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Growth Curve Analysis for a QTL Resource Family F_2 Intercross of the Oh-Shamo and White Leghorn Breeds of Chickens

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Abstract: A growth curve analysis was performed with 439 F_2 birds from an intercross of the Oh-Shamo (Japanese Large Game) and White Leghorn breeds of chickens. Individual body weight and shank length were measured at every week until 16 weeks of age. The Gompertz and Logistic models were examined to verify a proper growth curve function for both body weight and sank length in each sex. To estimate the curve parameters on both function models, the Nonlinear Fit Platform of JMP 5.01 was used. In the mean of both the body weight and shank length within sex, there was no significant difference at hatch. However, the significant differences appeared after 1 week of age and then the level of differences within sex increased by age in both traits. As the results of mathematical function analyses, both models significantly fitted to the actual growth with >0.96 coefficients of determinations (R^2) however, the Gompertz model showed slightly better fitting with 0.99 of R^2 on all of traits and sexes. Also, the Gompertz model was able to estimate the closer values to actual mature body weight and shank length than Logistic's one. The estimated inflecting points had no large deference between the Gompertz and Logistic functions. On the other hand, the growth curve for shank length had the inflecting point at younger age (4-7 weeks of age) than the growth curve for body weight (9-11 weeks of age). The growth speed of bone development estimated by the shank growth curve reached the maximum earlier than the body development. It indicated that the bone and the body have different growth patterns. As the results, the Gompertz model might be a proper growth curve function for growth analysis and the different growth pattern between bone and body may induce the detection of QTLs for bone and body development separately.

Key words: Growth curve, gompertz, logistic, quantitative trait loci, chickens, Japan

INTRODUCTION

Growth refers to a change of size over time (age) and every living entity on this planet has the own growth characteristic (Brody, 1945). The process of growth measured as body weight and/or shank length on a longitudinal time frame has often been summarized using mathematical equations fitted to growth curves. One of the objectives of the curve fitting is to describe the course of body weight and/or shank length increase over age with mathematical parameters that are biologically interpretable. Understanding the biology of model parameters and their relationships provides a sound basis for developing a breeding strategy to modify or change the trajectory of growth (Aggrey, 2002).

In a mathematical analysis for growth, the sigmoid curve functions such as Gompertz (Gompertz, 1825), Logistic, Von Bertalanffy (1938) and Richard (1959) are often used. The Gompertz model carries three parameters: upper asymptote, curve position and growth rate. The Logistics model also has the same parameters as the Gompertz model. The Bertalanffy model also contains three parameters but they are asymptote, growth rate and the initial time value as curve position. The Richards model has four parameters of asymptote, the maximum relative growth per time, the age at maximum rate of growth and the curve shape parameter.

Since, the Gompertz and Logistic functions have the same three parameters, Winsor (1932) logically compared the two models. The researchers summarized that the

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Logistics model meets good fits on materials having an inflection about the middle between lower and upper asymptotes and the Gompertz model will meet good fits on materials having an inflection about 37% point of the total growth. However, it does not appear either model has any substantial advantage over the other in the range of phenomena which will fit. Rickleft (1968) also indicated that the Gompertz and Logistic models have a fixed growth form with points of inflection at about 37 and 50% of the asymptote, respectively. In another study on the Gompertz equation, Barbato (1991) pointed out that the equation is a function of the asymptote (Mature).

The Richards model has a variable point of inflection specified by the curve shape parameter (m) (Richard, 1959). When m is equal to two third, the Richards function is likely to the Bertalanffy function. The Richards growth function is similar to the Gompertz growth function as m tends to 1. In addition, the Richards model shows a similarity to the Logistic model when m is equal to 2.

So far, a number of nonlinear models have been applied to describe the growth curve in chickens (Grossman and Bohren, 1985; Grossman and Koops, 1988; Akimoto, 1991; Anthony *et al.*, 1991; Barbato, 1991; Mignon-Grasteau *et al.*, 2000; Aggrey, 2002). Many of reports indicated that actual growth of body weight in chickens highly fit either Gompertz function or Logistics function. Akimoto (1991) used the Richards function analysis for the body weight growth in the Rhode Island Red. His results indicated that the model showed the highest fitting when the curve shape parameter m tended to 1. It means that the Gompertz model would be suitable to the growth expression. Aggrey (2002) also mentioned that the four-parameter model was difficult to be fitted to the growth, though the Richards model was attractive and flexible.

In the present study, it was designed to compare the Logistic and Gompertz function models using growth data of F_2 birds from a QTL resource family and to study which models would be suitable for a QTL analysis for growth curves.

