THESES OF THE DOCTORAL DISSERTATION

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Institute of Physiology and Nutrition
Department of Farm Animal Nutrition

Head of the Doctoral School
Prof. Dr. ANDRÁS SZABÓ, DSc

Supervisor
Dr. VERONIKA HALAS, PhD

GENERIC DYNAMIC MODEL TO SIMULATE PERFORMANCE AND BODY COMPOSITION OF BROILERS

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Written by
GALYNA DUKHTA

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DOCTORAL SCHOOL IN ANIMAL SCIENCE

Name: GALYNA DUKHTA

Discipline: ANIMAL SCIENCE

Head: Prof. Dr. ANDRÁS SZABÓ, DSc
full professor, head of Doctoral School in Animal Science
Department of Physiology and Animal Health
MATE, Institute of Physiology and Nutrition

Supervisor: Dr. VERONIKA HALAS, PhD
associate professor, head of Department of Farm Animal Nutrition
MATE, Institute of Physiology and Nutrition

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Approval of the Head of Doctoral School	Approval of the Supervisor(s)

1. RESEARCH BACKGROUNDS AND OBJECTIVE

Being a central and integral part of the scientific methods, mathematical modeling of individuals may be adequate for better understanding growth and mechanisms behind it. Models can be used as simplifications of reality by means of representations of applying concepts with structuring data and prior knowledge (*i.e.,* operational models and research models). By describing nutrient flows and thus the animal response to certain circumstances, the nutritional models can be used to simulate an individual animal or group responses to different nutritional regimens (Black, 2014). Prediction of animals' growth based on modelling of feed utilization process or, conversely, while defining the nutrients requirements of the expected growth and providing the necessary amount and quality of nutrients, is one of the most important preconditions for the sustainable and economical manufacturing of high-quality animal products (Babinszky *et al.,* 2019). Hence, modelling is a high-potential tool gaining more and more application not only in research but also in practice nowadays.

Growth is a complex phenomenon that is highly determined by dietary nutrient supply. One of the greatest challenges in precision livestock farming is to be able to precisely meet the animal's dietary nutrients according to its actual requirements – thus to apply precision feeding. Nutrient requirement is changing as the animal grows over time, depending on feed and genetic potential of the animal, as well as the environment. By considering interactions that occur between many factors, which influence growth and development, simulation models have the capacity to greatly simplify a certain phenomenon what is otherwise a part of a large and complex biological system. Simplification helps us to understand the mechanisms and through that to develop better feeding strategies as well as to define the appropriate environmental conditions.

Modeling captures the main characteristics of the process by introducing the most important and determinant pathways of the system. Thus, growth models in case of two kind of animals such as pig and chicken, can share the same core.

And, despite the anatomical differences, there are examples on using generic models in animal nutrition for both species as they display many similarities in their digestive (Létourneau-Montimy *et al.,* 2011; Roger *et al*., 2018) and metabolic processes (Emmans, 1981; Gous *et al*., 2006). The energy flow model is valid to all animals and even to human, and also the protein evaluation systems are very similar in monogastric animals.

There are a few, but very limited number of metabolic models with a trans-species approach that have proved to be reliable in simulating the animal performance: *i.e.*, Emmans (1981) to EFG (1995), or Emmans (1994) and Ferguson *et al*. (1997) to Avinesp (2015). Those models are, however, not transparent since they are used in commercial animal feeding extension service, thus the developer has no interest in making them (the internal equations) available. Therefore, the hypothesis of the present work is that an available, well-defined dynamic mechanistic and deterministic pig model core can be used in development of a broiler model. In the course of the model development, there is a need to develop specie specific equations when the pig model is transposed to poultry. Furthermore, if reliable Ca and P partitioning model is ought to be developed, it should be integrated into the energy and protein metabolism model. According to our knowledge that integrated model has not been developed yet for poultry.

A generic dynamic mechanistic model will help to understand the nutrients partitioning and their interactions, and can be used as a tool in education and practice to develop sustainable feeding strategies.

The Aim of Research

The main goal of the dissertation is to develop a generic, dynamic mechanistic and deterministic model that is able to simulate the rate of changes in nutrient partitioning and performance of domestic chicken (*Gallus gallus domesticus*) at different age over the certain period of time. Our hypothesis was that a model core valid for growing and fattening pigs could be used as a starting point for a broiler growth model. Thus, the further aim was to assess the extent to which a publicly available and widely used growth model for pigs can be transposed to broiler chickens.

The purpose of the metabolic model is to give a “calculation engine” for predicting the actual animal production in response to different nutrient supplies. To make a comprehensive simulation model, Ca and P partitioning was integrated into the basic protein and energy partitioning model. Thus, the specific objectives of this dissertation are:

1. To develop a post-digestive metabolic dynamic mechanistic model by using a generic approach to nutrient partitioning for broilers, predicting the chemical body composition without major changes in the core structure of the pig model.
2. To conduct sensitivity analysis and to challenge the broiler model with experimental datasets in order to study the model behaviour and its reliability.
3. To extend the energy and protein metabolism model with a module that is able to simulate the P partitioning thus the P retention and excretion in broilers from digestible P intake.
4. To provide case studies on the benefit of model application related to environmental footprint of broiler production.

2. MATERIALS AND METHODS

Despite their differences, pig and chicken share many similarities in physiological processes of digestion and metabolism. Considering that the stoichiometry of the underlying metabolic pathways is independent of the species, the common basis and the generic approach seems to be feasible. Thus, the InraPorc pig model (van Milgen *et al.*, 2008) core was used in the course of the development of the growth model for poultry (MsChick model) maintaining the same general principle but with some specific adaptations for broilers. Those adaptations needed in the broiler model are related to 1) chemical *vs.* anatomical body composition, 2) the protein partitioning in a view that feather is a significant contribution to total protein, and 3) to some extent, representation of energy metabolism. The anatomical body composition is less important for pig producers, therefore most pig models, including InraPorc, estimate the BW and the chemical composition of the body (and the gain) rather than, for example, the yield of ham. Broiler performance studies typically report on breast yield, since this is a principal trait used by the sector. Therefore, broiler model was developed to be able to estimate not only the body chemical composition but the valuable carcass parts as well.

In a generic approach and based on concepts of energy and protein flows, the MsChick model simulates the utilization and partitioning of digestible nutrients (*i.e.*, EAAs, fat, starch and sugars, Figure 1) according to the phenotypic potential of the bird fed *ad libitum*. The actual protein deposition will not surpass the phenotypic potential but can be lower due to an insufficient supply of essential amino acids (EAA). The net energy intake is used for maintenance and to sustain protein deposition, and the surplus energy is used for body lipid deposition. Based on protein and lipid deposition, growth performance is predicted on a daily basis and for the average individual.

