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Article

Defining growth curves with nonlinear models in seven sheep breeds in Mexico

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Abstract:

Characterizing growth in livestock is important when making management, marketing and genetic improvement decisions. Nonlinear models were tested to identify those with the best fit for growth curves in seven sheep breeds [Blackbelly (n= 19,084); Pelibuey (n= 39,025); Dorper (n= 35,814); Katahdin (n= 74,154); Suffolk (n= 10,267); Hampshire (n= 7,561); and Rambouillet (n= 7,384)]. Using breed registry databases, live weight was assessed from birth to 230 d of age. The SAS program was applied to test six nonlinear models: Brody, Verhulst, von Bertalanffy, Gompertz, Mitscherlich and logistic. The criteria for selecting the best-fit model were the average prediction error; the prediction error variance; the Durbin-Watson statistic; the coefficient of determination; the root-mean-square error; and the Akaike and Bayesian information criteria. For the Hampshire, Pelibuey and Suffolk breeds the best-fit model was the von Bertalanffy, with a sigmoid curve and an inflection point age between 40 and 57 d. For the Katahdin, Blackbelly, Dorper and Rambouillet breeds the best-fit models were the Brody and Mitscherlich models, with a continuous growth curve, no inflection point and constant growth rate. Marked differences were observed in adult weight between breeds, with average values (kg) of 44.6 for Blackbelly, 49.2 for Rambouillet, 52.9 for Pelibuey, 55.6 for Hampshire, 60.2 for Katahdin, 64.7 for Suffolk and 65.2 for Dorper; values tended to be highest in the Brody and Mitscherlich models, and lowest in the logistic and Verhulst models.

Key words: Growth rate, adult weight, model selection, von Bertalanffy, Brody, Nonlinear regression.

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Introduction

In Mexico the Organization of the Sheep Breeders National Unit (Organismo de la Unidad Nacional de Ovinocultores - UNO) encompasses producers of specialized and pure breed sheep. This organization coordinates genetic improvement plans in sheep breeds based on genealogical records and production controls of the variables included in each breed's selection criteria and objectives. Growth variables such as animal live weight are recorded at five points or ages(1). Live weight data for different ages is used to generate a points distribution over time. This allows analysis and characterization of growth patterns based on nonlinear mathematical models (NLM), which use biological interpretation to summarize variation in live weight over time through a small number of growth parameters and indicators(2,3).

Sheep production in Mexico occurs under various technological, agro-ecological and socioeconomic conditions. Organized and truthful documentation of events in the production unit, particularly financial variables, is essential for producers to determine unit profitability. Changes in animal live weight are influenced by genetic and environmental factors, with variable effects through time and during individual development. Each sheep breed has a characteristic growth pattern, requiring the testing of several NLM to identify that with the best fit for each breed. Identifying the NLM with the best fit provides objective and accurate growth pattern data which can be used by producers in decision-making regarding production, management and genetic improvement.

The present study objectives were: 1) To identify the best-fit NLM to describe the growth curve in four hair sheep breeds (Blackbelly, Pelibuey, Dorper and Katahdin) and three wool sheep breeds

(Suffolk, Hampshire and Rambouillet); and, 2) To generate growth indicators that can characterize and analyze these growth curves.

Materials and methods

The analyzed database includes live weight records for female lambs in seven UNO-registered breeds: Blackbelly (BB), Pelibuey (PE), Dorper (DR), Katahdin (KT), Suffolk (SF), Hampshire (HS) and Rambouillet (RB). Analyzed variables were live weight at birth, 75, 120, 150 and 210 d of age, with measurements taken at intervals of ± 20 d with respect to the reference age (Table 1). Weight at 75 d corresponds to weaning. Because males are sold beginning at 120 d, only data for females was used in the analyses.

Table 1: Number of records at each age for the seven evaluated sheep breeds

Breed	WB	W75	W120	W150	W210	Total
Katahdin	24,878	21,365	11,500	10,502	5,909	74,154
Pelibuey	14,164	11,796	5,301	4,993	2,771	39,025
Dorper	11,487	9,522	5,802	5,510	3,493	35,814
Blackbelly	7,151	5,439	2,475	2,416	1,603	19,084
Suffolk	3,636	2,836	1,542	1,459	794	10,267
Hampshire	2,597	2,177	1,236	1,056	495	7,561
Rambouillet	2,504	1,748	1,189	1,093	850	7,384

WB= live weight at birth; W75= live weight in 55 to 95 d interval; W120= live weight in 100 to 140 d interval; W150= live weight in 130 to 170 d interval; and W210= live weight in 190 to 230 d interval.