MATERIALS AND METHODS

Animals and trait measurements: An Oh-Shamo (Japanese Large Game, JLG) male and three White Leghorn (WL) females were mated to built a QTL resource family. Subsequently, 4 F_1 males and 22 F_1 females were mated in full-sib matings. As F_2 birds, 224 males and 215 females were obtained. This resource family partially contained F_2 birds in the earlier report (Tsudzuki *et al.*, 2007) nevertheless, more number of F_2 birds were added in the present research.

Body weight and shank length of each bird were measured at hatch (BW00, SH00) and every week until 16 weeks of age (BW01-BW16, SH01-SH16).

Growth function models

Gompertz model: The equation of the Gompertz growth curve is defined as follows:

$$L_G = K \exp(-a \exp(-b\,t))$$

Where the parameter K is upper asymptote of body weight or shank length that is the weight or length at an infinite age. The a explains curve position which is equal to ln (K/BW00) or ln (K/SH00) where BW00 and SH00 are the estimated hatching weight and the estimated hatching shank length, respectively. Growth (Maturation) rate on weight or length is estimated by the b. Since, the t places a time, weeks of age were put to use in the present study.

Logistic model: The following equation describes the Logistic growth curve:

$$L_L = K/(1+\exp(-a \exp(-b\,t)))$$

Where the parameter definitions are as the same as the Gompertz equation. To estimate the curve parameters on both function models, the Nonlinear Fit Platform of JMP 5.01 (SAS Institute Inc., Cary, NC, USA) was used. To calculate the other statistical matters, JMP 5.01 was used also.

RESULTS

Overall means and standard deviations for the body weight and shank length in both sexes are shown in Table 1. At hatch, the means of body weight in males and females were the same. The mean of shank length at hatch was slightly longer in males than in females but there was no significant difference. On the other hand at 1 week of age, the sex difference with a statistically significant level had already appeared in both the body weight and shank

Table 1: Means and Standard Deviations (SD) for the body weight and shank length on F_2 birds[a]

Weeks of age	Body weight		Shank length	
	Female	Male	Female	Male
0	35.0±2.3500	35.0±2.3900	26.2±0.81	26.5±0.82
1	51.9±6.3100	54.7±7.0600*	29.8±1.16	30.8±1.28*
2	73.1±14.530	79.7±18.310*	33.1±2.30	34.6±2.62*
5	211.6±53.790	245.1±59.710*	47.8±5.05	51.4±5.47*
10	669.3±125.71	831.5±157.42*	77.8±7.18	86.6±6.90*
16	1176.6±157.21	1577.5±224.05*	96.1±5.40	114.0±6.79*

Values are shown as Mean±SD; [a]N = 439 (224 males and 215 females); *Statistically significant between sexes ($p<0.01$)

Table 2: Estimated parameters in the Gompertz function (L_G) and Logistic function (L_L), the correlations between the actual measurements and the estimated functional values, the coefficients of determination and the inflecting points of age in the each growth curve in F_2 birds

	Body weight				Shank length			
	Female		Male		Female		Male	
Growth function	L_G	L_L	L_G	L_L	L_G	L_L	L_G	L_L
Parameters								
K (Asymptote)	1705.50	1305.90	2493.20	1803.60	125.16	108.57	159.53	131.58
a (Position)	4.46	3.29	4.77	3.47	1.70	1.27	1.91	1.46
b (Rate)	0.16	0.33	0.15	0.33	0.12	0.22	0.11	0.21
Correlation[a]	0.99	0.99	0.99	0.98	0.99	0.99	0.99	0.99
R^2[b]	0.99	0.99	0.99	0.96	0.99	0.98	0.99	0.99
Inflecting point[c]	9.58	9.86	10.64	10.51	4.29	4.76	5.79	6.94

[a]The correlations between the actual measurements and estimated functional values; [b]The coefficients of determination; [c]The inflecting point of age (weeks)

length. With weeks of age, the differences between sexes increased. Similarly, the standard deviation for both traits and sexes increased with age. At 16 weeks of age, the sex difference in body weight was >400 g and the difference in shank length was >17 mm.

The fitted parameters for each growth model are shown in Table 2. In comparing upper asymptote of each model, the Gompertz function estimated heavier body weight and longer shank length than the Logistic function. The curve position parameters resulted that the Gompertz curve showed earlier stage (age) position than the Logistic curve. The growth rate parameters of the Logistic function showed faster growth speed comparing with the Gompertz function.

The correlations between the actual measurements and estimated functional values are shown in Table 2. The correlation was >0.98 in all of the traits and all of the estimated growth curves. Also, the coefficients of determination (R^2) on each function are shown in the same table. Though the lowest value was indicated in the Logistic function model for the male body weight, the value of R^2 was 0.96.