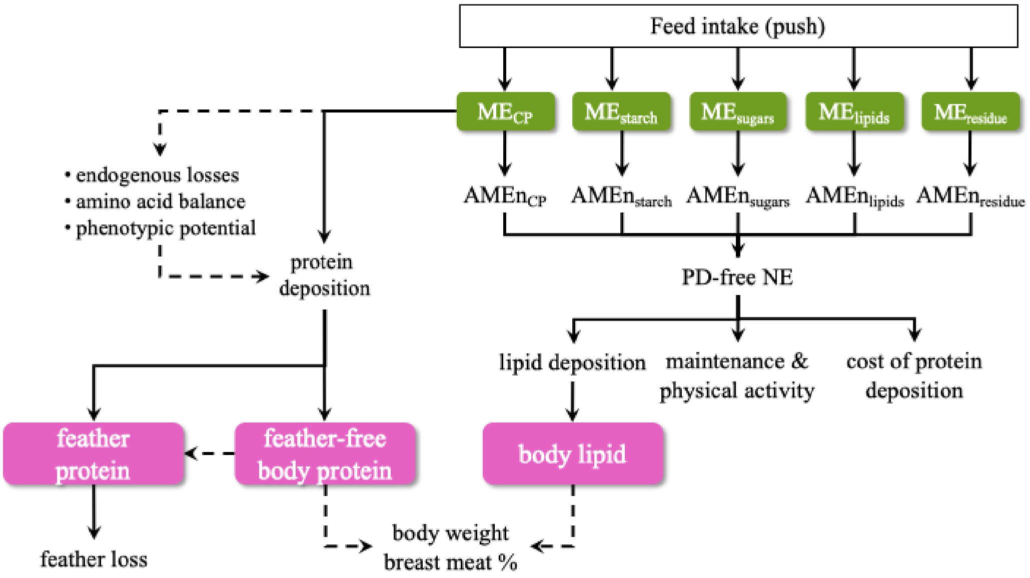

Figure 1. Flow-chart of the model concept on utilization of digestible nutrients including energy, protein / essential amino acids (ME$_{CP}$, ME$_{strach}$, ME$_{sugars}$, ME$_{lipids}$, ME$_{residue}$, AMEnCP, AMEn$_{strach}$, AMEn$_{sugars}$, AMEn$_{lipids}$, AMEn$_{residue}$ are metabolizable and apparent metabolizable N-corrected energy contents for crude protein, starch, sugars, lipids, and residue; PD-free NE – protein deposition free net energy)

The outputs of the simulation are: (1) the prediction of performance as body weight, daily gain and feed conversion ratio over time; (2) the net feather protein, empty feather-free body protein (BP) and empty feather-free body lipid gains (BL); (3) the partitioning of digestible EAAs supply in terms of requirements for maintenance, net accretion for BP as well as for feather protein (FP) for feather growth and losses, chemical body composition at any time point, dynamic EAA requirement, and N-excretion.

Model development

In the model approach it was assumes that daily feed intake (DFI) is the driving force for growth, it determines the growth but not *vice versa*, and thus the growth rate has no direct effect on DFI. The model is driven by daily digestible nutrient (crude protein, starch, sugars, lipids, and residue) supply calculated from daily feed consumption and digestible nutrient content of the feed. The voluntary DFI as a function of BW considers certain phenotypic traits and defines the energy intake quantity in multiples of energy for maintenance. The function has been shown to be able to estimate smoothly the FI pattern of an average pig (Vautier *et al.*, 2011; van Milgen *et al.*, 2015) and for an average broiler during its growth (Dukhta *et al.*, 2017).

Gompertz function, which is frequently used in growth models, describes protein gain and has been often parametrized to include the mature protein mass. The function was reparametrized and instead of using the mature protein mass, the model contains parameters that are easier to estimate or interpret for the young and growing animals. Two parameters are used in calculation of the potential protein deposition, the mean BP deposition (*meanBPD*) which is strongly related to the growth rate, and a *precocity* parameter – maturity rate – describing the concave shape of the protein deposition curve, like in InraPorc model (van Milgen *et al.*, 2008). In the model this function applied to define the phenotypic potential of the average bird for BP deposition in gram per day.

The phenotypic potential determines the maximum deposition rate, but the actual daily BPD could be limited by digestible EAA or/and energy supplies. However, in the case of modern broiler nutrition, the energy limitation is not applicable since broilers are fed *ad libitum* with a high-quality feed, and therefore the energy limitation is not implicit in the model. Supply of digestible AAs is used for maintenance needs and for protein deposition. The consumed energy, remaining above, is available for lipid deposition (BLD) in empty feather-free body (eFFB). The BL serves as an energy sink in the model. The eFFB is a sum BP, BL, eFFB ash and eFFB water. The eFFB ash was assumed to be 20% of BP and constant over time. The eFFB water calculated by allometric equations of BP using reliable experimental data (Vargas *et al.*, 2020). Empty BW in MsChick consist of eFFB and feather weights (FW).

The valuable body meat parts such as breast, thighs, drums, and wings are in allometry to the BP which is dependent on sex and independent of chicken breed by applying the equations from Danisman and Gous (2013).

General trend

The construction of MsChick had commenced with re-evaluating the model parameters, some of which relate (1) to down-scaling of a pig to a chicken (*e.g.*, DFI and potential BPD), (2) to poultry-specific aspects (*i.e.*, feathers, nutrient digestibility, dietary requirement for Arg), or (3) to interspecies differences (*e.g.*, efficiency of nutrient utilization, body composition). The model was built in Microsoft Excel software. The amount of daily NE intake (NEI, MJ/d) and DFI (kg/d) were estimated by considering the BW at the beginning of the simulated day *i*. It was assumed that BW at the end of the simulated day *i* is equal to BW at the beginning of the next day *i+1*.

Thus, there are five initial parameters for the MsChick model that can be modified or updated by the user to represent the phenotype. Three parameters of the growth equation, namely the *BW_init* (1) – initial body weight which is used to estimate the initial BP, *precocity* (2) – the shape parameter of Gompertz equation, and *meanBPD* (3) – a general parameter potential for BP deposition used to calculate final BP as well as BP at maturity (another Gompertz function parameters). The two additional parameters that can be estimated are “*FI_1*” and “*FI_2*” for the DFI equation, expressing NE intake (MJ/d) at 1 and 2 kg of BW, respectively.

Model calibration

Before running the simulation, the model was calibrated for the average broiler chicken according to the Aviagen (2017) and Cobb (2015) guidelines on nutrients requirements and performance objectives for males and females. The five initial parameters were set for each sex and genotype. The *BW_init, precocity*, and *meanBPD* based on observed (recommended in guideline) and predicted values on BW, as well as *FI_1* and *FI_2* based on recommended guideline values on FI, over 9 weeks of age. It was adjusted by Solver function in Microsoft Excel.

