

**Unique Features and Advantages of the New Database Paradigm
(Revised November 2009)**

It has been argued that there are numerous feed information databases available (both public and proprietary) and that the efforts of FeedAC are redundant. However, these databases often contain information from only one source or are compilations of information from multiple undefined sources. Both types of databases have problems with being unbiased sources of information with defined methodologies that can be universally accepted.

The initial attempt by FeedAC to define the best analytical methodologies and use them exclusively to generate the information in a new database would have been different and an improvement. However, FeedAC became bogged down in trying to identify what results should be included in the database and what methods should be used to generate those results. The vision apparently was to create a database similar to that in NRC bulletins that would be a standard with values based on defined methods. It is clear that there will never be agreement or even consensus on the correct way to measure constituents or even on which constituents to include in the database.

The new paradigm will be an open-ended database similar to the system of AAFCO in which results are reported in relation to the method used for measurement. Instead of dictating *the* method that must be used to measure an analyte, results for all alternative methods will be included in the database, each in its own field and each linked to a description of the specific method used to generate the results. Thus, there can and will be multiple values for protein, fiber, or any analyte. It will be up to the user to decide which method is appropriate for their application, which should not be dictated by a committee. The new paradigm will allow the comparison of alternative methods for measuring an analyte on exactly the same samples so that individual or consensus decision can be made about the most appropriate method or methods to be accepted for routine or specific usages.

The new feed information and sample system will have several unique features not contained in any current feed information database:

1. Analytes will be included in the database only if they are accompanied by a defined method written in a standard format,
2. Both the results for the analyte and the method used for measurement will be in the database,
3. Each analyte that is measured by a specific method will be identified by a unique acronym and stored in a unique field within the database,
4. Ten to twenty samples of each feed that encompass the diversity in the entire population of the feed will be identified and evaluated for the database and retained in storage,
5. Samples with unique information (e.g., in vivo evaluation) or unique characteristics will be retained and included in the database if they provide unique information,
6. Detailed, complete nutritional evaluation will be done on the same set of diverse samples for a particular feed,
7. Analyses for the same constituent and method will be replicated by multiple laboratories on the same set of samples,

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8. Replicated data within and among samples within a feed will allow database information to be edited and classified using objective statistical criteria,
9. Approximately 50 lb of the diverse feed samples will be stored for future use,
10. Diversity of the retained sample collection will be evaluated annually to determine if additional samples need to be collected and analyzed, and
11. Changes in feed information can be tracked by location, year, type, and method (some databases can track location and year, but typically only one method is used so interactions with method cannot be detected).

The unique features of the new feed information and sample system will provide the following advantages to sponsors and users that are not available in any other database system:

1. Data will only be included if the method is documented, and each constituent will have a unique acronym in the database for identification (if we cannot define how it was obtained, it will not be included in the database, and if it is included, it will have an acronym that uniquely establishes the terminology for that constituent group),
2. For the first time, methods will be described for all results in the database for quick reference (users can always find the method associated with any value and acronym),
3. The unique characteristics of a feed sample can be used to detect differences among subgroups (users could relate them to genotype and environment-location or year),
4. Complete data will be provided on exactly the same set of samples,
 - a. Results for different methods can be compared directly for the first time in a national database (e.g., the NDR method without sulfite can be compared to aNDF with sulfite across multiple samples and feeds),
 - b. Unique characteristics of diverse samples can be detected and used (samples with unique characteristics can be used to investigate the sources of variation or to challenge current or new analytical methods and nutritional models),
5. Complete information will be provided on individual samples of a feed,
 - a. Once samples are selected, complete information on each sample can be obtained on a competitive basis by submitting requests for bids to provide specific nutritional information (instead of trying to pay for detailed analyses on 100 samples, detailed analysis is done only on the 10 to 20 samples selected to represent the diversity of the feed population),
 - b. Averaged results for one constituent can be directly compared to averaged results for another constituent because all data is obtained on the same samples (as opposed to using the averages from 2000 CP values, 1500 NDF values, and 200 calcium values that may not be equally representative samples in a database),
 - c. Feed averages can be obtained by the user because the samples selected represent the diversity of the feed population,
 - d. Measured results from a feed can be matched to a specific sample in the database to obtain comparable values for unmeasured constituents (e.g., if a user had routine analysis for a corn sample indicating it contains 7% CP, he could search the database only for corn samples with similar CP and use the amino acid composition for those subsamples of corn to complete his results data set),
 - e. Relationships between and among constituents could be derived by the feed information and sample system for general use,

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6. Because analytes for the same sample can and should be replicated by multiple laboratories, the database can provide an accurate mean for an analyte with a measure of reproducibility,
 - a. For the first time, reproducibility of results among laboratories under practical conditions for the same sample can be determined,
 - b. These samples can be useful for a user who is evaluating alternative laboratories to determine if they can accurately reproduce results reported in the database,
 - c. These samples can be used by laboratories as standards for quality assurance programs (e.g., if it can be documented that at least three independent laboratories can obtain similar results for a sample and method, this sample can be used as a laboratory standard),
 - d. These samples can be used as references to cross-validate a new method with an old method or to relate methods of one type to another by an individual laboratory (e.g., a laboratory would like to determine if a new enzyme-based in vitro method gives information consistent with the ruminal in vitro data in the database),
 - e. Because sample retention is a big part of the new system, samples will be available for alternative uses as described in item 6 (samples could become a small, but significant, source of revenue),
7. Because of its specificity and consistency in editing, the user can be assured the data is as accurate as possible (e.g., if the database manager receives a result that is not consistent with similar results already in the database based on objective statistical criteria, the manager can reject the data or identify the discrepancy in methods used by the result generator and determine if a new acronym and method description should be added to the database), and
8. The database can be mined by in-house managers or users to discover underlying relationships, discrepancies among methodologies, and missing information that is needed for complete nutritional evaluation.