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Analytical Variation Between and Within Laboratories When Measuring Soybean Meal Composition and Quality

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Summary

Accurate laboratory analysis is critical for evaluating soybean meal composition and quality; however, differences in analytical procedures and laboratory practices can contribute to variability in reported nutrient values, creating challenges in diet formulation. Therefore, the objective of this study was to quantify between and within laboratory variation for common soybean meal quality analytical assays. One sample was collected from 27 US soybean processing plants and analyzed in quadruplicate for proximate analysis, neutral detergent fiber, calcium, phosphorus, trypsin inhibitor, and amino acid profile. Samples were analyzed at four laboratories: University of Missouri (Columbia, MO), Eurofins Food Chemistry Testing Center (Des Moines, IA), ATC Scientific (Little Rock, AR), and Midwest Laboratories (Omaha, NE), except for trypsin inhibitor, which was analyzed at USDA-ARS (Columbia, MO), Eurofins Food Chemistry Testing Center, and ATC Scientific. Data are presented through descriptive statistics as mean ± standard deviation, with corresponding minimum and maximum values to describe the range for each analysis within laboratory. To further evaluate analytical variation, the coefficient of variation (CV) was calculated for each analyte. Within laboratory CV was calculated using the mean and standard deviation of the four independent subsamples analyzed within each laboratory, representing analytical repeatability. Between laboratory CV was calculated using the mean values from each laboratory for a given analyte, with the standard deviation representing variation between laboratories, reflecting analytical reproducibility. Between laboratory variation was lowest for dry matter and crude protein, with CV values ranging from 0.33 to 0.76% and 0.05 to 1.49%, respectively, suggesting there was little variation between labs for these analytes. Moderate variation between laboratories was observed with CV values ranging from 1.84 to 12.92% for crude fiber, 2.55 to 9.64% for ash, 0.93 to 15.45% for calcium, and 1.22 to 6.87% for phosphorus, whereas ether extract and NDF exhibited the greatest variation between laboratories with CV values ranging from 1.52 to 32.67% and 2.03 to 23.07%, respectively. Amino acid variability between laboratories was analyte-dependent, ranging from 0.25 to 31.25%, with greater vari-

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ation observed for tryptophan and cysteine. Within laboratory variation indicated strong repeatability for most analyses, with dry matter and crude protein consistently below 3.54% CV and the majority of samples across assays had a CV below 10%. In contrast, trypsin inhibitor exhibited the greatest variability within laboratories with CV values ranging from 0.11 to 62.09%, and direct comparison between laboratories was not appropriate due to methodological differences. Quantifying analytical variation between and within laboratories provides insight into the repeatability and reproducibility of commonly used soybean meal assays and will help guide best practices when evaluating soybean meal for diet formulation.

Key words: analytical variation, soybean meal quality, trypsin inhibitor

Introduction

Soybean meal is the primary source of protein incorporated in animal diets due to the favorable amino acid profile and dependable supply. Accurate determination of soybean meal composition is critical for feed formulation, ingredient valuation, and quality control within the feed industry. As a result, nutritionists and feed manufacturers frequently rely on laboratory analyses to evaluate soybean meal composition and quality. Although standardized analytical procedures exist, variation can still occur both between and within laboratories due to differences in instrumentation, calibration procedures, sample preparation methods, and analytical techniques.

Evaluating both repeatability and reproducibility provides insight into the reliability of commonly used analytical methods and helps identify assays that may require greater standardization. In addition to analytical accuracy, practical considerations such as cost, turnaround time, and ease of implementation also influence assay selection in commercial settings. Quantifying analytical variation can help make informed decisions regarding which assays provide the most reliable information relative to their cost and practicality for routine soybean meal evaluation. Therefore, the objective of this study was to evaluate within and between laboratory variation for commonly used soybean meal analytical procedures using identical soybean meal samples analyzed in quadruplicate at four different laboratories.

Procedures

A representative sample was collected from 27 different US soybean processing plants between June and August 2025. Of the 27 plants, 25 were solvent-extracted and 2 plants were mechanically extruded-expelled.

Each plant received pre-labeled sampling bags (Whirl-Pak, Nasco, Fort Atkinson, WI) at the time of collection. Upon receipt of the sampling packages, an employee from each soybean processing plant collected a representative sample. Once collected, the samples were shipped to Kansas State University. All samples were stored at room temperature until analyses were performed. Each sample was ground to approximately 220 μm prior to subdividing into four independent sampling bags (Whirl-Pak, Nasco, Fort Atkinson, WI), such that each laboratory received four separate sample bags per original sample. In total, each laboratory received 108 samples (four subsamples from 27 plants). Laboratories were blinded to samples received.

Samples were analyzed in quadruplicate for proximate analysis, amino acid profile, neutral detergent fiber, calcium, phosphorus, and trypsin inhibitor. These measurements were selected because they represent key elements of soybean meal composition

for formulation and are frequently used to define soybean meal quality. Samples were analyzed in quadruplicate at four laboratories: University of Missouri (Columbia, MO), Eurofins Food Chemistry Testing Center (Des Moines, IA), ATC Scientific (Little Rock, AR), and Midwest Laboratories (Omaha, NE), except for trypsin inhibitor, which was analyzed in triplicate at USDA-ARS (Columbia, MO), and quadruplicate at Eurofins Food Chemistry Testing Center and ATC Scientific. These laboratories were selected as they are widely used commercial labs across the animal feed industry and offer a breadth of testing procedures; inclusion does not imply endorsement of these specific commercial laboratories.

