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Board Invited Review

BOARD INVITED REVIEW

ASAS-NANP SYMPOSIUM: RUMINANT/NONRUMINANT FEED COMPOSITION: Challenges and opportunities associated with creating large feed composition tables

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Abstract

Traditional feed composition tables have been a useful tool in the field of animal nutrition throughout the last 70 yr. The objective of this paper is to discuss the challenges and opportunities associated with creating large feed ingredient composition tables. This manuscript will focus on three topics discussed during the National Animal Nutrition Program (NANP) Symposium in ruminant and nonruminant nutrition carried out at the American Society of Animal Science Annual Meeting in Austin, TX, on July 11, 2019, namely: 1) Using large datasets in feed composition tables and the importance of standard deviation in nutrient composition as well as different methods to obtain accurate standard deviation values, 2) Discussing the importance of fiber in animal nutrition and the evaluation of different methods to estimate fiber content of feeds, and 3) Description of novel feed sources, such as insects, algae, and single-cell protein, and challenges associated with the inclusion of such feeds in feed composition tables. Development of feed composition tables presents important challenges. For instance, large datasets provided by different sources tend to have errors and misclassifications. In addition, data are in different file formats, data structures, and feed classifications. Managing such large databases requires computers with high processing power and software that are also able to run automated procedures to consolidate files, to screen out outlying observations, and to detect misclassified records. Complex algorithms are necessary to identify misclassified samples and outliers aimed to obtain accurate nutrient composition values. Fiber is an important nutrient for both monogastrics and ruminants. Currently, there are several methods available to estimate the fiber content of feeds. However, many of them do not estimate fiber accurately. Total dietary fiber should be used as the standard method to estimate fiber concentrations in feeds. Finally, novel feed sources are a viable option to replace traditional feed sources from a nutritional perspective, but the large variation in nutrient composition among batches makes it difficult to provide reliable nutrient information to be tabulated. Further communication and cooperation among different stakeholders in the animal industry are required to produce reliable data on the nutrient composition to be published in feed composition tables.

Key words: black soldier fly larvae, data mining, feed composition tables, stochastic formulation, total dietary fiber

Abbreviations

ADF	acid detergent fiber
BSFL	black soldier fly larvae
CP	crude protein
DM	dry matter
NASEM	the National Academies of Science, Engineering, and Medicine
NDF	neutral detergent fiber
PCA	principal component analysis
TDF	total dietary fiber

Introduction

One of the most successful examples of large datasets applied to animal production is the Animal Nutrition Series published by the National Research Council (currently, the National Academies of Science, Engineering, and Medicine [**NASEM**]). The Animal Nutrition Series has created systems to formulate balanced diets for different livestock species, such as poultry (NRC, 1994), dairy cattle (NRC, 2001), swine (NRC, 2012), and beef cattle (NASEM, 2016). The NASEM approach relies on two factors: 1) mathematical models used to predict the nutrient requirements of different classes of animals and 2) feed composition tables displaying nutrient composition values for different feedstuffs. Thus, from the estimated nutrient composition of feeds, nutritionists can formulate diets to match nutritional requirements, allowing proper use of feeds and nutrients.

Feed composition tables display nutritional information on hundreds of feeds commonly used in animal nutrition. All feed tables report means and some report standard deviations for different nutrients, such as protein, fat, carbohydrates (sugars and fiber), amino acids, and minerals. Most tables also report information on nutrient values that are dependent on the animal species being fed. Some examples include net energy, amino acid digestibility, and protein degradability (Sauvant et al., 2004; CVB, 2016; NASEM, 2016). Historically, the information provided by feed composition tables have been widely used to assist nutritionists in diet formulation tasks and are also used as tools to instruct students on the nutrient composition of different types of feeds and diet formulations. Similarly, feed composition datasets (used to construct feed composition tables) are widely used for developing and evaluating nutritional models (Rumburg et al., 2008; Cemin et al., 2019; Li et al., 2019).

Traditional static feed composition tables such as those published by NRC/NASEM (NRC, 2001, 2012), Institut National de la Recherche Agronomique (Sauvant et al., 2004), and Centraal Veevoederbureau (CVB, 2016) have been useful tools in animal nutrition; however, these traditional tables do not meet the rapidly changing needs of a dynamic feed industry and scientific community. Traditional feed composition tables are difficult to update (e.g., NRC animal nutrition series books are updated, on average, every 10 to 20 yr) and often become obsolete because of new production practices, changes in plants genetics, changes in analytical methods, and introduction and characterization of new feeds. Currently, there are several efforts to create feed composition tables using database-driven websites relying on large datasets (INRA-CIRAD-AFZ, 2019; NANP, 2020). Database-driven webpages display feed composition tables in a flexible platform to meet requirements of the industry and scientific community and store and display large amounts of information, with the potential to reach a large number of users. However, developing such online tools presents challenges associated with traditional feed composition tables such as editorial decisions on content (i.e., feed and nutrients to be displayed) as well as new challenges related to management and screening large datasets.

Considering the importance of feed composition tables to different aspects of the animal production industry, the objective of this paper is to discuss the challenges and opportunities associated with creating large feed ingredient composition tables. This manuscript will focus on three topics discussed during the National Animal Nutrition Program (NANP) symposium presented at the American Society of Animal Science (ASAS) Annual Meeting at Austin, TX, on July 11, 2019, namely:

- The value of feed composition tables providing accurate estimates of standard deviation in nutrient concentrations;
- Using feed composition tables as a tool for comparing and promoting methods to determine fiber in feeds; and
- Challenges and importance of including information on novel feeds (i.e., insects, algae, single-cell proteins) in feed composition tables.

The Value of Feed Composition Tables Providing Accurate Estimates of Standard Deviation in Nutrient Concentrations

Prior to about 2001, feed composition tables published in the NRC nutrient requirement series were based predominantly or exclusively on data acquired from university research labs. Although most of these tables did not include information regarding the number of samples, the data were likely based on a very small number of samples per feed. In the last years, farm-specific sampling and analysis of forages and other feedstuffs have become routine, which reduced the reliance on feed composition tables for diet formulation and other tasks. Paradoxically, the vast amount of data generated by commercial feed testing labs has the potential to improve the accuracy of statistics displayed in feed composition tables (i.e., average and standard deviations). Datasets created with data from commercial labs represent a valuable resource to the animal science and animal production communities. Samples from these labs reflect growing conditions from across the country, numerous manufacturing systems, different plant genetics, different storage and harvesting methods, among others. In addition, because sampling and analytical variation can be substantial for some feeds (e.g., forages), the low number of feed samples taken from a specific farm would limit the accuracy of nutrient composition used at the farm level (St-Pierre and Weiss, 2015). In this regard, an average value from a larger database may be more accurate for some feeds.

Good feed composition databases should provide more information than average concentrations such as accurate standard deviations in nutrient composition. Standard deviations are available in some feed composition tables (NRC, 2001; NASEM, 2016). However, some published standard deviations may not be accurate because data used to construct these tables were largely unfiltered.

