

# Evaluation of the inclusion of *Tenebrio molitor* meal in pig's diet

Alessandro Quiese<sup>1</sup>, Irene Ferri<sup>1</sup>, and Luciana Rossi<sup>1</sup>

<sup>1</sup>Department of Veterinary Medicine and Animal Sciences, - DIVAS, University of Milan, Lodi

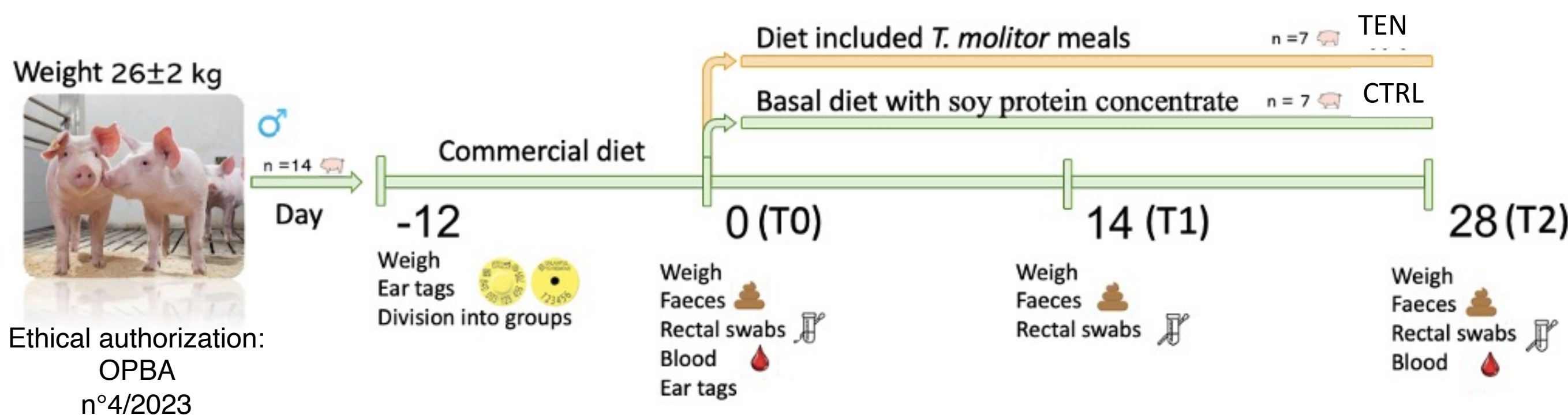
## Introduction

Insects are considered a valuable alternative to conventional protein sources in animal diets due to their low environmental impact and high nutritional value (Liceaga, 2022). One of the main achievable goals in pig livestock during the growing phase includes zootechnical performances. In addition, the quality of proteins is critically important for meeting the nutritional requirements. In this sense, *Tenebrio molitor* is an insect species characterised by an elevated protein and fat content, good digestibility and remarkable functional capacity (Jin et al., 2016; Shafique et al., 2021).

## Aim

The aim of this study was to evaluate the replacement of fermented soy protein concentrate with 5 % of *Tenebrio molitor* meals on performance, diet digestibility, and gut microbiota of growing pigs

## Materials and methods



14 piglets weaned at 26±2d were divided in two experimental groups fed for 28 days an isoenergetic and isoproteic diet differentiable for the substitution of soy protein concentrate and soybean oil with 5 % of *T. molitor* meals (CTRL and TEN group).

Individual body weight was recorded at day 0 (T0), 14 (T1), and 28 (T2).