Data were from flocks mainly distributed in three regions of Mexico. Half (50 %) of the flocks were from the country's central region and included primarily the SF, HS and RB breeds. The south-southeast region accounted for 22 % of the database, and corresponded to the PE, BB, DR and KT breeds. The north region represented 18 % of the data and included mostly the BB, DR and KT breeds. The remaining 10 % of the data was from flocks in other regions. Production systems in the central region are largely intensive or semi-intensive using stables combined with cultivated pastures. Systems in the north and south-southeast regions are semi-intensive and extensive, combining grazing with corrals. In the north, large arid and semi-arid areas with multispecies pastures and scrub are used, whereas in the south-southeast the tropical climate promotes wide availability of tropical grasses.

Seven NLM were evaluated: Brody (BRO), Verhulst (VER), von Bertalanffy (VBE), Gompertz (GOM), Mitscherlich (MIT) and logistic (LOG). All consisted of three regression coefficients (β_1, β_2 and β_3)[4,5,6]. In NLM equations (Table 2), $\boldsymbol{y_i}$ represents live weight (kg) measured at time $\boldsymbol{t}$; β_1 is the asymptotic value when $\boldsymbol{t}$ tends to infinity, interpreted as the adult weight parameter (AW); β_2 is a fit parameter when $\boldsymbol{y} \neq 0$ and $\boldsymbol{t} \neq 0$; and β_3 is growth rate (GR), expressing weight gain as a proportion of total weight[2,7]. The VER, VBE, GOM and LOG models describe growth based on a sigmoid curve, for which inflection point age (IPA) and weight (IPW) were estimated[8,9].

Table 2: Nonlinear models used to describe growth in registered sheep breeds

Models	**Equation**
Verhulst	$y_i = \beta_1*(1 + exp(-\beta_2*t))^{-\beta 3} + e_i$
Logistic	$y_i = \beta_1 / (1 + \beta_2*(exp(-\beta_3*t))) + e_i$
Von Bertalanffy	$y_i = \beta_1*((1 - \beta_2*(exp(-\beta_3*t)))**3) + e_i$
Gompertz	$y_i = \beta_1*(exp(-\beta_2*(exp(-\beta_3*t)))) + e_i$
Brody	$y_i = \beta_1*(1 - \beta_2*(exp(-\beta_3*t))) + e_i$
Mitscherlich	$y_i = \beta_1*(1 - exp(\beta_3*\beta_2 - \beta_3*t)) + e_i$

y_i= live weight in kg measured at time t; β_1= asymptotic value; β_2= integration constant; β_3= curve slope or growth rate.

Analyses were done using the Gauss-Newton method of the NLIN procedure in the SAS statistical program[10]. Selection of the model with the best fit was done based on seven criteria[11,12,13]: a) the Akaike information criterion [AIC = n*nl(sse/n) + 2k]; b) the Bayesian information criterion [BIC = n*nl(sse/n) + k*nl(n)]; c) the average prediction error [APE= $(\sum_{i=1}^{n}\left(\frac{lwi - ewi}{ewi}\right) * 100)/n$]; d) the prediction error variance [PEV = $\sum_{i=1}^{n}(ewi - lwi)^2/n$]; e) the Durbin-Watson statistic [DW= $2(1-\rho)$; $\rho = \frac{\sum_{t=2}^{n}(e_t - e_{t-1})^2}{\sum_{t=1}^{n} e_t^2}$]; f) the determination coefficient [$R^2 = (1 - (sse/tss))$]; and g) the general standard error or model error, from the root-mean-square error (GSE= $\sqrt{\frac{sse}{n-p-1}}$. Where: lwi = live weight (kg) at *i*-th age (d); ewi = estimated live weight (kg) at *i*-th age (d); n = total number of data; sse = sum-squared error; tss = total sum-squared; k = number of parameters in model; nl = natural logarithm. The APE analyzes the relationship between measured and estimated weight, and, as a function of the symbol, the NLM overestimates (+) or underestimates (-) the predictions. For APE, PEV, GSE, AIC and BIC, the model with the lowest value was considered to have the best fit; for R^2 it was the model with the highest value. The DW analyzes for auto correlations in the errors using scenarios: if 2<DW<4, there is a negative auto correlation; if 0<DW<2, there is no auto correlation; and if DW$\leq$0, there is a positive auto correlation.