One of the most direct ways to use measures of standard deviation in diet formulation is in the development of margins of safety. A margin of safety is defined as the degree to which a diet is formulated above nutrient requirements and aims to minimize the risk of nutrient deficiency (St-Pierre and Weiss, 2015). Similarly, stochastic formulation is used by some nutritionists to formulate concentrate mixes and by some

formulation software for poultry and swine diets (Saxena and Chandra, 2011). Stochastic formulation includes uncertainty in nutrient composition to formulate an optimal diet based on the risk the user is willing to accept. For example, a user might set a goal of providing adequate nutrients to produce a certain amount of milk 80% of the time (in contrast to 50% of the time when using conventional formulation methods). A diet based on that goal or any goal can only be formulated if the standard deviation of the nutrients in the feeds is known (D'Alfonso et al., 1992).

Knowing the standard deviation can also be useful when comparing the economic value of feeds. Various methods are available to compare the economic value of feeds (Ely et al., 1991; Bethard, 1998; St-Pierre and Glamocic, 2000), but these methods are based on the mean composition of the feedstuffs and do not incorporate the nutrient variability into their pricing systems. A feed with greater nutrient variability is worth less than a consistent feed with the same average nutrient composition. More variable feeds may require additional sampling and laboratory analyses and diets may need to be reformulated more often, all of which incur added costs (Bethard, 1998; Weiss, 2004). In addition, diets that include more variable feeds should have greater margins of safety, which will usually increase diet costs. The magnitude of the safety margin should be proportional to the variability in nutrient composition; therefore, variable feeds should be discounted more than consistent feeds.

Methods to obtain accurate standard deviation values in feed tables

The value of incorporating nutrient variability into diet formulation and feed pricing is predicated on the availability of accurate estimates of standard deviation. An adequate number of independent samples is needed to obtain an accurate estimate of the variability of a population. Many farms will not have an adequate number of samples of the feeds being fed to generate accurate population statistics, but large feed databases can.

To obtain accurate estimates of average and standard deviation, large feed composition datasets must be screened to eliminate erroneous data. Potential errors include simple data entry mistakes, incorrect units, analytical mistakes, bad sampling procedures, misidentification of feed, and feeds correctly identified but representing different populations because of genetics, processing, or region. Obvious errors (e.g., identifying wet corn gluten feed as corn gluten meal, Figure 1b) can be easily identified using histograms or box-plots. However, in many cases, errors are difficult to identify using data visualization (Figure 2a).

Errors in datasets can be corrected using statistical screening methods. Univariate methods are often used to screen feed composition datasets (NASEM, 2016). Univariate methods assume that variables in a dataset are independent and with identical and known distribution, that is, normal distribution (Ben-Gal, 2005). A commonly used univariate method consist on considering outliers all datapoints exceeding an arbitrary number of SD from the mean. Common values used as a threshold to classify a datapoint as outlier are 3.5 SD from the mean (NASEM, 2016) or in some cases, perform a double screening, first using a threshold of 3 SD from the mean and, if required, a second screening deleting values exceeding 2 SD from the mean (CVB, 2016). The INRA feed composition tables (Sauvant et al., 2004) eliminated values below the 5th percentile and above 95th percentile for every nutrient in a dataset. Although many published feed composition tables

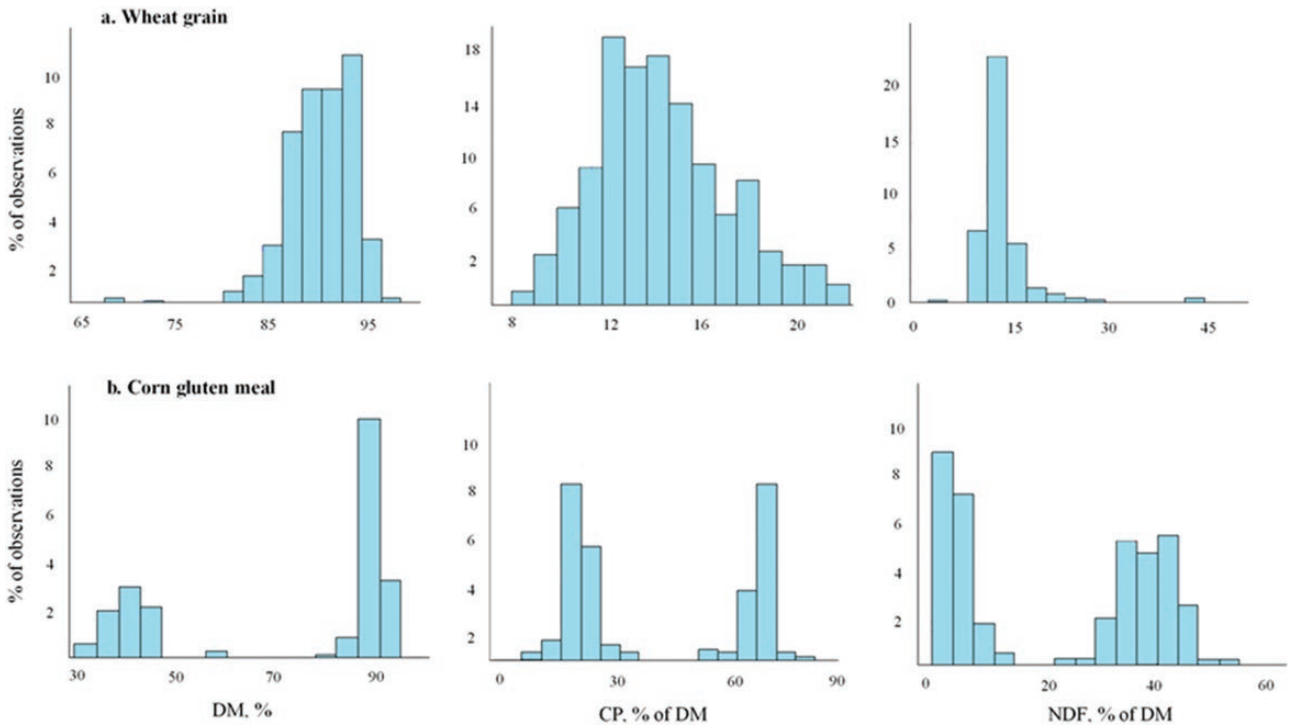

Figure 1. Histograms for DM (%), CP, and NDF concentrations for datasets initially identified as (a) wheat grain and (b) corn gluten meal. For wheat grain, mean and standard deviation are DM = 89.7% ± 3.3, CP = 14.6% ± 2.6, and NDF = 12.4% ± 4.1. Reference feed composition values for wheat grain are DM = 89.5% ± 2.5, CP = 14.7% ± 2.3, and NDF = 15.2% ± 8 (NANP, 2020). Histograms and statistics for the dataset identified as wheat grain suggest a low number of misclassified samples. For corn gluten meal, mean and standard deviation are DM = 72.8% ± 23.1, CP = 43.2% ± 23.2, and NDF = 23.2% ± 16.3. Reference feed composition values for corn gluten meal, DM = 91.5% ± 2.0, CP = 63.2 ± 7.8, and NDF = 9.1 ± 6.6 (NANP, 2020). The histograms for the dataset identified as corn gluten meal show a bimodal distribution containing misclassified feed samples. This is confirmed by the large standard deviation and mean values widely different from reference.

