



# **FEED-A-GENE**

Adapting the feed, the animal and the feeding techniques to improve the efficiency and sustainability of monogastric livestock production systems

# **Deliverable D3.2**

# A simulation model to evaluate the digestive use of compound feeds and nutrients in monogastric animals

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# 1. Summary

Regarding the context of animal production, monogastric livestock systems have to be more sustainable. For this, an increase in the efficiency of feed utilization is necessary. This requires a better understanding and prediction of the nutritional value of the feeds. Many experimental data provide the digestibility of nutrients in various conditions. However, very few studies describe the digestive mechanisms along the digestive tract and for all the nutrients contained in the diet. However, it seems very important to be able to identify the reasons why a diet is digested more efficiently than another and what the causes of differences in digestibility are in the digestive system. Consequently, a modeling approach seems a good way to integrate information available, be able to represent the digestive processes and predict the digestibility.

The work performed aimed at developing a model representing the transit, hydrolysis, fermentation and absorption/excretion of the main nutrients along the digestive tract. A similar structure was adopted for pig and poultry and only selected model parameters were adapted for each species. Parameters for pigs come from existing models and were then modified for the broiler based on biological knowledge and literature data. The transposition of a digestive model for pigs to a broiler has been done step by step to preserve the genericity and make only those modifications that are really needed. Modifications were driven either for biological reasons or to improve the predictive capacity of the model. For now, a generic model has been developed for growing pigs and broilers.

**Objectives:** The aim of the project was to develop a generic, dynamic and mechanistic model to represent transit and digestion in pigs and poultry and to integrate factors of variation of the nutritional value of feed in complex diets fed to animals at different physiological stages.

**Rationale:** Modelling is an appropriate tool to integrate knowledge, to represent biological mechanisms and to test hypotheses. It is also a very useful approach to understand how a biological system works and to predict responses of animals in various conditions (e.g. species, physiological status, diet composition). Several models have been developed to represent the digestive process in pigs but this type of model is scarce in poultry. Considering many similarities in feeds used for both species and that the main digestive functions can be represented in a same way, it seemed logical to use the same generic model concept to be able to carry out comparative studies on the digestive use of feeds and nutrients.

#### Teams involved:

Feed-a-Gene partner involved:

- INRA, AFZ
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#### Species and production systems considered:

The conventional pig and broiler production systems were considered.





# 2. Introduction

Regarding the context of animal production (e.g., increase in meat demand, international market, climate change, rarefaction of resources, competition between food, feed and biofuel production, consumers' expectations) monogastric livestock systems have to be more sustainable while maintaining or increasing their production efficiency. For this, it is necessary to better understand and predict the digestive use of feeds and nutrients by the animals. In pig and poultry production systems, feed formulation is mainly based on models in which the nutritional values of feedstuffs are considered fixed and additives. However, interactions exist between feed components within a diet and between the feed and the animal (Bedford 1995; Jiménez-Moreno et al., 2013; Quinsac et al., 2013). Considering this interaction in the estimation of the nutritional value of the diet could be a way to better predict multiple responses of the animal to a diet (e.g., growth performance, environmental impact through nutrient excretion) and thus better adapt the diet to the productive goals.

Modelling is an appropriate tool to integrate knowledge, to represent biological mechanisms and to test hypotheses. It is also a very useful approach to understand how a biological system works and to predict responses of animals in various conditions (e.g., specie, physiological status, diet composition). Several models have been developed to represent the digestive process in pigs but this type of model is scarce in poultry. In addition, the model developed and the approach used highly depends on the objective of the work. However, no existing models have fully responded to the goals of the current project.

The aim of the project was thus to develop a generic, dynamic and mechanistic model capable to predict the digestive utilization of feeds and nutrients. To ensure the predictive potential, the model should be able to predict nutrient digestibility of feedstuffs listed in common nutritional tables (e.g., INRA, CVB, or NRC), account for differences among and within livestock species in terms of digestive capacity, and have the potential to accommodate aspects of feed technology, including the use of by-products and advances in enzymology as addressed in WP1. The approach is mechanistic, but emphasis is given to the representation of processes that can be adequately parameterized, which is a significant improvement from current empirical approaches.

# 3. Results

The digestive model described here is based on concepts used in existing models (Bastianelli et al., 1996; Strathe et al., 2008 ; Létourneau-Montminy et al., 2011). It represents the transit, hydrolysis, fermentation and absorption of the different nutrients ingested in a dynamic way. The model was developed in Matlab (MATLAB R2015b). The integration time step is one minute and parameters have been those used in existing models, representative for a pig of 40 kg.