Results and discussion

The statistical criteria used for selection of the best-fit model for each breed showed that based on R^2 all the NLM explained 94 % or more of the variability in the analyzed data (Table 3). All the NLM also tended to underestimate the predictions (negative APE) without auto correlation in the residuals (0<DW<2). The PEV and APE results did not differ within breeds, but were higher for the LOG model in all breeds. Based on the AIC and BIC, the MIT and BRO model results did not differ within breeds and were the best fit for the KT, BB, DR and RB breeds. For the HS, PE and SF breeds, however, the best-fit model was the VBE, with epi between 40 and 57 d (Table 4), an age within the preweaning period. Based on the NLM, average IPW was 16.4 kg for PE, 20.2 kg for HS and 23.2 kg for SF.

Table 3: Statistics used for selection of best-fit nonlinear models

Breeds†	**Models**§	*PEV	*APE	*DW	*R^2	*GSE	*AIC	*BIC
BB	LOG	20.4	-17.8	0.66	0.95	4.3	55904	55927
	GOM	19.3	-10.5	0.58	0.95	4.2	54563	54587
	VBE	19.1	-8.4	0.56	0.95	4.1	54202	54225
	VER	19.9	-13.5	0.62	0.95	4.2	54942	54966
	MIT	18.8	-5.9	0.54	0.95	4.1	53757	53781
	BRO	19.0	-6.0	0.56	0.95	4.1	53757	53781
DR	LOG	44.3	-18.4	1.30	0.95	6.4	132665	132690
	GOM	41.7	-10.5	1.30	0.95	6.1	130012	130037
	VBE	41.1	-7.9	1.32	0.96	6.1	129282	129307
	VER	42.2	-9.8	1.31	0.95	6.2	130754	130779
	MIT	40.5	-5.4	1.36	0.96	6.0	128389	128415
	BRO	41.0	-5.8	1.39	0.96	6.0	128389	128415
HS	LOG	44.3	-12.4	0.04	0.95	5.7	26115	26135
	GOM	42.8	-7.3	0.04	0.95	5.6	25799	25820
	VBE	42.6	-6.3	0.04	0.96	5.6	25749	25770
	VER	43.7	-9.9	0.04	0.95	5.6	25876	25897
	MIT	42.8	-5.2	0.04	0.96	5.6	25755	25775
	BRO	42.8	-5.4	0.04	0.96	5.6	25755	25775
KT	LOG	37.1	-17.0	0.68	0.95	6.0	262113	262141
	GOM	35.6	-9.9	0.64	0.95	5.8	257855	257882
	VBE	35.3	-8.0	0.64	0.95	5.8	256792	256819

	VER	35.9	-9.1	0.66	0.95	5.9	259020	259048
	MIT	35.3	-6.1	0.68	0.95	5.7	255755	255782
	BRO	35.4	-6.1	0.67	0.95	5.7	255755	255782
PE	LOG	26.4	-15.1	0.26	0.94	4.6	118402	118428
	GOM	25.6	-9.3	0.24	0.94	4.5	116815	116841
	VBE	25.5	-7.0	0.24	0.94	4.5	116583	116608
	VER	26.1	-8.6	0.25	0.94	4.5	117161	117187
	MIT	25.6	-5.2	0.24	0.94	4.5	116745	116771
	BRO	26.2	-5.9	0.26	0.94	4.5	116745	116771
RB	LOG	19.8	-5.6	1.80	0.98	4.4	21873	21894
	GOM	18.7	-4.9	1.80	0.98	4.2	21119	21139
	VBE	18.5	-4.2	1.80	0.98	4.1	20914	20935
	VER	19.1	-5.1	1.81	0.98	4.0	21355	21376
	MIT	18.3	-3.5	1.80	0.98	4.0	20629	20650
	BRO	18.4	-3.7	1.82	0.98	4.0	20629	20650
SF	LOG	46.8	-9.1	0.04	0.95	6.4	37846	37867
	GOM	45.0	-7.3	0.04	0.96	6.2	37354	37376
	VBE	44.8	-6.1	0.06	0.96	6.2	37276	37298
	VER	45.9	-9.1	0.05	0.96	6.3	37467	37489
	MIT	44.8	-5.3	0.06	0.96	6.2	37277	37299
	BRO	44.9	-5.3	0.07	0.96	6.2	37277	37299

†Breeds: BB= Blackbelly; PE= Pelibuey; DR= Dorper; KT= Katahdin; SF= Suffolk; HS= Hampshire; RB= Rambouillet.

