



Comparison of equations to fit growth curves of Holstein, Jersey and Jersey x Holstein cows in a grazing system



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Abstract:

The objective of the study was to compare the goodness of fit of four nonlinear equations to describe the growth curves of Jersey, Holstein, and Jersey x Holstein cows in grazing. The Brody, Gompertz, von Bertalanffy, and Logistic equations were fitted to the data ($n= 2,315$) on weight and age of Jersey ($n= 54$), Holstein ($n= 6$) and Jersey x Holstein ($n= 30$) cows. For each animal, genotype and equation, the parameters A , b and k that generated the best-fit growth curves were estimated. In each of the four equations compared, parameter A corresponds to the upper asymptote of the curve and estimates the ‘mature weight’ of the animal, parameters b and k represent the integration constant and the maturation rate. For the growth curves of Jersey cows and Jersey x Holstein crosses, the Gompertz and von Bertalanffy equations produced the best fit. In contrast, the Logistic equation had the best fit for the growth curves of Holstein, followed closely by the Gompertz and von Bertalanffy equations. Under the management and feeding conditions of the animals in this study, the growth curves of the females of the three genotypes studied can be fitted with the von Bertalanffy equation.

Key words: Dairy cattle, Nonlinear models, Growth pattern.

Received: 15/08/2018

Accepted: 17/02/2021

When the weight of the same individual at regular age intervals, from birth to maturity, is available, it is possible to fit a function that describes the weight curve according to age. This curve that allows condensing the growth path of an individual into a few parameters is called the growth curve⁽¹⁾.

There are several equations that have been used to describe the growth of plants and animals⁽²⁾, including Brody's⁽³⁾, Gompertz's⁽⁴⁾, Logistic⁽⁵⁾ and von Bertalanffy's⁽⁵⁾, all special cases of Richards' equation⁽⁵⁾. Growth curves reflect the interrelationships between the individual's inherent impulse to grow and mature, and the environment in which these impulses are expressed⁽⁶⁾. Some of these equations have been used to describe the growth of several species of zootechnical interest, such as Pantaneira bovines in Brazil⁽⁷⁾, and Holstein females to predict their growth from birth to first calving⁽⁸⁾. These equations have also been used to describe the growth of sheep genotypes^(9,10,11), dairy cattle^(12,13), and horses⁽¹⁴⁾.

Under grazing milk production systems with low use of supplemental feed and a mixture of bovine genotypes that differ in mature size, the average weight of the cow largely determines the maximum stocking rate supported by the system. Different bovine genotypes may have different mature weights and metabolizable energy requirements for maintenance. Fitting a growth curve from birth to maturity can be useful for calculating maintenance requirements over the life of the animal. The individual growth curves of animals can be estimated by fitting mixed nonlinear models, even with incomplete records of the growth curve of the animals of the herd. The objective of this study was to compare the goodness of fit of four nonlinear equations to describe the growth curves of Jersey, Holstein, and Jersey x Holstein cows grazing on mixed meadows of alfalfa-perennial ryegrass-orchard grass-white clover.

The study was conducted in the Module of Organic Milk Production in Grazing of the Experimental Farm of the Chapingo Autonomous University, Mexico. Díaz⁽¹⁵⁾ details the development of the Module. Briefly, the module started with 10 Holstein cows and 25 Jersey cows of first calving in May 2000. The animals that make up the herd are Jersey cows from the New Zealand genetic line, Holstein cows from the North American genetic line and cows originating from the cross of Holstein cows with Jersey semen.

The feeding of the animals is based on the grazing on meadows, hay that is preserved from these and corn silage that is produced in meadow areas that are renewed every year. The animals are managed in intensive rotational grazing in strips on mixed meadows of alfalfa (*Medicago sativa*) variety Aragonese, orchard grass (*Dactylis glomerata*) variety Potomac, perennial ryegrass (*Lolium perenniale*) variety Linn and white clover (*Trifolium repens*) variety Ladino.