Sensitivity analysis

The traits such as BPD (g/d), BLD (g/d), CFI (kg), excess protein (g/d) eFFBwater (kg) and eFFBash (kg), and breast meat (% of BW) at 35 d of age were checked in sensitivity analysis in response to parameters of *meanBPD*, *precocity*, *FI_1* and *FI_2* and parameter "*c*" in DFI curve (multiples of maintenance) with deviation ± 20 %. The dietary EAAs were set to be not limited. Also, the model outputs such as BW (kg), FCR and BP and BL mass at slaughter (kg) at 42 days of age were checked in the course of changing *meanBPD* and *precocity*, *FI_1* and *FI_2*, as well as allometry coefficient of eFFBwater to BP. The values of those parameters were changed with ± 10-20 %.

Model validation

The calibrated model was validated by using dynamic data as well as literature data published during recent years. Dynamic, individual data from two trials were available: BW, DFI and chemical body composition for Ross, and BW and DFI for Cobb broilers. Both trials were carried out at INRAE PEAT experimental facility in the framework of the H2020 Feed-a-Gene project. The calibrated model was also tested with literature data published during recent years representing a total of 44 dietary treatments from 7 experiments (Table 1).

The model was challenged with diets containing graded levels of digestible lysine, methionine, or threonine. Furthermore, datasets on broilers fed with low protein diets supplemented with or without amino acids and/or dietary fat were tested.

The outputs of simulation on distinct performance data were compared to measured (*in vivo*) data available from literature, and the model was run both with simulated and measured daily FI in separate steps. To assess the quality of the model prediction, mean square prediction error (MSPE), was calculated according to Bibby and Toutenburg (1977).

$$MSPE = \frac{\Sigma\ (O_i - P_i)^2}{n}$$

where O_i and P_i are observed and predicted values; $_i$ = 1, …, n, and n is the number of experimental observations.

The root MSPE is a measure in the same units as the output and is also expressed as a percentage of the observed mean (relative MPSE, relMPSE). The MPSE partitioning between errors attributing to the overall bias (B%); deviation of regression slope from one (R%); and disturbance proportion (E%) was determined too.

Table 1. Collection of the broiler trials used for the model testing

Author	Year	Number of birds	Number of treatments	Measured parameters	Periods
Zhai *et al.*	2016	960	**4** *dig Met 3.04-5.32 g/kg*	FI, kg BW, kg	21-42 d
Li	2017	450	**3** *CP control 25.19 –20.1 g/kg* *CP low 19.19 – 14.1 g/kg* *CP +CAA 20.36 – 14.8 g/kg*	BW, kg	0-14 d 15-24 d 25-56 d
Liu *et al.*	2017a	240	**10** *5 dietary protein levels* *154 – 400 g/kg* *2 dietary ether extract levels* *46 vs. 85 g/kg*	FI, g BW, g	7-28 d
Liu *et al.*	2017b	336	**14** *Starch 313 – 503 g /kg* *CP 159 – 357 g/kg* *lipid 20.6 – 44.3 g/kg*	FI, g/bird BWG, g/bird	10-23 d
Najafi *et al.*	2017	288	**4** *dig Thr 6.5-9.7 g/kg*	FI, g/d BWG, g	1-14 d
Lee *et al.*	2018	480	**6** *dig Lys 9.8-14.8 g/kg*	ADFI, g/d ADG, g/d	1-10 d
Sigolo *et al.*	2019	270	**3** *Lys12.7 – 15.3 g/kg*	ADFI, g ADG, g	1-14 d 15-28 d 29-42 d

where: BW – body weight; DFI – daily feed intake; BWG – body weight gain; ADG – average daily gain; ADFI – average daily feed intake.

Model extension

Further, the validated model was extended with a so-called phosphorus (P) module. The module represents Ca and P metabolism and simulates the effect of dietary digestible P supply on P retention and urinary P excretion (Figure 2). The partitioning and utilization of dietary digestible P is based on the premise that animals need Ca and P for maintenance and production.

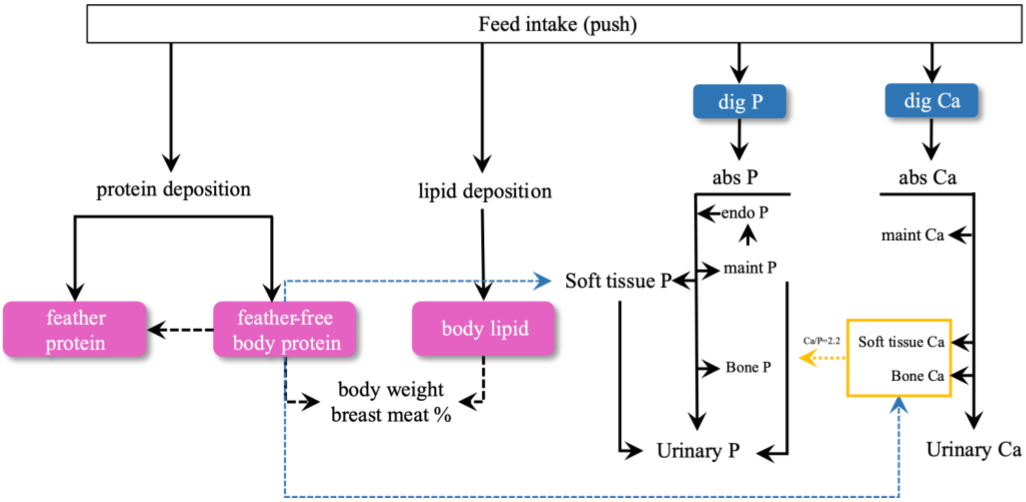

Figure 2. Flow-chart of the model concept on utilization of digestible phosphorus (P) and calcium (Ca)

The ingested digestible P is utilized for maintenance purposes, including to replenish gut and urinary endogenous losses, also used for feather growth, as well as for soft and bone tissues development. The available P (entered the metabolism) in excess over the amount that was used for maintenance and retention is excreted via urine. While integrated, P-module has feedback to the basic energy and protein metabolism model by correcting muscle growth if the P supply limits the development of the soft tissue.

Model application

The model simulates the utilization of daily digestible protein and available P intake, protein retention in the eFFB and P retention in soft body tissues and bones and feather. Due to the model structure the total N and P excretion and partitioning between faeces and urine can be determined.

The calibrated model was challenged with eight phases feeding schedule with more gradual decrease of dietary protein and available P levels during fattening (Table 2). Practically, MS Excel version was run separately with two feeding scenarios: Ross nutrition recommendation (Sc1) having 4 phases and the alternative strategy (Sc2). The ratio of EAAs to protein was set to be the same in both simulations, as well as energy content of the diets.