§Models: VER= Verhulst; LOG= Logistic; VBE= von Bertalanffy; GOM= Gompertz; BRO= Brody; MIT= Mitscherlich.

*Statistics for model selection: PEV= prediction error variance; APE= average prediction error; DW= Durbin-Watson statistic; R^2= determination coefficient; GSE= general standard error; AIC= Akaike information criterion; BIC= Bayesian information criterion.

Table 4: Regression coefficients and growth indicators in evaluated nonlinear models

Breeds†	**Model§**	**¥β1 ± se**	**¥β2 ± se**	**¥β3 ± se**	**£IPW**	**£IPA**
BB	LOG	33.1±0.13	7.37±0.08	0.0243±0.0001	16.6	82
	GOM	36.9±0.21	2.42±0.01	0.0139±0.0001	13.6	63
	VBE	40.0±0.28	0.575±0.01	0.0103±0.0001	11.9	53
	VER	35.2±0.17	3.35±0.02	0.0171±0.0002	17.6	86
	MIT	61.3±1.22	-13.11±0.03	0.0034±0.0002		
	BRO	61.2±1.31	0.955±0.02	0.0034±0.0002		
DR	LOG	48.8±0.14	7.61±0.07	0.0242±0.0001	24.4	84
	GOM	54.1±0.22	2.48±0.01	0.0140±0.0001	19.9	65
	VBE	58.6±0.29	0.586±0.01	0.0105±0.0001	17.4	54

	VER	51.8±0.17	3.43±0.01	0.0171±0.0001	25.9	88
	MIT	88.8±1.23	-11.52±0.22	0.0035±0.0001		
	BRO	88.9±1.22	0.959±0.0	0.0036±0.0001		
HS	LOG	45.4±0.24	6.99±0.13	0.0285±0.0003	22.7	68
	GOM	50.0±0.37	2.31±0.02	0.0163±0.0002	18.3	51
	VBE	53.2±0.48	0.552±0.03	0.0125±0.0001	15.8	40
	VER	48.0±0.31	3.22±0.03	0.0201±0.0002	24.0	71
	MIT	68.6±1.36	-12.31±0.49	0.0054±0.0002		
	BRO	68.6±1.36	0.935±0.01	0.0054±0.0001		
KT	LOG	43.5±0.09	7.42±0.04	0.0241±0.0001	21.8	83
	GOM	48.6±0.15	2.44±0.01	0.0138±0.0001	17.9	65
	VBE	52.9±0.21	0.581±0.01	0.0102±0.0001	15.7	54
	VER	46.3±0.12	3.38±0.01	0.0171±0.0002	23.2	86
	MIT	84.9±1.01	-12.83±0.17	0.0032±0.0001		
	BRO	84.9±0.98	0.959±0.01	0.0032±0.0001		
PE	LOG	35.9±0.01	8.48±0.07	0.0256±0.0001	17.9	83
	GOM	40.7±0.18	2.57±0.01	0.0141±0.0001	14.9	67
	VBE	44.7±0.24	0.597±0.01	0.0102±0.0001	13.2	57
	VER	38.7±0.14	3.55±0.02	0.0174±0.0001	19.4	88
	MIT	78.9±1.40	-12.01±0.22	0.0029±0.0001		
	BRO	78.9±1.41	0.966±0.01	0.0029±0.0001		
RB	LOG	42.7±0.16	6.05±0.09	0.0259±0.0002	21.4	69
	GOM	45.9±0.23	2.14±0.02	0.0157±0.0001	16.9	48
	VBE	48.1±0.28	0.524±0.02	0.0124±0.0001	14.3	36
	VER	44.5±0.19	3.00±0.02	0.0191±0.0001	22.3	70
	MIT	56.8±0.62	-13.96±0.32	0.0064±0.0001		
	BRO	56.9±0.61	0.915±0.01	0.0064±0.0001		
SF	LOG	51.7±0.23	7.67±0.13	0.0276±0.0002	25.8	74
	GOM	57.5±0.36	2.42±0.02	0.0155±0.0001	21.1	57
	VBE	61.6±0.49	0.571±0.01	0.0117±0.0001	18.3	46
	VER	55.1±0.36	3.38±0.02	0.0191±0.0001	27.6	77
	MIT	84.0±1.61	-12.03±0.35	0.0046±0.0001		
	BRO	84.0±1.61	0.945±0.01	0.0046±0.0001		