Chemical analysis

At ATC Scientific (Little Rock, AR), proximate composition was determined including dry matter (Method Ba 2a-38; AOCS), crude protein (Method Ba 4f-00; AOCS), ether extract (Method Ba 3-38; AOCS), crude fiber (Method Ba 6a-05; AOCS), and ash (Method Ba 5a-49; AOCS), as well as neutral detergent fiber (ANKOM 6 Technology). Complete amino acid profile (Method 994.12, 988.15, 982.30; AOAC), mineral analysis by inductively coupled plasma–atomic emission spectrometry (Method 2011.14; AOAC) and trypsin inhibitor (Method 14902; ISO, 2001) were also determined.

At Eurofins Food Chemistry Testing Center (Des Moines, IA), proximate composition was determined including dry matter (Method Ba 2a-38; AOCS), crude protein (Method 990.03; AOAC), ether extract (Method Ba 3-38; AOCS), crude fiber (Method 962.09; AOAC), and ash (Method 942.05; AOAC), as well as neutral detergent fiber (A2000 ANKOM Technology). Complete amino acid profile (Method 982.30, 988.15; AOAC), mineral analysis by inductively coupled plasma optical emission spectroscopy (Method 985.01; AOAC), and trypsin inhibitor (Ba 12a-2020; AOCS) were also determined.

At Midwest Laboratories (Omaha, NE), proximate composition was determined including dry matter (Method 930.15; AOAC), crude protein (Method 990.03; AOAC), ether extract (Method 2003.05; AOAC), crude fiber (Method Ba 6a-05; AOCS), and ash (Method 942.05; AOAC), as well as neutral detergent fiber using ANKOM technology (Method 2001.11; AOAC). Complete amino acid profile (Method 994.12, 988.15; AOAC) and mineral analysis by inductively coupled plasma optical emission spectroscopy (Method 985.01; AOAC) were also determined.

At the University of Missouri (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 (Method 982.30 E (a, b, c), 988.15; AOAC, 2006), and mineral analysis by inductively coupled plasma optical emission spectroscopy (Method 985.01 A, B, and D; AOAC) were also determined. Each soybean meal sample was submitted for analysis of trypsin inhibitor units in triplicate at USDA-ARS (Columbia, MO) using procedures outlined by Kim and Krishnan (2023).[3]

[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.

Statistical analysis

Descriptive statistics were used to visualize means and standard deviations of each analytical criterion within soybean meal type and laboratory analyzed. Additionally, the range was included, which represented the minimum and maximum values for each analytical criterion within the soybean meal type and laboratory. The range was based on an individual analysis and does not represent the values of a sample analyzed in quadruplicate. To further evaluate analytical variation, the coefficient of variation (CV) was calculated for each analyte. The CV expresses the standard deviation as a percentage of the mean and provides a standardized measure of variability that allows comparisons among analyses with different units and concentration ranges. Lower CV values indicate greater consistency among measurements, whereas higher CV values indicate greater analytical variability. Within laboratory CV was calculated using the mean and standard deviation of the four independent subsamples analyzed within each laboratory, representing analytical repeatability. Between laboratory CV was calculated using the mean values from each laboratory for a given analyte, with the standard deviation representing variation between laboratories, reflecting analytical reproducibility.

Results and Discussion

Mean ± standard deviation and ranges for each analysis by laboratory are presented in Tables 1 to 5, whereas between laboratory variation (Figures 1 to 3) and within lab variation (Figures 4 and 5) are illustrated using CV. Together, these metrics provide complementary insight into the repeatability and reproducibility of each analytical method.

Between laboratory variation

Dry matter and crude protein demonstrated the lowest between laboratory variation of the analytes, as indicated by the lowest CV values. Across both solvent-extracted and extruded-expelled samples, CV for DM ranged from 0.33 to 0.76% and CV for crude protein ranged from 0.05 to 1.49%. Several criteria demonstrated moderate between laboratory variation, with CV values ranging from 1.84 to 12.92% for crude fiber, 2.55 to 9.64% for ash, 0.93 to 15.45% for calcium, and 1.22 to 6.87% for phosphorus. Similar procedures were used across laboratories for these analyses, indicating that differences in technician or laboratory equipment may be driving the moderate CVs reported. In contrast, ether extract and NDF had the greatest between laboratory variation with CV values ranging from 1.52 to 32.67% and 2.03 to 23.07%, respectively. For ether extract, there were differences in the methodology used by each laboratory, potentially leading to the between laboratory CVs reported. Select laboratories used a continuous solvent extraction procedure, which is better suited for analysis of oilseeds; however, it is a more time-consuming assay. Another method used by laboratories was a two-step procedure which includes a boiling and then rinsing step. This method is better suited for cereal grains and forages, and is a faster, less time-consuming methodology. Unlike ether extract, a similar analytical method was used to determine NDF across laboratories. However, NDF is sensitive to slight deviations in procedures (amylase application, filter bag techniques, and sulfite usage) leading to significant discrepancies between laboratories, likely leading to the wider ranges in CVs reported in this survey.