Table2. Nutrient composition of diets in scenario 1 (Sc1, Ross 308 recommendations) and scenario 2 (Sc2, multiple phases feeding)

	Ross recommendation (Sc1)				Multiphase feeding (Sc2)							
	0-10	*11-24*	*25-39*	*40+*	*0-10*	*11-14*	*15-19*	*20-23*	*24-27*	*28-32*	*33-39*	*40-42*
AMEn	12.55	12.97	13.39	13.39	12.55	12.92	12.95	12.98	13.37	13.39	13.39	13.39
CP	23.0	21.5	19.5	18.3	23.0	21.5	20.0	18.0	17.0	16.0	14.0	13.0
digP	4.8	4.35	3.9	3.75	4.6	4.5	4.3	3.9	3.7	3.4	3.1	2.8
digCa	9.6	8.7	7.8	7.5	9.2	9	8.6	7.8	7.4	6.8	6.2	5.6

Where, AMEn – apparent metabolizable energy corrected for zero nitrogen balance; CP – crude protein; digP – digestible phosphorus (the amount of dietary P that is absorbed by the gut until the end of the ileum; requirement for digestible P for growing poultry can be calculated by use of the equation: digP = (Pmaintenance + Pgrowth) / feed intake); digCa – dietary digestible calcium.

The actual levels of dietary protein and digestible P were defined based on Sc1 and were kept on the same level when calculating the dietary composition for Sc2. Two scenarios were compared on N and P excretion as well as partitioning of excreted N and P, while keeping the desired level of birds' performance in both cases. Furthermore, scenario to check the model response to shifts in protein digestibility ± 5%, was also applied in a separate simulation. The outputs were checked for N retention and partitioning of excreted N in terms of g/d in each day as well as cumulative total, fecal and urinary N excretion.

3. RESULTS AND DISCUSSION

Model calibration, output, and sensitivity analysis

The model was calibrated based on datasets from nutrition specifications and performance objectives of Aviagen (2017) and Cobb (2015) broiler breeders' guidelines. Thus, the input parameters for calibration – BW and DFI over 9 weeks (63 days) of age – were differentiated by considering different sexes (male and female) and genotypes (Ross 308AP and Cobb 500). The simulation of performance outputs fitted well to the performance data from the guidelines (Figure 3) with low relative mean square predicted error (relMSPE) being 0.006%, 0.005%, 0.139%, and 0.048% for Ross males and females, and Cobb males and females. Most of MSPE is explained by the disturbance proportion (E%) representing the proportion of MSPE unrelated to the errors of model prediction and less by the overall bias (B%) or the deviation from regression (R%).

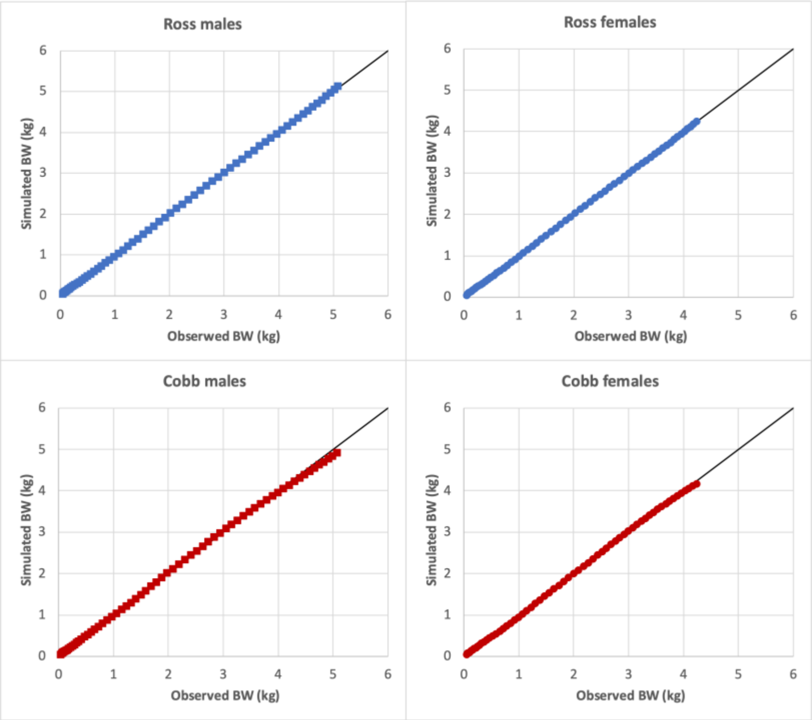

Figure 3. Simulated versus observed data (taken from management guidelines) for Ross and Cobb males and females

The simulation calibrated for Ross males was used to demonstrate the model outputs and sensitivity analysis further. Figure 4 demonstrates the body weight (BW, kg), cumulative feed intake (CFI, kg), feed conversion ratio (FCR, kg/kg), actual and potential empty feather-free body protein depositions (BPD actual, BPD potential, g/d) and empty feather-free body lipid deposition (BLD, g/d) over 9 weeks of age. The yellow curve presents the BPD (g/d), showing the highest rate at the end of 5th week, and descending further. As concerns the BLD graph, it is increasing until 9th week of age and probably reaching its maximum rate further in time. Lipid deposition is undertaking the function of an energy sink and is depending on energy intake from the diet.

According to the model simulation on day 35 there are 13.6 g/d of BPD and 21.5 g/d of BLD into the empty feather-free body for males, whereas 11.7 and 16.9 g/d, respectively, for females. Those depositions correspond to 141.8 g/kg feather-free body protein and 137.8 g/kg body fat content for males, or 144.4 and 138.9 g/kg protein and fat content of feather-free body, for females, respectively. The model output for the 35 day of age is shown in the Table 3.

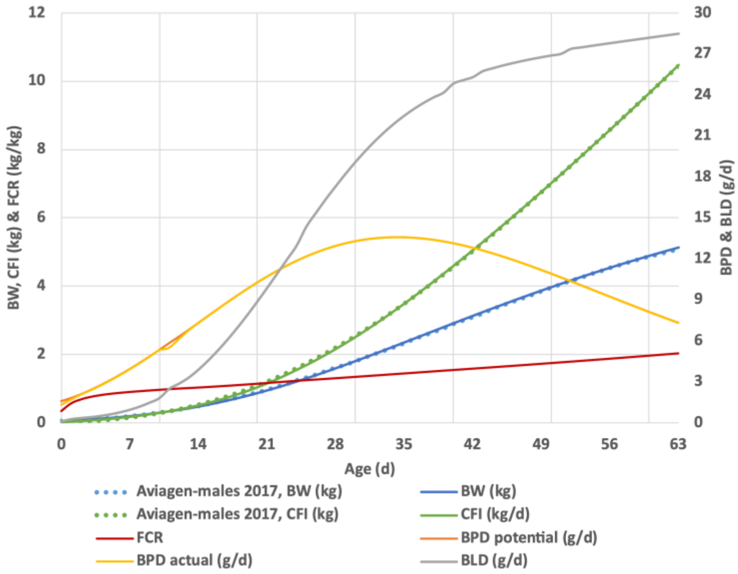

Figure 4. Simulated and observed BW (kg, left axis), CFI (kg, left axis). FCR (kg/kg, left axis) and simulated daily depositions (right axis) for potBPD (g/d), BPD actual (g/d) and BLD (g/d) over 9 weeks of age for an average broiler