The animals of the herd are managed in three groups: lactating, dry and growing animals. Depending on the growing conditions of the meadow, paddocks are assigned by group or grazing is carried out with the scheme of leaders and followers, the leaders are the cows in production and the followers the group of dry cows and growing cattle.

With this grazing scheme, the animals are provided with production conditions that guarantee sufficient freedom of movement, area for rest, fresh air, adequate light and temperature, clean water and sufficient food for the productive stage of the animal. In addition to the meadow forage, animals are provided with a freely accessible mineral mixture. This mixture was formulated based on a diagnosis of the mineral status of animals and meadow forage, with tests on blood, forage, feces, hair and milk⁽¹⁶⁾.

Cows give birth on the meadow, in the group of dry cows, providing them with assistance only when necessary. The calf remains with the mother in the meadow for the first two days of life consuming colostrum freely. On the third day, the mother joins the group of lactating cows, the calf is sent to a rearing room with natural ventilation, and it is assigned an individual cage with a raised floor. Only for females, a card is opened on which identification of the calf, date and weight at birth, identification of the mother and father are recorded. The identification of the calf consists of a tattoo on the right ear and earring on the left ear, using a four-digit system. During the first two weeks of life, the calves receive four liters of whole milk divided into two doses. Subsequently, in addition to milk, the calves have access to the meadow forage. Weaning is done at three months of age⁽¹⁵⁾.

The weight and age records of the animals of the genotypes studied were generated from the dates of birth, weighing dates and individual records of the live weight of animals at different stages of their life, from birth to maturity. The animals were periodically weighed at regular intervals of about 30 d. A Tru-Test digital scale (Tru-Test, Palmerston North, NZ), EC 2000 System with GP 600 Bars, with a capacity of 1,500 kg and an accuracy of 0.5 kg, was used. The live weight data used in this study were recorded from 2012 to 2016. The animals included in the study were weighed at birth, weaning, and monthly.

In total, there were 2,315 records of weight (kg) and age (d) generated by 54 Jersey, 6 Holstein, and 30 Jersey x Holstein cows, with ages ranging from 1 to 6,597 d.

The Brody⁽³⁾ model, a modified version of the Gompertz⁽⁴⁾ function, the Logistic⁽⁵⁾ and von Bertalanffy⁽⁵⁾ models were fitted to the weight and age data of the cows.

$$\text{Brody: } Y_t = A(1 - be^{-kt})$$

$$\text{Gompertz: } Y_t = Ae^{-e^{(b-kt)}}$$

$$\text{Logistic: } Y_t = A(1 + be^{-kt})^{-1}$$

$$\text{von Bertalanffy: } Y_t = A(1 - be^{-kt})^3$$

In all cases, Y_t is the live weight (kg) recorded at age t (days); parameter A corresponds to the upper asymptote, which estimates the mature weight (kg) of the animal; parameter b is an integration constant related to the initial weight; parameter k is the maturation rate; and e is the base of natural logarithms⁽¹²⁾.

With the information of weight and age, descriptive statistics were calculated in different sections of the herd growth curve. Nine age intervals were generated: three that covered the interval from birth to one year, and six that covered the interval from two to twelve years, with two years apart. A similar partition was made to describe the growth curve of North American Angus cattle⁽¹⁷⁾. Descriptive statistics were obtained using the MEANS procedure of SAS⁽¹⁸⁾.