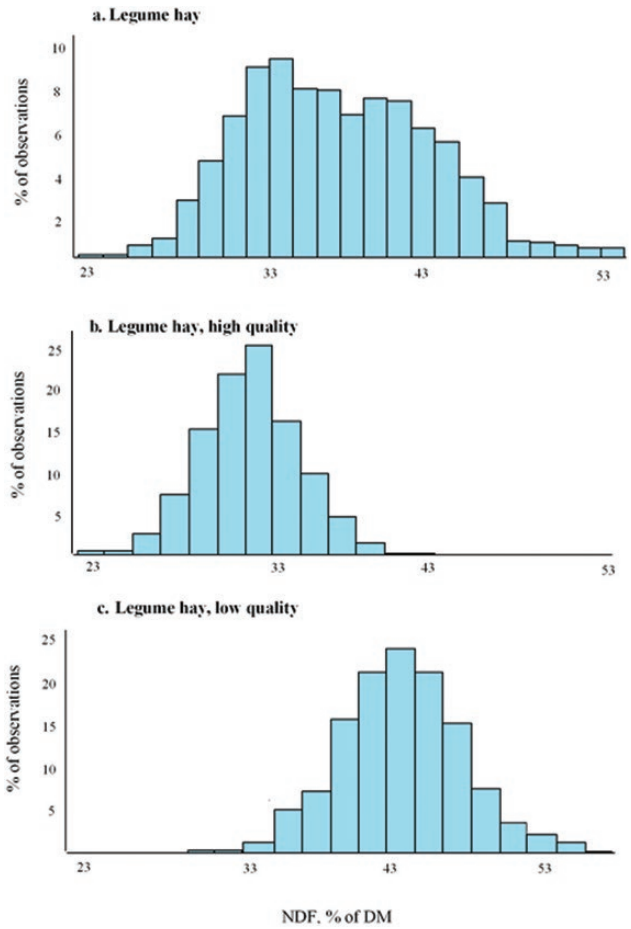

Figure 2. Histograms of NDF concentrations for a dataset initially identified as legume hay (a). The population had 432 observations with mean and standard deviations NDF = 38.0% ± 6.1. After PCA + clustering screening procedure (Yoder et al., 2014), two subpopulations were identified as (b) legume hay, high quality with a mean NDF = 34.2% ± 3.4 and (c) legume hay, low quality with a mean NDF = 43.0% ± 4.2.

rely on univariate methods for detecting errors, these statistical methods are not always the right choice. Poorly defined feeds (e.g., legume hay) may have very large standard deviations (Figure 2), which makes identifying outliers difficult. Univariate methods are appropriate for normal distributions (Ben-Gal, 2005), but many nutrients follow a skewed distribution. Lastly, univariate methods do not take advantage of the covariance among nutrients to identify outliers and misclassified feeds.

In the case of commercial lab datasets, a common error is the misclassification of feed samples. For example, a sample submitter may confuse corn gluten meal with corn gluten feed (Figure 1b). Misclassification of feeds can impact population statistics depending on the number of misidentified observations and how different the misidentified feed is from the correctly identified feed. Misclassification also occurs because of broad and often ambiguous definitions of feeds. For example, bakery byproducts can include waste from bread bakeries, breakfast cereal companies, cookie bakeries, etc. The byproducts resulting from these different manufacturing operations can differ markedly in nutrient composition. Cookie waste is high in fat and sugar, whereas bread waste would typically be mostly starch with low concentrations of sugar and fat. Although these feeds may be identified as bakery byproducts, they are often available for sale as specific products (e.g., bread waste). Finally, the classification of forages can be especially problematic because quality or maturity classes are ambiguous. Forages classes exist as a continuum without a clear nutritional difference between classes and could be identified quite differently by different users as shown in the histograms in Figure 2. Although commercial labs have very large datasets of the nutrient composition of forages, the data may not be useful for feed price comparisons or stochastic programing because inconsistent and often poorly defined classification criteria can produce erroneous estimates of average and standard deviations. The undefined classifications may also be so broad (e.g., legume silage vs. late bud legume silage) that the mean and standard deviation will not be specific enough to be useful. When data from one feed are contaminated with data that belong to another feedstuff, both means and standard will be affected, and often the data follow nonnormal distributions (Figure 1b).

Separation of misclassified feed has been done manually using histograms of dry matter (**DM**; NASEM, 2016). However, this approach is not always useful because it is time-consuming and it is based on a univariate approach (i.e., using a single variable such as DM). A different approach to separate misclassified feeds relies on different machine learning techniques. According to Samuel (1959), machine learning is defined as "the study that gives computers the ability to learn without being explicitly programmed." Machine learning procedures are widely used to predict and classify parameters in datasets (Géron, 2017). Yoder et al. (2014) developed an unsupervised machine learning procedure to screen large feed datasets using a multivariate approach. Unsupervised machine learning methods can identify hidden groups within a large dataset when data labeling (i.e., feed name) is unreliable or inexistent. The Yoder et al. (2014) method was modified to increase automation and tested on large data commercial datasets by Tran et al. (2020). Prior to applying the Yoder et al. (2014) method, the raw data must be screened to remove clearly erroneous observations such as duplicate entries and feeds where measured nutrients summed to greater than 100%. A more difficult task at this step is to standardize feed names, which is especially critical when collating data from multiple labs. This step has not been automated and requires input from someone with knowledge of feeds. The standardization of terms required about 60% of the total time needed to produce final feed composition tables from raw lab data (Tran et al., 2020). After the initial screening, data were subjected to a univariate screening, followed by principal component analysis (**PCA**) and finally cluster analysis as discussed by Yoder et al. (2014).

Besides identifying misclassified feeds that have a clear separation such as corn gluten meal vs. corn gluten feed (Figure 1), the procedure was useful to eliminate less obvious outliers. Unsupervised machine learning procedures such as PCA and cluster analysis can identify outliers using a multivariate approach based on highly improbable relationships (i.e., covariance) among nutrients. For example, based on the mean and standard deviation for a corn silage population (data not shown), approximately 30% of the samples would be expected to have a starch concentration greater than 39%, and 30% of the samples would be expected to have a neutral detergent fiber (**NDF**) concentration greater than 45%. A sample of corn silage with an NDF of 45% and a starch concentration of 39% would not be identified as an outlier using univariate statistics. However, starch and NDF in corn silage have a strong negative correlation so that a sample with high starch and high NDF is extremely unlikely. Based on the covariance in this dataset (r = –0.88), a

sample with 39% starch and 45% NDF will only occur about twice out of 1,000 samples. Multivariate analysis would identify this sample as an outlier.