Table 3. Model output for the day 35 on empty feather-free body and feather weights, its chemical and physical compartments

Age – 35 days	Ross 308		Cobb 500	
	males	females	males	females
BW (kg)	2.35	2.12	2.33	2.09
eFFBW (kg)	2.11	1.90	2.10	1.87
CFI (kg)	3.27	3.08	3.43	3.09
FCR	1.42	1.49	1.50	1.52
BWG (g/d)	110.21	91.18	108.95	91.02
FP (g/d)	3.02	2.79	2.85	2.69
BP (g/kg eFFBW)	141.83	144.37	138.72	143.84
BL (g/kg eFFBW)	137.79	138.93	160.24	150.58
Breast meat (% eBW)	21.58	21.12	20.90	20.88
Thighs (% eBW)	8.46	8.53	8.27	8.50
Drums (% eBW)	7.30	7.37	7.14	7.34
Wings (% eBW)	5.73	5.82	5.61	5.80

where: BW – body weight, eFFBW – empty feather-free body weight, CFI – cumulative feed intake, FCR – feed conversion ratio, BWG – body weight gain, FP – feather protein, BPD – empty feather-free body protein deposition, LD – empty feather-free body lipid deposition, eBW – empty body weight

The driving force of the model is DFI, and the model's core is the BP. The results of the sensitivity analysis as regards the BW, feed efficiency, protein and lipid mass are most affected by the initial model parameters and thus determine the phenotypic potential of the bird. Basically, by the model's logic, if the intake of AAs is adequate to fulfil the requirements determined by the phenotypic potential (Gompertz function parameters *meanBPD* and *precocity*), the growth trajectory will not be disturbed. These changes in the above-mentioned parameters will influence the simulation in a direct way, with increase of the parameters, the treats output values will increase as well. If BP value has grew, all the treats in linear or allometric relation to BP – eFFBwater, eFFBash, BW, FW, breast meat – will grow too. Gradual change in coefficients of the efficiency of AA utilization for protein deposition affects the actual BPD (g/d).

The lipid deposition is dependent on energy intake, which is at the "beginning of the day", and is regulated by parameters *FI_1* and *FI_2* which are fixing the amount of energy to be consumed at certain metabolic BW per day.

Since, the DFI is depending on energy intake, if to decrease both *FI_1* and *FI_2* the BL and BLD values will decrease.

From another side, if to decrease the energy content of the diet, thanks to the established energy intake level by *FI_1* and *FI_2*, in simulation the animal will increase the quantity of the diet intake, keeping the BLD (g/d), and thus, BL (kg) almost at the same level. Nevertheless, the manipulations with maintenance parameters – FHP, activity level, kBR – acting in inverse way regarding the BL (kg) and BLD (g/d), with decrease in maintenance energy needs, the amount of fat deposition will increase.

Model validation with dynamic datasets

The advantage of the dynamic datasets is that both feed intake and the body weight were continuously measured during the trial, therefore the reliability of the model in time could be tested. Results show that simulations fit well the observed broilers' performance for each experimental group (Figure 5), however, with underprediction for males with maximum relMSPE 1.28 and 1.06 % in control and precision dietary treatments. Also, chemical body analysis was done in 5 time points during the 33 days long study. The simulation output for the comparison of measured values (5th, 11th, 16th, 23rd and 33rd days of age) versus simulated performance (over 30 days of age). An example for Ross 308 females fed control diet is shown in Figure 6.

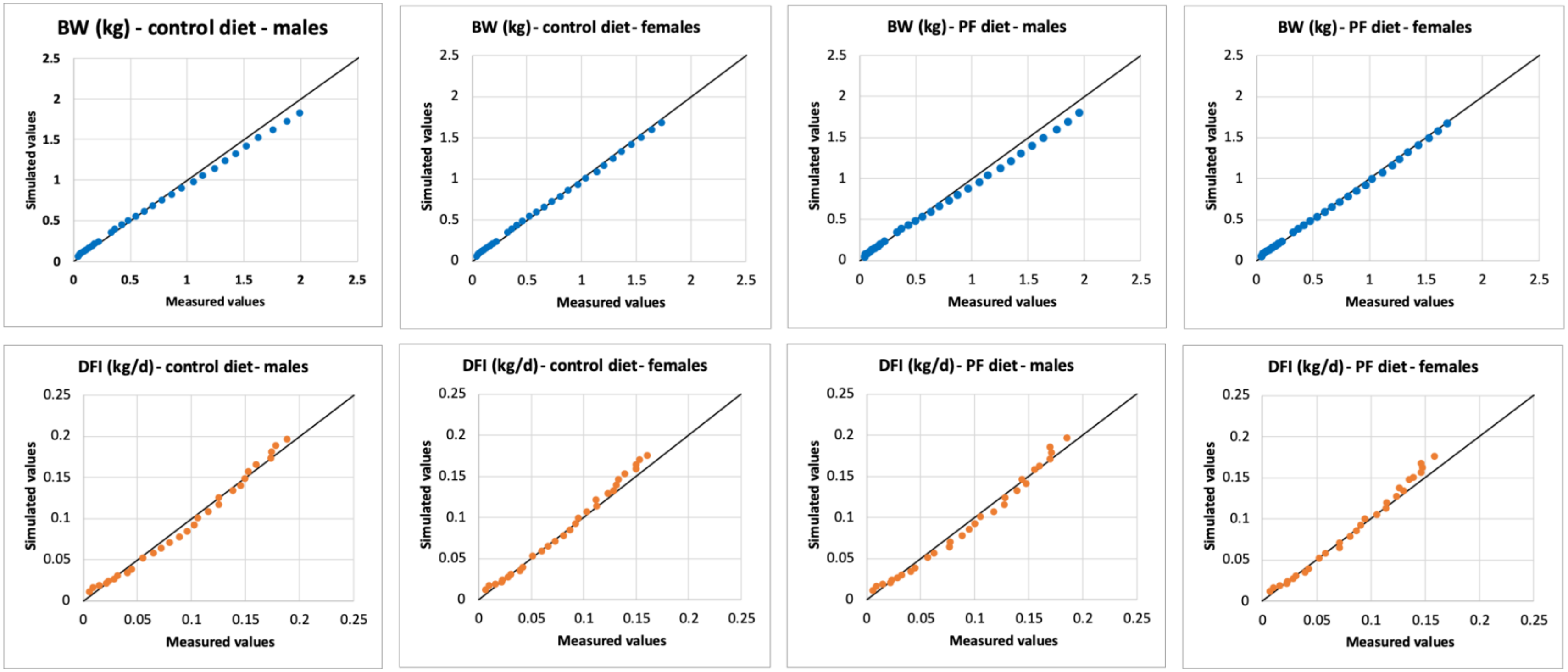

Figure 5. Comparison of simulated performance versus observed: body weight (upper graphs in blue, BW, kg) and daily feed intake (in orange, DFI, kg/d) for Ross 308 males and females fed control (C) and precision feeding (PF) diets over 30 days of age