The inflecting points of age in each growth curve are shown in Table 2. Within the same sex and the trait, the inflecting points were similar between the functions. However, the trait difference and sex difference were observed. In the body weight, the female had the inflecting point at younger age (9.58 and 9.86 weeks of age in the Gompertz and Logistic, respectively) than the male (10.64 and 10.51 weeks of age in the Gompertz and Logistic, respectively). Also, in the shank length, the female had the inflecting point at younger age (4.29 and 4.76 weeks of age in the Gompertz and Logistic, respectively) than the male (5.79 and 6.94 weeks of age on Gompertz and Logistic, respectively). Comparing the traits, the shank length had the inflecting point at younger age (4.29-6.94 weeks of age) than the body weight (9.58-10.64 weeks of age).

DISCUSSION

As shown in Table 1, there was no sex difference in the body weight and shank length at week zero (at hatch). It indicates that the body mass and body frame in newly hatched chicks are similar regardless of sexes. However, the growth differences in sexes started soon after hatch and the level of differences increased with age. At the molecular level, the dissimilarity between males and females will be in the sex chromosome. It is thought that a gene (*locus*) related to growth on the sex chromosome starts to work after hatch.

In comparing the growth curves between the body weight and shank length, they showed different sigmoid shapes because of the trait unlikeness. The results clearly indicated that the shank length developed faster than the body weight. The curve position of the growth curve for the shank length was located at earlier stage than for the body weight and the inflecting point of the growth curve for the shank length appeared at earlier age than for the body weight. It indicates that the bone grows first and then the other body compositions such as the muscle and internal organs, grow. Furthermore, the results induced similar conclusion to that of Koops (1986), Koops *et al.* (1987) and Grossman and Koops (1988) indicating that growth has two stages with development of bones at the first stage and accumulation of muscle and fat at the second stage. If QTL analysis is separately applied to the body weight and shank length development, it may be possible to detect different QTLs for body weight development and shank growth (bone development).

In the estimation of growth curves in the present study, the results showed highly fitted growth curves in both the Gompertz function model and Logistic function model. The correlations between the actual measurements and estimated functional values were >0.98 in all of conditions. Moreover, the coefficients of determination (R^2) in all functions were >0.96. Previous studies on growth curve analysis also indicated good fitting results. For example in chickens, Akimoto (1991) applied the

Gompertz function for growth of the body weight and the estimated growth curve had 0.99 of R^2. Aggrey (2002) applied several growth curve functions to the growth of the body weight and the R^2 from both Logistic and Gompertz models was 0.98. Namely, the growth curve function information (Parameters) can be as good as a phenotypic value and the information may provide a summary of entire growth such as the growth speed and the possible mature values of the trait.

In the present study, the heritabilities of the growth curve parameters were not estimated. However, some of studies estimated the heritabilities. Barbato (1991) reported that Logistic function values were moderately heritable with 0.18. On the other hand, Mignon-Grasteau *et al*. (2000) estimated the heritability values of the Gompertz function and they were 0.42 in the male chicken and 0.47 in the female chicken. Therefore, it may be considerable that the growth curve information is heritable one.

Another issue of the present study was that which growth function (Gompertz or Logistic) model might provide better information for QTL analysis. Correlations between the actual measurements and the estimated curve values showed no superiority between the two models. The R^2 also indicated that both functions worked equally however, the Logistic function model for the male body weight showed the lowest fitting value of R^2 as 0.96. Accordingly, the Gompertz curve model is thought to be slightly better than the Logistic curve model.

In other points of view, the Gompertz model might also be better than the Logistics. The upper asymptote (K) in the two growth models showed large differences in both the body weight and shank length. The Gompertz function estimated heavier mature body weight and longer shank length than the Logistics function. Considering the actual mature body weight and shank length in chickens, the K of the Gompertz model was closer to the actual phenotypic values. This phenomenon might be based on the characteristics of the functions.

The Logistic model has a fixed growth form with points of inflection at about 50% of the asymptote and the curve shows a symmetrical line with respect to the inflection point (Rickleft, 1968). Because of these characteristics of the Logistic function, the record values at 16 weeks of age were counted as the values near to maximum for the asymptote parameter estimation. As the result, the Logistic function possibly showed smaller K than the actual mature body weight and shank length.

On the other hand, Barbato (1991) indicated that the Gompertz equation is a function of the asymptote (Mature). In the present study, the data of the body weight and shank length were available until 16 weeks of age. They had not reached the mature age yet but >37% of the growth which indicates the inflection point of the Gompertz curve (Winsor, 1932; Rickleft, 1968) had already been completed in each trait before 16 weeks of age. The records until 16 weeks of age might provide good enough data to estimate the K value. Therefore, it would be better to use the Gompertz model to analyze the growth.

CONCLUSION

The growth curve information might be useful phenotypic values indicating entire body development and shank growth. Moreover, the function parameters (as the curve information) would be useful phenotypic traits information to be applied to QTL analysis. Using the Gompertz function information may provide QTL detection affecting entire body development and shank growth (as bone development) at rearing periods in chickens.

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