The described unsupervised machine learning procedure was also useful when a feed class lacks distinct breakpoints in the data. A dataset of legume hay has a continuous range in NDF concentrations (Figure 2a). It could be manually partitioned into higher and lower quality by setting a specific NDF cutoff similar to what was done in the NRC (2001) feed composition tables. Setting a cutoff of less than 40% NDF for immature legume hay will result in a nonnormal distribution and the mean and SD may be incorrect. Using the unsupervised machine learning procedure, the samples were partitioned into two classes: one was higher-quality legume hay with a lower mean concentration of NDF and greater concentration of crude protein (CP) compared with the lower-quality legume hay. The distributions were normal with some overlap (Figure 2b and c). Wet brewers' grains provide another example of the value of unsupervised machine leaning procedure (Table 1). In the dataset of Tran et al. (2020), the univariate procedure eliminated 16 observations, and another 11 and 59 observations were eliminated by PCA and cluster analysis, respectively (a total of 8.5% of the initial observations). This elimination had essentially no effects on mean concentrations of DM (full dataset vs. screened dataset; 25.0% vs. 24.4%), CP (29.5% vs. 29.4%), NDF (50.1% vs. 49.9%), and ash (5.0% vs. 4.9%); however, the SD decreased for some nutrients (DM; 5.4% vs. 3.7%), NDF (6.4% vs. 5.2%), and ash (1.7% vs. 0.8%). Furthermore, the analysis revealed that within the large screened dataset, there were three large clusters with 273, 183, and 482 observations in each cluster (Table 1). Although specific identification of the clusters was not possible (they might reflect specific breweries or types of beer), the clusters had unique characteristics. The SD was generally much less for the generated clusters than for the initial screened population. If those clusters could be identified, a broad, variable classification (wet brewers' grains) would become three feeds with more precisely identified nutrient composition.

The described unsupervised machine learning procedure was useful to generate accurate estimates of population statistics, but the procedure has some limitations. First, the procedure eliminated a large number of records (about 46% from the initial dataset); second, because cluster identification had to be done manually, the procedure was time-consuming (Tran et al., 2020). Recently, Schlageter-Tello and Miller (2019) proposed two supervised machine learning procedures (i.e., decision tree and random forest) for automatic feed classification using the feed dataset created by Tran et al. (2020). Supervised machine learning procedures can identify hidden groups within a large dataset but require labeled data (i.e., feed names; Géron, 2017). The proposed procedures were able to classify 10 different corn grain feeds with a correct classification rate ≈90% (range = 89% to 100%) for most feeds. Steam-flaked corn grain and corn screenings had a correct classification rate < 80% (range = 68% to 77%). Both steam-flaked corn and corn screenings were consistently misclassified as corn grain dry. The classification rate for corn feeds could be improved by including physical characteristics of feeds into the classification parameters; however, they are not commonly reported by laboratories. Another option to improve classification rates is to try different supervised machine learning methods such as neural networks. Further work is required to develop these supervised machine learning methods to screen and classify datasets for most feeds used in animal nutrition.

Feed Composition Tables as a Tool for Comparing and Promoting Methods to Determine Fiber in Feeds

Animal nutrition is an evolving discipline and, as such, decisions on the nutrients included in feed composition databases/tables are difficult. One example of this constant evolution is related to the different methods to assess fiber content of feeds. Fiber is the common term assigned to a group of complex molecules (i.e., cellulose, lignin, hemicelluloses, pectins, β-glucans, etc.) contained in the cell wall of plant cells. Different livestock species can digest fiber to different extents. Traditionally, fiber was considered to be an important source of energy for ruminants (NRC, 2001) and an antinutritional factor for nonruminants. Today, fiber holds a more prominent role in animal nutrition than in years past, as new properties and methods to assess fiber are discovered (Gaggìa et al., 2010; Bach Knudsen, 2014). In this regard, feed composition tables could be used to compare and promote the different methods used to assess fiber content of feeds, recognizing that seasonality and stage of plant growth affect the chemical composition and contribute to the chemical variation noted in feed libraries.

Importance of fiber in animal nutrition

Ruminant and equine nutrition researchers still conduct in-depth studies of fiber from forages, pastures, byproduct feeds, and fiber supplements in hopes of optimizing the nutritional value of these dietary ingredients that are so critical to efficient animal production, health, and well-being. In the case of nonruminants, fiber is viewed by some as an "antibiotic proxy" and a "metabolic modifier" (Jha et al., 2019). For example, in swine nutrition, greater incorporation into swine diets of byproduct feeds containing elevated fiber concentrations is occurring. Examples include

Table 1. Nutrient composition and variability of wet brewers grains following a three-step screening procedure[1]

	Initial dataset		Cluster 1		Cluster 2		Cluster 3	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
N[2]	983		273		183		482	
DM, %	24.4	3.7	22.7	2.2	29.5	2.3	23.5	3.2
CP, %	29.4	4.8	33.0	2.1	34.7	1.8	25.3	2.6
NDF, %	49.9	5.2	47.4	3.1	47.4	3.5	52.2	5.8
Ash, %	4.87	0.83	4.52	0.54	4.47	0.51	5.26	0.91

[1]The identities of the clusters are unknown but may represent different breweries or residues from different types of beer.
[2]The three clusters sum to less than the full dataset because clusters containing less than 10% of records from the initial dataset are deleted (Yoder et al., 2014).

distillers dried grains with solubles (Stein and Shurson, 2009) and other grain byproducts (Kerr and Shurson, 2013). The use of no or lower concentrations of antibiotics in swine diets results in fiber being supplemented for its effects as a microbiota management agent and an immunomodulator (Stein, 2007). Other outcomes affected by fiber inclusion in swine diets include increased satiety and reduced occurrence of stereotypic behavior in pregnant sows (Ramonet et al., 1999; Kerr and Shurson, 2013)

In poultry nutrition, moderate concentrations of dietary fiber stimulate gastrointestinal tract development and hydrochloric acid and enzyme production (Yokhana et al., 2015). High-fiber diets have value in welfare-friendly molting programs for laying hens and may replace complete feed withdrawal (Ricke et al., 2013). The need for the controlled growth of pullets and turkey breeders makes fiber useful in these phases of poultry production. In addition, partial control of stereotypic behavior expressed as feather pecking is achieved with dietary fiber (Rodenburg et al., 2013). Finally, the gut microbiota, most of which are found in the crop and paired ceca of poultry, are modulated by fiber inclusion in the diet (Jha et al., 2019).

Fiber is a critical component of the diet of pet animals (dogs and cats) in that it aids in optimizing gut health outcomes (de Godoy et al., 2013). Unlike livestock and poultry with finite lifespans, many pets live until the end of their natural lives. Pet owners desire longevity for their pets. They desire that their pets live long, healthy lives. Fiber figures prominently in the various nutrient-based health platforms that exist today in pet animal nutrition, whether it be digestive health, cognitive development, immune support, weight and diabetes management, among others. The fact that the dog and the cat coexist with humans in the home represents a diet formulation challenge as regards fiber, which can decrease digestibility and increase the frequency of defecation. The source of the fiber, the concentration used in the diet, and the ratio of insoluble:soluble dietary fiber are critical in the development of food formulas that will work well for the pet and the pet parent (de Godoy et al., 2013).