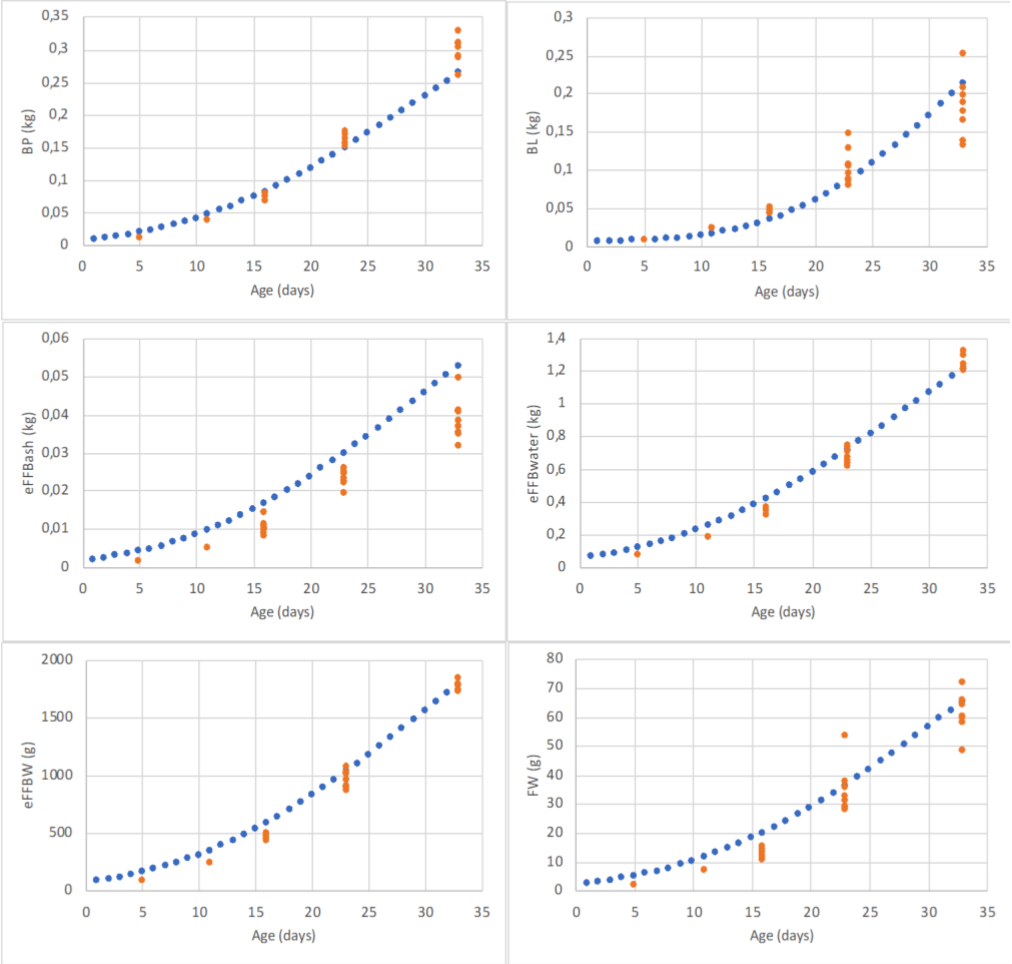

Figure 6. Comparison of measured values (5th, 11th, 16th, 23rd and 33rd days of age) versus simulated performance (over 30 days of age) for Ross 308 females fed control diet: empty feather-free body protein (eBP, kg), empty feather-free body lipid (eBL, kg), empty feather-free body ash (eFFBash, kg), empty feather-free body water (eFFBwater, kg), empty feather-free body weight (eFFBW, g), and feather weight (g)

It can be seen from the graphs in Figure 6, that the model simulation for males fed control diet slightly overpredicts the BP during the first 3 weeks, and underpredicts it in later age. Also, the eFFBash is overpredicted for the first three time points, and it is in range within observed values for 23rd day, whereas it overpredicts the measured values for the day 33. The eFFBwater, eFFBW and FW are following a similar tendency with overprediction the first three points of time, while for the days 23 and 33 it is in range for the estimated values. BL, however, seems to be in range within observed values, with a little overprediction over the 33rd day.

Validation with independent datasets from the literature

In this section evaluation of the broiler model in terms of body weight or average body weight gain response to different energy and protein levels as well as dietary AAs is presented. The model was challenged by comparing the animal *vs*. the model responses to different dietary treatments in specific time intervals as reported in the relevant studies. The root mean square prediction error (root MSPE) and relative MSPE (relMSPE, %) for the simulations run with experimental diets from the literature data are presented *in* the Table 7.

Table 7. Root mean square prediction error (root MSPE) and relative MSPE (relMSPE, %) for the simulations run with experimental diets from the literature data

Article	Diagnostic trait	Root MSPE	relMSPE (%)	B (%)	R (%)	E (%)
Li, 2017	BW	0.243	16.46	0.17	38.98	60.85
Lee *et al.*, 2018	BW	0.003	20.472	0.000	74.017	25.983
Sigolo *et al.*, 2019	BWG	0.017	33.208	89.909	1.903	8.188
Zhai *et al.*, 2016	BWG	0.037	1.288	95.238	4.656	0.107
Najafi *et al.*, 2017	ADG	0.106	59.352	59.533	28.568	11.899
Liu *et al.*, 2017a	ADG	0.047	3.310	22.719	2.493	74.788
Liu *et al.*, 2017b	ADG	0.215	47.913	25.723	71.389	2.887

where: BW – body weight, BWG – body weight gain, ADG – average daily gain; rootMSPE – root mean square prediction error, measure in the same units as the output and is also expressed as a percentage of the observed mean as a relative MSPE – relMSPE, B% – represent the proportion of MSPE due to a consistent over- or underestimation of the experimental observations by the model predictions, R% – represents the proportion of MSPE due to inadequate simulation of differences among experimental observations, E% – represents the proportion of MSPE related to the undefined errors of model prediction.