[†]Breeds: BB= Blackbelly; PE= Pelibuey; DR= Dorper; KT= Katahdin; SF= Suffolk; HS= Hampshire; RB= Rambouillet.

[§]Models: VER= Verhulst; LOG= Logistic; VBE= von Bertalanffy; GOM= Gompertz; BRO= Brody; MIT= Mitscherlich.

[¥]Regression coefficients in nonlinear models: β_1= asymptotic value (kg); β_2= fit parameter; β_3= growth rate; se= standard error.

[£]Growth indicators: IPA= inflection point age (d); IPW= inflection point weight (kg).

The growth curves based on the best-fit models showed the differences in growth pattern by breed (Figures 1 and 2). The growth curve describes and represents the evolution of live weight over time. Analysis of growth curves generates information that can be used in management, feeding and genetic improvement programs. The NLMs express the growth curve according to several components: adult weight, growth rate, degree of maturity, and inflection point age and weight, among others[2,7]. Modifying or altering growth therefore requires strategies that improve these components[14,15]. The VBE model is characterized by a sigmoid curve (Figure 2), with the inflection point being where the GR transitions from an acceleration process to a deceleration phase. The BRO and MIT models, in contrast, describe a continuous growth curve with no inflection point (Figure 1), and in which the GR as a proportion of the AW is constant over time[3,16].

Figure 1: Growth curves for Katahdin (KT), Blackbelly (BB), Dorper (DR) and Rambouillet (RB) sheep breeds based on Brody model

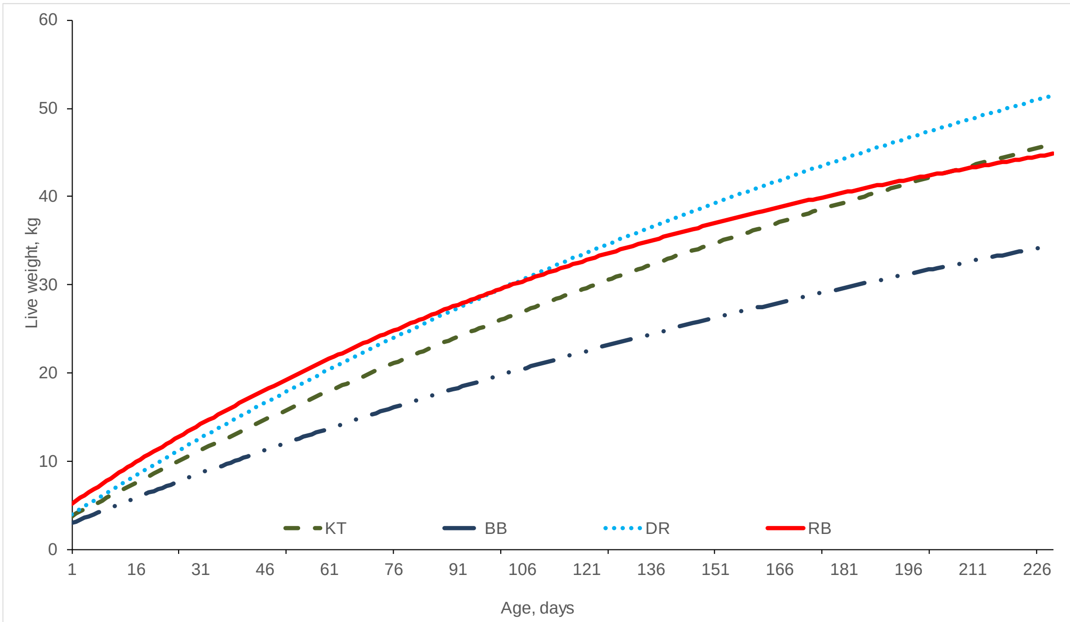
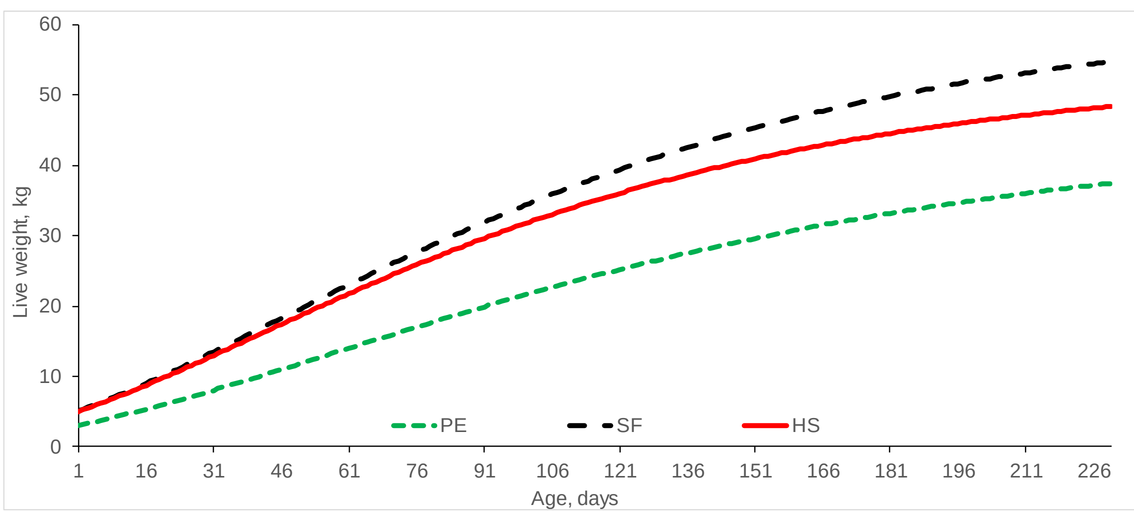