There are several health-related outcomes mediated by fiber for nonruminant animal species. First, fiber affects gut structure and function. Gastrointestinal tract hypertrophy as a result of increased fiber ingestion leads to a more metabolically active gut as demonstrated by increased energy and amino acid requirements for maintenance and high cell turnover in the epithelial lining of the gut (Kerr and Shurson, 2013; Jha et al., 2019). These events are thought to be mediated through the production of short-chain fatty acids from the fermentation of fiber. Second, fiber stimulates the secretion of mucins in the ileum, resulting in enhanced barrier function. Mucin secretion is caused, in part, by mechanical irritation resulting from the ingestion of insoluble dietary fiber and it reduces the incidence and severity of gastric ulcers. The particle size of the fiber may also play a role (Jha et al., 2019). Finally, fibers modulate the gut microbiota (Hamaker and Tuncil, 2014). Different fibers affect the gut microbiota in different ways, but in general, the effect is positive for all dietary fibers. Microbiota utilization of fibers is complex and is affected by many factors, including fiber source, monosaccharide composition, linkage types, chain length, particle size, anomeric form, epimeric form, and the interaction of other compounds associated with the fiber itself (Hamaker and Tuncil, 2014).

Methods to determine fiber concentrations and their limitations

Dietary fiber is made up of structural carbohydrates (cellulose, hemicelluloses, pectins, and β-glucans) and lignin that are resistant to hydrolytic digestion by mammalian small intestinal enzymes. In addition, components other than structural carbohydrates and lignin, to include "animal fiber" (mostly connective tissue made up of hyaluronic acid and chondroitin sulfate), resistant starch, and nondigestible oligosaccharides (prebiotic fibers), are now among the mix of compounds referred to as "dietary fiber" (Figure 3). Many isolated and synthetic fibers also exist today and are sometimes used to provide an optimal balance of fibers in animal diets, although these are used mostly in human food matrices (Institute of Medicine, 2001).

Recognition of the importance of fiber as a dietary component demands that a definable, accurate, and repeatable method for its analysis be available. But fiber is nutritionally, chemically, and physically heterogeneous, however, making this the most difficult task, and accurate methodologies have been slow in coming. In addition, the fact that the feed industry has chosen to retain the crude fiber analysis as the method of choice for reporting dietary fiber concentrations on feed labels has hindered the advancement of the science in this area. Fahey et al. (2019) prepared an in-depth review of the factors crucial to the successful measurement of dietary fibers and provided suggestions on how to overcome potential analytical problems with the various assays. A brief summary follows.

Crude fiber is one of the components of the proximate analysis system developed by Henneberg and Stohmann (1864) at the Weende Agricultural Experiment Station in Germany. Crude fiber has been an Association of Official Agricultural Chemists method (AOAC, 2006) since 1916 and remains so yet today (AOAC method 930.10 relates to crude fiber in plant tissues and AOAC methods 962.09 and 978.10 relate to crude fiber in animal feed and pet food, respectively). Shortcomings of the method were recognized nearly from the beginning but were not summarized in any organized fashion until the publication of the paper by Nordfeldt et al. (1949). The crude fiber method was developed specifically for the nutritional analysis of ruminant feeds, including silages. Van Soest and McQueen (1973) determined that this method loses a significant amount of the hemicelluloses (as much as 80%), lignin (as much as 60%), and cellulose (as much as 50%) during the extraction process. All soluble dietary fibers (e.g., pectins, β-glucans, gums, mucilages, oligosaccharides) are lost as well (Figure 3). Although it remains the feed industry standard, the food industry has moved totally away from its use.

The case for the unacceptability of the use of crude fiber was explained in Van Soest (1966) and detergent fiber methodology was proposed. Two major detergent methods were developed—acid detergent fiber (**ADF**) and NDF. ADF was intended for the isolation of the less fermentable fractions of forages (cellulose, lignin, acid-insoluble ash) by using an acidic medium containing cetyltrimethylammonium bromide. It was developed in collaboration with the AOAC (Van Soest, 1973) and given final approval in 1977. The concept behind NDF analysis is that plant cells can be divided into the less digestible cell walls (cellulose, hemicelluloses, lignin) and the highly digestible cell contents (starch, sugars; Figure 3). The procedure involves the extraction of samples with a hot solution of sodium lauryl sulfate with the subsequent gravimetric determination of the residue retained on a fritted glass filter (Goering and Van Soest, 1970). Mertens (2002) included a heat-stable amylase with the original NDF method that used sodium sulfite to obtain the amylase-treated NDF (AOAC 2002.04) that can also be used to measure ash-free NDF. Soluble dietary fiber components are not quantified using this method (Figure 3).

The impetus for the establishment of the total dietary fiber (**TDF**) methodologies was the passage of the Nutrition

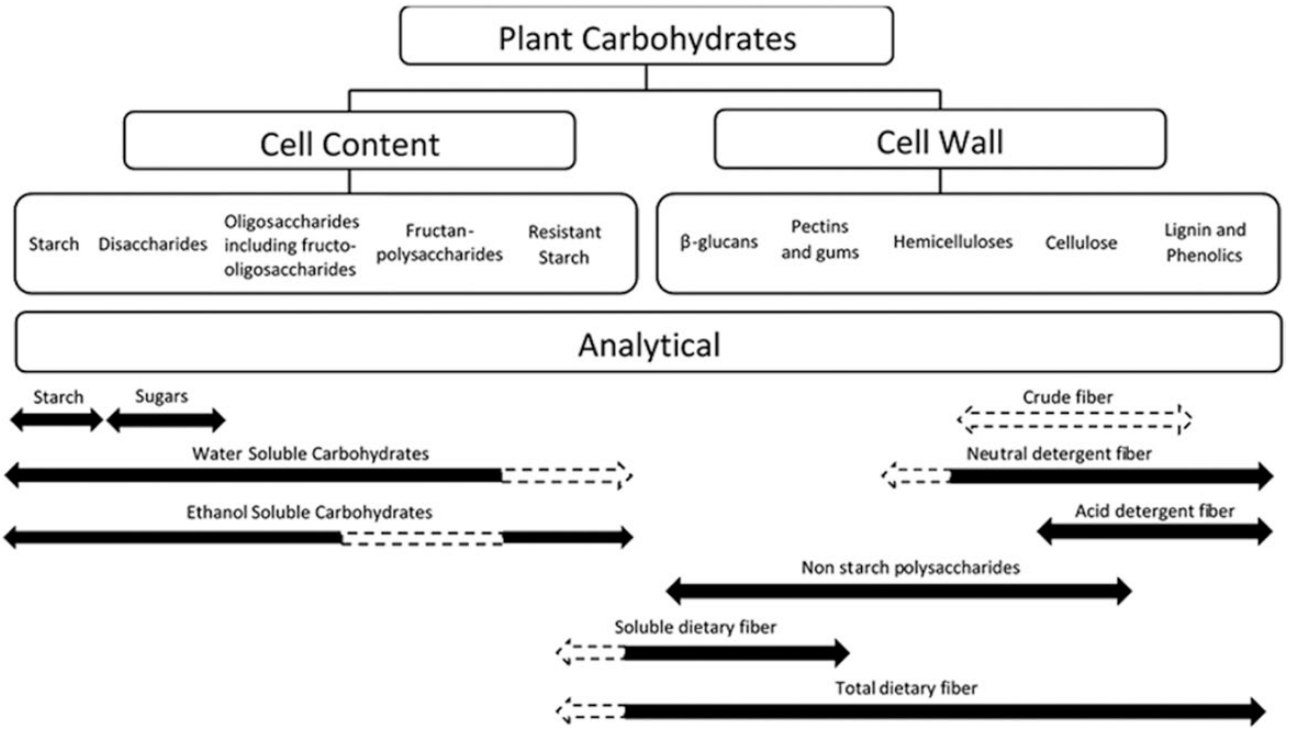

Figure 3. Scheme of carbohydrates structure in vegetal cells and analytical methods to estimate their concentrations. Dashed lines indicate that the recovery of included compounds may be incomplete. Adapted from NRC (2007).