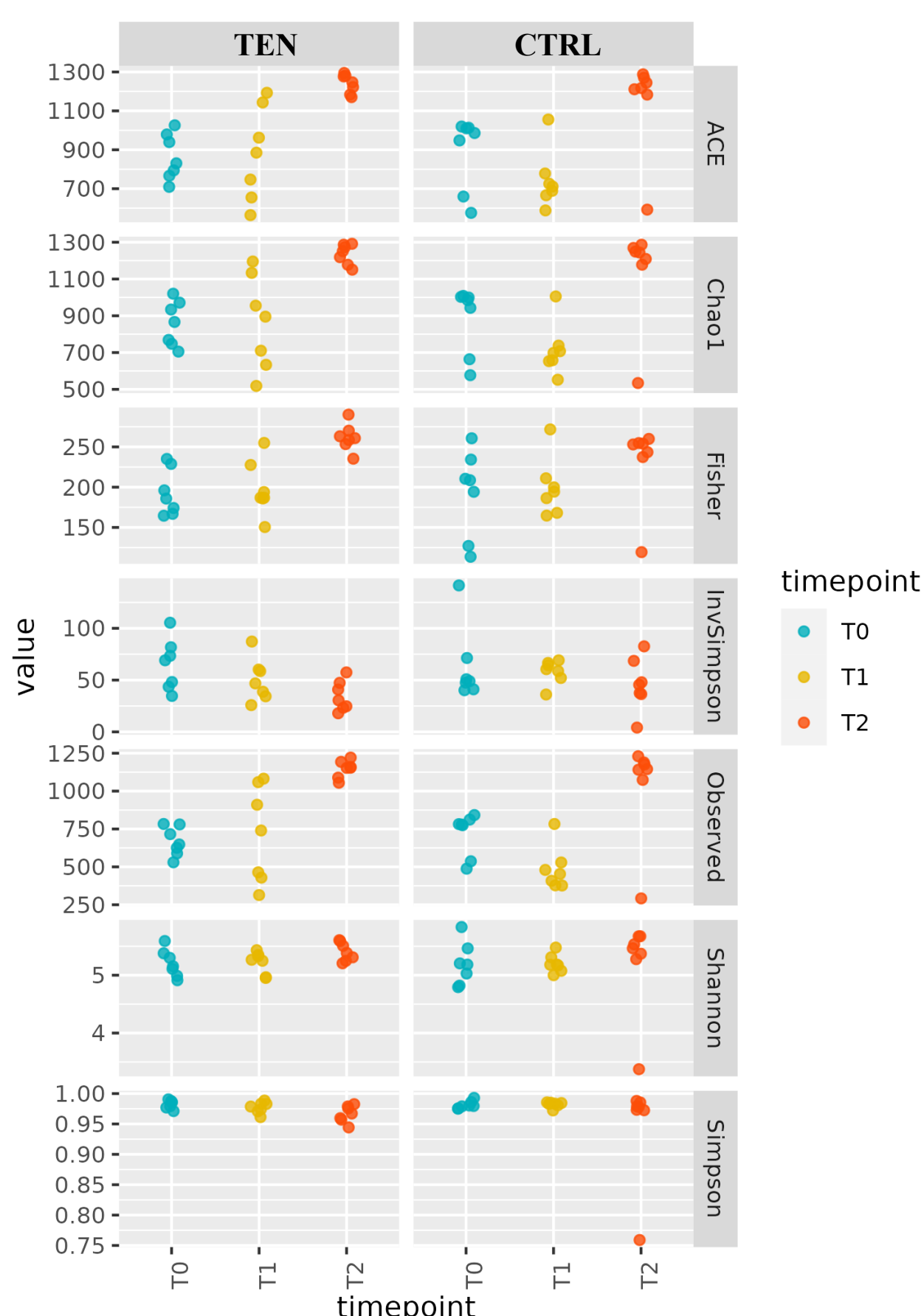
Faecal and blood samples were collected for the evaluation of nitrogen and lipid digestibility and serum metabolic profile through chemical and enzymatic colourimetric analysis, respectively. Microbial DNA was extracted from faecal swabs to evaluate the gut microbiota by 16s rRNA gene sequencing (Miragoli et al., 2021) using Bray Curtis index.

Statistical analysis was performed using GraphPad Prism ver 9.0 statistical software and means were considered different when  $p \leq 0.05$ . QIIME2 and R software were used for Bioinformatic and biostatistic analysis.

