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Predicting empty body weight in growing goats: A meta-analytic approach

Letícia Marra Campos, Amélia Katiane Almeida, Bruno Biagioli, Kleber Tomas Resende, Izabelle Auxiliadora Molina Almeida Teixeira*

Universidade Estadual Paulista (UNESP), Department of Animal Science, Jaboticabal, SP 14884-900, Brazil

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ABSTRACT

The objective of this study was to develop statistical models to predict empty body weight (EBW) by body weight (BW), testing the influence of sex (females, intact males or castrated males), type of diet (suckling or post-weaning), and genotype (Saanen, ½ Boer × ½ Saanen, ¾ Boer × ¼ Saanen, and Indigenous goats). Individual records of 311 goats combined from 10 studies, with BW ranging from 4.3 to 47.4 kg were used. The EBW was computed as the BW at slaughter minus the weight of the contents of the digestive tract, urinary bladder, and biliary vesicle. Linear regression analyses were performed to develop the models, considering sex, type of diet, and genotype as fixed effects and random effect of study. CONTRAST statements were used to conduct all pairwise comparisons of fixed effects and all the statistical analyses were performed using SAS. The present study revealed that sex did not affect both intercept ($P = 0.53$) and slope ($P = 0.19$). On the other hand, the EBW prediction was affected by type of diet ($P < 0.01$), and genotype ($P = 0.02$). Therefore, were proposed different equations to predict EBW from BW for suckling and post-weaning Saanen goats, where gastrointestinal tract content (g/kg EBW) in suckling goat kids increased as they grew, oppositely it remained slightly constant in post-weaning goats. The effect of genotype on the EBW:BW relationship was tested considering only post-weaning goats, and one equation was proposed for each genotype. In general, gastrointestinal tract content (g/kg EBW) decreased as goat kids grew in all genotypes but Indigenous goats. The results also highlighted different gastrointestinal relative capacity between genotypes. The development of these equations would enable producers and researchers to predict the animal EBW, and develop strategic plans in a goat herd.

1. Introduction

The decision-making in production system is often based on weight gain of the animals. In this regard, accurate body measurement of weight is crucial in assessing animal performance *in vivo*, and assisting the strategic management in a herd (i.e., formulating diets, reproductive management, weight gain projections, carcass yield, etc). However, in ruminants, the accuracy of the body weight (BW) measurement can be mainly affected by gastrointestinal content variation (Gionbelli et al., 2015; Meyer et al., 1960). The gastrointestinal tract (GIT) content represents from 8 up to 19% of animals' BW (Chay-Canul et al., 2014). This variation may be due to many factors: feed quality, intake level, sex, maturity degree, physiological state and evolutionary adaptations (Beranger and Robelin, 1978; Chay-Canul et al., 2014; Clauss et al., 2016; Gionbelli et al., 2015). Aiming to reduce the variation due to GIT content, Owens et al. (1995) suggested the empty body weight (EBW) should be used to better describe animal size (i.e., rather than BW). For instance, the standard method for determining the nutritional requirements in goats, (i.e., the comparative slaughter) generates EBW-based recommendations (Ferreira et al., 2015; Figueiredo et al., 2016b; Sampelayo et al., 1990; Teixeira et al., 2015).

However, the estimation of EBW is a time- and work-demanding and expensive method (Lofgreen et al., 1962), requiring the slaughter of the animal, and the digestive tract emptying. Considering that strategies management in research and production is done with live animals, it is desirable to develop models designed to make EBW usable.

