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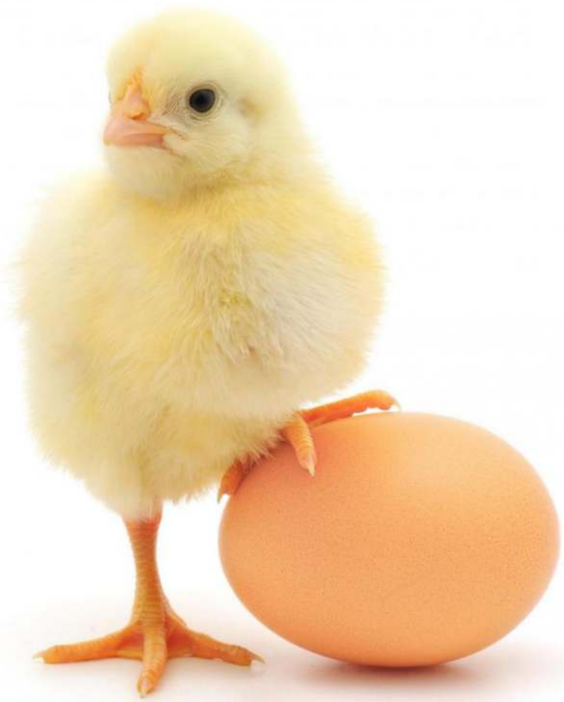

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Models to Estimate Amino Acid Requirements for Broiler Chickens: A Review[1]

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Abstract: Computerized growth models can be a useful tool to determine more profitable and accurate concentrations and balance of dietary amino acids and other nutrients for broiler chickens. The methodology of mathematical modeling can be rapidly accepted in poultry nutrition and research due to the complexity of nutrient requirement estimations in practical and economical terms, and the necessity to have some quantitative margin of safety in the prediction of broiler performance for decision-making applications in the poultry industry. This paper reviews the current problems related to the methodologies for amino acid requirement estimation for growing chickens, the development of mathematical modeling of growth and their applications in poultry nutrition, and a short chronological review of the evolution of computer growth models.

Key words: Broilers, modeling, growth, amino acid requirements

Introduction

Even though the essential amino acid requirements for broiler chickens have been well documented (Sibbald, 1987; Rhodimet, 1993; NRC, 1994; Rostagno *et al.*, 2000), the prediction of performance in practical and useful terms to be used in deciding the most advantageous dietary amino acid patterns is still difficult, even when the digestibility or availability of each amino acid is specified. This difficulty is partly due to the non-linearity of growth responses to changes in dietary amino acid concentrations (Phillips, 1981; Mercer, 1982), interactions between or among amino acids, classified as imbalance, antagonism or toxicity (D'Mello, 1994), interactions of some amino acids with other nutrients or antinutritive factors (Austic, 1986) and variations in metabolism due to environmental conditions or genetic potentials (Boorman and Burgess, 1986).

Problems in determining accurate amino acid needs of chickens: Amino acid requirements of broilers have been determined with growth variables, carcass analysis (Gous, 1986; Hruby *et al.*, 1999), radioactive isotope studies, plasma amino acid analysis (Prieto *et al.*, 1994) and rates of amino acid oxidation (Austic, 1986). The most common methodology is the empirical evaluation of broiler performance as a function of graded levels of a particular amino acid, or factorial combinations of amino acids that are offered in the diet, during a given age and pre-determined feeding period corresponding to a fixed feeding schedule. These levels are obtained either by addition of synthetic amino acids or by the dilution technique (Gous and Morris, 1985). The concentration of the amino acid(s) in the diet producing the maximum body weight gain, the best feed conversion ratio, the best carcass traits or the adequate plasma levels is determined as being the requirement for that amino acid or amino acids, and normally is expressed as a fixed concentration of the diet. These fixed values of amino acids are compiled in tables of requirements and utilized for feed least-cost formulation. These tables do not consider factors such as genetic diversity in potential rate of growth or carcass composition (Gous, 1986; 1998). With fixed requirements it is impossible to predict the effect on rate of growth, feed intake, or carcass composition by the manipulations of the concentration and balance of dietary amino acids. Furthermore, single fixed numbers of requirements are not useful to apply to an accurate cost-benefit analysis. Because the responses of birds to dietary energy, protein, and amino acids are a diminishing returns phenomena, they should be evaluated economically as such to estimate economic optimum levels, rather than as biological maximums (Parks, 1982; Fawcett, 1986; Pesti and Miller, 1997).