and Education Act of 1990 by the U.S. Congress that required the concentration of "dietary fiber" to be listed on the Nutrition Facts Panel of human foods. The methodology was developed by a consortium of researchers in the United States and Europe leading to the AOAC Official Method 985.29 (referred to as the "Prosky TDF method") and to subsequent modifications to include the AOAC Official Method 991.43 that allowed individual measurement of the "insoluble dietary fiber" and "soluble dietary fiber" fractions (Fahey et al., 2019). Many new AOAC-approved methods have come about since the original methods were established, all dealing with either improvements to the methodology or allowing more and more fibrous fractions to be measured as either single entities (e.g., fructooligosaccharides, AOAC 997.08 and 999.03) or as one portion of the TDF (e.g., AOAC 2009.01 and 2011.25). These are described in detail in Fahey et al. (2019). These methods enable detailed analysis of sugars, starches, nondigestible oligosaccharides, noncellulosic polysaccharides, cellulose, and lignin and often are used for the analysis of complex food matrices that include isolated/extracted fiber (e.g., inulin) and (or) synthetic fiber (e.g., resistant maltodextrins) in addition to intrinsic and intact natural ingredient fiber sources (e.g., wheat bran, beet pulp). They quantify, for all practical purposes, all components of dietary fiber present in a substrate (Figure 3). Although these methods were initially applied to human foods and their ingredients, animal nutritionists are now using these methods to quantify fibers in complete feeds, feed ingredients, and byproduct feeds.

Fiber classification methods that should be used for different animal species

First and foremost, crude fiber should be abandoned for research, feed labeling, or regulatory purposes as the method of choice to represent the fiber concentration of feedstuffs fed to animals. It is unconscionable that a method known for over 100 yr to result in grossly inaccurate nutritional information should be the one accepted yet today by feed control officials to represent the concentration values of such an important dietary constituent as fiber.

The detergent system of fiber analysis is the one used most often by the animal nutrition community. It accurately quantifies the insoluble dietary fiber components but does not quantify the soluble dietary fiber components. Therefore, NDF values always underestimate the true fiber content of the many animal feed ingredients that contain a soluble dietary fiber component. In cases where little soluble dietary fiber is present (e.g., corn and corn byproducts), the NDF value is very similar to the TDF value. But in today's ruminant and nonruminant animal feeding systems, many ingredients containing significant soluble dietary fiber are fed, causing the detergent fiber system to come up short as regards quantification of the total fiber component. Soluble dietary fiber would be rapidly and extensively fermented in the reticulorumen of ruminants, whereas the soluble dietary fiber fraction would exert its effects primarily in the cecum/large intestine of nonruminant animals.

The accuracy of the TDF methodology, the ability to quantify the insoluble and soluble dietary fibers separately, and the many updated AOAC approved methods that allow literally all fibers to be quantified either separately or as an integrated unit make this technology the way of the future in the field of dietary fiber analysis. To be sure, the methods are more complicated and expensive than either crude fiber or detergent fiber analyses. But fiber is a complicated chemical and physical entity that today takes many forms (intrinsic and intact, extracted, isolated, synthetic), so more complicated procedures are needed to assay it properly. Given that fiber is the major food for the gut microbiota, and given the importance of the gut microbiota in

host animal physiology and health, it is imperative that fiber be assayed accurately in order to optimize its use in animal diets.

Inclusion of Novel Ingredients in Feed Composition Tables

The type of feeds to be included in feed composition databases/tables can be a dilemma. Currently, most livestock species are fed with combinations of corn, soybean meal, and forages. It is estimated that feed production uses 75% of all agricultural land and 8% of global drinking water. As the world population grows and, along with it, the demand for meat consumption grows (Godfray et al., 2010, 2018), new solutions are needed to improve food/feed production and sustainability. Natural resources are also required for an increasing demand for bio-fuels and direct human food. Thus, new sustainable feed sources are required for livestock production. There are a number of ingredients that are receiving interest as alternative protein sources, including insect-derived ingredients (Makkar et al., 2014), algal proteins (Madeira et al., 2017), and single-cell proteins, to name just a few (Øverland et al., 2010). Insects have a high feed conversion efficiency and can transform waste biomass into high-value feeds (Makkar et al., 2014). Similarly, algae can transform simple carbon structures into a biomass rich in proteins, vitamins, fatty acids, minerals, and pigments (Madeira et al., 2017). Both insect and algae production still need to overcome several challenges before being widely used as feed for livestock species (e.g., being produced and processed on a large scale). The problem with including insects and algae in feed composition databases/tables currently is that there are few data sources and a lack of information on nutrient digestibility for different species and, therefore, it is difficult to confirm the accuracy of information to be published. This section provides a brief overview of novel ingredients, particularly their potential application in animal feeding systems as well as concerns that remain about their use.

Insect-derived ingredients

Several species of insects are being commercialized for animal (and human) consumption. Black soldier fly larvae (**BSFL**, *Hermetia illucens*), mealworm larvae (*Tenebrio molitor*), and crickets (nymphs and adults, *Acheta domesticus*) are the primary species being commercialized (Koutsos et al., 2019). Insects are good candidates for large-scale rearing efforts due to their fast lifecycle (e.g., BSFL birth to reproductive maturity in ~40 d); ability to be farmed vertically, which dramatically increases yield potential per unit area; a large proportion of edible material due to lack of bones, hide, and other structural components; and high concentrations of essential nutrients.

The proximate and amino acid compositions of several insect meals are presented in Table 2. In general, CP and amino acids profile from different insect-derived feeds is similar to profiles reported by soybean meal and fishmeal menhaden (Table 2). Methionine and cysteine tend to be the first-limiting amino acids for most agricultural species (Finke and Oonincx, 2017; Table 2), although arginine and threonine may be limiting for some companion animals (Do et al., 2020). Amino acid digestibility is generally good for insect meals, ranging from 70% to 86% (De Marco et al., 2015). For BSFL meal,

Table 2. Proximate and amino acid composition (± standard deviation) of insect meals and typical protein ingredients[1,2]