Amino acid profile analysis demonstrated moderate to high between laboratory variation depending on the specific amino acid evaluated, as illustrated by CV distributions ranging from 0.25 to 31.25% across amino acids. Mean values for most amino acids

were generally comparable among laboratories; however, notable differences in both range and CV were observed, indicating variability in analytical reproducibility. Among essential amino acids, histidine and lysine exhibited relatively low between laboratory variation, with CV values below 6%, whereas isoleucine, tryptophan, and valine all had CVs with values greater than 10%. As expected, tryptophan exhibited the greatest between laboratory variation among essential amino acids with CV values ranging from 0.95 to 15.13%, although this analysis was not part of the standard amino acid profile package for Lab B. This increased variability of tryptophan is consistent with the requirement for alkaline hydrolysis, which differs from the standard acid hydrolysis used for most amino acids. For nonessential amino acids, glutamic acid and proline demonstrated low variation with CV values ranging from 0.74 to 5.97% and 1.00 to 5.88%, respectively. In contrast, cysteine and tyrosine demonstrated greater variability, with CV values ranging from 2.37 to 31.25% and 5.58 to 13.55%, respectively, likely due to their sensitivity to oxidation and degradation during sample preparation and analysis.

Trypsin inhibitor exhibited substantial variability across laboratories; however, interpretation of these results requires consideration of methodological differences among laboratories. Due to variation in analytical procedures and reporting units such as trypsin inhibitor units versus trypsin inhibitor activity used to quantify trypsin inhibitor, a direct comparison of TI values across laboratories by calculation of between laboratory CV was not appropriate. Instead, mean and standard deviation can be found in Table 5.

Within laboratory variation

Within laboratory variation represents the repeatability of values reported by each laboratory for the submitted soybean meal samples. As expected, DM and crude protein had the lowest observed CV, with a maximum value of 0.98% and 3.54%, respectively. With a CV of less than 5% typically considered 'excellent' for intra-assay precision, both DM and crude protein fell well below this range, regardless of laboratory. These assays are relatively straightforward and highly standardized, requiring minimal sample manipulation, which contributes to their strong precision within laboratories. Similarly, ash and phosphorus had a high level of precision indicated by low CVs ranging from 0.23 to 8.34% and 0.00 to 12.72%, respectively, with the majority of samples below a CV of 5% for both assays. Despite wide ranges of CV for ether extract from 0.32 to 30.27%, crude fiber from 1.55 to 16.30%, and calcium from 0.21 to 33.85%, over 80% of the samples for each analyte were below a CV of 10%, demonstrating moderate within laboratory variation. Intra-assay precision is typically considered 'good' with a CV below 10% and is well within the commonly accepted range of 20%.[4] Furthermore, NDF and trypsin inhibitor analysis had a high within laboratory variation, largely driven by one laboratory for each assay. Although the majority of samples for both NDF and trypsin inhibitor analysis had a CV below 10%, ranges extended from 0.77 to 25.47% and 0.11 to 62.09%, respectively. For NDF, this variability likely reflects the inherent sensitivity of the assay to small procedural inconsistencies during analysis, including minor differences in detergent extraction efficiency, filter bag integrity, and completeness of residue recovery, all of which can influence final values even when performed within the same

[4] Reed, G. F., F. Lynn, and B. D. Meade. 2002. Use of coefficient of variation in assessing variability of quantitative assays. Clin. Diagn. Lab. Immunol. 9:1235–1239. doi:10.1128/CDLI.9.6.1235-1239.2002.

laboratory. Similarly, trypsin inhibitor analysis is also sensitive to procedural inconsistencies including sample homogeneity and particle size, but is also highly influenced by the assumption of the trypsin reagent purity, likely driving a majority of the within laboratory variation seen in this survey.

Within laboratory variation for amino acid analyses was generally low to moderate but varied depending on the specific amino acid evaluated. Cysteine was only analyzed at Labs A and D as part of the standard amino acid packages and exhibited moderate within laboratory variation, with CV values ranging from 0.72 to 69.63%. Although occasional extreme values were observed, the average CV was 5.52%. Branched-chain amino acids such as isoleucine and valine demonstrated moderate within laboratory variation, with CV values ranging from 0 to 11.32% and 0.22 to 23.82%, respectively. However, lysine exhibited relatively low within laboratory variation, with CV values averaging 2.69%, indicating strong repeatability of this analysis. Methionine and tryptophan were not analyzed across all laboratories, as they were not included in standard amino acid packages at Lab B. Methionine and tryptophan exhibited moderate to high within laboratory variation relative to other amino acids, with methionine CV values ranging from 0.78 to 11.19% and tryptophan CV values ranging from 0.68 to 16.57%.

In conclusion, dry matter and crude protein were consistently the most reliable analyses, demonstrating low variation both between and within laboratories. In contrast, ether extract, NDF, trypsin inhibitor, and select amino acids showed greater variation between laboratories, reflecting sensitivity to analytical methodology and laboratory specific procedures. Across a majority of the assays, precision was acceptable, regardless of laboratory, with CVs largely below 20%. However, the trypsin inhibitor assay varied greatly in precision depending on the analyzing laboratory, indicating importance in lab selection for this particular assay. These findings highlight that although most soybean meal analyses are reproducible, both between and within laboratory sources of variation exist. Understanding which assays exhibit inherently low variability, as well as which are more variable due to differences in methodology, equipment, and laboratory procedures, is essential when interpreting soybean meal composition and quality for diet formulation.