## Results

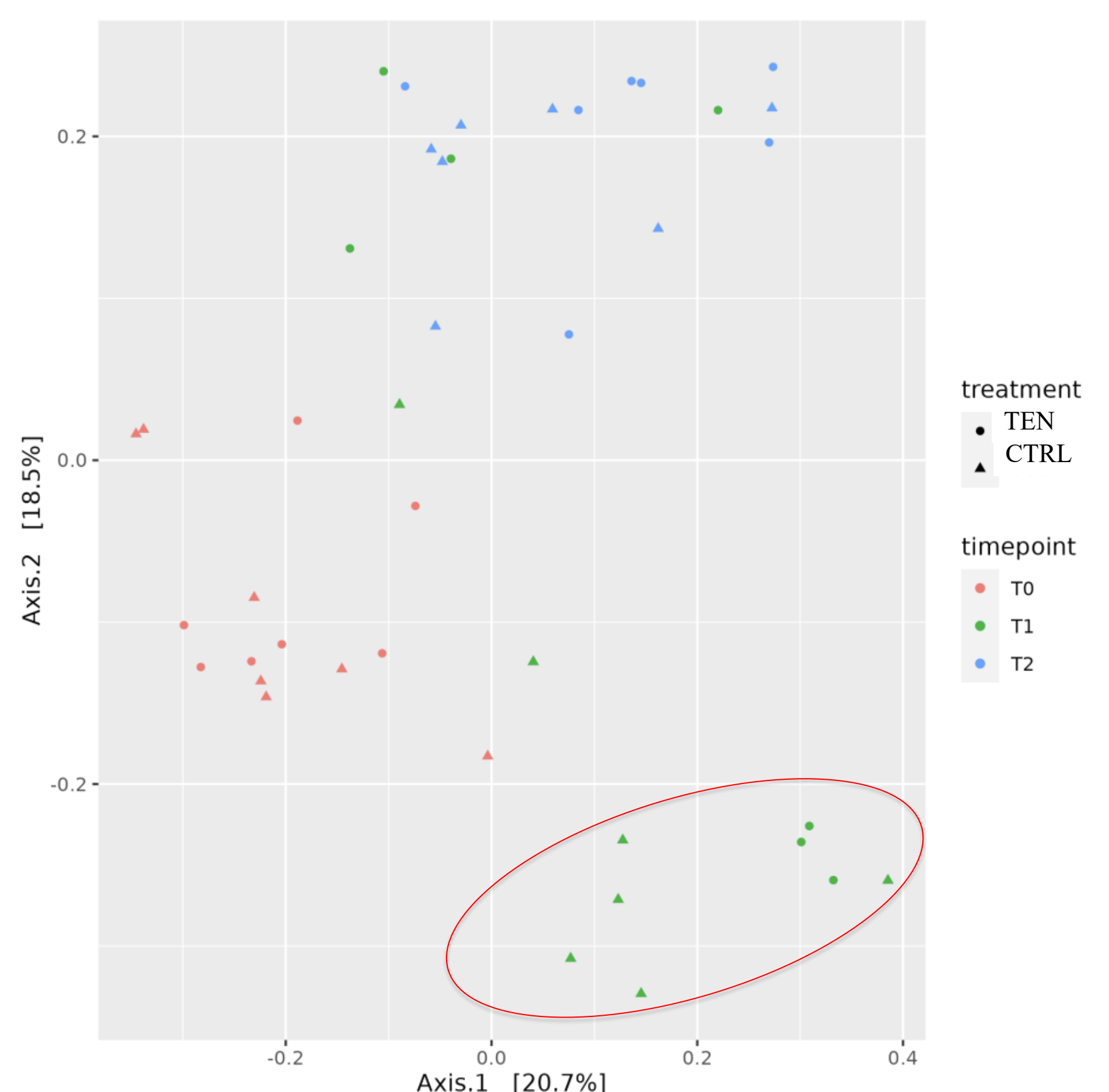
- Body weight in the CTRL ( $48.44 \pm 3.41$ ) and TEN ( $48.41 \pm 4.52$ ) group was comparable at the end of the trial ( $p > 0.05$ ). No differences were highlighted in the zootechnical performance of TEN group compared to CTRL group during the whole experimental period.
- Comparable results were observed between the two experimental groups in apparent nutrient digestibility and blood serum metabolites ( $p > 0.05$ ).

Fecal microbiota diversity showed no significant results within the two experimental groups (alpha-diversity).



Indexes of alpha-diversity. Data are presented for treatment by timepoint for six indexes used for alpha-diversity (ACE; Chao1; Fisher; InvSimpson; Observed; Shannon; Simpson) of gut microbiota of the control (CTRL) and treatment groups (TEN) at day 0 (T0), 14 (T1) and 28 (T2) of the trial.

The beta-diversity showed a significant difference after 14 days of trial (PERMANOVA analysis,  $R^2$  0.0384,  $p$  value = 0.0260) comparing CTRL and TEN groups.



Principal coordinates analysis obtained by PERMANOVA approach for Bray-Curtis index for control (CON) group and treatment (TM) group at day 0 (T0), 14 (T1) and 28 (T2) ( $R^2$  0.1418,  $p$ -value = 0.03197).

## Conclusions

- The inclusion of 5 % of *T. molitor* meals as partially substitute of soy protein concentrate did not negatively affect growth performance and feed intake in growing pigs.
- Comparable protein and lipid digestibility was observed between the two experimental groups.
- *T. molitor* could modulate the gut microbiota in growing pigs.
- It significantly increased beta diversity after 14 days of trial.