For each genotype, each of the equations evaluated was fitted by the NLMIXED procedure of SAS⁽¹⁸⁾. Only the parameter related to mature weight (A) was fitted as a random effect in the respective equation; the remaining parameters of the growth curve (b and k) were considered fixed. A procedure similar to that of other studies, in which stochastic models were fitted to describe individual variation in farm animal growth, was followed^(19,20,21). The inclusion of a random term (a_i) associated with parameter A of the growth equations compared was done as described by Craig and Schinckel⁽¹⁹⁾ when fitting growth curves in pigs. Thus, the statistical model fitted within genotype, for each of the equations compared in the present study, included a random term related to the mature size of the cow, it is expressed as follows:

$$\text{Brody: } Y_{i,t} = (A + a_i)(1 - be^{-kt}) + \varepsilon_{i,t}$$

$$\text{Gompertz: } Y_{i,t} = (A + a_i)e^{-e^{(b-kt)}} + \varepsilon_{i,t}$$

$$\text{Logistic: } Y_{i,t} = (A + a_i)(1 + be^{-kt})^{-1} + \varepsilon_{i,t}$$

$$\text{von Bertalanffy: } Y_{i,t} = (A + a_i)(1 - be^{-kt})^3 + \varepsilon_{i,t}$$

where $Y_{i,t}$ is the live weight of the animal i recorded on day t of age, e is the base of the natural logarithms (i.e. 2.718281), A is the predicted mature weight, a_i is the random effect of the animal i for the parameter of the growth curve related to the mature weight (A) of the animal $\sim Normal(0, \sigma_A^2)$, t is the age of the animal in days, b is an integration constant related

to the initial weight of the animal, k is the maturation rate and $\varepsilon_{i,t}$, is the residual of the model $\sim Normal(0, \sigma_\varepsilon^2)$.

The fitting of these models generated, in addition to the estimators of the parameters of the growth curve, estimators of variance for parameter A (σ_A^2) and residual variance (σ_ε^2). The fitting of the model also generated estimators of $-2 \log$ likelihood, the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC), which were used as goodness-of-fit criteria to compare the four fitted equations.

The fitting of each of the models to the three genotypes studied generated the coefficients of parameters A , b and k , to generate the individual growth curves of animals. In the SAS code used, an expression was also included to generate the coefficients of the fixed regression to describe the average growth curve of each genotype studied. These coefficients were used to generate, in each equation and genotype, the predicted values of live weight to generate the individual curves of the animals and the average growth curves per cow genotype, using the SGPLOT procedure of SAS⁽¹⁸⁾.

The descriptive statistics of the live weight for different age intervals of the growth curve of the genotypes evaluated are shown in Table 1. In general, it is observed that the weight increases markedly in the first three to four years, subsequently, it remains relatively constant. The standard deviation increases as the age of the animal advances; this is explained by a greater variation in adult weight in the different genotypes⁽²²⁾.

Table 1: Descriptive statistics of weight (kg) grouped by age of Jersey, Holstein and Jersey x Holstein females managed in grazing

Age (days)	Jersey			Holstein			Jersey x Holstein		
	n	Mean	SD	n	Mean	SD	n	Mean	SD
0- 30	10	26.2	6.6	--	--	--	7	26.0	3.4
30- 120	19	56.1	11.9	--	--	--	2	69.5	21.9
121- 200	44	81.6	14.2	2	110.5	2.1	27	104.2	34.4
201-365	92	128.4	29.5	5	136.2	24.9	72	151.4	35.1
366-730	201	245.9	46.3	12	276.0	56.6	157	255.3	58.9
731-1460	404	338.5	54.3	28	490.5	66.5	269	365.0	60.4
1461-2190	213	358.5	51.1	43	477.0	42.5	138	441.7	56.3
2191-2920	103	384.4	33.4	55	512.0	37.0	23	480.7	55.1
>2920	235	403.0	58.0	130	527.2	44.5	11	464.0	28.9

SD = standard deviation.

The estimators of the goodness of fit of the model, $-2 \log$ likelihood, the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) are shown in Table 2. According to the magnitude of these estimators (smaller values indicate better fit), the von

Bertalanffy and Gompertz models were the ones that best fitted the growth curves of females of the Jersey genotype. For the growth curves of the Jersey x Holstein crosses, the best fit was obtained with the von Bertalanffy equation, and for Holstein with the Logistic, followed very closely by the Gompertz and von Bertalanffy equations.