In the same way, when fixed requirements are used, it is also difficult to evaluate how or even whether these levels of nutrients should change with the available genotypes. In fact, relatively little research has been done taking in consideration changes imposed by broiler genetic selection, even though these may have altered dietary requirements (Emmans, 1995). It has been assumed that faster-growing broilers exhibit a higher feed intake, which would compensate for the lower-than-required amino acid content of the diet. However, Morris and Njuru (1990) demonstrated that

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these broilers might not consume more feed.

It is difficult then to visualize a feasible solution, if for each amino acid and every new set of circumstances it is necessary to accomplish an experiment in order to determine the right solution (Gous, 1998; MacLeod, 2000). In order to solve this problem several different approaches have been taken. Among them, the ideal protein formulation, the partitioning of the requirement to match physiological functions, and the modeling approach are the most widely evaluated. Baker (1994) proposed to express amino acid requirements for poultry as an ideal ratio to lysine. Although multiple factors (diet, environment, sex and genetics) affect the amino acid requirement, the ideal ratio of indispensable amino acids to lysine should remain largely unaffected by these variables, according to Baker. Several ideal ratios have been proposed (Austic, 1994; Baker, 1996; Mack *et al.*, 1999). However, some research has indicated that these ideal ratios can change according to the objective to be evaluated (Fritts *et al.*, 2000), and still there is no way to predict the responses to these changes.

On the other hand, Whittemore (1983) has suggested that nutrient requirements should not be stated in fixed terms but instead should describe levels of energy, protein, amino acids and other nutrients that are required to satisfy a target response in the animal consistent with the animal's genetic potential and environment. One method of estimating the need for a specific amino acid to meet a targeted response is to separate its requirement into two fractions, maintenance plus performance (Owens and Pettigrew, 1989). This methodology can provide an accurate determination of amino acid requirements, improvement in nitrogen accretion efficiency and reduction in nitrogen excretion (Baker, 1991; Hruby *et al*, 1999). Wang and Fuller (1989) developed an ideal amino acid profile for both gain and maintenance in growing pigs by determining the changes in nitrogen retention using a deletion method. The researchers removed a proportion of each amino acid in the diet and measured the changes in urine nitrogen.

In poultry, Hruby *et al.* (1995) estimated the pattern of amino acids needed by growing broilers for maintenance and tissue accretion using performance variables, weekly comparative slaughter methods and nitrogen excretion assay. The analysis of muscle and feather protein together with an estimate of amino acid levels for maintenance published by Emmans and Fisher (1986) were employed for amino acid requirement calculations. These maintenance and growing requirements have been reviewed in additional research (Hruby *et al.*, 1999). These authors have concluded that the best way to express daily maintenance requirements for different sizes of broilers would be to use mg amino acid/kg carcass protein instead of using the traditional mg/day/kg $BW^{0.75}$.

Modeling as a tool for amino acid requirement estimation: It has been observed that the traditional empirical estimation of nutrient requirements applies only to the conditions under which the requirements were established. Another philosophy of requirement estimation relies on the mathematical description by equations of biological complex phenomenons such as growth (Hurwitz *et al.*, 1978; Emmans, 1981; Parks, 1982). Mathematical modeling can quantitatively describe the relationships among dietary nutrient inputs and outputs, and the development of tissues as a function of time or as affected by environmental conditions. From the adequate and dynamic description of carcass and feather growth and composition it is possible to determine accurate amino acid requirements for chickens that can be applied for a wider variety of conditions (Munks, *et al.*, 1945; Hurwitz *et al.*, 1978; 1980; Fisher and Scougall, 1982) avoiding approximations and margins of safety in the formulation actually made when no research data is available for a given condition (Zhang and Coon, 1994).

It seems more feasible to accumulate information that allows higher precision in requirement estimations. It is necessary in the estimation model to integrate information about the bird, the feed and the environment (Emmans and Fisher, 1986; Emmans, 1987; 1995) in order to simulate all the possible conditions and with this make accurate predictions of feed intake, live weight gain, feed efficiency utilization and changes in body composition as affected by the environment and the diet (Gous and Morris, 1985). In this way, utilizing mathematical optimization techniques, we can estimate the most profitable level and method to feed a specific flock under a wide range of economic conditions.