It has been realized in the model testing that the reliability of the prediction of DFI determines the accuracy of the simulation in terms of estimated BW or average daily gain. Thus, it can be stated that the main variation factor in the model is DFI, and the model output is becoming closer to the observed values if the adjustment is applied. It has been repeatedly shown that the FI is a multivariate trait depending not only on the genetic potential of the animal, but vary importantly by environmental factors such as dietary composition, ambient temperature, and number of stress factors. In the present model, the DFI is a phenotypic trait represented by two values (*FI_1* and *FI_2*) and it is based on the premise that birds eat according to consume desired amount of energy described by multiples of maintenance. Thus, in the model nothing else but dietary energy content and the BW determine the DFI which is likely an oversimplification of the phenomena. However, the more precise model outputs in case of adjusted DFI in most tests confirm the reliability of the nutrient partitioning model. The inaccuracy of DFI prediction is likely not critical, since real-time on-farm systems are being developed to measure actual DFI, thus those data might be used as inputs in a nutrient partitioning model when adopted to farm situation (Guettier *et al., 2022*).

Phosphorus module extension

The phosphorus (P) module is a useful tool to estimate the P requirement of the animals, and to predict the optimal level of the digestible P in the feed for different sexes or strains. An example of a model simulation for Ross male and female broilers is shown in Figure 7. Females, due to their lower potential to deposit protein from approximately 15 days of age, need less digestible P compared to males.

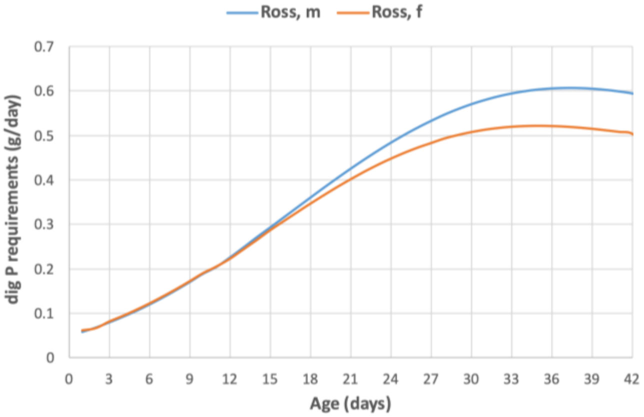

Figure 7. Simulation of the digestible phosphorus (P) requirement of Ross broilers for males (blue line) and females (orange line) in grams per day

The digestible P requirement is derived from the P that can be utilized by the chicken. The model is able to show the partitioning of P in terms of retention into soft and bone tissue, feather as well as the maintenance P needs. Also, P partitioning of surplus and obligatory losses for maintenance needs is estimated by the model, thus it is a useful tool to evaluate feeding strategies to mitigate P footprint of the poultry sector. The comparison of results shows that model is following the tendency for decreasing N and P retention when feed is low in crude protein, total P, and Ca. The model displays similar tendency with the data from study of Imari *et al.* (2020), demonstrating the reduction in FI and BW, when dietary available P reduced by 30% commencing from early age in starter period. In comparison of the simulation with the data of Konieczka *et al.* (2020), the rate of P and the N retention is reliably estimated.

To conclude, the model gives a reliable simulation and follows the main trends about P retention reported in the literature. However, further improvements may be needed, in particular, more detailed datasets would be useful to evaluate the P retention and P partitioning in dynamic datasets in order for the prediction to be in accordance with the metabolic model part.

Model application

A case study is shown in the dissertation. Two scenarios are presented, Sc1 is the 4 phases feeding strategy as recommended by the breeder (Aviagen, 2017) and Sc2 is 8 phases feeding program adjusted according to the breeders' guideline based calibrated model output. The dietary digestible crude protein (CP) and P contents fed in the feeding programs Sc1 and Sc2 and the simulated "actually" required levels of digestible CP and digestible P are graphically represented on Figures 8. It is shown that Sc2 feeding strategy with multiple phases leaves smaller differences between dietary and required levels of N and P comparing to recommended Sc1. Dietary protein and P above the digestible protein and P requirement will be excreted via urine that can be quantified by the model. Since CP is one of the most, or probably the most expensive nutrient in compound feeds, overfeeding of dietary protein increases the feeding cost with extra load on ammonia emission.

The Sc2 values are very closely approach the model estimated requirements. This is reasonable, because the most accurate way to cover an area under the curve (in

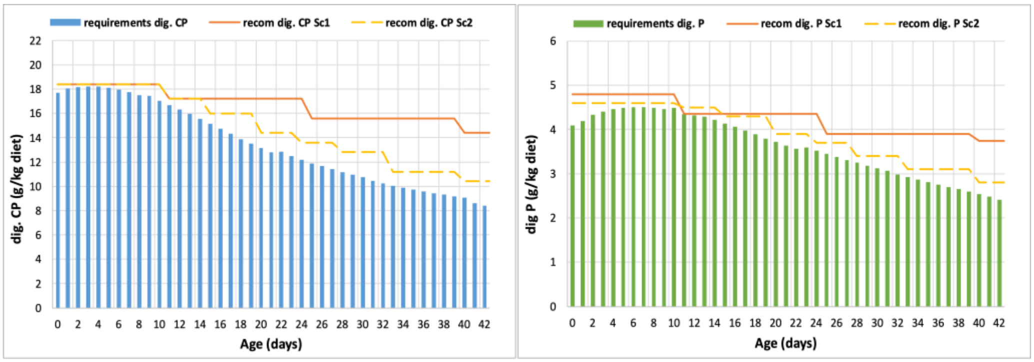

Figure 8. Estimation of actual digestible crude protein (CP, left figure) and phosphorus (P, right figure) requirements for Ross 308 hybrid (requirement dig CP / dig P), and digestible CP / P content recommended by the breeder (Sc1 – Ross recommendations) and that in the feeding strategy developed based on the model (Sc2 – multiple phases feeding)

this case, the nutrient requirements) is to use multi-phase feeding. Considering that N excretion is an energy demanding process, in case of more phases the dietary energy level ought to be changed with more cautious. In the simulation, diets used for both strategies were isoenergetic. Thus, the protein-to-energy ratio changed in Sc2, which promoted more energy retention as fat, since the protein content of the diet in relation to the total energy is the main factor determining the amount of fat deposited in the body. The lower the protein-to-energy ratio, the greater the fat content of the bird. Lower CP level in the Sc2 diet resulted in 3.4% more body fat of simulated performance, compared to one in Sc1. This agrees with literature data when an excess dietary CP results in a leaner bird but reduces feed efficiency, whereas a less-than-optimal protein content increases feed intake but also consumed an excessive amount of energy in this process (Buyse *et al.*, 1992; Buyse and Decuypere, 2015).