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Table 1. Solvent-extracted soybean meal composition means and ranges by laboratory (as-is basis)[1,2]

	Lab A	Lab D
Item, %	Mean[3]	Range
Dry matter	87.99 ± 0.44	87.21 - 89.71
Crude protein	46.85 ± 0.76	44.16 - 48.66
Ether extract	2.03 ± 0.70	1.08 - 4.35
Crude fiber	3.46 ± 0.41	2.51 - 4.67
Ash	6.27 ± 0.37	5.66 - 7.03
Neutral detergent fiber	6.54 ± 0.75	5.44 - 12.26
Calcium	0.41 ± 0.15	0.22 - 0.83
Phosphorus	0.66 ± 0.03	0.53 - 0.77

[1] One sample from each plant collected from June to August 2025 was ground and sent for analysis in quadruplicate at ATC Scientific (Little Rock, AR), Eurofins Food Chemistry Testing Center (Des Moines, IA), Midwest Laboratories (Omaha, NE), and University of Missouri (Columbia, MO).

[2] There were 100 samples analyzed per laboratory, representing four replicate samples from each of the 25 processing plants.

[3] Means represent the average value ± standard deviation for each individual assay within laboratory.

[4] The range is the minimum and maximum value for each individual assay within laboratory.

Table 2. Extruded-expelled soybean meal composition means and ranges by laboratory (as-is basis)[1,2]

	Lab A
Item, %	Mean[3]
Dry matter	91.92 ± 2.63
Crude protein	41.34 ± 4.22
Ether extract	9.48 ± 0.46
Crude fiber	5.54 ± 0.56
Ash	5.37 ± 0.47
Neutral detergent fiber	9.59 ± 0.71
Calcium	0.29 ± 0.01
Phosphorus	0.56 ± 0.03

[1] One sample from each plant collected from June to August 2025 was ground and sent for analysis in quadruplicate at ATC Scientific (Little Rock, AR), Eurofins Food Chemistry Testing Center (Des Moines, IA), Midwest Laboratories (Omaha, NE), and University of Missouri (Columbia, MO).

[2] There were 8 samples analyzed per laboratory, representing four replicate samples from 2 of the processing plants.

[3] Means represent the average value ± standard deviation for each individual assay within laboratory.

[4] The range is the minimum and maximum value for each individual assay within laboratory.

Table 3. Solvent-extracted soybean meal amino acid profile means and ranges by laboratory (as-is basis)[1,2]

	Lab A		Lab B		Lab C		Lab D	
Amino acid, %[3]	Mean[4]	Range[5]	Mean	Range	Mean	Range	Mean	Range
Essential								
Arginine	3.32 ± 0.15	2.85 - 3.61	3.32 ± 0.09	3.03 - 3.55	3.58 ± 0.34	2.34 - 4.46	3.39 ± 0.15	3.13 - 4.00
Histidine	1.20 ± 0.05	1.06 - 1.34	1.22 ± 0.02	1.11 - 1.29	1.20 ± 0.06	1.04 - 1.41	1.26 ± 0.05	1.19 - 1.43
Isoleucine	2.16 ± 0.08	1.81 - 2.31	2.19 ± 0.05	2.01 - 2.28	1.92 ± 0.17	1.57 - 2.28	2.29 ± 0.11	2.13 - 2.72
Leucine	3.53 ± 0.16	3.12 - 3.89	3.66 ± 0.07	3.36 - 3.79	3.36 ± 0.15	2.89 - 3.79	3.65 ± 0.15	3.42 - 4.27
Lysine	2.98 ± 0.12	2.50 - 3.19	2.94 ± 0.06	2.73 - 3.08	3.01 ± 0.21	2.59 - 4.01	3.07 ± 0.11	2.89 - 3.54
Methionine	0.60 ± 0.04	0.51 - 0.76	---	---	0.63 ± 0.03	0.52 - 0.70	0.65 ± 0.03	0.61 - 0.79
Phenylalanine	2.33 ± 0.08	2.10 - 2.49	2.39 ± 0.05	2.19 - 2.47	2.21 ± 0.08	1.98 - 2.36	2.46 ± 0.12	2.25 - 2.95
Threonine	1.77 ± 0.11	1.25 - 1.95	1.87 ± 0.05	1.74 - 1.97	1.68 ± 0.07	1.43 - 1.93	1.86 ± 0.10	1.74 - 2.29
Tryptophan	0.63 ± 0.06	0.51 - 0.77	---	---	0.63 ± 0.08	0.50 - 0.82	0.63 ± 0.03	0.54 - 0.71
Valine	2.21 ± 0.08	1.86 - 2.36	2.26 ± 0.05	2.09 - 2.37	2.05 ± 0.21	1.63 - 2.82	2.36 ± 0.09	2.16 - 2.71
Non-essential								
Alanine	2.04 ± 0.07	1.80 - 2.20	2.03 ± 0.04	1.88 - 2.12	2.02 ± 0.12	1.72 - 2.46	2.05 ± 0.08	1.95 - 2.36
Aspartic acid	6.10 ± 0.37	5.06 - 6.97	5.38 ± 0.12	4.92 - 5.63	5.57 ± 0.28	4.86 - 6.20	5.35 ± 0.24	5.04 - 6.40
Cysteine	0.68 ± 0.15	0.35 - 1.55	---	---	---	---	0.72 ± 0.05	0.64 - 0.90
Glutamic acid	8.89 ± 0.44	6.47 - 9.72	8.59 ± 0.18	7.81 - 8.95	8.74 ± 0.43	7.40 - 9.88	8.82 ± 0.44	8.25 - 10.90
Glycine	1.93 ± 0.08	1.65 - 2.13	1.99 ± 0.04	1.85 - 2.06	2.08 ± 0.14	1.75 - 2.46	1.99 ± 0.08	1.88 - 2.32
Hydroxylysine	< 0.050	< 0.050	---	---	---	---	0.06 ± 0.02	0.03 - 0.14