### 3.1 Structure of the model

The model contains four compartments that represent different anatomical sections of the digestive tract:

- Stomach
- Proximal small intestine (duodenum and proximal jejunum)
- Distal small intestine (distal jejunum and ileum)
- Large intestine

The separation of the small intestine is the same as that described by Bastianelli et al. (1996); Strathe et al. (2008) and Létourneau-Montminy et al. (2011). The first part of the small intestine is supposed to account for 9% of the mean residence time of the small intestine (Bastianelli, 1996). This part was separated from the rest of the small intestine because of its particular importance in hydrolysis and absorption (Bastianelli et al., 1996). Also Strathe et al. (2008) considered the first part of the small intestine of particular importance because of endogenous secretions and the high rate of hydrolysis. The second part of the small intestine is anatomically a long tube. It was represented in the model as a single compartment but with the introduction of a delay to account for digesta flow (Bastianelli et al., 1996). It is the primary site for absorption (Strathe et al., 2008). Regarding minerals, the separation of the small intestine into two parts is also of importance. The first part of the small intestine is a section of intense Ca and P absorption, especially due to the low pH that allows minerals to be solubilized. In the distal part, non-phytic phosphorus (NPP) and Ca can also be absorbed but because of the increase in the pH in this section, NPP and Ca are not fully solubilized and therefore cannot be absorbed (Létourneau-Montminy et al., 2011). This representation is a simplification that seems the best compromise between biological complexity and model simplification. Indeed, it was important to consider the small intestine as two distinct parts to represent biological phenomena that change along the small intestine. Representing these phenomena through more compartments would result in a more complicated model requiring more parameters without the insurance to improve the predictive ability of the model.

The diagram of the model is represented in Figure 1 and is explained in following sections. The flow chart of the model shows that nutrients are hydrolyzed (or fermented) in the different compartments. The rates of hydrolysis and absorption are different, and the outflow of a compartment (of non-absorbed nutrients) is the major inflow for the following compartment.







Figure 1. Diagram of the model. Stomach (STO), Proximal small intestine (SI1), Distal small intestine (SI2), Large intestine (LIC). Proteins (PRO), Amino Acids (AA), Non-protein nitrogen (NPN), Starch (ST), Soluble sugars (SS), Potentially degradable (DF) and undegradable fibres (UF), Lipids (LIP), Fatty acids (FA), Volatile fatty acids (VFA), non-solubilized calcium of animal and mineral origins (CAamns), non-solubilized calcium of plant origin (CAvns), non-solubilized calcium of all origins (Cans), solubilized calcium (CAs), non-solubilized phytic phosphorus (PPns), solubilized phytic phosphorus (PPs), solubilized non-phytic phosphorus (NPPs), non-solubilized non-phytic phosphorus (NPPns), microorganisms (MIC) and residuals (RES). Transit flows are represented by solid arrows between compartments. Hydrolysis flows are represented by solid arrows between two different nutrients. Solubilized calcium or phosphorus. Fermentation in the large intestine is represented by solid lines with white arrows. Endogenous flows are represented by dotted lines which came from "Endo" boxes. Absorption flows are represented by dotted lines which reached "Abs" boxes.

## 3.2 Inputs of the model

The inputs of the model are the quantitative and qualitative description of nutrient feed intake, representing daily dry matter and nutrient intake.

#### Qualitative description of the feed

The dietary nutrients considered in the model are proteins, free amino acids, lipids, starch, soluble sugars, fiber, calcium and phosphorus. These come from the concepts of the three existing models on which this model is based. The model is able to simulate the effect of plant and microbial phytase.



To represent the action of phytase, the approach of Letourneau-Montminy et al. (2011) was used.

The amount of each nutrient is expressed as a percentage of the dry matter intake. In this way it was not necessary to consider the moisture content of the diet and water consumption through the day. According to Bastianelli et al. (1996), traits such as transit time are affected by the water content of the diet. However, for simplicity reasons it was assumed that the water content was constant for conventional diets, thereby having no impact on the transit time and digestibility (Bastianelli et al., 1996).

The nutrient content of the feed is taken from table values (INRA-AFZ, 2004). Once the amount of proteins, amino acids, lipids, starch, sugars, fiber, calcium and phosphorus have been calculated, some additional calculations are required to fit the inputs required by the Matlab model (Table 1).