Gous (1986; 1998) has proposed the simulation modeling technique as the only defensible way in which nutritionists can use research results to improve and optimize the efficiency of feeding broilers under a wide range of conditions (Talpaz *et al.*, 1986). Growth modeling techniques allow nutritionists and poultry researchers to predict dynamic or daily amino acid requirements, by a process which seems to be more adequate than the use of fixed requirements for starter, grower, and finisher periods published in several tables of recommendations (Hruby *et al.*, 1994) opening the evaluation of other feeding schedules that can be more adequate and profitable in certain conditions.

Development of mathematical models: The process of modeling includes defining the objectives, building a flowchart to identify the principal factors involved in the system to model, formulating the adequate mathematical functions, collecting data to estimate parameters, solving equations, evaluating and verifying the model, and programming the simulation software (Baldwin, 1995; Black, 1995). Descriptions made by models must be based on parameters estimated from data of careful research or field collection analyzed with the right statistical procedures.

Many relationships between the variables involved in dietary amino acid effects can be described by linear and nonlinear regression models, or by response surface regression equations resulting from amino acid interactions as a whole (Curnow, 1986). One important characteristic of some methods such as the response surface, from the point of view of economic decision-making, is the shape of the curve around the point at which the requirement of the average individual in the flock is met that allows determination of optimums (Curnow, 1973; Gous, 1986; Pesti *et al.*, 1986). The model can be classified as static, deterministic and empiric, if the model estimates only a single value for a specific age or period based on the data input and output without explanations of the process. However, if it can predict values as a function of time or age, corresponding to the data probability distribution, describing the processes involved, this model can be categorized as dynamic, stochastic and mechanistic (Zoons *et al.*, 1991; France and Thornley, 1984; Baldwin, 1995; Black, 1995).

To mathematically describe changes in bird growth and carcass traits the Gompertz function seems to be the best fit (Lehmann, 1980; Tzeng and Becker, 1981; Gous, 1986; 1998; Emmans, 1995; Hruby *et al.*, 1996). The Gompertz equation currently utilized by most broiler models is given in the form:

$$W_t = W_o\, e^{(L/K)\,(1 - e^{(-Kt)})}$$

Where: W_t = Weight at time t,
W_o = Hatch weight,
L = Initial growth rate,
K = Rate of exponential decay of L.

In this form, the mature weight is described as $A = W_o e^{(L/K)}$ (Hruby *et al.*, 1994). In its pure form the Gompertz curve is empirical as it shows what maximum growth will be at any point in time with the provided nutritional and environmental conditions. This empirical model describes a mathematical relationship between a dependent variable and an independent variable based on theoretical assumptions concerning growth, without any explanation of the biological processes involved. The theoretical assumptions can be that the growth rate is proportional to the live weight W with a proportionality u and the effectiveness of growth decays with time t according to first-order kinetics, giving exponential decay (Zoons *et al.*, 1991).

Although the Gompertz equation is often used in empirical models, Emmans (1981) concluded that the Gompertz function is frequently chosen in mechanistic models for its mathematical properties, biological meaning of parameters and its reasonable fit. However, a better description of the realized growth of the tissues (muscle, feathers and fat) is a result of potential growth (genetically determined) and its interaction with nutrient intake and environment factors becomes a necessity.

To interpret growth response curves of flocks, the best way is to reduce the growth curve to that of an individual at a specific time, and then to integrate such curves for all of the individuals in a population over time or age (Emmans and Fisher, 1986). Separate population response curves can then be constructed for each day of the growing period and feeding strategies can be optimized (Gous, 1998). In this way, it is possible to consider the probability distributions such as variation and covariation of the population in the model, making this stochastic.

It is well known that amino acids and protein affect in a different manner such parameters as carcass fat deposition (Cabel and Waldroup, 1991), individual muscle development, and feather growth (Fisher *et al.*, 1981; Boorman and Burgess, 1986; Pesti and Miller, 1997). Consequently, to describe these effects, carcass and feather chemical growth must be represented in the model. The ash, water, and lipid content of broilers predicted by allometric relations with body protein are accepted since a linear relationship exists between these. The lipid gain predictions are a problem because the carcass lipid is greatly influenced by feed composition and environmental temperature (Tzeng and Becker, 1981; Hruby *et al.*, 1994; Yahav *et al.*, 1996). Supplying separate feather and carcass yields combined with composition permit nutrient requirements for production of these two components to be calculated. Growth curves for live weight and feather yield vary between strain-crosses and sexes and the adequate estimation of parameters is necessary (Stilborn, *et al.*, 1994; Hancock *et al.*, 1995; Gous *et al.*, 1999).

