Prediction of the total and standardized ileal digestible amino acid contents from the chemical composition of soybean meals of different origin in broilers

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ABSTRACT The objective of this experiment was to determine total amino acid (**TAA**) content, standardized ileal digestibility (**SID**) of crude protein, and standardized ileal amino acid digestibility in 9 sources of soybean meal (**SBM**) of different origin and to subsequently establish equations for predicting the TAA content and concentration of standardized ileal digestible amino acids (**SIDAA**) based on their protein content and other proximate components. Concentration of SIDAA of the samples was also predicted using TAA values. A total of 160 1-day-old male broiler chicks were randomly assigned to 10 dietary treatments consisted of 9 semipurified diets containing one SBM (200 g of crude protein/kg) as the only source of dietary amino acid (**AA**) and one N-free diet to determine endogenous ileal AA flow. The birds were fed with a standard diet from 0 to 18 D of age, and experimental diets were fed from 19 to 24 D of age. The fitness of the models of the study was tested using the adjusted coefficient of determination (R^2) value, P-value regression and coefficients, and standard error of prediction (**SEP**). The coefficient of SID for Lys and Cys among SBM varied from 86.7 to 96.3 and 74.1 to 89.3, respectively, with significant difference ($P < 0.05$). In equations based on protein content, the adjusted R^2 value ranged from 40.7 (Ile) to 99.6 (Met) and 37.2 (Met + Cys) to 99.6 (Met) for TAA content and concentration of SIDAA, respectively. Inclusion of other proximate components of test samples (e.g., crude fiber, neutral detergent fiber, acid detergent fiber, ash, gross energy, and so on) into the regression equation increased the adjusted R^2 value and decreased the SEP. The results of linear regression revealed that it is possible to satisfactorily estimate the TAA content and concentration of SIDAA of SBM through its protein content and other proximate components, but the prediction equations based on other proximate components were more accurate in terms of reflecting the measured results; however, additional time and costs were associated with this approach. It is also possible to estimate the concentration of SIDAA through TAA values with reasonable accuracy and lower SEP.

Key words: prediction equation, amino acid, broiler, standardized ileal digestibility, soybean meal

INTRODUCTION

There is a broad range of dietary feedstuffs providing protein and amino acids (**AA**). The availability of AA is vastly different, especially for those in processed feed or by-products (NRC, 1994). The nutrient compositions of feedstuffs are changing owing to raw material changes and new processing methods. Soybean meal (**SBM**) is commonly used as a source of AA because it has a consistent nutrient profile with high protein levels. The chemical composition and quality of SBM protein depend on bean genotype (Cromwell et al., 1999; Palacios et al., 2004), origin, environment in which the beans were grown (Goldflus et al., 2006; Van Kempen et al., 2006), and heat processing conditions of the beans (Waldroup et al., 1985; Parsons et al., 1992). However, these factors are not considered in most tables on nutrient compositions of ingredients (NRC, 1994; INRA, 2002; De Blas et al, 2003; Feedstuffs, 2014). Serrano et al. (2012) reported a significant difference in growth performance of broilers fed with diets based on 4 different sources of SBM.

Protein and AA are the most expensive parts of a poultry ration, and accurate knowledge of digestible AA contents of feedstuffs is necessary because formulation of diets on a digestible AA basis may decrease feed costs, feed safety margins, and nitrogen excretion into the environment and increase profitable production (Applegate et al., 2008). Rostagno et al. (1995) reported that formulating broiler diets with digestible AA gives a better prediction of dietary protein quality and bird performance than total amino acid (**TAA**)–based formulation. NRC (1994) and Feedstuffs (2014) have presented the AA digestibility coefficients for only a source of SBM (dehulled, solvent extracted with 48% protein), and maybe the different processing conditions can change the AA digestibility coefficients. However, SBM from various regions of the world are different in nutrient composition and in their AA digestibility potential for broilers (Frikha et al., 2012). The ileal digestibility measurements have been suggested as reasonable estimates of availability because standardized ileal digestibility (**SID**) can be used for growing broilers, enables ad libitum feeding, and accounts for age-appropriate basal endogenous losses (Lemme et al., 2004; Bryden and Li, 2010). But there is limited information on standardized ileal amino acid digestibility (**SIAAD**) for conventional feedstuffs and variation in determining the digestible AA coefficient, such as the type and age of birds, methodology used, and so on (Baker, 1994; Lemme et al., 2004; Garcia et al., 2007; Applegate et al., 2008). Furthermore, formulating broiler diets based on estimates of concentration of standardized ileal digestible amino acids (**SIDAA**) results in rations that more closely match the birds' requirements and reduce excess nutrients (Adedokun et al., 2009).

The classic method using high-pressure liquid chromatography and digestibility trials using live animals have become the most common techniques for assessing AA but are expensive and time-consuming. Therefore, nutritionists are highly interested in finding rapid, inexpensive, and accurate methods for assessing TAA content and concentration of SIDAA contents of feedstuffs. Several studies have shown that digestible AA of feedstuffs is correlated with its chemical composition (Ebadi et al., 2005, 2011; Soleimani Roudi et al., 2012). Previously, regression equations have been used to predict the TAA content in feed ingredients based on chemical composition (NRC, 1994; Cravener and Roush, 1999). Information about TAA content of feedstuffs is important; however, it is more essential for nutritionists to know the concentration of SIDAA in feed ingredients when formulating poultry diets (Ebadi et al., 2011). Regarding the fact that the equations presented in NRC (1994) date back to the studies of many years ago and conditions in which soybean cultivating have been changed, defining an appropriate prediction regression equation for TAA content and concentration of SIDAA based on conventional SBM and broiler strains would be necessary. Therefore, the main objective of this study was to evaluate the chemical composition of different samples of SBM and determination of SIAAD in a growing broiler chick bioassay and to use these data to develop prediction equations for estimating TAA content and concentration of SIDAA based on its protein content and other proximate components.

MATERIALS AND METHODS

Dietary Treatments

A total of 9 batches of SBM were collected for this study. Two of the batches were obtained from commercial suppliers and were imported from Brazil and Argentina. The other SBM samples were obtained directly from the suppliers (edible oil–manufacturing plants) and were processed by solvent process and dehulled solvent process. Ten dietary treatments consisted of 9 semipurified diets containing a single SBM as the only source of AA and one N-free diet for determination of basal endogenous AA losses. The diets were based on corn starch and the SBM tested (43.22–46.90% of inclusion in the diet according to their protein content). The proportion of corn starch in the test diet varied so that the assay diet contained approximately 200 g of crude protein (**CP**) per kg. In the N-free diet, corn starch and dextrose were used as energy sources (Table 1). All the diets were balanced in terms of calcium and phosphorus and supplemented with equal amounts of vitamin and mineral premix (NRC, 1994). Celite (Celite 281), a source of acid-insoluble ash (**AIA**), was added to all diets at a concentration of 1% as an indigestible marker. The analyzed CP and AA contents of the diets are reported in Table 2. All diets were fed in mash form.