	Abbreviation	Definition	Unit
	QPHYmFEED	Activity of microbial phytase in the feed	FTU/kg DM
	QPHYvFEED	Activity of plant phytase in the feed	FTU/kg DM
	PAAFEED	Proportion of free amino acids in the feed	%
	PPROFEED	Proportion of proteins in the feed	%
L L	PLIPFEED	Proportion of lipids in the feed	%
iti	PSTFEED	Proportion of starch in the feed	%
OSİ	PSSFEED	Proportion of soluble sugars in the feed	%
d	PUFFEED	Proportion of potentially undegradable fibers in the feed	%
E	PDFFEED	Proportion of potentially degradable fibers in the feed	%
CO	PCAamnsFEED	Proportion of non-soluble calcium in the feed of animal and mineral origin	%
e e	PCAvnsFEED	Proportion of non-soluble calcium in the feed of plant origin	%
Fe	PCAsFEED	Proportion of soluble calcium in the feed	%
	PPPnsFEED	Proportion of non-soluble phytic phosphorus in the feed	%
	PNPPnsFEED	Proportion of non-soluble non-phytic phosphorus in the feed	%
	PNPPsFEED	Proportion of soluble non-phytic phosphorus in the feed	%
	PRESFEED	Proportion of residuals (other components) in the feed	%
	N_days	Duration of the entire simulation	days
_	H_meal_morning	Within each day, time at which the morning meal is given	min
attern	H_meal_day_interval	Interval between regularly spaced meals during the day (in between the morning meal and the evening one) (when left empty [which will mean "NaN" in MATLAB] disables "during the day" meals)	min
	H_meal_evening	Within each day, time at which the evening meal is given	min
ec	Du_meal	Duration of a meal	min
Fe	DailyDMInt	Daily dry matter intake (morning meal + meals in the day + evening meal)	g
	P_meal_morning	Proportion of daily intake eaten during the morning meal	%
	P_meal_evening	Proportion of daily intake eaten during the evening meal	%
	BW	Body weight	kg

Table 1 : Inputs

Regarding the **fiber** part of the diet, chemical analysis or information available in nutritional tables usually gives NDF, ADF, ADL (lignin). However, in the model, inputs are potentially degradable and



undegradable fiber (Bastianelli et al., 1996; Strathe et al., 2008). The potentially degradable fiber represents 70% (Bastianelli et al., 1996) or 80% (Strathe et al., 2008) of the fiber fraction. The fiber fraction was assumed to be represented by the NDF content in Bastianelli et al. (1996). However, as reported in Figure 2, the NDF fraction does not represent the total fiber content of the diet.



Figure 2 : Classification of the fiber

It was assumed that the potentially degradable fiber fraction is 70% of the total dietary fiber (TDF). This is calculated by equation 1 and the potentially degradable and undegradable fiber contents are then calculated by equations 2 and 3 respectively.

TDF (%) = 1.03 \* NDF(%) + 0.05 (1) (Le Gall et al., 2011)

Degrdable fiber (PDFFEED, %) = 0.7 \* TDF (%) (2)

Undegradable fiber (PUFFEED, %) = 0.3 \* TDF (%) (3)

#### Regarding the **minerals**:

In the model, absorption of two minerals, Ca and P is simulated. In the feed, calcium can be of plant, animal or mineral origin. Plant calcium is considered to be non-soluble whereas calcium from animal and mineral origin can be found in solubilized or non-solubilized forms (Létourneau-Montminy et al., 2011). In this version of the model, it is assumed that the diet does not contain any feedstuffs of animal origin. Regarding the mineral source of calcium, a coefficient of solubilisation in the stomach of 1 was used (Létourneau-Montminy et al., 2011). Indeed, in nutritional value tables, calcium carbonate is considered as the reference and has a biological value of 100%. Due to little available information on the other sources of calcium, only one solubilisation coefficient was used. Consequently, the non-soluble part of mineral calcium is considered to be totally solubilized in the stomach (Létourneau-Montminy 2009). For the models inputs:

- PCAamnsFEED = 0
- PCAvnsFEED = calcium from plant origin
- PCAsFEED = calcium from mineral origin





Similarly, phosphorus can come from plant, animal or mineral origin and can be found as phytic or non-phytic phosphorus.

• Phytic phosphorus comes from plants only and is calculated from INRA table values by equation 4. It is non-soluble.

Phytic phosphorus (g/kg) = Total phosphorus (g/kg) \* Phytic phosphorus/Total phosphorus (%) (4)

• Non-phytic phosphorus comes from plant, mineral and animal origin. Coefficients of solubilization defined by Létourneau-Montminy et al. (2011) are used (Figure 3).



Figure 3 : Different forms of phosphorus in the diet. \* phytic phosphorus in feedstuffs is calculated by equation 4

For the model inputs:

- PPPnsFEED = phytic phosphorus calculated by equation 4 for each feedstuff
- PNPPnsFEED = non-phytic phosphorus non-solubilized from plant, animal or mineral origin
- PNPPsFEED = non-phytic phosphorus solubilized from plant, animal or mineral origin

**Residuals** represent the dry matter that is not represented explicitly by nutrients in the model. Thus, PRESFEED is calculated by equation 5.