	Mealworm larvae meal (n = 5)[3]	BSFL meal (n = 3)	Partially defatted BSFL meal (n = 3)	Cricket meal (*Acheta domesticus*) (n = 3)	Soybean meal (48%)	Fishmeal (menhaden)
CP, %	55.8 ± 0.89	43.0 ± 4.81	65.5	59.9	47.5	61.3
Arginine, %	2.80	2.04 ± 0.34	2.70	4.28 ± 0.16	3.48	3.68
Histidine, %	1.68	1.38 ± 0.30	1.63	1.74 ± 0.07	1.28	1.42
Isoleucine, %	2.21	2.09 ± 0.57	2.40	2.48 ± 0.12	2.12	2.28
Leucine, %	3.15	3.47 ± 0.93	3.67	3.97 ± 0.21	3.74	4.16
Lysine, %	3.18 ± 0.06	2.73 ± 0.76	2.52	3.46 ± 0.15	2.96	4.51
Methionine, %	0.54 ± 0.04	0.75 ± 0.22	0.86	1.40 ± 0.07	0.67	1.63
Phenylalanine, %	1.88	2.00 ± 0.54	2.18	2.18 ± 0.09	2.34	2.21
Threonine, %	1.34 ± 0.09	1.63 ± 0.56	2.18	2.49 ± 0.12	1.87	2.46
Tryptophan, %	1.75	0.52 ± 0.05		0.79 ± 0.08	0.74	0.49
Valine, %	2.82	2.86 ± 0.71	3.45	3.56 ± 0.12	2.22	2.77
Alanine, %	3.89	4.00 ± 1.39	4.37	4.80 ± 0.27		
Aspartic acid, %	4.37	4.03 ± 0.77	4.88	6.73 ± 0.73		
Cysteine, %	1.25	0.32 ± 0.08	0.02	1.40 ± 0.12	0.72	0.57
Tyrosine, %	3.28	2.81 ± 0.60	3.41	1.79 ± 0.01	1.93	1.8
Crude fat, %	25.2 ± 1.1	35.1 ± 6.24	18.0	22.1	1.0	9.4
Ash, %	4.8 ± 0.33	8.6 ± 1.65	9.3	3.57	7.33	20.98
Apparent metabolizable energy, kcal/kg	3,626.6 ± 319.6[4]	4,250.8 ± 363.4[4]	3,883.8 ± 193.8[5]		2,440.0	2,820.0
Apparent metabolizable energy, Nitrogen-corrected (AMEn), kcal/kg	3,446.0 ± 312.9[4]	4,060.0 ± 355.8[4]	3,554.0 ± 205.6[5]		2,485.0	2,977.0

[1]All values are presented on a DM basis; values in the table for insect meals obtained from: Finke (2002, 2015), Collavo et al. (2005), De Marco et al. (2015), Taufek et al. (2016), Schiavone et al. (2017), and Jajić et al. (2019); EnviroFlight internal data.
[2]Values in the table for soybean meal (48% protein) and fishmeal (manhaden) obtained from poultry NRC (1994).
[3]n = sample size; n in the header is applicable to all data in the column unless specified with superscript. In values without standard deviation n = 1.
[4]n = 10.
[5]n = 5.

amino acid digestibility tends to be negatively correlated with fat content (Schiavone et al., 2017). In addition, nitrogen could be in the form of chitin, which may be digested only if animals possesses endogenous chitinase enzymes, but if not digested chitine may also act as a probiotic or as a fiber-like source (Tabata et al., 2018). This nonprotein nitrogen may impact the assessment of CP from nitrogen assays (Janssen et al., 2017).

Additional nutrients in insect meals include essential fatty acids that may be synthesized by the insect (e.g., linoleic acid) or diet-derived (e.g., *n*-3 fatty acids) and short-chain fatty acids with potential for improved digestibility and(or) immunomodulatory functions (e.g., lauric acid 12:0; Spranghers et al., 2018). Minerals are often adequate in insects, except for calcium that is low in insects other than fly larvae species. However, fly larvae can bio-accumulate other minerals and heavy metals, which should be considered and analyzed in commercial animal feeds (Diener et al., 2015; Spranghers et al., 2016). Insects are generally a good source of water-soluble vitamins and vitamin D3 and may be a source of vitamin E and carotenoids depending on the feedstock upon which the insects were raised (Koutsos et al., 2019). Carotenoid-enriched insect ingredients may provide pigmentation to meat and eggs (Dalle Zotte et al., 2019). Digestibility and availability of nutrients from insect meals can be impacted by the processing method, so this should be considered during insect ingredient evaluation (Poelaert et al., 2018).

Considerable research has been conducted to examine the value of insect-derived ingredients in the diets of agricultural species, in addition to pets and exotic animals (Rumpold and Schlüter, 2013; Makkar et al., 2014; Sánchez-Muros et al., 2014; Henry et al., 2015; Irungu et al., 2018; Khan, 2018). In general, insect meal can be used as a replacement for soybean meal, or high-quality animal proteins, when dietary amino acid profiles are balanced. Insect oils have potential in nursery pigs and other young animals, particularly those insect oils enriched in lauric acid (Zentek et al., 2011).

Algal-derived ingredients

Algal-derived ingredients represent another alternative protein source (Shields and Lupatsch, 2012, Admassu et al., 2015). Algal-derived ingredients may be derived from seaweed, macroalgae, and microalgae. Algal-derived ingredients may vary significantly in composition. The proximate and amino acid compositions of several algae are presented in Table 3. Algae-derived protein, seaweed digestibility, in particular, can be much lower than many microalgae species due to its high content of indigestible polysaccharides (Ventura et al., 1994). Algal protein and amino acid digestibility tend to be similar to that of legumes (Bleakley and Hayes, 2017). For example, the essential amino acid digestibility of *Chlorella* in salmon was 79% to 90% and was improved by rupturing the algal cell walls (Tibbetts et al., 2017). Some of the nitrogen extracted from algal sources is nonprotein, from nucleic acids, amines, glucosamides, and cell wall materials (Becker, 2007); thus, traditional methods of measuring N × 6.25 for CP assessment may overestimate the actual protein levels. Lysine and tryptophan in algae meals tend to be limiting for agricultural species (Bleakley and Hayes, 2017).

Algae not only tend to be enriched in linoleic and linolenic acid (Lipstein and Hurwitz, 1980) but also can be a source of long-chain *n*-3 polyunsaturated fatty acids and arachidonic acid (Patil et al., 2007), making these ingredients very appealing as alternatives to fish oil. Vitamins and carotenoid pigments may also be enriched in algae, and the latter can have impacts on the pigmentation of meat and eggs (Lipstein and Hurwitz, 1980, Altmann et al., 2018). Concerns with algal-derived ingredients include cell wall polysaccharides and phenolics that may impact digestibility (Tibbetts et al., 2016). There is a risk of mineral and heavy metal accumulation, including As, I, Al, Pb, and Hg (Chekroun and Baghour, 2013), which often is greater in macroalgae grown in seawater. Like insects, the base feedstock, the method of production, and the type of processing also impact nutrient composition and digestibility (Bleakley and Hayes, 2017).