Bird Husbandry

This project was approved by the Animal Care Committee of the University of Tehran, Iran. In this trial, 160 1-day-old Ross 308 male chicks were obtained from a commercial hatchery and received vaccinations for Newcastle disease (7, 18 D) and infectious bronchitis (1 D). Chicks were weighed and randomly allotted into 40 grower battery cages so that each cage of chicks had a similar initial weight and cage weight distribution (4 replicates and 4 birds per cage; 0.18 m^2/bird), and each cage was equipped with a trough feeder and a trough waterer. Battery cages were located in a solid-sided house with temperature control. The temperature was set to $33°C$ at placement and was decreased gradually to $24°C$ by the end of experimentation, with continuous fluorescent lighting. Chicks were allowed ad libitum access to a corn–SBM starter diet until 18 D of age. On day 19, after an overnight fast, chicks were given ad libitum access to the experimental SBM–starch diets and N-free diet. On day 24, all of the birds were euthanized by CO_2 asphyxiation, and ileal digesta were collected from the distal two-thirds of the ileum (portion of the small intestine from Meckel's diverticulum to approximately 1 cm anterior to the ileocecal junction) by flushing with distilled water (Kluth and Rodehutscord, 2005). Collected ileal samples from 3 birds within a cage were pooled and stored in a freezer at $-20°C$ for further analyses of AIA and AA. Frozen digesta samples were thawed, lyophilized, and

Table 1. Ingredient composition of diets fed to broilers from 19 to 24 D of age for determination of SIAAD (%, as-fed basis).

Item	Diets[1]									
	SBM-1	SBM-2	SBM-3	SBM-4	SBM-5	SBM-6	SBM-7	SBM-8	SBM-9	N-Free
Ingredient										
SBM	43.90	45.84	45.15	46.90	45.52	45.19	43.22	45.23	43.91	-
Corn starch	46.31	44.37	45.06	43.31	44.69	45.02	46.99	44.98	46.30	45.65
Dextrose	-	-	-	-	-	-	-	-	-	43.00
Soybean oil	5.00	5.00	5.00	5.00	5.00	5.00	5.00	5.00	5.00	1.00
Dicalcium phosphate	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.00	2.50
Limestone	0.83	0.83	0.83	0.83	0.83	0.83	0.83	0.83	0.83	0.85
Salt	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.36	0.40
Vitamin–mineral premix[2]	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.60	0.60
Solka Floc[3]	-	-	-	-	-	-	-	-	-	5.00
Celite	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Total	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000	1,000
Calculated energy and nutrient										
AME_n, kcal/kg	3,044	3,020	3,028	3,006	3,024	3,028	3,053	3,027	3,044	3,191
Protein, %	20.00	20.00	20.00	20.00	20.00	20.00	20.00	20.00	20.00	-
Ca, %	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87	0.87
Available P, %	0.44	0.44	0.44	0.44	0.44	0.44	0.44	0.44	0.44	0.44
Sodium, %	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18	0.18

Abbreviation: SIAAD, standardized ileal amino acid digestibility.

[1]The soybean meals (SBM) were obtained from different origin: Golestan (dehulled, solvent process), Argentina (solvent process), Khorasan (solvent process), Aksdanh (solvent process), Kalhor (solvent process), Modalal (solvent process), Khavrdsht (dehulled, solvent process), Brazil (solvent process), Nabdanh (dehulled, solvent process), respectively.

[2]Provided the following per kilogram of diet: vitamin A (trans-retinyl acetate), 10,000 IU; vitamin D3 (cholecalciferol), 2,000 IU; vitamin E (alpha-tocopherol acetate), 20 IU; vitamin K (bisulfate menadione complex), 3 mg; riboflavin, 5 mg; pantothenic acid (d-calcium pantothenate), 10 mg; nicotinic acid, 30 mg; pyridoxine (pyridoxine·HCl), 3 mg; thiamine (thiamine mononitrate), 1 mg; vitamin B12 (cyanocobalamin), 12 µg; d-biotin, 0.15 mg; choline (choline chloride), 300 mg; folic acid, 0.5 mg; Se (Na_2SeO_3), 0.1 mg; I (KI), 2.0 mg; Cu ($CuSO_4 \cdot 5H_2O$), 10 mg; Fe ($FeSO_4 \cdot 7H_2O$), 30 mg; Mn ($MnSO_4 \cdot H_2O$), 100 mg; Zn (ZnO), 100 mg; and ethoxyquin, 110 mg.

[3]Purified cellulose (contains dietary fiber).

ground using an electric coffee grinder to obtain a finely ground sample while avoiding significant loss.

Chemical Analyses

Dry matter (**DM**), ash, CP, crude fiber (**CF**), and ether extract (**EE**) were analyzed according to AOAC International (2000) analytical methods (930.15, 920.39, 990.03, 978.10, and 942.05, respectively). Neutral detergent fiber (**NDF**) analysis was performed as described by Van Soest et al. (1991), and sequentially, acid detergent fiber (**ADF**) analysis was performed as described by Robertson and Van Soest (1981). Gross energy (**GE**) was measured using an adiabatic bomb calorimeter.

Table 2. Analyzed amino acid and CP composition of the semipurified diets fed to broilers from 19 to 24 D of age (%, as-fed basis).[1]