PRESFEED (%) = 100 - (PAAFEED + PPROFEED + PLIPFEED + PSTFEED + PSSFEED + PUFFEED + PDFFEED + PCAamnsFEED + PCAvnsFEED + PCAsFEED + PPPnsFEED + PNPPnsFEED + PNPPsFEED)(5)

Once the nutrient composition and other preliminary calculations have been performed in Excel, inputs were transferred to the Matlab model.



#### Quantitative description of the feed intake

The quantitative description of feed intake is first the amount of the daily dry matter intake (g) and then how it is ingested along the day. In the model, the feed intake pattern within a day is set up as an input. For this, several criteria have to be defined:

- Hour of the morning meal (*H\_meal\_morning*)
- Hour of the evening meal (*H\_meal\_evening*)
- Meals in between are defined by a regular interval between meals (meal frequency)
   (*H\_meal\_day\_interval*)
- Duration of the meal

The model assumes that all meals have the same duration. A value of 15 min was used as done by Bastianelli et al. (1996). Meals occurring between morning and evening meals are defined by a regular interval which is not always very well represented when the time interval between morning and evening meals cannot be divided by the interval defined in input (see following examples no. 3 and 4).

In a classic pig production system as well as in digestibility studies, animals are usually fed restrictively using two meals per day. To represent this, *H\_meal\_morning* and *H\_meal\_evening* are the times (in minutes) at which the morning and evening meals occur. However, to introduce some flexibility in the feeding pattern, more than two meals can be represented. For this, *H\_meal\_day\_interval* has to be defined. It calculates the regular interval between morning and evening meals. Some examples are given below:

#### Example no. 1: Two meals per day at 08:00 am and 04:00 pm

- H\_meal\_morning = 480 (08\*60 to represent 08:00 am in minutes)
- H\_meal\_evening = 960 (16\*60 to represent 04:00 pm in minutes)
- H\_meal\_day\_interval = 0

#### Example no. 2: One meal per hour between 08:00 am and 04:00 pm

- H\_meal\_morning = 480
- H\_meal\_evening = 960
- H\_meal\_day\_interval = 60

This works well when the interval defined fits with the difference between evening and morning meals. However, in cases where the interval between evening and morning meals cannot be divided by the interval given in input, meals are not evenly spaced (Examples no.3 and 4).

#### Example no. 3: Two meals at 08:00 am and 04:00 pm and meals every 6h in between

- H\_meal\_morning = 480
- H\_meal\_evening = 960
- H\_meal\_day\_interval = 360 (6\*60)

The interval between 08:00 am and 04:00 pm (8 hours cannot be divided by 6). In this way, the model defines the meals at 08:00, 02:00 pm (6 hours after the morning meal) and 04:00 pm (defined





in input). In this case meals are not evenly spaced.

Example no. 4: Two meals at 08:00 am and 04:00 pm and meals every 3h in between

- H\_meal\_morning = 480
- H\_meal\_evening = 960
- H\_meal\_day\_interval = 180

The model defines meals at 08:00 am, 11:00 am, 02:00 pm and 04:00 pm. As in the previous example, the 8 hours between morning and evening meals cannot be divided by 3 (interval defined in input). In this way, the model applies the request whenever this is possible (until 02:00 pm) but meals are not evenly spaced.

This approach might be further improved, however, the representation of the feed intake pattern as it is now in the model can be sufficient for the digestive model.

Regarding the amount of feed intake, three inputs have to be defined:

- DailyDMInt
- P\_meal\_morning
- P\_meal\_evening

**DailyDMInt** corresponds to the amount of dry matter intake during the day. Then **P\_meal\_morning** and **P\_meal\_evening** are the proportions of the DailyDMInt that are ingested during the morning and evening meals respectively.

Once these inputs are defined, the model calculates the DM intake that is not ingested during morning and evening meals and share it equally between the other meals performed during the day.

Example with feeding pattern no. 4 (meals occurring at 08:00 am, 11:00 am, 02:00 pm and 04:00 pm).

- DailyDMInt = 1600 g
- P\_meal\_morning = 30%
- P\_meal\_evening = 20%

50% of the DailyDMInt are not ingested in morning and evening meals and will be shared: 25% at 11:00 am and 25% at 02:00 pm.