Table 2: Values of the criteria used to compare the fit of the equations to the weight and age records of bovines of three genotypes

Genotype	Model	Indicator of the goodness of fit of the model ¹		
		-2 log likelihood	AIC	BIC
Jersey (J)	Brody	12963	12973	12983
	von Bertalanffy	12892	12902	12912
	Gompertz	12891	12901	12911
	Logistic	12920	12930	12940
Holstein (H)	Brody	2945	2955	2954
	von Bertalanffy	2915	2925	2924
	Gompertz	2909	2919	2918
	Logistic	2895	2905	2904
JH	Brody	7143	7153	7260
	von Bertalanffy	7111	7121	7128
	Gompertz	7122	7132	7139
	Logistic	7151	7161	7168

¹AIC and BIC are the Akaike (AIC) and Bayesian (BIC) Information Criteria for assessing the goodness of fit of the respective model (lower values indicate better model fit).

In a study of bovine growth in Brazil, the Brody equation generated the best fit to describe the growth curve of Nellore bovines in confinement⁽²³⁾. Likewise, the Brody equation best fitted the growth curves of Tropicarne bovines, which implies for this genotype a slow maturation rate, characteristic of the growth of bovines under grazing conditions in the tropics⁽²⁴⁾. Brown *et al*⁽²⁵⁾ reported that the Brody equation best fitted the growth curve in several bovine genotypes under different management and feeding conditions. In contrast, other researchers⁽²⁶⁾ indicate that the Gompertz and von Bertalanffy equations best fitted to describe the growth of Hereford steers, which is consistent with what was found in this study for the Jersey and Jersey x Holstein genotypes.

The estimators of parameters *A*, *b* and *k* of the growth models evaluated, as well as the estimators of the variances of 'mature weight' and residual are presented in Table 3. Parameter *A*, which represents mature weight, was different in each genotype, depending on the equation used. The Brody equation fitted for the three genotypes the highest value of mature weight, which is consistent with what was obtained in other studies⁽²³⁾, in which it is also mentioned that this equation overestimates mature weight. Herrera *et al*⁽²⁷⁾ indicated that groups of animals with higher *A* value are less precocious. For Holstein, the von Bertalanffy

and Logistic equations produced practically the same A value (512 kg). This value of mature weight for cows of the Holstein genotype is well below the estimators of 591, 566 and 543 kg obtained in Ireland under grazing conditions for two lines from Holstein-Friesian from North America-Europe and Holstein-Friesian from New Zealand, respectively⁽¹³⁾. The Brody equation yielded the lowest value of k . A small value of k represents a slower growth rate to reach asymptotic weight from initial weight, or slower maturation rates^(7,24,28).

Table 3: Parameters of the growth curve (\pm standard error), estimators of residual and mature weight variances after fitting the equations to the weight and age records of three bovine genotypes