Item	Diets[2]									
	SBM-1	SBM-2	SBM-3	SBM-4	SBM-5	SBM-6	SBM-7	SBM-8	SBM-9	N-Free
CP	20.02	19.58	20.35	20.77	19.36	21.43	19.81	19.85	20.24	0.27
Essential AA										
His	0.465	0.494	0.433	0.447	0.439	0.504	0.433	0.416	0.446	0.003
Thr	0.728	0.728	0.904	0.792	0.870	0.756	0.874	0.871	0.939	0.003
Arg	1.338	1.308	1.333	1.456	1.284	1.378	1.294	1.245	1.402	0.005
Val	0.713	0.767	0.722	0.778	0.696	0.762	0.697	0.701	0.761	0.005
Met	0.342	0.316	0.356	0.382	0.303	0.319	0.320	0.300	0.314	0.000
Phe	0.920	0.927	0.842	1.002	0.828	0.945	0.816	0.851	0.859	0.005
Ile	0.724	0.786	0.845	0.775	0.840	0.782	0.819	0.825	0.905	0.003
Leu	1.397	1.461	1.421	1.468	1.401	1.522	1.375	1.448	1.512	0.009
Lys	0.983	1.100	1.115	0.932	1.312	1.238	1.277	1.303	1.163	0.005
Nonessential AA										
Asp	2.228	2.233	2.462	2.410	2.409	2.390	2.398	2.415	2.612	0.006
Glu	3.645	3.624	3.593	3.791	3.516	3.877	3.475	3.507	3.746	0.014
Ser	0.993	0.981	0.998	1.016	0.936	1.057	0.920	0.872	1.026	0.005
Gly	0.777	0.792	0.829	0.850	0.760	0.842	0.755	0.767	0.819	0.005
Ala	0.790	0.792	0.891	0.842	0.842	0.828	0.836	0.830	0.904	0.006
Tyr	0.636	0.670	0.595	0.681	0.574	0.701	0.561	0.604	0.632	0.001
Cys	0.294	0.245	0.279	0.257	0.341	0.235	0.326	0.218	0.279	0.000
Pro	0.945	0.960	0.984	0.933	0.931	0.998	0.890	0.894	1.075	0.001

Abbreviations: AA, amino acid; CP, crude protein.

[1]Values reported from the analysis conducted at the chemical laboratory, Institute for Food and Agricultural Research and Technology (IRTA), Catalonia, Spain. Samples were analyzed in duplicate.

[2]The soybean meals (SBM) were obtained from different origin: Golestan (dehulled, solvent process), Argentina (solvent process), Khorasan (solvent process), Aksdanh (solvent process), Kalhor (solvent process), Modalal (solvent process), Khavrdsht (dehulled, solvent process), Brazil (solvent process), and Nabdanh (dehulled, solvent process), respectively.

These were analyzed in the chemical laboratory of the College of Agriculture and Natural Resources, University of Tehran, with 3 replications. Nitrogen-free extract was determined by mathematical calculation. For AA analysis, samples (meals, diets, and digesta) were prepared by 6 N HCL hydrolysis for 24 h at 110°C, followed by neutralization with 15 mL of 9.8 N NaOH, and then cooled to room temperature. Afterward, sodium citrate buffer was added, and the mixture was equalized to a 100-mL volume (AOAC International, 2000). Methionine and cysteine (sulfur-containing AA) were analyzed by performic acid oxidation at 0°C, followed by acid hydrolysis (Moore, 1963). The AA in the hydrolyzate were determined by high-pressure liquid chromatography Agilent 1100 and 1260 (Institute for Food and Agricultural Research and Technology, IRTA Mas Bové, Tarragona, Spain) using reverse phase chromatography with precolumn derivatization with ortho-phthalaldehyde with 2 replicates. Acid-insoluble ash concentration of diets and ileal digesta was analyzed after ashing the samples and then boiling the ash with 4 N HCl in duplicate based on the method reported by Van Keulen and Young, 1977.

Apparent ileal AA digestibility (**AIAAD**) was calculated using the following equation (Lemme et al., 2004): AIAAD = [(AA/AIA) diet − (AA/AIA) digesta]/(AA/AIA) diet. Ileal endogenous AA (**IEAA**) flow in broilers fed with the N-free diet was calculated as milligrams of AA flow per kilogram of DM intake (**DMI**) using the following equation (Adedokun et al., 2008): IEAA, mg/kg of DMI = ileal AA, mg/kg × [(AIA)diet/(AIA) digesta]. Apparent ileal AA digestibility coefficients were standardized using the determined IEAA flows using the following equation: SIAAD = AIAAD [(IEAA flow g/kg of DMI)/(AA content of the diet, g/kg of DM)] × 100.

Statistical Analyses

Data were analyzed using a randomized complete block design (SAS Institute, 2003). Pen location was the blocking factor. The general linear model procedure and least-squares means method were used to compare mean SIAAD coefficients.

Simple and multiple linear regression were used to predict TAA content and concentration of SIDAA in SBM samples using SPSS version 19 with the following model (Statistic, 2011). The input variables were CP and other proximate components and also TAA in the SIDAA equations. Each individual TAA content and concentration of SIDAA were the output variable:

$$y_i = \beta_0 + \beta_{1 \times 1} + \beta_{2 \times 2} + \ldots + \varepsilon_i,$$

where y_i is the TAA content and concentration of SIDAA, β_0 is the intercept of the regression equation, β_j is the regression coefficient, x_j is the CP and other proximate components, and ε_i is the random error of the regression model. The coefficient of determination (R^2), adjusted R^2, P-value regression, P-value coefficients, and standard error of prediction (**SEP**) were used to define the equation with the best fit. Statistical significance was considered at $P \leq 0.05$.

The SEP was calculated using the following equation (Yegani et al., 2013):

$$SEP = \sqrt{\frac{\sum (Y - \acute{Y})2}{N}}$$

where Y is the TAA content and concentration of SIDAA determined in the chick bioassay, $\acute{Y}$ is the predicted TAA and SIDAA values based on the in vitro data, and N is the number of SBM samples tested.

RESULTS AND DISCUSSION

The CP contents of the experimental diets were close to expected values (Table 2). For CP, the calculated value was the same (20.0%) for all diets, and the determined values ranged from 21.4% (Modalal) to 19.3% (Kalhor). In the present study, AA composition of the diets cannot be directly compared because inclusion levels of SBM varied among diets, but these data are in close agreement with 6 SBM samples (inclusion level of 44% SBM) reported by De Coca-Sinova et al. (2008).

The standardized ileal crude protein digestibility and SIAAD coefficients for the 9 SBM samples with their mean are presented in Table 3. The standardized ileal crude protein digestibility values ranged from 92.05% for Khavrdsht to 87.77% for Golestan, with that of the other SBM being intermediate. The SIAAD values differed also among SBM samples, with the greatest value for Khavrdsht and the least for Golestan. There were significant differences ($P \leq 0.05$) in digestibility coefficients for Lys, which ranged from 96.30% (Khavrdsht) to 86.78% (Golestan), with an average of 91.81%, and for Cys, which ranged from 89.31% (Kalhor) to 74.12% (Brazil), with an average of 80.74%. The mean of SIAAD values was similar to that reported by Loeffler et al. (2013) for Lys (92%), Met (91.7%), Thr (89%), Val (89.4%), and Cys (79.6%) for commercial SBM in 22-day-old birds but was relatively less than that reported by Frikha et al. (2012) and Serrano et al. (2013). Processing conditions might affect the digestibility of AA in SBM (Parsons et al., 1992). In addition, the differences might be related to the methodology used. Toghyani et al. (2015) studied SIAAD of expeller-extracted canola meal subjected to different processing conditions and reported that processing conditions affected CP and AA digestibility, likely because of formation of indigestible complexes of AA with fiber.