Finally the animal eats:

- 08:00 30% DailyDMInt = 480 g (32 g / min as the meal duration is 15 min)
- 11:00 25% DailyDMInt = 400 g (26.7 g/min)
- 02:00 25% DailyDMInt = 400 g (26.7 g /min)
- 04:00 20% DailyDMInt = 320 g (21.3 g /min)

This gives the amount of dry matter intake at each time step of the simulation.



## 3.3 Model: representations and calculations

#### Feed intake calculations

At each time step, the model calculates the amount of nutrients ingested (Equation 6).

Nutrient intake (g)

= proportion of the nutrient in the diet on dry matter basis (%)
\* dry matter intake (g) (6)

#### Representation of the digestive phenomena

For growing pigs, all equations and parameters come from Bastianelli (1996), Bastianelli et al. (1996), Létourneau-Montminy (2009) and Létourneau-Montminy et al. (2011).

Digestion is represented by four main functions that are transit of the digesta, hydrolysis, fermentation and the absorption of nutrients. All nutrients that are not absorbed are excreted in the feces. To represent the main biological phenomena and have a global overview of the process of digestion from ingestion to excretion it was necessary to keep a simple representation and not to represent the mechanisms in too much detail. The objective was to be able to:

- represent the amount of each nutrient in each compartment and at each time step

- predict the ileal and fecal digestibilities for each nutrient

- predict the amount of each nutrient absorbed at each time step (inputs for the metabolic model, WP3, task 3.2)

#### Representation of the transit

The transit or the flow of nutrient from one compartment to another is represented by a mass action law considering that the transit at time t depends on the amount of the nutrient in the compartment at time t-1 (Equation 7). For simplification, it was assumed that all nutrients follow the same transit as dry matter (Bastianelli et al., 1996).

Output flow from compartment A to B(t)

- = proportion of the nutrient in the dry matter (t 1) in A \* flow of dry matter from A to B (t)
- = (quantity of nutrient (t 1)/quantity of dry matter (t 1)) in A \* constant \* quantity of dry matter (t 1) in A
- = constant \* quantity of nutrient (t-1) in A(7)

The constant value represents the fractional rate of dry matter flow and equals:

- 0.0058%/min from stomach to small intestine 1
- 0.05%/min from small intestine 1 to small intestine 2
- 0.005%/min from small intestine 2 to large intestine
- 0.0005%/min from large intestine to feces

These coefficients are the inverse of the mean retention time (MRT) of dry matter in the compartment (Fractional rate = 1/MRT).

In the distal small intestine, a delay of 30% of the retention time in that compartment (60 min for growing pigs, Bastianelli et al., 1996; Létourneau-Montminy et al., 2011) was added to smooth the passage of nutrients. It is represented by a flow through three virtual compartments in the distal





small intestine.

In the large intestine, the output flow of nutrient (transit from large intestine to feces) is represented by equation 8 because a higher ileal dry matter flow decreases the residence time in the large intestine. The fractional rate of the large intestine emptying is an exponential function rather than a linear function of the dry matter content in the large intestine.

Output flow from Large intestine to Feces (t) = constant \* quantity of dry matter in the large intestine (t - 1) $* \exp((quantity of dry matter in the large intestine <math>(t - 1) - a)/b)$  (8)

With a = 450 and b = 250 (Bastianelli, 1996)

#### Representation of the hydrolysis

The hydrolysis of a nutrient by endogenous enzymes at each time t is considered to be related to the nutrient quantity considered at the time t-1 and this holds for all the digestive compartments. It is defined by Equation 9.

*Hydrolysis of nutrient* (t) = constant \* amount of nutrient <math>(t - 1) (9)

One constant value is defined for each nutrient and for each digestive compartment (Bastianelli et al., 1996).

Equation 9 represents the hydrolysis by endogenous digestive enzymes. For the minerals, the hydrolysis results from endogenous enzymes but also from plant and microbial phytase. Hydrolysis due to plant and microbial phytase is represented by a Michaelis-Menten law (Létourneau-Montminy et al., 2011, equation 10).

Hydrolysis of minerals by plant/microbial phytase (t)  

$$= \frac{(quantity of nutrient (t - 1) * Vmax)}{(quantity of nutrient (t - 1) + Km)} \quad (10)$$

With Vmax and Km parameters (Létourneau-Montminy et al., 2011).

#### Solubilization and insolubilization of minerals

In the stomach and in the distal part of the small intestine, solubilization and insolubilization of minerals occur (see Figure 1). This is represented by considering the effect of the pH on the solubility of minerals. The equations and parameters used come from Létourneau-Montminy et al. (2011).