Hydroxyproline	0.25 ± 0.07	0.14 - 0.44	---	---	---	---	0.07 ± 0.02	0.00 - 0.18
Ornithine	0.12 ± 0.08	0.07 - 0.21	---	---	---	---	0.04 ± 0.01	0.03 - 0.08
Proline	2.32 ± 0.08	2.09 - 2.50	2.39 ± 0.07	2.21 - 2.57	2.39 ± 0.14	2.10 - 2.93	2.42 ± 0.15	1.71 - 2.83
Serine	2.36 ± 0.14	1.43 - 2.78	2.38 ± 0.05	2.16 - 2.49	2.29 ± 0.20	1.58 - 2.68	2.11 ± 0.14	1.94 - 2.86
Taurine	< 0.050	< 0.050	---	---	---	---	0.12 ± 0.02	0.07 - 0.20
Tyrosine	1.83 ± 0.15	1.39 - 2.15	1.49 ± 0.05	1.35 - 1.63	1.68 ± 0.06	1.47 - 1.84	1.69 ± 0.12	1.38 - 2.03

[1]One sample from each plant collected from June to August 2025 was ground and sent for analysis in quadruplicate at ATC Scientific (Little Rock, AR), Eurofins Food Chemistry Testing Center (Des Moines, IA), Midwest Laboratories (Omaha, NE), and University of Missouri (Columbia, MO).

[2]There were 100 samples analyzed per laboratory, representing four replicate samples from each of the 25 processing plants.

[3]Values not reported (---) indicate the analyte was not included in standard amino acid analysis package.

[4]Means represent the average value ± standard deviation for each individual assay within laboratory.

[5]The range is the minimum and maximum value for each individual assay within laboratory.

Table 4. Extruded-expelled soybean meal amino acid profile means and ranges by laboratory (as-is basis)[1,2]

	Lab A		Lab B		Lab C		Lab D	
Amino acid, %[5]	Mean[3]	Range[4]	Mean	Range	Mean	Range	Mean	Range
Essential								
Arginine	2.86 ± 0.32	2.44 - 3.24	2.87 ± 0.32	2.51 - 3.20	2.98 ± 0.36	2.62 - 3.49	2.96 ± 0.34	2.56 - 3.30
Histidine	1.06 ± 0.11	0.93 - 1.22	1.07 ± 0.10	0.97 - 1.17	1.05 ± 0.11	0.91 - 1.18	1.12 ± 0.12	0.98 - 1.26
Isoleucine	1.87 ± 0.19	1.65 - 2.09	1.90 ± 0.20	1.68 - 2.11	1.79 ± 0.19	1.43 - 2.00	2.01 ± 0.23	1.74 - 2.25
Leucine	3.08 ± 0.32	2.73 - 3.55	3.21 ± 0.29	2.91 - 3.50	3.01 ± 0.26	2.70 - 3.29	3.20 ± 0.31	2.83 - 3.52
Lysine	2.61 ± 0.28	2.26 - 2.94	2.59 ± 0.26	2.33 - 2.85	2.54 ± 0.27	2.26 - 2.93	2.71 ± 0.29	2.41 - 3.02
Methionine	0.52 ± 0.04	0.48 - 0.58	---	---	0.58 ± 0.05	0.52 - 0.65	0.58 ± 0.05	0.52 - 0.63
Phenylalanine	2.04 ± 0.23	1.79 - 2.35	2.08 ± 0.22	1.86 - 2.31	1.97 ± 0.22	1.67 - 2.19	2.15 ± 0.23	1.83 - 2.39
Threonine	1.54 ± 0.14	1.40 - 1.75	1.67 ± 0.15	1.51 - 1.82	1.42 ± 0.16	1.16 - 1.63	1.63 ± 0.16	1.45 - 1.83
Tryptophan	0.53 ± 0.09	0.42 - 0.69	---	---	0.45 ± 0.08	0.37 - 0.53	0.55 ± 0.06	0.47 - 0.63
Valine	1.92 ± 0.19	1.71 - 2.15	1.96 ± 0.20	1.75 - 2.18	1.86 ± 0.18	1.49 - 2.05	2.07 ± 0.24	1.78 - 2.32
Non-essential								
Alanine	1.81 ± 0.19	1.58 - 2.10	1.80 ± 0.17	1.62 - 1.98	1.74 ± 0.17	1.57 - 2.06	1.80 ± 0.17	1.62 - 1.99
Aspartic acid	5.24 ± 0.58	4.40 - 5.93	4.72 ± 0.46	4.24 - 5.17	4.61 ± 0.48	4.11 - 5.37	4.65 ± 0.48	4.15 - 5.21
Cysteine	0.60 ± 0.04	0.56 - 0.66	---	---	---	---	0.66 ± 0.04	0.61 - 0.71
Glutamic acid	7.61 ± 0.67	6.73 - 8.46	7.48 ± 0.70	6.77 - 8.20	7.31 ± 0.81	6.47 - 8.50	7.58 ± 0.78	6.75 - 8.43
Glycine	1.71 ± 0.18	1.50 - 1.99	1.79 ± 0.18	1.61 - 1.96	1.78 ± 0.18	1.60 - 2.06	1.79 ± 0.18	1.58 - 1.98