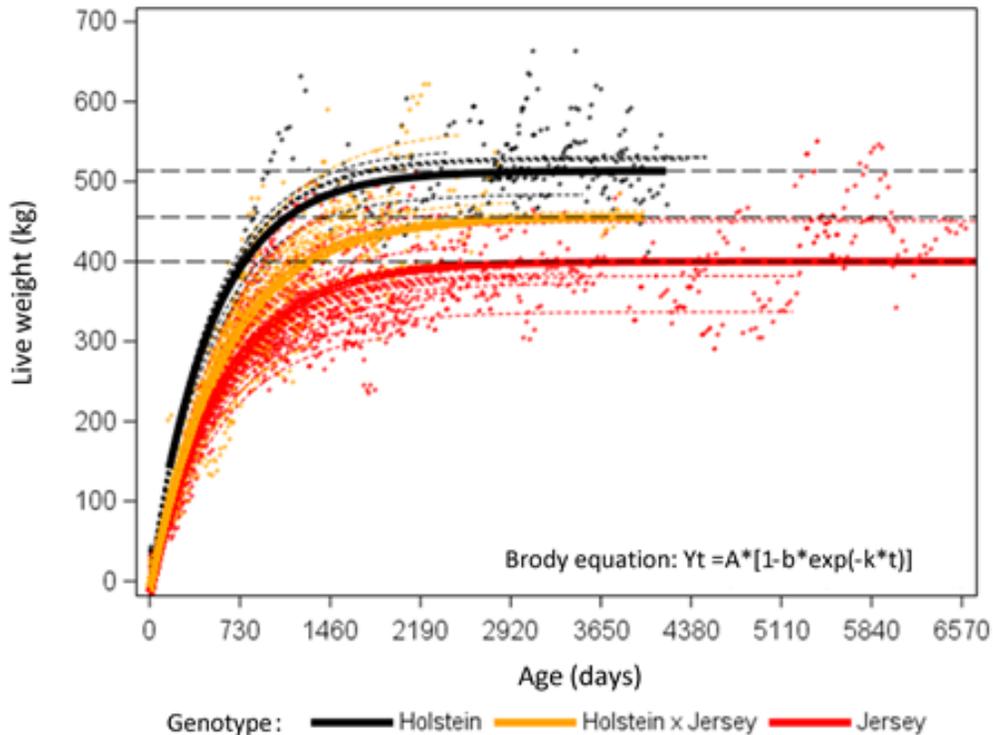
Parameter	Jersey	Holstein	Jersey x Holstein
Brody equation			
A	400.0 \pm 6.5	513.5 \pm 13.6	455.8 \pm 9.4
b	1.04 \pm 0.01	0.99 \pm 0.03	1.02 \pm 0.02
k	1.71E ⁻³ \pm 5.6E ⁻⁵	1.95E ⁻³ \pm 0.01	1.65E ⁻³ \pm 8.1E ⁻⁵
σ_A^2	1005.0 \pm 156.8	800.0 \pm 617.0	803.0 \pm 121.0
σ_e^2	1075.0 \pm 43.7	1875.0 \pm 154.2	1497.5 \pm 100.0
Gompertz equation			
A	383.5 \pm 5.6	510.6 \pm 15.0	426.6 \pm 7.9
b	0.98 \pm 0.03	1.30 \pm 0.01	0.84 \pm 0.04
k	3.19E ⁻³ \pm 9.6E ⁻⁵	3.86E ⁻³ \pm 3.42E ⁻⁴	2.97E ⁻³ \pm 1.27E ⁻⁴
σ_A^2	918.7 \pm 140.2	904.8 \pm 2598.0	952.4 \pm 143.2
σ_e^2	996.4 \pm 39.7	1731.2 \pm 148.4	1238.0 \pm 68.0
Logistic equation			
A	373.5 \pm 5.3	512.3 \pm 10.2	413.8 \pm 7.5
b	7.31 \pm 0.41	13.2 \pm 2.86	5.55 \pm 0.39
k	4.69E ⁻³ \pm 1.39E ⁻⁴	5.43E ⁻³ \pm 4.02E ⁻⁴	4.26E ⁻³ \pm 1.83E ⁻⁴
σ_A^2	900.8 \pm 134.4	500.6 \pm 437.7	958.7 \pm 138.7
σ_e^2	1000.4 \pm 39.3	1661.5 \pm 141.8	1282.7 \pm 70.6
von Bertalanffy equation			
A	388.4 \pm 5.9	512.0 \pm 10.6	432.3 \pm 8.6
b	0.64 \pm 0.02	0.92 \pm 0.16	0.59 \pm 0.02
k	2.70E ⁻³ \pm 8.3E ⁻⁵	3.45E ⁻³ \pm 3.92E ⁻⁴	2.57E ⁻³ \pm 1.07E ⁻⁴
σ_A^2	1013.7 \pm 163.9	512.2 \pm 411.7	1153.9 \pm 191.7
σ_e^2	998.1 \pm 39.8	1778.0 \pm 152.0	1135.3 \pm 57.6

¹ A is the parameter of the growth curve that corresponds to the upper asymptote, which estimates the mature weight (kg) of the animal; b is an integration constant; k is the maturation rate; (σ_A^2) is the variance of the mature weight (kg²) of the animal estimated by the fitted model; (σ_e^2) is the residual variance (kg²).