Considering the wide range of factors that may affect the EBW:BW ratio, the hypothesis to be tested is that female and male goats exhibit differences in EBW:BW ratio due to differences in their growth (Burrin et al., 1992; Ferrell and Jenkins, 1998), as well as their feed intake (Ingvartsen et al., 1992; NRC, 2007). Additionally, suckling goats are functionally non-ruminants, then it is expected their GIT content would be lighter compared with post-weaning animals (Khan et al., 2011; Sampelayo et al., 1990). It is also worthy to test differences among genotype in the EBW:BW relationship because dairy breeds, would require greater intake capacity to support milk production (Backes et al., 2006), resulting in greater GIT. Thus, the objective of this meta-analytic study is to develop statistical models for the prediction of EBW by the

* Corresponding author at: Universidade Estadual Paulista (UNESP), Via de acesso Prof. Paulo Donato Castellane s/n, CEP 14884-900, Jaboticabal, Brazil.
E-mail address: izabelle@fcav.unesp.br (I.A.M.A. Teixeira).

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Table 1
Database and characteristics of studies included in this meta-analysis.

Study	Reference	Genotype	Sex	Type of Diet[a]	Body weight range, kg	Number of animals
1	Almeida et al. (2015)	Saanen	Intact male	Post-weaning	27.6–46.6	14
		Saanen	Castrated male	Post-weaning	27.8–47.4	16
		Saanen	Female	Post-weaning	27.4–44.9	17
2	Bompadre et al. (2014)	Saanen	Intact male	Suckling/Post-weaning	4.7–16.6	19
		Saanen	Castrated male	Suckling/Post-weaning	4.7–16.7	16
		Saanen	Female	Suckling/Post-weaning	4.6–16.4	18
3	Fernandes et al. (2007)	¾ Boer ¼ Saanen	Intact male	Post-weaning	20.2–36.6	20
4	Ferreira et al. (2015)	Saanen	Castrated male	Post-weaning	20.6–35.5	27
5	Figueiredo et al. (2016a)	Saanen	Female	Post-weaning	29.5–46.0	18
6	Figueiredo et al. (2016b)	Saanen	Intact male	Post-weaning	15.7–34.0	20
		Saanen	Castrated male	Post-weaning	15.3–32.5	20
		Saanen	Female	Post-weaning	14.8–31.7	18
7	Medeiros et al. (2014)	Saanen	Intact male	Suckling/Post-weaning	5.1–21.6	23
8	Resende (1989)	Indigenous	Intact male	Suckling/Post-weaning	5.0–27.8	12
9	Ribeiro (1995)	Indigenous	Intact male	Suckling/Post-weaning	4.9–17.0	14
10	Teixeira et al. (2015)	½ Boer ½ Saanen	Intact male	Suckling/Post-weaning	4.3–16.2	19
		½ Boer ½ Saanen	Intact male	Post-weaning	14.6–26.3	20

[a] Post-weaning refers to studies that involved goat kids receiving just solid diet and Suckling/Post-weaning refers to studies that involved goat kids receiving milk and solid diet.

BW, testing the influence of genotype, sex, and type of diet (suckling or post-weaning).

2. Materials and methods

2.1. Database

A database of 311 individual records of body weight and empty body weight of goat kids was used. It comprised goat kids of different sexes (intact males, $n = 161$; females, $n = 71$; and castrated males, $n = 79$), genotypes (Saanen, $n = 226$; Boer × Saanen crossbreds: ½ Boer × ½ Saanen or ¾ Boer × ¼ Saanen, $n = 59$, and Indigenous goats, $n = 26$), and types of diet (suckling/post weaning, $n = 121$ and post-weaning, $n = 190$). Afterwards the suckling/post weaning goat kids will be referred as suckling. The BW of the goat kids ranged from 4.3 to 47.4 kg. This database was combined from 10 studies (Table 1): Almeida et al. (2015), Bompadre et al. (2014), Fernandes et al. (2007), Ferreira et al. (2015), Figueiredo et al. (2016a), Figueiredo et al. (2016b), Medeiros et al. (2014), Resende (1989), Ribeiro (1995), and Teixeira et al. (2015. These studies were conducted at the Goat Facility of the Universidade Estadual Paulista (UNESP, campus of Jaboticabal, SP, Brazil; 21°14′05″S and 48°17′09″W, altitude 595 m). Animals were fed similar diets under *ad libitum* regimen, diets (DM basis% ± SD) were comprised of dehydrated corn plant (46.6 ± 0.57%) or grass hay (41.7 ± 24.0%; studies 5, 8, and 9), corn grain (29.6 ± 7.9%), soybean meal (17.5 ± 3.7%), soybean oil (1.1 ± 0.46%), wheat bran (9.0%; study 5), molasses (4.3 ± 0.09%; studies 2, 3, 4, 7, and 10), mineral supplement (3.0 ± 1.1%), and ammonium chloride (0.5 ± 0.57%; studies 5 and 6). For further details regarding diets within studies see supplementary material. All experimental procedures were followed in accordance with the University's Animal Care Committee, under protocols described in the published sources.