Hydroxylysine	< 0.050	< 0.050	---	---	---	---	0.07 ± 0.02	0.04 - 0.10
Hydroxyproline	0.26 ± 0.06	0.19 - 0.35	---	---	---	---	0.09 ± 0.02	0.07 - 0.12
Ornithine	0.05 ± 0.01	0.00 - 0.08	---	---	---	---	0.04 ± 0.02	0.02 - 0.07
Proline	2.06 ± 0.21	1.83 - 2.35	2.16 ± 0.21	1.91 - 2.38	2.02 ± 0.18	1.86 - 2.41	2.16 ± 0.23	1.84 - 2.48
Serine	2.03 ± 0.18	1.82 - 2.28	2.08 ± 0.21	1.84 - 2.29	1.80 ± 0.35	1.24 - 2.43	1.84 ± 0.18	1.64 - 2.08
Taurine	< 0.050	< 0.050	---	---	---	---	0.15 ± 0.03	0.11 - 0.19
Tyrosine	1.63 ± 0.18	1.46 - 1.95	1.23 ± 0.16	1.05 - 1.44	1.46 ± 0.15	1.28 - 1.64	1.50 ± 0.16	1.21 - 1.71

[1] One sample from each plant collected from June to August 2025 was ground and sent for analysis in quadruplicate at ATC Scientific (Little Rock, AR), Eurofins Food Chemistry Testing Center (Des Moines, IA), Midwest Laboratories (Omaha, NE), and University of Missouri (Columbia, MO).

[2] There were 8 samples analyzed per laboratory, representing four replicate samples from 2 of the processing plants.

[3] Values not reported (---) indicate the analyte was not included in standard amino acid analysis package.

[4] Means represent the average value ± standard deviation for each individual assay within laboratory.

[5] The range is the minimum and maximum value for each individual assay within laboratory.

Table 5. Soybean meal trypsin inhibitor means and ranges by soybean meal processing type and laboratory (as-is basis)[1,2]

	Lab A, TIA mg/g		Lab B, TIU/mg		Lab D, TIU/mg	
Type	Mean[3]	Range[4]	Mean	Range	Mean	Range
Samples, n	108		108		81	
Solvent-extracted	2.18 ± 0.86	0.55 - 4.39	5.61 ± 1.13	2.37 – 7.85	4.94 ± 0.45	1.98 - 9.43
Extruded-expelled	3.59 ± 1.23	1.18 - 5.12	13.83 ± 1.50	11.70 – 16.10	13.88 ± 2.50	12.66 - 15.09

[1] One sample from each plant collected from June to August 2025 was ground and sent for analysis in quadruplicate at ATC Scientific (Little Rock, AR) and Eurofins Food Chemistry Testing Center (Des Moines, IA) and was analyzed in triplicate at USDA-ARS (Columbia, MO).

[2] A representative sample was collected from 27 different US soybean processing plants between June and August 2025. Of the 27 plants, 25 were solvent-extracted and two were mechanically extruded-expelled.

[3] Means represent the average value ± standard deviation for each individual assay within laboratory.

[4] The range is the minimum and maximum value for each individual assay within laboratory.