Determined chemical composition, TAA content, and concentration of SIDAA of the 9 SBM samples were variable (Table 4). The GE ranged from 4,568 to 4,261 kcal/kg (CV = 2.01%); ash ranged from 5.8 to 6.47% (CV = 5.91%); CP ranged from 46.27% for the Khavrdsht (SBM-7) to 42.64% for the Aksdanh (SBM-4), and the CV was lower (CV = 2.36%). However, EE ranged from 0.97 to 2.23% (CV = 26.18%), CF ranged from 4.8 to 8.13% (CV = 15.73%), and in addition, the NDF and ADF varied widely from 10 to 18.93% (CV = 17.52%) and from 10.47 to 16.23% (CV = 11.43%), respectively. The range

Table 3. Coefficient of standardized ileal crude protein digestibility (%; SICPD) and standardized ileal amino acid digestibility (SIAAD) of the diet in broilers of 24 D of age.[1]

Item	Soybean meal[2]									P-value	SEM	Mean
	SBM-1	SBM-2	SBM-3	SBM-4	SBM-5	SBM-6	SBM-7	SBM-8	SBM-9			
CP	87.77	88.56	89.05	89.69	90.84	90.86	92.05	89.00	89.13	0.719	0.515	89.66
Essential AA												
His	90.14	91.28	90.26	92.18	92.88	93.15	93.95	89.95	92.38	0.415	0.464	91.80
Thr	86.94	91.56	89.16	86.30	92.24	90.26	93.19	91.75	90.34	0.100	0.604	90.19
Arg	92.19	93.47	93.40	93.42	95.16	95.42	95.87	93.52	94.64	0.440	0.386	94.12
Val	87.68	89.45	88.58	91.34	91.16	91.44	92.36	90.47	90.46	0.705	0.570	90.33
Met	84.71	91.43	88.64	92.08	91.48	92.27	93.37	90.19	90.98	0.703	0.911	90.23
Phe	89.91	91.75	90.87	93.51	92.76	93.73	93.48	91.65	92.24	0.575	0.446	92.21
Ile	88.37	90.90	91.57	90.43	93.21	92.31	93.79	92.21	92.82	0.262	0.474	91.73
Leu	88.99	91.23	90.69	91.81	92.63	92.79	93.60	92.07	91.77	0.510	0.442	91.73
Lys	86.78[d]	94.17[a,b]	87.92[c,d]	90.02[b,c,d]	95.90[a]	93.58[a,b]	96.30[a]	89.59[b,c,d]	91.99[a,b,c]	0.0008	0.688	91.81
Nonessential AA												
Asp	86.61	88.77	89.54	87.50	90.92	90.00	91.91	87.34	90.24	0.245	0.512	89.20
Glu	91.12	92.98	92.99	93.66	93.96	94.29	94.95	91.03	93.37	0.233	0.376	93.15
Ser	87.16	88.72	89.55	91.93	91.13	90.21	92.10	89.35	89.39	0.645	0.581	89.95
Gly	83.27	85.79	85.22	87.55	87.68	87.37	88.69	85.23	87.30	0.711	0.620	86.46
Ala	87.54	88.65	88.91	90.98	91.70	90.55	92.42	90.71	90.34	0.599	0.553	90.20
Tyr	89.42	91.34	90.28	92.85	92.22	92.92	93.37	91.86	91.75	0.760	0.507	91.78
Cys	80.43[a,b]	80.76[a,b]	79.26[a,b]	75.49[b]	89.31[a]	75.80[b]	88.70[a]	74.12[b]	82.83[a,b]	0.026	1.330	80.74
Pro	86.62	89.52	89.86	88.02	91.07	90.33	91.99	87.57	90.04	0.454	0.555	89.45

[a–d]Means within a row, not sharing a common superscript, are significantly different ($P \leq 0.05$).

Abbreviations: AA, amino acid; CP, crude protein.

[1]There were 4 cages of 4 chicks each per treatment.

[2]The soybean meals (SBM) were obtained from different origin: Golestan (dehulled, solvent process), Argentina (solvent process), Khorasan (solvent process), Aksdanh (solvent process), Kalhor (solvent process), Modalal (solvent process), Khavrdsht (dehulled, solvent process), Brazil (solvent process), and Nabdanh (dehulled, solvent process), respectively.

in CP contents of SBM in the present study was lower, and in ash, EE, and CF, the range was similar to that observed by De Coca-Sinova et al. (2008) and Frikha et al. (2012). The range in GE and NDF was higher than that observed by De Coca-Sinova et al. (2008). Average contents of CP (44.5%), DM (91.2%), and ash (6.48%) in the present study were in good agreement with those reported by NRC, 1994 and Feedstuffs, 2014.

The TAA profile varied also among SBM samples (Table 4). The Lys content was the highest for Golestan meal (3.17%) and the least for Aksdanh meal (2.21%), the Met content varied from 0.759% for Golestan meal to 0.598% for Kalhor, and the Thr content was the highest for Golestan meal (1.54%) and the least for Aksdanh meal (1.44%). In general, the mean AA profile of the SBM was similar to that reported in the literature (NRC, 1994; Feedstuffs, 2014), but the variability was higher than expected, especially for Lys (CV = 11.5%) and Cys (CV = 16.3%). Frikha et al. (2012) found high variability in Lys (56.5–63.4 g/kg) and Cys (12.6–15.2 g/kg) content of SBM samples. In addition, Bandegan et al. (2010) reported high variability (CV) in Lys and Cys than the other AA.

Regression equations obtained by SPSS to predict TAA values based on the protein content and other proximate components of 9 SBM samples are shown in Table 5. The protein content and TAA content of the test samples were related, and adjusted R^2 values ranged from 40.7 (Ile) to 99.6 (Met). The prediction equation, for example, for TMet developed from this regression was as follows: TMet = 0.016 × CP (adjusted R^2 = 99.6; SEP = 0.046; $P < 0.0001$). This equation

predicted TMet of the test samples in a simple and rapid manner. The inclusion of other proximate components of the test samples into the equations increased the accuracy and precision of the most of the TAA value predictions. Inclusion of NDF and ash (adjusted R^2 = 99.6; SEP = 0.039; $P < 0.0001$) decreased SEP of prediction of the TMet. As shown in Table 5, inclusion of CP, CF, ADF, GE, and moisture content of the samples together significantly decreased the SEP compared with the other 2 equations (adjusted R^2 = 94.2, SEP = 0.008, $P = 0.011$). In the equations based on the other proximate components, it was reported that 2 prediction equations can be used to predict the TAA values in SBM samples; one of them according to the simplicity of the equation as well as the accuracy of the prediction. Chemical compositions previously were used in some studies to estimate the TAA content of SBM samples via the regression method (NRC, 1994; Cravener and Roush, 2001). The National Research Council (NRC, 1994) presented the following equations to predict the TMet value of a SBM: Met = 0.127 + 0.0111 × CP and Met = 0.1754 + 0.0079 × CP + 0.0221 × ash. The accuracy of the regression equations reported in NRC (1994) for predicting the amount of AA in ingredients is variable and low in some equations ($R^2 < 0.5$). Mottaghitalab et al. (2015) predicted Met (R^2 = 75%) and Lys (R^2 = 76%) contents from chemical composition (CP, EE, ash, CF, and moisture) in SBM using artificial neural network and found positive correlation with CP and negative correlation with CF. Cravener and Roush (1999) used the multiple linear regression and artificial neural network models to predict the AA content in feed ingredients based on