2.2. Slaughter procedures

All studies adopted similar slaughter procedures and chemical analyses. The animal's BW was recorded immediately before the slaughter; for those studies that adopted fasting before slaughter, it was used the BW recorded in the previous day, before fasting (studies 3, 4, 5, 7, 8, 9, and 10; Table 1). At slaughter, animals were stunned with a captive bolt pistol, followed by severing of the jugular vein and carotid artery. Blood and organs were collected and weighed. The digestive tract was weighed full and empty. The EBW was computed as the BW at slaughter minus the weight of the contents of the digestive tract, urinary bladder, and biliary vesicle.

2.3. Statistical analyses

Linear regression analyses (Eq. (1)) were performed to develop the models, considering sex (intact males, castrated males, and females), genotype (Saanen, ½ Boer × ½ Saanen, ¾ Boer × ¼ Saanen, and Indigenous goats), and types of diet (suckling and post-weaning) as fixed effects and random effect of study. The variance due to study was considered using the RANDOM statement of MIXED procedure in SAS while fitting the regression equations (St-Pierre, 2001).

$$Y_{ijk} = \beta_{0i} + \beta_{1j} \times BW_{ijk} + s_j + e_{ijk} \quad (1)$$

In which, Y_{ijk} is the EBW (kg) for the k[th] goat of the i[th] level of tested fixed effect in the j[th] study, β_0 and β_1 are the parameters to be estimated for each of the i[th] level of tested fixed effect (i.e., i = 1, 2, 3 sexes, i = 1, 2 types of diet or i = 1, 2, 3, 4 genotypes), s_j is the random effect of the j[th] study $\sim N(0, \sigma_s^2)$, and e_{ijk} is the residual error $\sim N(0, \sigma^2)$.

If the linear regressions slope differed between suckling and post-weaning Saanen goats, a segmented model (i.e., broken line, Eqs. (2) and (3)) was used to identify the BW in which the slope changed (i.e., breakpoint; Ryan and Porth, 2007).

$$EBW = \beta_0 + \beta_1 \times BW; \quad \text{for } BW \le \beta_2 \quad (2)$$

$$EBW = [\beta_0 + \beta_2 \times (\beta_1 - \beta_3)] + \beta_3 \times BW; \quad \text{for } BW \le \beta_2 \quad (3)$$

In which; *EBW* is the empty body weight in kg, β_0 and β_1 are, respectively, the intercept and slope of linear fit to data below breakpoint, β_2 is the breakpoint (i.e., the point in which the slope change), and β_3 is the slope of the linear fit to data above breakpoint.

In this case, the variance due to study was considered at the RANDOM statement of PROC MIXED, as explained by Almeida et al. (2016), generating an adjusted database before fitting the segmented model using PROC NLIN (see supplementary material for further details). The MARQUARDT convergence method was used, and the HOUGAARD option was requested to generate skewness values (Hougaard 1982, 1985).

When sex, type of diet or genotype was found significant ($P < 0.10$), indicating a different intercept for at least one of tested fixed effects, CONTRAST statements were used to conduct all pairwise comparisons of fixed effects. Likewise, CONTRAST statements were used to conduct all pairwise comparisons when the interaction between fixed and regressor effects was found to be significant ($P < 0.10$), indicating a different slope for at least one of the tested interaction. The statistical analyses were performed using SAS (SAS Institute Inc., Cary, NC 9.4).