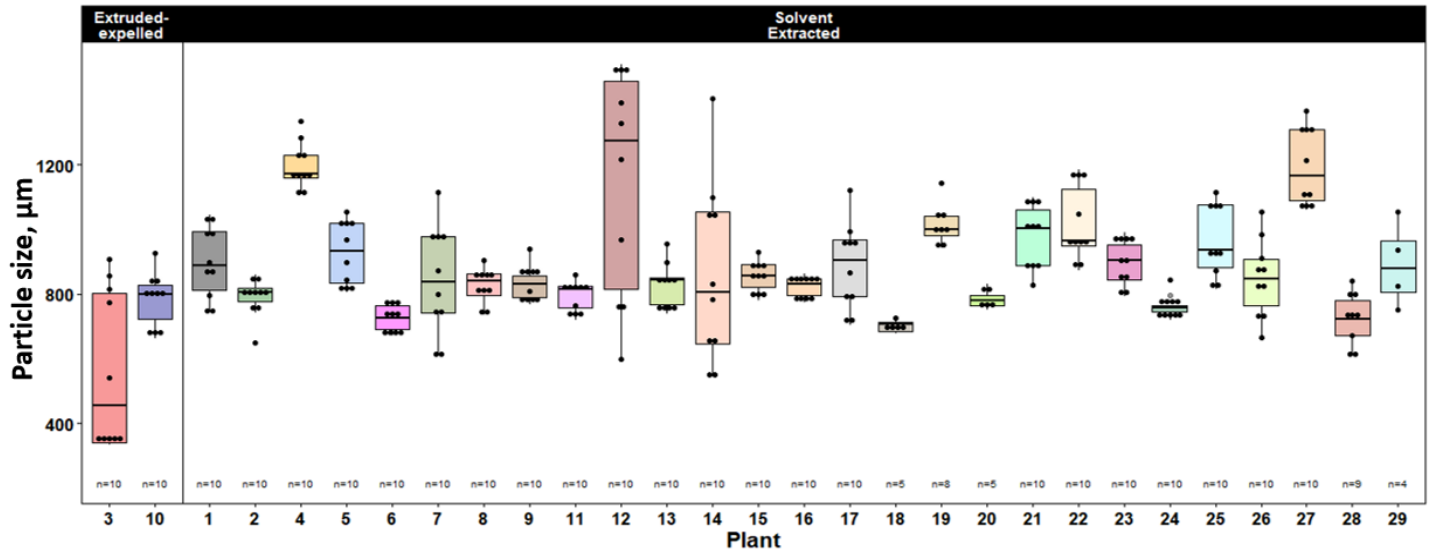



**Figure 4.** Particle size of soybean meal samples by soybean processing type and plant (as-is basis). Individual boxplots are presented for each soybean processing plant where each data point represents a sample analyzed in singlet. The line within the boxplot represents the median, the lower and upper bounds represent the 25th and 75th percentiles, respectively, the lower and upper whiskers represent the minimum and maximum data points within 1.5 times the interquartile range, and individual data points outside the whiskers represent points exceeding 1.5 times the interquartile ranges.

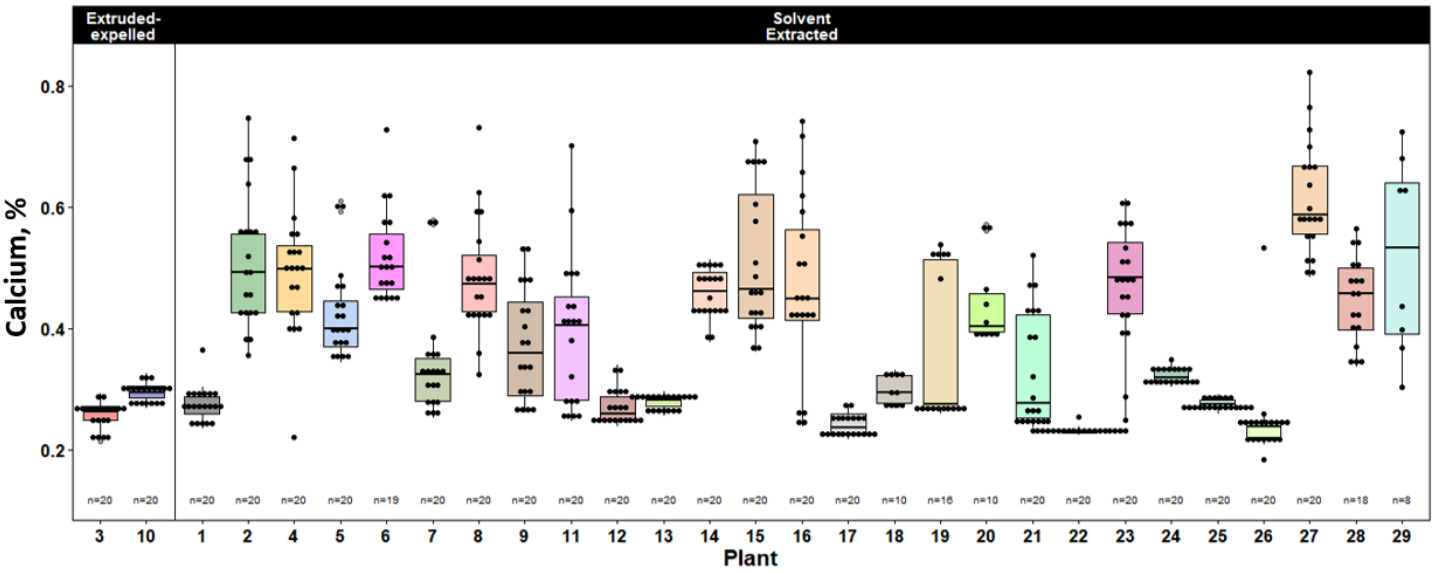



**Figure 5.** Calcium of soybean meal samples by soybean processing type and plant (as-is basis). Individual boxplots are presented for each soybean processing plant where each data point represents a sample analyzed in singlet. The line within the boxplot represents the median, the lower and upper bounds represent the 25th and 75th percentiles, respectively, the lower and upper whiskers represent the minimum and maximum data points within 1.5 times the interquartile range, and individual data points outside the whiskers represent points exceeding 1.5 times the interquartile ranges.