Figure 9 represents the comparison of the model simulations for the reference *vs*. higher digestibility protein feeds. The N retention is quite the same in the simulations (blue curves). Comparison of simulation outputs shows that the improvement in protein digestibility did not change the total N excretion (78 g over the 42 days). Since the AA requirement of the genetic potential was fulfilled in the default simulation, there was no extra N retention even if more AAs entered the

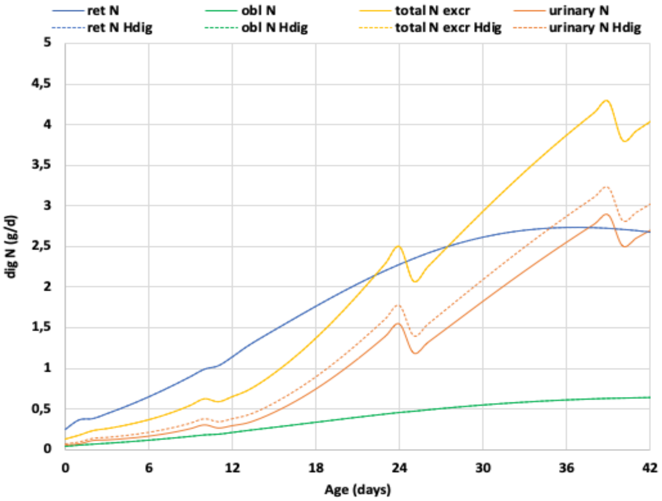

Figure 9. Effect of higher (85% *vs.* 80%) dietary crude protein digestibility (Hdig) on N-excretion and its partitioning: ret N – retained nitrogen (g/d); obl N – obligatory urinary nitrogen loss (g/d); total N excr– sum of fecal and urinary N excretions (g/d); urinary N – urinary nitrogen excretion, (g/d)

metabolism. By improving protein digestibility the form of excreted N was shifted, and resulted in reduced faecal to urinary N ratio from 0.63 to 0.41. It has been confirmed that an increase in protein digestibility without adjusting the feed CP to the digestible AA requirements increased the N excess, the surplus was actually increased by more than 18% from default 35.08 to 43.07 g. The lower faecal N to urinary N ratio results in higher total ammonia N in both absolute and relative terms. It can be concluded that using feed supplements or specific feed processing technology to improve protein digestibility is beneficial only if the diet is formulated on digestible protein and AA basis (Dukhta and Halas, 2023).

In conclusion, the baseline emission of N or P is vary depending on lots of factors such as the concentration of other nutrients in the diet and its digestibility as well as physiological, health and management factors. The current approach allows a better understanding of the concept of feed use mechanism for the decision to be taken. The model is an excellent tool to design alternative feeding strategies for animal production with a low environmental footprint. A systematic approach enables to reconsider the insights of N and P utilization, and therefore it gives a tool to reduce environmental pollution of broiler production.

4. CONCLUSIONS AND RECOMMENDATIONS

From the present dissertation, the following main conclusions are be drawn:

1. Although pigs and poultry (broilers) are different species, this work has confirmed that it is possible to develop a model to predict broiler production which is based on a well-elaborated pig growth model.
2. In order to develop this broiler model, new species-specific parameters and equations have been appointed, and dynamic mechanistic and deterministic model simulation has been built for chicken (*Gallus gallus domesticus*). This developed model is called: “Model Simulation for Chicken” (MsChick).
3. The MsChick model, based on the feed (Net energy) intake, simulates the post-digestive utilization of energy and amino acids, and predicts the growth performance, as well as changes in chemical body composition of the individual birds over time. The model was extended for simulation of calcium (Ca) and phosphorus (P) metabolism too.
4. The growth model can be used for estimation of the protein, fat, and water deposition (g/d) in the body, as well as for determination the amount of valuable meat parts, but the fat to protein ratio as a trait of meat quality has not been evaluated.
5. Based on testing with independent data, the model simulation is reliable when different feeding schedules and nutrient supplies are estimated. The body weight and the average daily gain are well predicted in general, as well as the chemical body composition in time. The accuracy of the model is highly determined by the accuracy of feed intake estimation.
6. The model is sensitive to the parameters related to the model core – empty feather-free body protein: *meanBPD* and *precocity*, as well as to parameters related to daily feed intake: *FI_1* and *FI_2*. Besides initial parameters, it is

also sensitive to *empty-feather-free body water allometry* and *c* parameters of the feed intake's representation as multiples of energy.

7. In addition to the chemical body composition and performance of the broiler, the model is able to simulate N- and P-retention, urinary N- and P-excretion upon different dietary supply and digestible protein and P-requirement of *Gallus gallus domesticus* at different body weights.
8. The model allows testing different feeding schedules, as well as might serve as a great educational and/or decision support tool. Therefore, it is useful in education for demonstrating certain problems and finding solutions, and probably could help to formulate *in vivo* experiments to confirm or reject certain theories.
9. The model is able to determine quantitatively the environmental load of a feeding strategy. It has been shown that using multiple phases defined through the model, the N and P excretion can be significantly reduced without compromising the growth performance. The broiler growth model in the present state is a useful tool to determine the amount and partitioning of N and P excretion, and thus can support the development of feeding strategies to mitigate the environmental footprint of poultry sector.
10. It has been confirmed that an oversupply of dietary protein – either due to the use of safety margin or the underestimation of protein digestibility – will increase the total ammonia N in the manure and thus the N emission potential of poultry meat production.
11. It is necessary to continue to challenge the model with real-time dynamic datasets to improve its mechanistic approach and thus the accuracy of prediction.

5. THE NEW SCIENTIFIC RESULTS

1. A mechanistic-dynamic model for broilers has been successfully developed. It simulates the body chemical composition and production parameters of the bird with high accuracy. Therefore, it can be used for estimation of the protein, fat, and water deposition (g/d) in the body, as well as for the determination of the amount of valuable meat parts.

2. In general, the reliability of the model is sufficient, in terms of animal response in time to different feeding strategies. The model has a goodness of fit to observed data, however, its predictive power can be improved if feed intake curve is adjusted to and/or replaced by real-time on-farm data.

3. The developed dynamic mechanistic model can estimate the standardized ileal digestible amino acid requirement, and particularly the amino acid pattern of ideal protein of different strains at different points of time.

4. The developed model is able to simulate the tendency of P-retention, urinary P-excretion at different body weights upon different P supply, as well as digestible P-requirement of *Gallus gallus domesticus*.

5. Compared to the use of static table values of breeder recommendation, the application of a dynamic model to define optimal levels of dietary nutrients is worthwhile. The broiler growth model in its present state is a useful tool to determine the amount and partitioning of N and P excretion and thus can support the development of feeding strategies to mitigate the environmental footprint of poultry sector.

6. The model has confirmed that an oversupply of dietary protein – either due to the use of safety margin or the underestimation of protein digestibility – will increase the total ammonia N in the manure and thus the N emission potential of poultry meat production.

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