#### Endogenous secretions

Endogenous secretions are represented (see Figure 1) and are assumed to be a function of the dry matter. It is calculated by multiplying the flow of dry matter entering the compartment by a constant (Equations 11 and 12). In this way, any increase in the dry matter (either by an increase in feed intake or by a decrease in digestibility) induces an increase in the endogenous secretion (Bastianelli et al., 1996).



For the endogenous secretions in the stomach:

Endogenous secretions (t) = constant \* dry matter intake (t - 1) (11)

For the other compartments:

Endogenous secretions in B (t) = constant \* dry matter flow from compartment A to B (t) = constant \* (constant \* amount of dry matter in compartment A (t - 1))(12)

With constant values from Bastianelli et al. (1996) and Létourneau-Montminy et al. (2011).

#### Representation of fermentation

The fermentation process is represented in a very simple way with a microbial sub-compartment in the large intestine. The composition of the microflora is one defined as given by Bastianelli et al. (1996). The growth and maintenance of the microbes requires uptake of soluble sugars, fatty acids, amino acids and non-protein nitrogen. The uptake of each one of these four nutrients is represented by equation 13.

Uptake of nutrient for microbial compartment (t) = constant \* quantity of soluble sugars in the large intestine (t - 1)(13)

The microbial compartment produces volatile fatty acids (equation 14).

*VFA* production 
$$(t) = constant * quantity of soluble sugars in the large intestine  $(t - 1)$  (14)$$

#### Representation of the absorption

The absorption process is supposed to be saturable and for this a Michaelis-Menten representation is used. Absorption in the stomach is considered to be negligible and was not represented except for phosphorus. In the other compartments, it is represented by equation 15 for amino acids, soluble sugars, fatty acids.

Absorption (t) = 
$$\frac{(quantity of nutrient (t-1)*Vmax)}{(Km+quantity of nutrient (t-1))}$$
 (15)

Parameters Vmax and Km are those proposed by Bastianelli et al. (1996) for each nutrient and each compartment. For minerals, active and passive absorption are represented by equations and parameters defined by Létourneau-Montminy et al. (2011).

## 3.4 Outputs of the model

#### Amount of nutrients in the compartment at each time step

The amount of nutrient in each digestive compartment and at each time step is the difference between the inflow (intake, transit, endogenous secretions and hydrolysis) and the outflow from the compartment (hydrolysis, transit, absorption, excretion). This can be generalized by equation 16.



Amount of nutrient in each compartment (t) = amount (t - 1) + amount in (t) - amount out (t) (16)

#### Amount of nutrients absorbed at each time step

The amount of nutrient absorbed at each time step (for the total digestive tract) is calculated by summing the amount of nutrient absorbed in each compartment. This information is useful for the metabolic model. The figure 4 illustrates the amount of nutrients absorbed in function of time.



Figure 4 : Dynamic of the quantity of nutrients absorbed along the day for a growing pig. The daily dry matter intake was 1924 g shared in two meals (start times = 1 and 721 min, duration = 15 min) represented by the red lines. Diet composition was wheat (87.25%), soybean meal (10%), dicalcium phosphate (0.7%), calcium carbonate (1.1%), salt (0.45%) and other vitamins and minerals (0.5%) as described in Cozannet et al., 2010.

#### Digestibility

For the digestibility calculations, the transit flow from large intestine to feces was calculated for different classes of nutrients:

- crude protein = protein + amino acids + protein from microbes
- total nitrogen = crude protein + non-protein nitrogen + nitrogen from microbes
- lipids = lipids + fatty acids + lipids from microbes
- sugars = starch + soluble sugars + VFA + sugars from microbes

The digestibility is calculated only for the last day of simulation and the right value to consider is the one of the last minute (when steady-state is achieved). The amount of nutrient excreted is obtained by summing the flow on the 24h. It is represented by equation 17.

Apparent Digestibility =  $1 - \frac{\text{cumulated amount excreted (g)}}{\text{daily amount ingested (g)}}$  (17)

For the ileal digestibility, the amount excreted is the flow of nutrient from distal small intestine to





large intestine and for the fecal digestibility, it is the flow from large intestine to feces.



The figure 5 illustrates the apparent ileal digestibility obtained with five different diets.

Figure 5 : Apparent ileal digestibility of dry matter, crude protein, calcium and phosphorus for different diets. Simulations were performed with two meals per day occurring à 1 and 721 min (duration of the meals = 15 min) with 50% of the daily feed intake ingested at each meal. Daily dry matter intake and diet compositions are available in Annex 1.