Applications of algal-based ingredients in animal feeds have primarily been focused not only on aquaculture species but also in poultry and livestock (Yaakob et al., 2014). Inclusion rates are generally lower (<1%) when algal sources are being utilized as a specific nutrient source (e.g., docosahexaenoic acid); intermediate when used to promote carcass characteristics,

Table 3. Proximate and amino acid composition (± standard deviation) of algal-derived ingredients and typical protein ingredients[1,2]

	Laminaria sp.(brown algae) (*n* = 34)[3]	*Porphyra columbina* (red algae) (*n* = 7)	*Ulva clathrata* (green algae) (*n* = 3)	*Chlorella vulgaris* (whole-cell)	*Spirulina platensis* (*n* = 1)	Soybean meal (48 %)	Fishmeal (menhaden)
CP, %	8.24 ± 2.09	24.61 ± 0.21	23.0 ± 0.10	30.4 ± 0.10	58.2	47.5	61.3
Arginine, %	0.27 ± 0.04	1.52 ± 0.04	1.40 ± 0.02	1.67 ± 0.01	3.96	3.48	3.68
Histidine, %	0.18 ± 0.03	0.31 ± 0.02	0.29 ± 0.01	0.52 ± 0.02	1.00	1.28	1.42
Isoleucine, %	0.31 ± 0.08	0.67 ± 0.01	0.72 ± 0.02	0.94 ± 0.01	3.06	2.12	2.28
Leucine, %	0.22 ± 0.07	1.83 ± 0.03	1.23 ± 0.02	2.05 ± 0.03	4.84	3.74	4.16
Lysine, %	0.33 ± 0.12	1.50 ± 0.02	0.78 ± 0.01	1.41 ± 0.02	2.72	2.96	4.51
Methionine, %	0.07 ± 0.02	0.42 ± 0.02	0.30 ± 0.01	0.45 ± 0.00	1.98	0.67	1.63
Phenylalanine, %	0.26 ± 0.08	0.92 ± 0.01	0.97 ± 0.02	1.38 ± 0.00	2.50	2.34	2.21
Threonine, %	0.29 ± 0.05	1.45 ± 0.03	0.87 ± 0.01	1.29 ± 0.07	2.84	1.87	2.46
Tryptophan, %	0.04 ± 0.04	0.16 ± 0.00	0.15 ± 0.01	0.02 ± 0.00	0.07	0.74	0.49
Valine, %	0.31 ± 0.08	5.85 ± 0.03	1.11 ± 0.03	1.51 ± 0.01	3.34	2.22	2.77
Cysteine, %	0.10 ± 0.02	1.44 ± 0.01	0.35 ± 0.01	0.29 ± 0.00	0.72	0.72	0.57
Tyrosine, %	0.14 ± 0.02	0.63 ± 0.01	0.45 ± 0.01	1.03 ± 0.00	2.58	1.93	1.8
Crude fat, %	1.10 ± 0.33	0.25 ± 0.06	3.5 ± 0.30	26.0 ± 0.70	2.6	1.0	9.4
Ash, %		6.46 ± 0.09	45.8 ± 0.30	3.3 ± 0.10	8.44	7.33	20.98

[1]Data are presented on a DM basis; values in the table obtained from: Lourenço et al. (2002), Dawczynski et al. (2007), El-Deek and Brikaa (2009), Alvarenga et al. (2011), Peña-Rodríguez et al. (2011), Cian et al. (2014), and Tibbetts et al. (2016, 2017).
[2]Values in the table for soybean meal (48% protein) and fishmeal (manhaden) obtained from poultry NRC (1994).
[3]*n* = sample size; *n* in the header is applicable to all data in the column unless specified next to a particular nutrient value.

Table 4. Proximate and amino acid composition (± standard deviation) of single-cell protein-derived ingredients and typical protein ingredients[1,2]

	Bacterial meal (natural gas grown)	Brewers yeast	Soybean meal (48%)	Fishmeal (menhaden)
CP, %	70.2 ± 4.53	49.8 ± 4.61	47.5	61.3
Arginine, %	4.43 ± 0.21	2.21	3.48	3.68
Histidine, %	1.55 ± 0.14	1.05	1.28	1.42
Isoleucine, %	3.09 ± 0.28	2.13	2.12	2.28
Leucine, %	5.27 ± 0.14	2.96	3.74	4.16
Lysine, %	3.94 ± 0.28	3.05	2.96	4.51
Methionine, %	1.83 ± 0.14	0.75	0.67	1.63
Phenylalanine, %	2.95 ± 0.14	1.73	2.34	2.21
Threonine, %	3.02 ± 0.21	2.15	1.87	2.46
Tryptophan, %	1.55 ± 0.56	0.53	0.74	0.49
Valine, %	4.08 ± 0.21	2.36	2.22	2.77
Alanine, %	4.99 ± 0.28	3.97		
Aspartic acid, %	5.98 ± 0.28	4.45		
Cysteine, %	0.49 ± 0.07	0.31	0.72	0.57
Tyrosine, %	2.53 ± 0.21	4.24	1.93	1.8
Crude fat, %	9.0	4.2 ± 1.18	1.0	9.4
Ash, %	7.35 ±1.63	7.6 ± 1.18	7.33	20.98

[1]Data are presented on a DM basis; values in the table obtained from: Schøyen et al. (2007), Øverland et al. (2010), and Shurson (2018).
[2]Values in the table for soybean meal (48% protein) and fishmeal (manhaden) obtained from poultry NRC (1994).

resistance to heat stress, and immunomodulatory activity (Saker et al., 2004); and high (5% to 10%) when utilized as a protein or energy source.

Single-cell proteins

Single-cell proteins encompass bacterial proteins (primarily methanotrophs), fungal proteins, and yeast proteins. These are very broad classes of potential ingredients, and composition varies (Table 4). Bacterial protein digestibility is reportedly greater than or equal to 85% (Schøyen et al., 2007) and has broad application in animal feeding systems, including aquaculture, swine, poultry, and pet diets (Øverland et al., 2010). There are many yeast and yeast-derived ingredients that also have applications in animal nutrition. Viable yeasts (e.g., active dry yeast) are generally utilized for probiotic function, nutritional yeasts (derived from *Saccharomyces cerevisiae*) and specialty yeasts (e.g., Se-yeast, Cr-yeast) are utilized for specific nutrient composition and for immunomodulatory properties (Jensen et al., 2008), and fractionated yeast products (e.g., yeast soluble, condensates, hydrolysates, extracts, cell walls) are used as a source of β-glucans and mannans. General concerns about this class of ingredients include high nucleotide levels (>5%; (Fabregas and Herrero, 1985) that can impair performance at high levels, although at lower levels, nucleotides may enhance performance and gut health (Sauer et al., 2011). Endotoxin and mycotoxin contamination based on production systems, particularly with fungal protein production (Ritala et al., 2017), is another concern.

In general, relative to novel ingredients discussed in this section, there is considerable variation in ingredient composition of insect-derived ingredients, even within species or ingredient type. This may be due to the feedstock the organism is grown on, the life stage at which it is harvested, and the method of further processing. As these industries mature, we can anticipate that refinement of nutrient composition will occur, but until then, routine monitoring and close communications between suppliers and feed manufacturers will be critical for the successful incorporation of alternative protein sources into animal feeds.

Conclusions

Feed composition tables have been a useful tool for the livestock industry. The development of online database-driven feed composition tables has resulted in new uses of feed composition tables. Feed composition tables could be used as a source of good quality information about the nutrient content in feeds to be used for ration formulation, as a tool to promote accurate methods to analyze fiber in feeds, and for promoting novel feed sources, such as insects, algae, and single-cell protein. However, important limitations related to the lack of data available to partition variation associated with measuring protocol (i.e., analytical and sampling variation) exist. For TDF and novel feed sources, inadequate data are available to create large datasets to be used by the animal industry. In this regard, further communication and cooperation within different stakeholders of the animal industry are required to produce the data on nutrient composition to be published in feed composition tables.

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Conflicts of interest statement

The authors declare no conflict of interest.

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