Some diets that are nutritionally inadequate at the start of a growth period may become adequate as the broiler grows (Parks, 1982; Gous, 1986). Models based on the premise that growth rate determines requirements based on some fixed rate of nutrient utilization do not adequately represent the biological phenomena involved (Pesti and Miller, 1997). The curvature in response to such dietary treatments will differ depending on the length of the trial period. Some dietary treatments will, of course, be inadequate throughout the experimental period, whereas others will always be adequate, but it is the intermediate diets that create an additional source of curvature of the response curve. In order to interpret the responses to amino acids in growing animals, it is essential to separate out these confounding effects of time on the shape of the response curve (Zoons *et al.*, 1991; Gous, 1998). Dynamic models take time into account as a variable, given the possibility to determine optimal age of slaughtering or optimal age to stimulate certain growth of tissue. Models to estimate amino acids must also describe effects of feed restriction on growth and compensatory gain (Talpaz *et al*., 1991).

On the other hand, it is known that with certain amino acids the response measured would differ if the levels of interacting nutrients in the diet were altered (Gous, 1986; Muramatsu *et al*., 1991). Examples of some of the better-known interactions are those between lysine and arginine; leucine, isoleucine and valine; choline and methionine; nicotinic acid and tryptophan; and between vitamin E, selenium and cystine (Austic, 1986; D'Mello, 1994). These effects also should be included in models to increase the accuracy of estimation of requirements and prediction of responses. The ideal model to predict accurately amino acid requirements should be dynamic, stochastic and mechanistic. However, the model should be simple enough to describe just the principal factors that influence the response, such as interaction with other amino acids, environmental temperature and composition of the diet. Mechanistic models can help to understand complex metabolic pathways of amino acids and identify specific points to improve the whole animal performance (Clifford and Müller, 1998) as it has been studied for arginine in Japanese quails (Šnejdárková and Otto, 1983).

History of computerized models to determine amino acid needs: Modeling of animal growth and nutritional needs is very antique. Gompertz (1825) as cited by Parks (1982) published some of the first work in this area. Later research was mostly limited to developing prediction equations (Combs, 1964; Thomas, 1967; Fisher *et al*., 1973; Macleod, 2000) and standard growth curves for various animals that reflect responses to management, genetic selection and dietary treatments. More recently, the focus has changed to the production of commercially available software that could be used by the poultry industry to estimate different nutrient requirements, simulate responses of chickens and help in decision-making for production strategies.

All of these models are in some phase of development, validation and evaluation. To use them, all require a calibration process to make the parameters closer to the actual conditions. Most of them take in consideration factors such as gender, body weight gain, intake of some nutrients, feed efficiency, environmental temperature and husbandry conditions as variables for calibration. The evaluation process includes determination of its accuracy (how closely the model estimates real data); its precision (how variable are these estimations); and its bias (how much it is influenced by the errors of estimation) (Harlow and Ivey, 1994).

Curnow (1973) developed one of the first partition models for laying hens at the University of Reading in England. The "Reading Model" determines layer flock amino acid requirements to maximize profits based on the relation between amino acid cost and both product value and standard deviations of egg size and body weight of layers in the flock. Researchers at Edinburgh University (Emmans, 1981; 1987; Emmans and Fisher, 1986) proposed an early attempt for a commercial model. The program utilized projected Gompertz growth curves of the maximum genetic potential for broilers and partitioned the response to dietary energy and protein consumed for daily maintenance, muscle and feather growth. It was later commercialized for personal computers as the FORTEL™ model, which included improvements in the theoretical aspects of the program and modifications of the user interface.

Concurrent to the work at Edinburgh, Hurwitz and coworkers at Hebrew University in Israel developed another model (Hurwitz *et al*., 1978; Talpaz *et al*., 1986; Talpaz *et al*., 1991). This model was designed with computed determinations of amino acid and energy requirements for growth and maintenance on a daily basis. Feed cost was estimated for each day's incremental gain, which was then utilized to develop the economical optimum growth trajectory. This program was commercially available under the name CHICKPOT™. The model was evaluated for broiler chickens (Hurwitz *et al*., 1980; Jackson, 1987) and growing turkeys (Hurwitz *et al*., 1983a; Hurwitz *et al*., 1983b). The NRC accepted this model as a good estimator of requirements for some amino acids for which no experimental results were available (NRC, 1994).