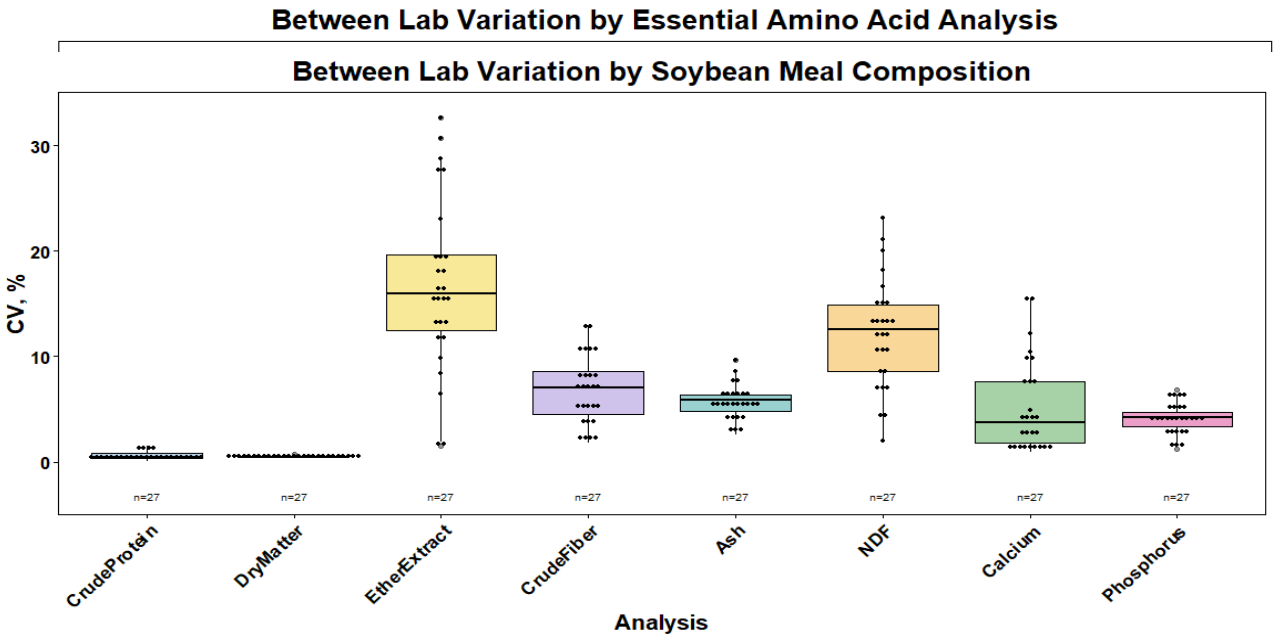


Figure 1. Between laboratory coefficient of variation (CV) of soybean meal composition characteristics by analysis. Individual boxplots are presented for each analysis where each data point represents the CV calculated for a single soybean processing plant across four laboratories. Between laboratory CV was calculated using the mean values from each laboratory for a given analyte, with the standard deviation representing variation between laboratories, reflecting analytical reproducibility.

Figure 2. Between laboratory coefficient of variation (CV) of soybean meal essential amino acids by analysis. Individual boxplots are presented for each analysis where each data point represents the CV calculated for a single soybean processing plant across four laboratories. Between laboratory CV was calculated using the mean values from each laboratory for a given analyte, with the standard deviation representing variation between laboratories, reflecting analytical reproducibility.

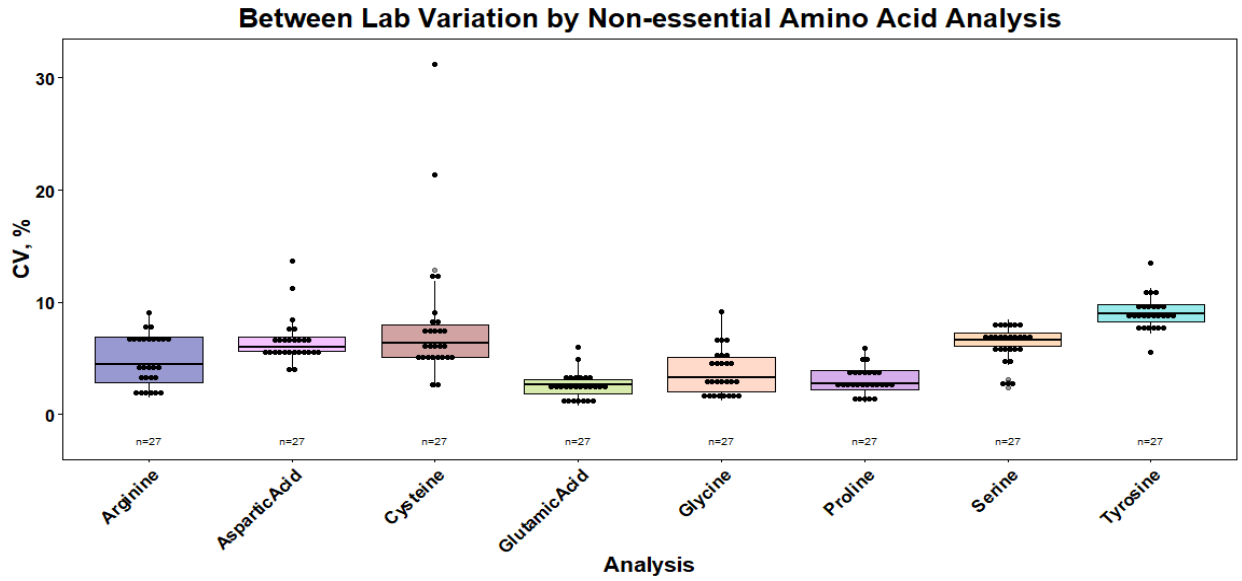
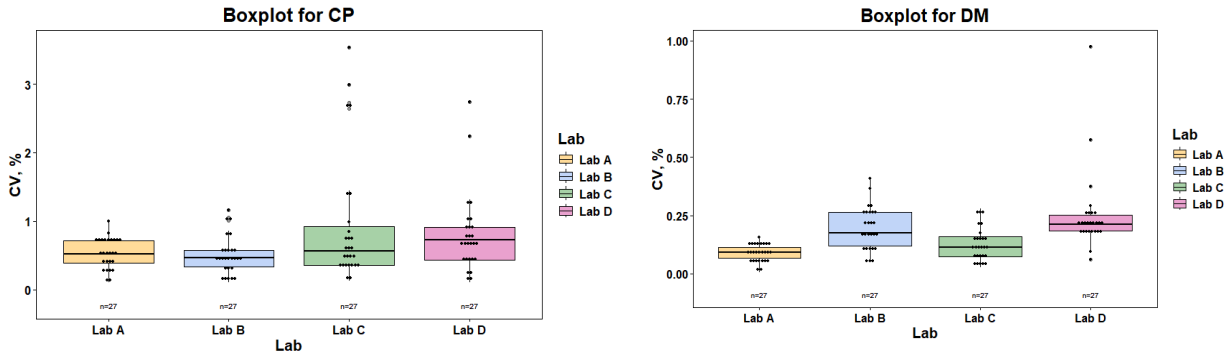


Figure 3. Between laboratory coefficient of variation (CV) of soybean meal non-essential amino acids by analysis. Individual boxplots are presented for each analysis where each data point represents the CV calculated for a single soybean processing plant across four laboratories. Between laboratory CV was calculated using the mean values from each laboratory for a given analyte, with the standard deviation representing variation between laboratories, reflecting analytical reproducibility.