The fit of the Brody equation to the weight and age data of the three genotypes studied is shown in Figure 1. In the present work, the availability records from birth to weaning at the

beginning of the project was low. For the Jersey and Jersey x Holstein genotypes, the Brody equation, in the case of the present work, predicted negative values for birth weight, while for Holstein, it estimated positive but low weights. This is consistent with what was estimated by Mgbere and Olutogun⁽²⁹⁾, who argue that the Brody equation underestimates weight during the first days of life of N'Dama cattle, but that it fits well at ages greater than six months. Similarly, Berry *et al*⁽¹³⁾ found that the Brody equation predicts negative weights at early ages when used to fit the growth curves of Holstein cows from the North American, European Holstein and Holstein-Friesian genetic lines, managed under semi-grazing conditions. In Brazil⁽³⁰⁾, they found that the Brody and Gompertz equations had the best fit of the growth curve from birth to adulthood of Caracu cows. This is consistent with the best fit of the Brody equation to describe the growth curve of Lagune beef cattle under grazing conditions⁽³¹⁾.

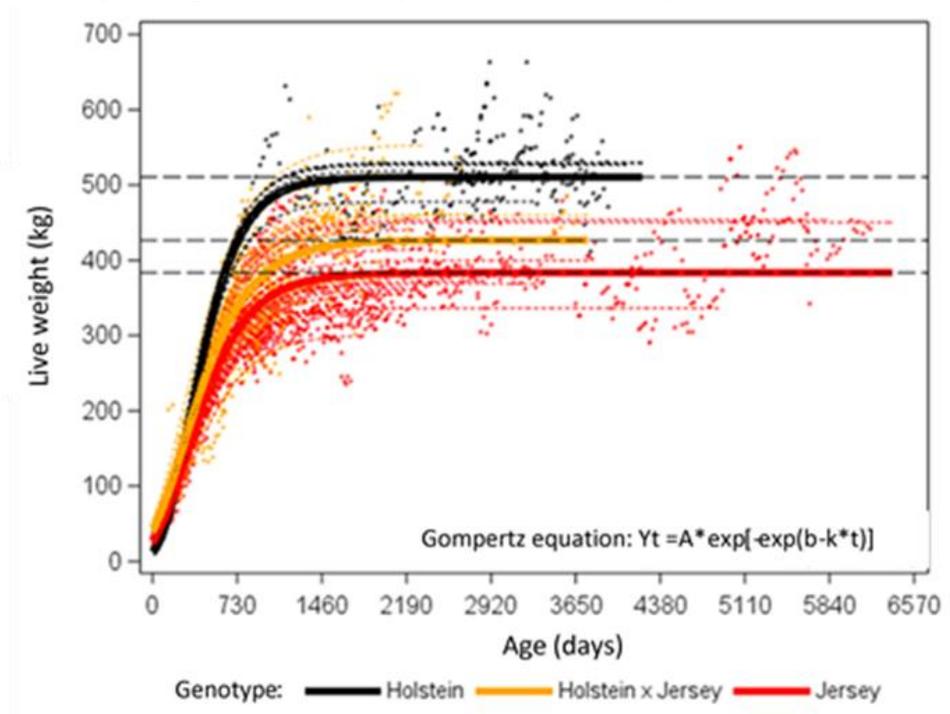
Figure 1: Scatter plot for weights and ages of the fit of the growth curves generated by the Brody equation for Jersey, Holstein and Jersey x Holstein females