Figure 2: Growth curves for Pelibuey (PE), Suffolk (SF) and Hampshire (HS) sheep breeds based on von Bertalanffy model



Other studies highlight how different NLM provide the best fit for different sheep breeds. Similar studies with the Baluchi(5), Hemsin(17), and West African Dwarf(18) sheep breeds reported that the

BRO model was best fitted to describe growth. In an analysis of growth in Morada Nova sheep[4], the Meloun I and Meloun III models were found to have the best fit, with growth patterns similar to those in the BRO and MIT models used in the present study. However, in the Segureñas[9] and Awassi breeds[19] the VBE model has been found to have the best fit.

Marked differences were observed in AW in the seven evaluated breeds (Table 4). This parameter tended to be highest in the BRO and MIT models, and lowest in the LOG and VER models. Average values were 44.6 kg in BB, 49.2 kg in RB, 52.9 kg in PE, 55.6 kg in HS, 60.2 kg in KT, 64.7 in SF and 65.2 in DR. Increases in female AW affect maintenance, reproduction and waste value needs. Given that a large percentage of lamb production costs occur in ewes, increasing ewe size can raise production costs; however, asymptotic weight can be kept constant in selection programs while GR is maximized[14,20]. Since GR refers to the velocity of growth relative to AW, high GR can result in AW being attained at a younger age. Growth rate (GR) is financially important because it can be used to determine the optimal moment for slaughter, which is usually when the animal has reached maximum GR[13,21].

The correlations between AW and GR are essential in strategies aimed at modifying growth curves[15,21]. All correlations between AW and GR in the present study were negative and high (-0.70 to -0.99). These negative correlations suggest certain growth curve characteristics: a) older AWs do not derive from high GRs; b) a lower GR may lengthen the time to reach AW; and c) in genetic improvement schemes, GR can be increased without affecting AW[7,15,22].

Conclusions and implications

For the Hampshire, Pelibuey and Suffolk breeds, a nonlinear model based on the von Bertalanffy model produced sigmoid type growth curves with an inflection point at 40 to 57 d. For the Katahdin, Blackbelly, Dorper and Rambouillet breeds, a nonlinear model based on the Brody model resulted in growth curves with a continuous growth rate and no inflection point. The differences observed between the breeds as manifested in curve pattern and growth indicators express varying genetic potential, which can be exploited in different production systems.

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