## 3.5 Transposition from pigs to broilers

The aim of the project was to develop a generic model that could be suitable for pigs and poultry. The work described above is a model representing digestion in pigs and is largely based on existing concepts. The second step of the work was to transpose this model to broiler chickens. For this and in an objective of genericity, a step-by-step method was adopted. The general structure of the model remains the same. Despite some anatomical differences between pigs and broilers, it was assumed that digestive functions described for the pig model were suitable for the broiler. The objective was thus to quantify the digestive mechanisms represented in the model to be able to simulate digestion in growing broilers by changing as few parameters as possible (and needed).

The first step was to change the daily dry matter intake (on average 82 g/d). Results indicated an overestimation of the apparent ileal and fecal dry matter digestibility by 7 and 8 points respectively. This result suggests that parameters have to be changed to be able to represent a broiler, keeping the structure of the pig model.

Changing parameters requires the quantification of these for the broiler. For this, data from literature were used. Articles investigating ileal and fecal digestibility of dry matter, starch, crude protein, ether extract, calcium and phosphorus in broilers as a function of diet composition (amount of nutrients) from years 2000 to 2015 were selected. The database included 128 experimental treatments in 20 published articles. Chickens ranged from 18 to 29 days of age and from 445 to 1365 g of body weight. Daily dry matter intake ranged from 45 to 148 g/d. Diet composition was: starch



from 0 to 52.3% of DM, soluble sugars from 0 to 51.9% of DM, crude protein from 7.3 to 29.6% of DM, total dietary fibres from 2.8 to 17.4% of DM, lipids from 2.9 to 13.9% of DM, calcium from 0 to 6.7% of DM, and phosphorus from 0 to 3.6% of DM.

As indicated above, simulating dry matter intake of chicken with pig parameters induced an overestimation of the apparent ileal and fecal digestibility. As the digestibility depends on the ingested and excreted amount of dry matter and because dry matter intake was measured in literature articles, this overestimation was hypothesized to be due to an underestimation of output transit flows. The only parameters used to calculate the output flow is the constant (fractional rate, Equation 7). As the fractional rate is the inverse of the mean retention time (fractional rate = 1/MRT), a decrease in MRT would increase the output flow. In addition, it is known that the total tract mean retention time is about 8 times shorter in broilers compared to growing pigs (5 h vs 39 h; Ouhida et al., 2000 ; Wilfart et al., 2007). This confirms the need to change the mean retention time for broilers.

#### <u>Step 1 : Quantification of the mean retention time for broilers</u>

Keeping in mind that the objective of the model is to represent the animal along its productive life and to represent pigs and broilers in a generic way, the mean retention time was changed by making it a function of body weight (BW).

The mean retention time is the ratio of *the indigestible dry matter in transit* and *the indigestible dry matter intake* (Van Der Klis et al., 1990).

 $Mean retention time (h) = \frac{Undigestible dry matter in transit (kg/h)}{Undigestible dry matter intake (kg)} (19)$ 

*The indigestible dry matter in transit* linearly increases with gut capacity (Clauss et al., 2007; Steuer et al., 2011).

Undigestible dry matter in transit 
$$(kg) = a * gut \ capacity \ (kg) \ (20)$$

The gut capacity increases linearly with body weight (Parra et al., 1978; Demment and Van Soest, 1985).

$$Gut \ capacity \ (kg) = b * BW \ (kg) \ (\mathbf{21})$$

Consequently, the indigestible dry matter in transit can be expressed in function of the body weight.

Undigestible dry matter in transit (kg) = a \* b \* BW (kg) (22)

Feed intake is considered to be related to the energy requirement, which can be scaled to the metabolic body weight.

Feed intake 
$$(kg) = c * Metabolic Body Weight = c * BW^{d} (kg)(23)$$

with d = 0.6 for pig and 0.7 for broiler (Dukhta et al., 2017).

The indigestible dry matter intake is a proportion of the feed intake. Consequently, by combining equations 22 and 23, the mean retention time is expressed as:



Mean retention time 
$$(h) = \frac{a * b * BW}{e * BW^d} = A * \frac{BW}{BW^d} = A * BW^{(1-d)} (kg)(24)$$

Based on literature data, it was possible to define the mean retention time as a linear function of metabolic body weight with an exponent of 0.3 for broiler and 0.4 for pigs. This theoretical equation was adjusted to literature data (Equation 25, Figure 4).



*Mean retention time* (h) = 4.24 \*  $BW^{0.3}(kg)(25)$  with R<sup>2</sup> = 0.61

Figure 6 : Linear relationship between the mean retention time and the metabolic body weight in broiler.