Table 4. Determined chemical composition, concentration of TAA, and concentration of SIDAA of the SBM samples tested (%, DM basis).[1]

Component	SBM-1	SBM-2	SBM-3	SBM-4	SBM-5	SBM-6	SBM-7	SBM-8	SBM-9	Mean	CV[3]%
DM	91.67	91.63	90.97	91.40	90.77	91.47	91.07	91.20	91.27	91.27	0.31
Moisture	8.33	8.37	9.03	8.60	9.23	8.53	8.93	8.80	8.73	8.73	3.47
GE, kcal/kg	4,412	4,481	4,261	4,315	4,335	4,445	4,381	4,346	4,568	4,394	2.01
CP	45.56	43.67	44.30	42.64	43.93	44.42	46.27	44.22	45.55	44.51	2.36
EE	1.47	1.27	0.97	1.23	2.23	1.33	1.13	1.03	1.43	1.34	26.18
CF	4.80	6.03	5.13	5.97	5.97	8.13	5.80	5.67	5.03	5.84	15.73
NDF	12.47	14.53	12.87	17.03	15.97	18.93	13.07	15.10	10.00	14.44	17.52
ADF	12.23	13.43	12.07	12.70	13.73	16.23	12.63	13.87	10.47	13.04	11.43
Total ash	6.07	6.10	5.80	6.47	5.97	6.33	6.10	6.37	5.87	6.48	5.91
NFE	33.77	34.56	34.77	35.09	32.66	31.24	31.76	33.91	33.38	33.46	3.77

	SBM-1		SBM-2		SBM-3		SBM-4		SBM-5		SBM-6		SBM-7		SBM-8		SBM-9		Mean		CV%	
	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID	Total	SID
Essential AA																						
His	1.060	0.956	1.015	0.926	0.980	0.885	0.936	0.862	0.987	0.917	1.003	0.935	1.024	0.962	0.942	0.847	1.043	0.964	0.999	0.917	4.23	4.71
Thr	1.548	1.346	1.466	1.342	1.453	1.296	1.442	1.244	1.460	1.347	1.463	1.320	1.550	1.445	1.477	1.355	1.547	1.398	1.490	1.344	3.04	4.25
Arg	2.904	2.677	2.696	2.520	2.678	2.502	2.685	2.508	2.677	2.548	2.711	2.587	2.903	2.784	2.632	2.461	2.876	2.722	2.751	2.590	3.98	4.32
Val	1.565	1.372	1.534	1.372	1.439	1.274	1.418	1.295	1.479	1.348	1.510	1.380	1.545	1.427	1.543	1.396	1.573	1.423	1.512	1.365	3.65	3.83
Met	0.759	0.643	0.696	0.636	0.729	0.646	0.726	0.668	0.598	0.547	0.677	0.625	0.744	0.695	0.651	0.587	0.717	0.652	0.700	0.631	7.23	6.98
Phe	1.976	1.776	1.864	1.710	1.801	1.637	1.811	1.693	1.836	1.703	1.887	1.769	1.958	1.831	1.890	1.732	1.941	1.790	1.885	1.738	3.37	3.41
Ile	1.614	1.426	1.550	1.409	1.463	1.340	1.465	1.325	1.516	1.413	1.571	1.450	1.579	1.481	1.596	1.472	1.602	1.487	1.551	1.423	3.68	4.11
Leu	3.039	2.705	2.944	2.686	2.814	2.552	2.793	2.565	2.937	2.721	2.967	2.753	3.002	2.810	2.989	2.752	3.042	2.792	2.947	2.704	3.04	3.38
Lys	3.178	2.758	2.426	2.285	2.750	2.418	2.219	1.997	2.463	2.362	2.887	2.702	2.981	2.871	2.610	2.338	2.966	2.729	2.720	2.496	11.5	11.4
Nonessential AA																						
Asp	5.401	4.678	4.997	4.436	4.724	4.230	4.883	4.273	5.120	4.655	4.991	4.493	5.218	4.797	4.948	4.322	5.232	4.721	5.057	4.512	4.08	4.65
Glu	8.682	7.911	8.244	7.665	7.464	6.941	7.830	7.333	8.432	7.923	7.956	7.502	8.463	8.036	8.021	7.302	8.485	7.923	8.175	7.615	4.74	4.87
Ser	2.111	1.840	2.000	1.775	1.979	1.772	1.949	1.792	2.021	1.842	2.027	1.829	2.119	1.952	1.983	1.772	2.076	1.856	2.030	1.826	2.96	3.17
Gly	1.671	1.392	1.581	1.356	1.637	1.395	1.561	1.367	1.570	1.377	1.650	1.442	1.675	1.485	1.617	1.378	1.673	1.461	1.626	1.406	2.81	3.23
Ala	1.676	1.467	1.582	1.403	1.605	1.427	1.560	1.419	1.551	1.422	1.590	1.440	1.670	1.543	1.579	1.433	1.611	1.456	1.603	1.445	2.86	2.86
Tyr	1.359	1.216	1.355	1.238	1.298	1.172	1.285	1.193	1.316	1.214	1.332	1.237	1.343	1.254	1.367	1.256	1.381	1.267	1.337	1.227	2.42	2.55
Cys	0.823	0.662	0.552	0.446	0.563	0.466	0.615	0.465	0.487	0.435	0.540	0.409	0.669	0.594	0.573	0.425	0.672	0.557	0.611	0.493	16.3	18.0
Pro	1.913	1.658	1.841	1.648	1.951	1.753	1.915	1.686	1.951	1.777	1.879	1.697	2.071	1.905	2.005	1.756	2.128	1.916	1.962	1.755	4.70	5.63

Abbreviations: AA, amino acid; ADF, acid detergent fiber; CF, crude fiber; CP, crude protein; EE, ether extract; GE, gross energy; NDF, neutral detergent fiber; NFE, nitrogen-free extract; SID, standardized ileal digestibility; SIDAA, standardized ileal digestible amino acids; TAA, total amino acids.