The fit of the Gompertz equation to the weight and age data of the three genotypes studied is shown in Figure 2. In the present study, birth weights for Holstein, predicted with the fit of the Gompertz equation, were very close to zero, while for Jersey and Jersey x Holstein, a better fit was observed. Several researchers⁽³²⁾ used this equation to describe the growth of dairy cattle, as it was the one that best fitted their data. Berry *et al*⁽¹³⁾ also found that the

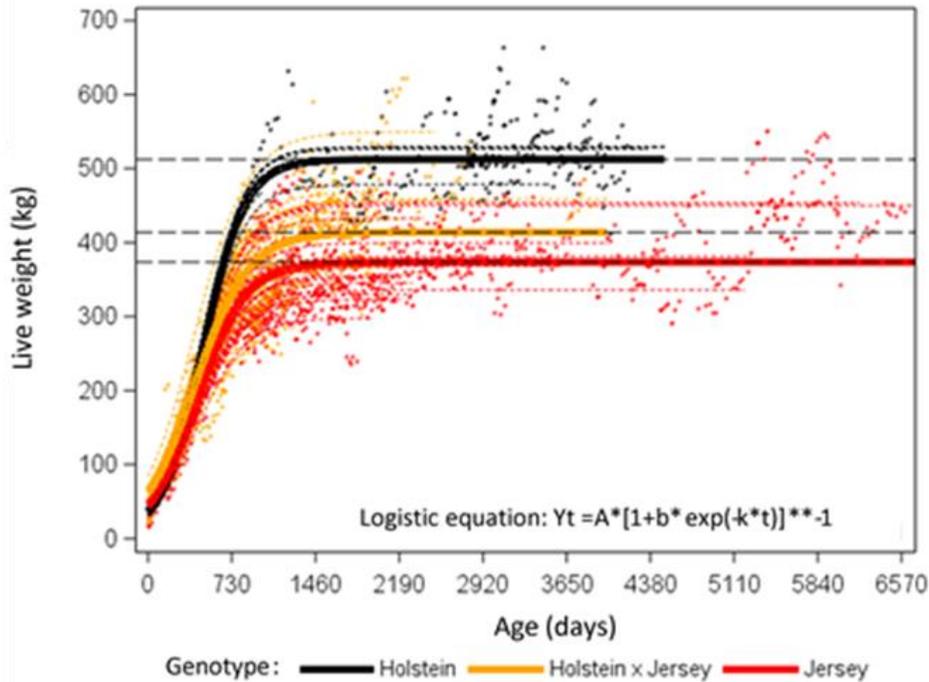
Gompertz equation better fitted the growth curves of American Holstein, European Holstein and Holstein-Friesian cows, managed under grazing conditions, better than Brody's.

Figure 2: Scatter plot for weights and ages of the fit of growth curves generated by the Gompertz equation for Jersey, Holstein and Jersey x Holstein females