A) Crude Protein

B) Dry Matter

Figure 4. Within laboratory coefficient of variation (CV) of soybean meal A) crude protein and B) dry matter. Individual boxplots are presented for each laboratory where each data point represents the CV calculated for a single soybean processing plant analyzed in quadruplicate. Within laboratory CV was calculated using the mean and standard deviation of the four independent subsamples analyzed within each laboratory, representing analytical repeatability.

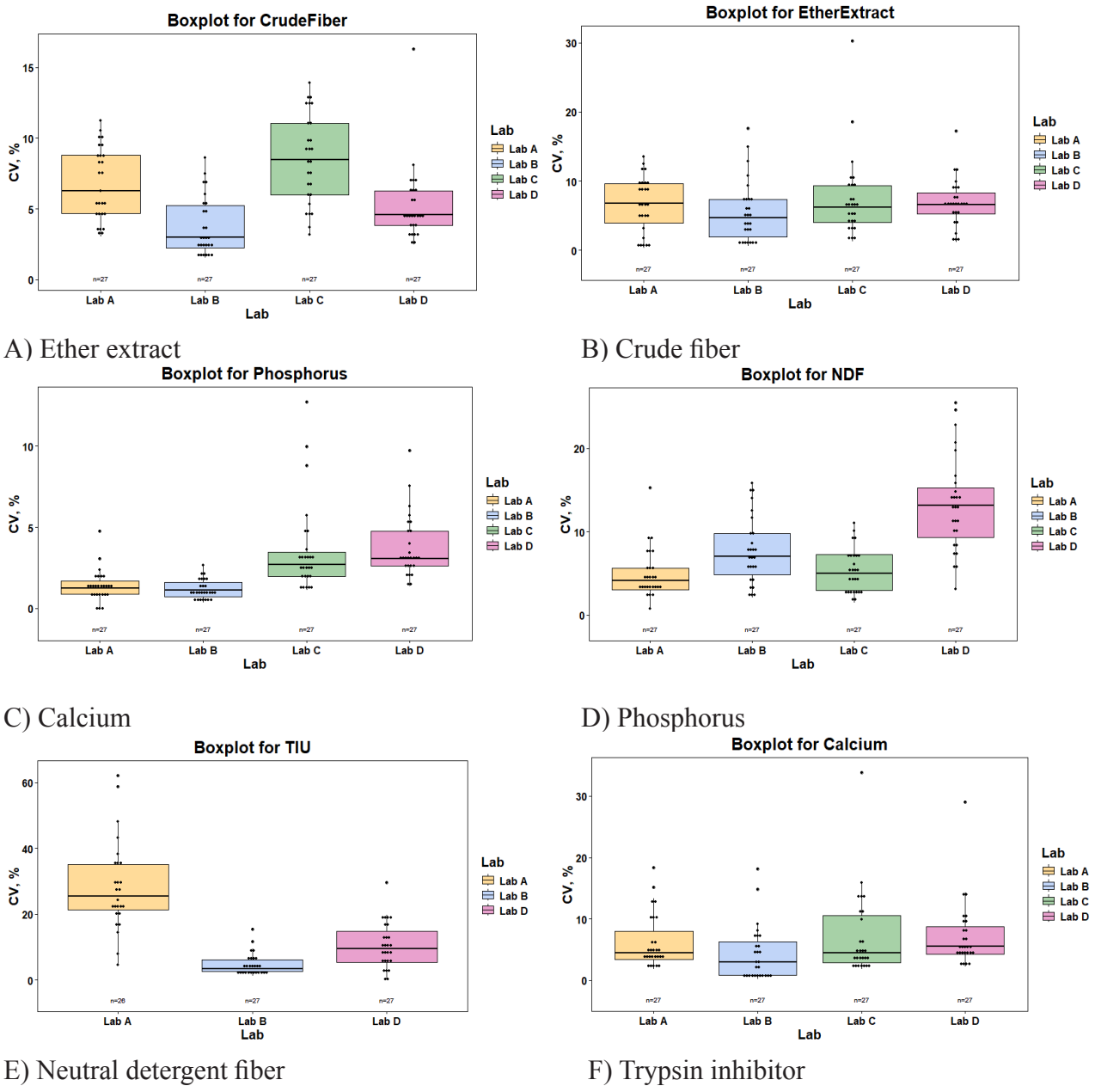


Figure 5. Within laboratory coefficient of variation (CV) of soybean meal A) ether extract, B) crude fiber, C) calcium, D) phosphorus, E) neutral detergent fiber, F) trypsin inhibitor. Individual boxplots are presented for each laboratory where each data point represents the CV calculated for a single soybean processing plant analyzed in quadruplicate. Within laboratory CV was calculated using the mean and standard deviation of the four independent subsamples analyzed within each laboratory, representing analytical repeatability.