[1]Amino acids were analyzed in duplicate samples, and other nutrients were analyzed in triplicate samples.

[2]The soybean meals (SBM) were obtained from different origin: Golestan (dehulled, solvent process), Argentina (solvent process), Khorasan (solvent process), Aksdanh (solvent process), Kalhor (solvent process), Modalal (solvent process), Khavrdsht (dehulled, solvent process), Brazil (solvent process), and Nabdanh (dehulled, solvent process), respectively.

[3]Coefficient of variation.

Table 5. Regression equations for prediction of total amino acid (TAA) composition of SBM from protein content and other proximate components (DM basis).[1]

Amino acids	Basis	Prediction equations	R^2	Adjusted R^2	P-value regression	P-value coefficients		SEP (%)
TMet	CP	Y = 0.016 × CP	99.6	99.6	0.000	CP	0.000	0.046
	CP, CF, ADF, GE, moisture	Y = 3.466 + 0.028 × CP + 0.058 × CF − 0.0497 × ADF − 0.0005138 × GE − 0.166 × Moisture	97.8	94.2	0.011	CP	0.009	0.008
						CF	0.015	
						ADF	0.006	
						GE	0.006	
						Moisture	0.003	
	Ash, NDF	Y = 0.157 × Ash − 0.018 × NDF	99.7	99.6	0.000	Ash	0.000	0.039
						NDF	0.032	
TCys	CP	Y = 0.014 × CP	98.0	97.8	0.000	CP	0.000	0.087
	CP, CF, ADF, NDF, moisture	Y = −1.542 + 0.098 × CP − 0.086 × CF + 0.0597 × NDF − 0.0579 × ADF − 0.208 × Moisture	98.8	96.7	0.005	CP	0.003	0.011
						CF	0.012	
						NDF	0.008	
						ADF	0.018	
						Moisture	0.002	
	CP, moisture, CF	Y = 0.052 × CP − 0.166 × Moisture − 0.0435 × CF	99.6	99.3	0.000	CP	0.002	0.041
						Moisture	0.015	
						CF	0.048	
TMet+Cys	CP	Y = 0.029 × CP	99.2	99.1	0.000	CP	0.000	0.122
	Moisture, GE, ADF, NFE	Y = 16.310 − 0.568 × Moisture − 0.001233 × GE − 0.1104 × ADF − 0.095 × NFE	98.9	97.8	0.000	Moisture GE	0.000	0.015
						ADF	0.001	
						NFE	0.000	
							0.000	
	CP, moisture,	Y = 0.077 × CP − 0.245 × Moisture	99.6	99.5	0.000	CP	0.004	0.088
						Moisture	0.035	
TLys	CP	Y = −8.632 + 0.255 × CP	82.7	80.3	0.001	CP	0.001	0.122
	NDF, NFE	Y = 8.830 − 0.150 × NFE − 0.076 × NDF	65.0	53.3	0.043	NFE	0.042	0.174
						NDF	0.038	
	CP, NFE	Y = 0.129 × CP − 0.0908 × NFE	99.6	99.5	0.000	CP	0.002	0.172
						NFE	0.038	
TThr	CP	Y = −0.151 + 0.0368 × CP	83.2	80.8	0.001	CP	0.001	0.017
	Moisture, CF, NFE	Y = 3.664 − 0.075 × Moisture − 0.052 × CF − 0.036 × NFE	95.1	92.2	0.001	Moisture	0.005	0.014
						CF	0.000	
						NFE	0.000	
	CP, ADF, ash, moisture, EE	Y = −0.187 + 0.037 × CP − 0.012 × ADF + 0.0596 × Ash − 0.028 × Moisture + 0.0258 × EE	99.5	98.7	0.001	CP	0.000	0.031
						ADF	0.004	
						Ash	0.015	
						Moisture	0.024	
						EE	0.017	
TIle	CP	Y = −0.032 + 0.0355 × CP	48.2	40.7	0.038	CP	0.038	0.038
	CF, ash, CP, GE, ADF	Y = −2.487 − 0.060 × CF + 0.0907 × Ash + 0.0318 × CP + 0.0004411 × GE + 0.0367 × ADF	97.8	94.1	0.011	CF	0.018	0.008
						Ash	0.047	
						CP	0.010	
						GE	0.007	
						ADF	0.019	
	Ash, NDF	Y = 0.3106 × Ash − 0.024 × NDF	99.9	99.8	0.000	Ash	0.000	0.053
						NDF	0.035	

Statistical parameter[2]

Table 5. (*continued*)

Amino acids	Basis	Prediction equations	Statistical parameter[2]					SEP (%)
			R^2	Adjusted R^2	P-value regression	P-value coefficients		
TLeu	CP	Y = 0.254 + 0.0605 × CP	56.8	50.6	0.019	CP	0.019	0.055
	CF, ADF, NFE, GE	Y = 1.154 − 0.132 × CF + 0.058 × ADF − 0.044 × NFE +0.0007487 × GE	96.8	93.6	0.003	CF	0.003	0.018
						ADF	0.010	
						NFE	0.004	
						GE	0.002	
	Ash, NDF	Y = 0.586 × Ash − 0.044 × NDF	99.9	99.8	0.000	Ash	0.000	0.104
						NDF	0.044	
THis	CP	Y = −0.276 + 0.0286 × CP	57.3	51.2	0.018	CP	0.018	0.026
	Moisture, ash, CF, NFE	Y = 3.589 − 0.108 × Moisture − 0.122 × Ash − 0.017 × CF − 0.0237 × NFE	97.8	95.5	0.001	Moisture	0.001	0.010
						Ash	0.003	
						CF	0.026	
						NFE	0.002	
TVal	CP	Y = −0.098 + 0.036 × CP	53.6	46.9	0.025	CP	0.025	0.036
	CP, GE	Y = −1.026 + 0.0003141 × GE + 0.026 × CP	77.9	70.6	0.011	GE	0.042	0.024
						CP	0.045	
	GE, CF, ADF, EE, NFE	Y = −0.027 + 0.0005382 × GE − 0.088 × CF + 0.0395 × ADF − 0.040 × EE − 0.023 × NFE	98.9	97.1	0.001	GE	0.001	0.007
						CF	0.002	
						ADF	0.005	
						EE	0.026	
						NFE	0.006	
TArg	CP	Y = −0.932 + 0.0827 × CP	71.0	66.9	0.004	CP	0.004	0.055
	Moisture, ADF, NFE	Y = 7.6562 − 0.178 × Moisture − 0.068 × ADF − 0.073 × NFE	92.0	87.2	0.004	Moisture	0.013	0.036
						ADF	0.001	
						NFE	0.002	
	CP, moisture, NDF, ADF	Y = 0.097 × CP − 0.134 × Moisture +0.033 × NDF − 0.066 × ADF	99.9	99.8	0.000	CP	0.000	0.028
						Moisture	0.017	
						NDF	0.041	
						ADF	0.019	
TPhe	CP	Y = −0.273 + 0.048 × CP	72.8	68.9	0.003	CP	0.003	0.037
	CP, moisture	Y = 0.403 + 0.049 × CP − 0.0826 × Moisture	88.3	84.4	0.002	CP	0.001	0.030
						Moisture	0.030	
	GE, CP, CF, NDF, EE	Y = −3.872 + 0.0005774 × GE + 0.071 × CP − 0.093 × CF + 0.043 × NDF − 0.031 × EE	99.9	99.7	0.000	GE	0.000	0.023
						CP	0.000	
						CF	0.000	
						NDF	0.000	
						EE	0.003	