A model proposed by Pesti *et al*. (1986) was based upon a response surface quadratic approach describing the live response data obtained in growth trials in which combinations of energy, protein and some essential amino acids levels were tested. The concept expressed in this model was that a bird could be grown to a specified target weight on either high/low protein or energy regimes, and that the resultant trade-offs in time and nutrient intake could be resolved based upon the relative economics. Through mathematical manipulation, the result was a single diet with a predicted feed intake that gave the least expensive bird to a given target weight.

In 1989 Novus[2] presented the Ivey Growth Model (IGM®), a commercial broiler growth model program. Its accuracy, precision and bias have been tested in experimental and field conditions (Harlow and Ivey, 1994). The IGM is based on differential equations for growth, and quantifies nutritional and/or environmental effects that reduce performance from theoretical genetic optimum. The IGM includes an "optimizer", that allows

[2] Novus International, Inc., St. Charles MO 63304.

for the unlimited generation of differing "least-cost" options, rather than simply predicting the result of a single dietary program input.

In 1996, Novus acquired the rights of the model developed by Hurwitz and coworkers. This model, commercially available as OmniPro® II, has been tested with field data with a high degree of accuracy for live performance prediction (Fancher, 1999; Ivey, 1999). The model is calibrated with the growth curves of the genetic line according to sex and environmental constraints (temperature, flock density, feed restriction, feeding schedule, etc.). The model is used for economical analysis and optimization processes. Dietary amino acid profiles can be either an input variable or a pattern to be calculated by the software. Protein and amino acid requirements are calculated essentially using the same model proposed by Hurwitz *et al.* (1978). OmniPro® II divides overall amino acid requirements into three components, maintenance, carcass growth and feather growth. The model only considers the sum of irreversible losses and amino acid tissue accretion, divided by the efficiency of intestinal absorption to obtain the total needs. Considering that feed intake is dependent on energy requirements, the daily amino acid needs are divided by the calculated energy needs to determine the adequate concentration in the diet.

Parallel to the development of this program, the EFG Software® of Natal, South Africa, has launched software to estimate the optimum concentration of amino acids and energy to determine the economical optimum feeding program for broilers and other species (Gous and Fisher, 2001; Gous, 2001). This program utilizes a growth model designed according to the theoretical concepts developed by several years of research at Edinburgh University (Emmans, 1981, 1987; Emmans and Fisher, 1986), and includes several tools of economic analysis as well as an optimizer under an experimental idiom to compare several treatments. The growth model simulates an individual broiler using its genetic parameters of the Gompertz function, diet composition, feeding schedule, feed restriction, environmental temperature, stocking density and other husbandry factors that can limit the maximum genetic potential for growth. To maximize the overall performance, the best amino acid concentrations and the amino acid to energy ratios, in each of the feeds, are determined as functions of available lysine, and all other amino acids are determined by ideal protein ratios. Individual efficiencies of utilization of each one of the essential amino acids are considered.

Liebert and coworkers (2000) have been working on a model to evaluate the utilization of limiting amino acids and derivation of requirements based on the pattern of nitrogen balance in growing animals and target amounts of daily protein deposition. The model depends on nitrogen intake and feed protein quality described by an exponential equation. Finally, King (2001) has described a model developed to estimate the effects of dietary amino acid changes in the carcass composition and growth of chickens. This growth simulation program called BPHL is a mechanistic, deterministic and dynamic model that uses the initial age and live weight of the bird, number of days over which the diet is to be fed, feed intake, protein and amino acid densities of the diet, and dietary metabolizable energy. The program gives the daily accumulated deposition of body chemical composition, total live, carcass and feather weight, feed intake, feed conversion ratio, heat loss and limiting amino acids estimations. The model utilizes first-limiting amino acid coefficients relating to accretion efficiency and dietary concentration to define the limits of protein retention, and equations to describe patterns of feed intake and fat loss to describe strain traits.

Although many of these programs have a high degree of development to model broiler growth and dietary amino acid effects, they have had limited utilization by poultry nutritionists. Careful research evaluation and validation of the models can help to make them of more broad use. However, several factors such as the interactions among amino acids described previously should be included in these models to increase their accuracy in estimation of amino acid and other nutrient requirements.

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