Equation 25 allowed estimating the mean retention time according to the body weight. For each simulation, the mean retention time and consequently the fractional rate of the output of nutrients are better adapted to the animal simulated. However, this modification resulted in an underestimation of the apparent ileal and fecal digestibility of dry matter ranging from 29 to 56 points and from 19 to 28 points respectively. This underestimation may result from the distribution of the mean retention time between the different parts of the gastro-intestinal tract (as a percentage of total retention time) which also differs between pigs and chickens (Rougière, 2010).

#### Step 2 : Modification of the distribution of the total tract mean retention time

As a percentage of the total tract MRT, the MRT in the stomach and small intestine is higher for chickens than for growing pigs. This result in increased hydrolysis and absorption of nutrients for the broiler compared to the growing pig and also leads to a lower fermentation of dietary fiber. For broilers, the distribution of the total MRT was estimated as 22% in the stomach (compared to 11% in pigs), 53% in the small intestine (9% in pigs) and 25% in the large intestine (80% in pigs; Dänicke et al., 1999; Shires et al., 1987). The distribution of the mean retention time in the small intestine was not changed (9% in the proximal part and 91 % in the distal part). With this modification the apparent ileal and fecal digestibility of dry matter were underestimated from 0 to 17 points and from 5 to 13 points respectively.

Considering that the output flows were quantified better, it was hypothesized that this underestimation may be due to other digestive processes (i.e. hydrolysis, fermentation, absorption). To identify which parameters have the greatest impact on the dry matter ileal and fecal digestibility, a sensitivity analysis was carried out. Parameters involved in hydrolysis, fermentation and absorption



for each nutrient and each compartment were increased or decreased by 25, 50 or 75% of their default values (Bastianelli et al., 1996; Létourneau-Montminy et al., 2011). Results indicated that the ileal and fecal digestibility of dry matter are most sensitive to the hydrolysis rate. Consequently, this parameter was modified.

#### Step 3 : Modification of the hydrolysis rate

Endogenous secretions are more important in broilers than in growing pigs. Endogenous secretions include digestive enzymes which further justifies the choice to increase the hydrolysis rate in broilers compared to the default value of pigs. Firstly, to simplify, the same coefficient of correction was applied to hydrolysis rates for all nutrients (multiplying by 2). With this modification, the predicted ileal digestibility of dry matter varies from an underestimation of 5 points to an overestimation of 3 points. After having obtained a reasonably good prediction of dry matter ileal and fecal digestibility, the digestibility of each nutrient is currently tested.

# 4. Conclusions

Based on existing digestion models for pigs, the first part of the work consisted in combining information from these pig models. This pig model has then been transposed to broilers. The developed model is an interesting research tool to describe the digestive steps for the main nutrients in growing pigs and broilers, and it can be used to determine the nutritive value of feedstuffs and mixed feeds. The digestive model is available for the DSS development in T3.5.

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# 6. Annex 1: Information used for simulations (Figures 4 and 5)

	Body weight (kg)	Daily Dry Matter Intake (g)
Cozannet et al. 2010	67.5	1923.5
Le Goff et al. 2002	45.2	1106.7
Wilfart et al. 2007	48.0	1747.4
Ramonet et al. 1999	68.3	1919.0
Brestensky et al., 2016	36.5	1343.5

#### **Diet compositions**

Cozannet et al., 2010	%
Wheat	87.25
Soybean meal	10.00
CaHPO <sub>4</sub>	0.70
CaCO₃	1.10
NaCl	0.45
Other minerals and vitamins	0.50

Le Goff et al., 2002	%
Wheat	89.90
Isolated soybean protein	6.85
CaHPO <sub>4</sub>	1.20
CaCO <sub>3</sub>	1.10
NaCl	0.45
Other minerals and vitamins	0.50

Wilfart et al., 2007	%
Wheat	41.05
Barley	41.05
Soybean meal	14.00
Rapeseed oil	0.70
CaHPO <sub>4</sub>	1.10
CaCO <sub>3</sub>	1.00
NaCl	0.30
Other minerals and vitamins	0.50
TiO <sub>2</sub>	0.30





Ramonet et al., 1999	%
Wheat	65.63
Barley	16.18
Soybean meal	11.24
Molasses	3.00
CaHPO₄	1.10
CaCO₃	1.30
NaCl	0.45
Other minerals and vitamins	1.00
Cr <sub>2</sub> O <sub>3</sub>	0.10

Brestensky et al., 2017	%
Corn	58.69
Soybean meal	20.00
Barley	17.41
Lysine	0.20
Threonine	0.02
Ca(H <sub>2</sub> PO <sub>4</sub> ) <sub>2</sub>	0.10
CaCO₃	1.59
NaCl	0.40
Other minerals and vitamins	0.30
Cr <sub>2</sub> O <sub>3</sub>	0.30
CELITE	0.99