Abbreviations: ADF, acid detergent fiber; CF, crude fiber; CP, crude protein; DM, dry matter; EE, ether extract; GE, gross energy; NDF, neutral detergent fiber; NFE, nitrogen-free extract; R^2, adjusted coefficient of determination; SBM, soybean meal; SEP, standard error of prediction.

[1]Analyzed using SPSS statistical software and stepwise procedures and interprocedures.

[2]R^2 is the coefficient of determination, Adjusted R^2 adjusted for the number of predictors in the model, P-value <0.05 is statistically significant (Yegani et al., 2013).

Table 6. Regression equations for prediction of concentration of standardized ileal digestible amino acids (SIDAA) of SBM from protein content and other proximate components (DM basis).[1]

Amino acids	Basis	Prediction equations	R^2	Adjusted R^2	P-value regression	P-value coefficients		SEP (%)
SID Met	CP	$Y = 0.014 \times CP$	99.6	99.6	0.000	CP	0.000	0.039
	Ash, NDF	$Y = 0.1348 \times Ash - 0.013 \times NDF$	99.7	99.6	0.000	Ash	0.000	0.037
						NDF	0.050	
SID Cys	CP	$Y = -2.119 + 0.0586 \times CP$	54.4	47.8	0.023	CP	0.023	0.057
	CP, CF, moisture	$Y = 0.041 \times CP - 0.045 \times CF - 0.124 \times Moisture$	99.4	99.1	0.000	CP	0.003	0.040
						CF	0.031	
						Moisture	0.033	
	CP, ADF	$Y = 0.0205 \times CP - 0.032 \times ADF$	98.8	98.5	0.000	CP	0.001	0.055
						ADF	0.004	
SID Met + Cys	CP	$Y = -2.041 + 0.071 \times CP$	45.0	37.2	0.048	CP	0.048	0.083
	Ash, NDF	$Y = 0.289 \times Ash - 0.044 \times NDF$	99.5	99.4	0.000	Ash	0.000	0.078
						NDF	0.013	
SID Lys	CP	$Y = -8.273 + 0.242 \times CP$	89.9	88.4	0.000	CP	0.000	0.085
	CP, NFE	$Y = -4.702 + 0.2047 \times CP - 0.057 \times NFE$	95.0	93.3	0.000	CP	0.000	0.061
						NFE	0.048	
	NFE, NDF	$Y = 9.4765 - 0.180 \times NFE - 0.066 \times NDF$	86.5	82.0	0.002	NFE	0.002	0.099
						NDF	0.007	
SID Thr	CP	$Y = -0.587 + 0.043 \times CP$	71.7	67.7	0.004	CP	0.004	0.033
	NFE, NDF	$Y = 2.6017 - 0.015 \times NDF - 0.031 \times NFE$	79.4	72.5	0.009	NDF	0.010	0.024
						NFE	0.009	
SID Ile	CP	$Y = -0.2464 + 0.0375 \times CP$	51.1	44.1	0.030	CP	0.030	0.133
	Ash, NDF, ADF	$Y = 0.216 \times Ash - 0.054 \times NDF + 0.0675 \times ADF$	99.9	99.8	0.000	Ash	0.000	0.131
						NDF	0.003	
						ADF	0.013	
SID Leu	CP	$Y = 0.210 + 0.056 \times CP$	46.9	39.3	0.042	CP	0.042	0.251
	Ash, NDF, ADF	$Y = 0.415 \times Ash - 0.0868 \times NDF + 0.1087 \times ADF$	99.9	99.9	0.000	Ash	0.000	0.252
						NDF	0.009	
						ADF	0.033	
SID His	CP	$Y = -0.378 + 0.029 \times CP$	55.8	49.5	0.021	CP	0.021	0.090
	Moisture, ash, NFE	$Y = 3.294 - 0.088 \times Moisture - 0.1387 \times Ash - 0.0226 \times NFE$	85.7	77.1	0.015	Moisture	0.022	0.079
						Ash	0.011	
						NFE	0.010	
SID Val	CP	$Y = -0.067 + 0.032 \times CP$	47.0	39.4	0.042	CP	0.042	0.158
	Ash, NDF, ADF	$Y = 0.218 \times Ash - 0.047 \times NDF + 0.054 \times ADF$	99.9	99.9	0.000	Ash	0.000	0.154
						NDF	0.004	
						ADF	0.024	
SID Arg	CP	$Y = -1.266 + 0.0866 \times CP$	74.4	70.8	0.003	CP	0.003	0.172
	Moisture, ADF, NFE	$Y = 7.479 - 0.1277 \times Moisture - 0.0648 \times ADF - 0.0875 \times NFE$	94.9	91.8	0.001	Moisture	0.022	0.165
						ADF	0.001	
						NFE	0.000	
SID Phe	CP	$Y = -0.076 + 0.0407 \times CP$	59.0	53.1	0.016	CP	0.016	0.152
	Ash, NDF, NFE	$Y = 2.103 + 0.2097 \times Ash - 0.0227 \times NDF - 0.039 \times NFE$	93.8	90.1	0.002	Ash	0.004	0.134
						NDF	0.002	
						NFE	0.001	

Abbreviations: ADF, acid detergent fiber; CF, crude fiber; CP, crude protein; DM, dry matter; NDF, neutral detergent fiber; NFE, nitrogen-free extract; R^2, adjusted coefficient of determination; SBM, soybean meal; SEP, standard error of prediction; SID, standardized ileal digestibility.
[1]Analyzed using SPSS statistical software and stepwise procedures and interprocedures.
[2]R^2 is the coefficient of determination, Adjusted R^2 adjusted for the number of predictors in the model, P-value <0.05 is statistically significant (Yegani et al., 2013).

proximate analysis and suggested the AA contents of feedstuffs are related to the sample proximate analysis.