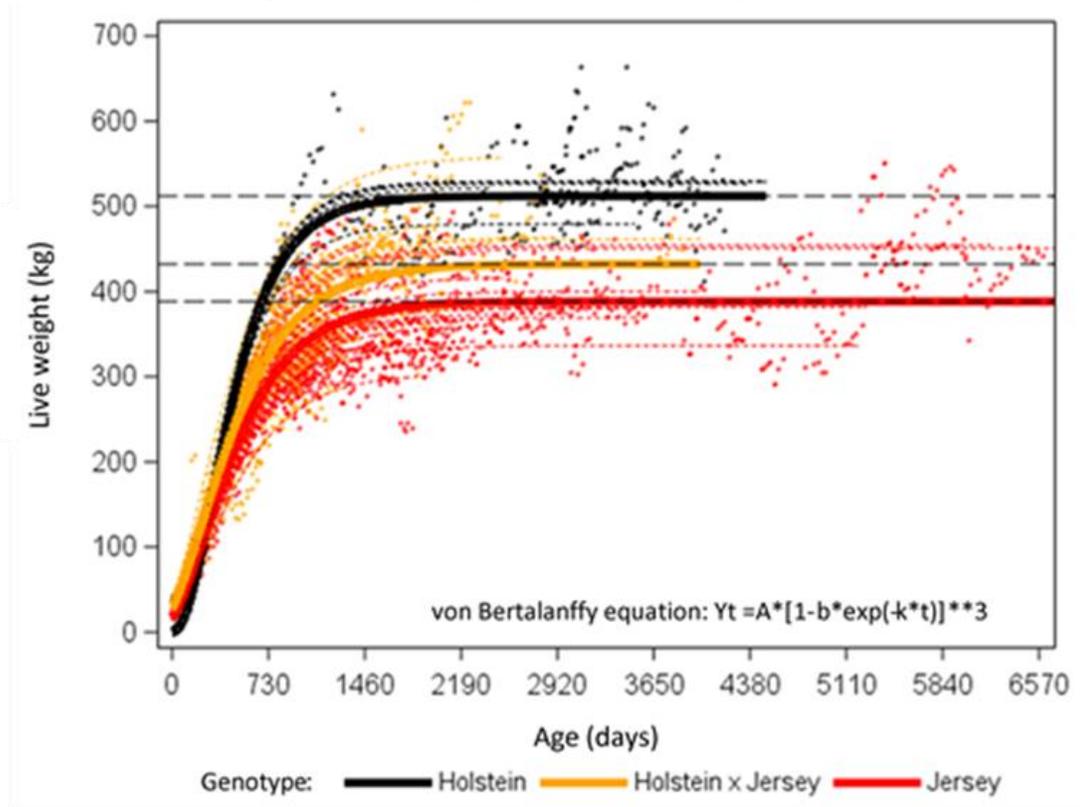
The fit of the Logistic equation to the weight and age data of the three genotypes studied is shown in Figure 3. In previous studies describing the growth curve of dairy cattle, the Logistic equation underestimated the mature weight of the animals⁽¹²⁾. In this study, the Logistic equation yielded values identical to those of von Bertalanffy for this growth curve parameter.

Figure 3: Scatter plot for weights and ages of the fit of growth curves generated by the Logistic equation for Jersey, Holstein and Jersey x Holstein females



The fit of the von Bertalanffy equation to the weight and age data of the three genotypes studied is shown in Figure 4. This equation fitted the live birth weights of Holstein with negative values and of Jersey and Jersey x Holstein, with weights close to zero, which differs from what was reported in other studies in which the von Bertalanffy equation overestimated the weight at early ages in N'Dama cattle⁽²⁹⁾. Spanish researchers⁽³³⁾ compared the Brody, Richards and von Bertalanffy equations to describe the growth curves of Retinta beef cows under extensive grazing conditions in Spain, finding that the von Bertalanffy equation had the best fit for the growth pattern of this genotype. In the present study, the von Bertalanffy equation generated the best fit in the growth curves of Jersey and Jersey x Holstein cows, and for Holstein cows, it produced parameters identical to those of the Logistic equation, which produced the best fit for the growth curves of this genotype.

Figure 4: Scatter plot for weights and ages of the fit of growth curves generated by the von Bertalanffy equation for Jersey, Holstein and Jersey x Holstein females



In conclusion, the Gompertz and von Bertalanffy equations best describe the growth curve of Jersey cows; that of von Bertalanffy, that of Jersey x Holstein females; and the Logistics, that of Holstein females, followed by those of Gompertz and von Bertalanffy. For the management and feeding conditions of the animals in this study, and in order to adequately describe their growth pattern, the growth curves of the females of the three genotypes studied can be fitted with the von Bertalanffy equation.

Acknowledgements

To the National Council for Science and Technology (CONACYT) for the financial support granted to the first author to carry out Master of Science studies at Universidad Autónoma Chapingo.

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