In addition to TAA content, equations were developed to predict the concentration of SIDAA in SBM from its protein content and other proximate components (Table 6). Owing to some difficulties, such as time and cost, in determination of concentration of SIDAA before feed formulation, mathematical equations are one of the important candidates for solving the problem. Therefore, the results of this test may provide the efficient and reliable solution for this problem. The adjusted R^2 values for the equations based on the protein content ranged from 99.6% (SID Met) to 37.2% (SID Met + Cys) and for equations based on the other proximate components ranged from 99.9% (Leu, Val) to 72.5% (Thr). Inclusion of other proximate components such as NDF, ADF,

ash, nitrogen-free extract, and so on into the prediction equation also increased the R^2 value and decreased SEP in the present study. The protein content traditionally was used to estimate AA digestibility coefficients (Angkanaporn et al., 1996; Short et al., 1999; Bryden and Li, 2003; Bryden et al., 2009). The prediction of true ileal digestible AA contents of protein concentrates was tested by van Kempen and Bodin (1998), with high R^2 values (higher than 80%) for digestible Met and Lys in feeds of animal origin and medium to low R^2 values (lower than 64%) for the prediction of the same AA in SBM. Frikha et al. (2012) reported the coefficients of SID of CP and Lys of the SBM were positively correlated with CP ($R^2 = 51.4$; $P < 0.05$ and $R^2 = 37$; $P = 0.09$, respectively). Ebadi et al. (2011) showed that chemical composition (CP, CF, EE, ash, and total phenols) of

Table 7. Regression equations for prediction of concentration of SIDAA of SBM from TAA values (DM basis).[1]

Amino acids	Prediction equations	Statistical parameter[2]				
		R^2	Adjusted R^2	P-value regression	P-value coefficient	SEP (%)
SID Met	$Y = 0.080 + 0.788 \times$ TMet	82.0	79.5	0.001	0.001	0.018
SID Cys	$Y = -0.014 + 0.831 \times$ TCys	87.3	85.5	0.000	0.000	0.030
SID Met + Cys	$Y = 0.094 + 0.788 \times$ TMetCys	90.2	88.9	0.000	0.000	0.035
SID Lys	$Y = 0.1636 + 0.857 \times$ TLys	88.7	87.1	0.000	0.000	0.090
SID Thr	$Y = -0.1489 + 1.002 \times$ TThr	62.5	57.1	0.011	0.011	0.032
SID Ile	$Y = 0.0039 + 0.9148 \times$ TIle	79.9	77.0	0.001	0.001	0.128
SID Leu	$Y = 0.0047 + 0.9157 \times$ Tleu	80.7	77.9	0.001	0.001	0.243
SID His	$Y = -0.052 + 0.970 \times$ THis	88.9	87.4	0.000	0.000	0.082
SID Val	$Y = 0.0708 + 0.856 \times$ TVal	81.2	78.5	0.001	0.001	0.147
SID Arg	$Y = -0.089 + 0.9737 \times$ TArg	90.7	89.4	0.000	0.000	0.161
SID Phe	$Y = 0.1368 + 0.849 \times$ TPhe	82.8	80.3	0.001	0.001	0.148

Abbreviations: DM, dry matter; R^2, adjusted coefficient of determination; SBM, soybean meal; SEP, standard error of prediction; SID, standardized ileal digestibility; SIDAA, standardized ileal digestible amino acids; TAA, total amino acids.

[1]Analyzed using SPSS statistical software and stepwise procedures and interprocedures.

[2]R^2 is the coefficient of determination, Adjusted R^2 adjusted for the number of predictors in the model, P-value < 0.05 is statistically significant (Yegani et al., 2013).

sorghum grain is a good parameter for digestible AA determination by multiple regression equations with reasonable accuracy (e.g., Met $= 0.3885 - 0.2454 \times$ total phenols $- 0.0109 \times$ CP $- 0.0336 \times$ EE $- 0.0158 \times$ CF $+ 0.0830 \times$ ash, $R^2 = 72\%$). Soleimani Roudi et al. (2012) used mathematical models to predict apparent ileal digestible AA values via protein content of wheat samples and indicated that CP can be used as a single model input to predict apparent ileal digestible AA values in wheat samples (e.g., Met $= -0.033 + 0.015$ CP, $R^2 = 76.6\%$). In most of the equations based on other proximate components, a strong negative effect of NDF content ($P < 0.05$) was observed because NDF may be responsible for the changes in SIAAD of SBM for poultry. De Coca-Sinova et al. (2008) reported a correlation coefficient of -0.745 ($P < 0.001$) between NDF and the coefficient of SID for Lys in a study with 6 SBM samples.

Linear regression also was used to determine the concentration of SIDAA in SBM samples from TAA values (Table 7). Adjusted R^2 values for these equations ranged from 57.1 (Thr) to 89.4 (Arg). The concentration of SIDAA of Met was predicted using the following equation: % SID Met $= 0.080 + 0.788 \times$ TMet (adjusted $R^2 = 79.5$, SEP $= 0.018$). The SEP values for these equations were relatively lower than those for 2 other equations using protein content and the other proximate components. The prediction equations of digestible AA from TAA concentration were reported by Urriola et al. (2009) in distillers' dried corn with solubles in growing pigs. They found a low correlation between the concentration and digestibility of AA, for example, digestible Lys $= 0.06 + 0.55 \times$ total Lys ($R^2 = 66\%$), and they suggested that it is necessary to develop in vitro procedures to predict digestible AA concentration. This observation differs from that reported by Van Kempen et al. (2002) for SBM in growing swine, wherein the amount of digestible CP and AA could be predicted from its total concentration (digestible Lys $= 0.227 + 0.834 \times$ total Lys, $R^2 = 96\%$).

It is concluded that TAA content and concentration of SIDAA can be predicted using the equations established in the present study based on protein content and other proximate components, but the prediction equations based on other proximate components were more accurate in terms of reflecting the measured results; however, additional time and costs were associated with this approach. The high adjusted R^2 and low SEP values between TAA content and concentration of SIDAA indicated that it is possible to predict the concentration of SIDAA from TAA content of SBM. As a result, the equation developed in the present study can serve as a reference analysis to develop calibration equations for the prediction of TAA content and concentration of SIDAA of SBM for broiler chickens such as near-infrared reflectance spectroscopy.

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