

## Genetic Parameters of Growth Curve Parameters and Weekly Body Weights in Japanese Quails (*Coturnix coturnix japonica*)

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**Abstract:** This study was carried out to estimate heritabilities of growth curve parameters, weekly body weights and genetic-phenotypic correlations among the traits of growth in Japanese quail. Body weight data taken from hatching to 6 weeks of age of approximately 500 quails of both sexes from 40 sires and 120 dams were utilized to estimate genetic parameters. Restricted maximum likelihood estimation was applied for variance-covariance structures of a multiple trait pooled (sire and dam) components model using SAS PROC MIXED and SAS/IML. Growth curves for individual quail were fitted using the Gompertz model. Mean and heritability estimates of Gompertz model parameters  $\beta_0$ ,  $\beta_1$ ,  $\beta_2$  were 227.57, 3.44, 0.084 and 0.42, 0.21, 0.40, respectively. Heritability estimates of weekly live weights ranged from 0.42-0.62. Means and heritabilities for weight and age at the inflection point were estimated as 83.72, 15.23 and 0.36, 0.08 g, respectively. All genetic correlations were higher than phenotypic correlations. Genetic and phenotypic correlations between the growth curve parameters were relatively high and negative with one exception. The only positive correlation was between  $\beta_1$  and  $\beta_2$ . Genetic and phenotypic correlations between the parameter  $\beta_0$  and body weights were positive and moderate to high. The genetic and phenotypic correlation estimates of parameter  $\beta_2$  among weekly body weights were generally negative.

**Key words:** Quail, gompertz, body weight, multiple trait, heritabilities, genetic correlations

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### INTRODUCTION

There are two main reasons of the great development, which has taken place in the last 50 years in the broiler industry. The first reason is obtaining hybrid chicks, which have superior genetic structure and the second reason is the improvement of the environmental conditions. Chicken meat makes up 86.41% of the consumption of poultry meat in the world (FAO, 2009). In countries, where poultry meat consumption is high, broiler consumption rate is below the world average. The increase in the consumption of poultry meat, such as Turkey, duck and goose does not decrease the total amount of broiler meat consumption. On the contrary, it increases the total consumption of poultry meat and as a result, it provides more cheap animal protein sources for consumers. An increase in poultry species production can take place only if breeding levels improve.

The Japanese quail is used in commercial production for its meat and egg due to qualities such as the short-time generation interval, low feed consumption, high breeding ability, capacity to have a great number of quails per unit area, low breeding costs and high resistance to diseases. Egg production is important in Far East and Asian countries, whereas meat production is

important in Europe (Minvielle, 2004). Most of the commercial quail breeding companies are small-scale. Usually genetic improvement is not performed for breeding flocks used in these companies. However, in the studies carried out to improve the live weight and egg productivity of quails, successful results could be acquired in the short-term.

The essential traits used in breeding programs to increase poultry meat production are for live weight and feed consuming. In evaluations regarding growth, live weights measured in fixed ages, growth curve and live weight-gain are used. Almost all the quantitative genetic studies carried out with the aim of increasing quail meat production have been performed to increase the live weight at fixed ages in early periods. With these methods, lines whose live weights were increased by 300% could be acquired as a result of long-term selection application. In consequence of the rapidly increasing live weight, undesired results such as decline in the number of fertilized eggs and devolution in feed utilization appeared (Minvielle, 2004).

Growth curves reveal time-dependent non-linear changes of the body or organ weights in animals. Growth curves usually express the growth achieved generally with 3 or 4 parameters and with the biologically

interpretable values calculated from these parameters. There are additive and non-additive genetic variations between breeds, lines and individuals in terms of growth curve parameters (Akbas and Oguz, 1998). Growth curve parameters and some values calculated from a model can be used as the criteria in index, independent culling and BLUP applications in poultry breeding.

Studies to determine the most convenient non-linear regression model used in modeling the growth patterns of animal breeds, have been carried out for several years. The most commonly used growth models for this purpose are Gompertz, Richards, Bertalanffy, Brody, Logistic, Negative Exponential, Morgan-Mercer Flodin and recently Hyperbolic models (Knizetova *et al.*, 1991; Aggrey, 2002; Golian and Ahmadi, 2008). In many studies carried out to model the growth data of Japanese quails, the best model was found to be the Gompertz Model with three parameters in terms of the goodness of fit criteria (Tzeng and Becker, 1981; Anthony *et al.*, 1991; Barbato, 1991; Akbas and Oguz, 1998; Mignon-Grasteau *et al.*, 1999).

The Gompertz Growth Model has three parameters, which are defined as asymptotic weight, integration constant and growth rate. The parameter determining the maximum value of the characteristic, whose time-dependent change is measured, when the time reaches to infinite is called the asymptotic weight parameter. The scaling parameter is defined as the integration constant. The amount of change measured in a unit of time is called the growth rate and the parameter expressing this change rate is called the growth rate parameter (Akbas and Oguz, 1998). The inflection point divides the growth curve into two terms, which are the increasing growth rate term (accelerating period) and the decreasing growth rate term (decelerating period).

Some studies have been carried out to analyze the quail growth patterns with the Gompertz model. Following long-term selection research, Marks (1978), Hyankova *et al.* (2001), Aggrey *et al.* (2003) and following short-term selection research Akbas and Oguz (1998) and Balcioglu *et al.* (2005) analysed the growth patterns of the lines they achieved with the Gompertz Model. There are few studies performed to estimate heritabilities and genetic correlations of Gompertz growth curve parameters for Japanese quails (Mignon-Grasteau *et al.*, 1999; Akbas and Yaylak, 2000).

In order to establish a breeding program, it is essential to estimate genetic parameters for improving the traits. The scale of the genetic parameters can show the amount of improvement by selection. Although, several methods for genetic parameters estimation can be applied as realized heritability or parent-offspring regression, the

most frequently used method is the variance component estimation with REML estimator (Firat, 1996; Saatci *et al.*, 2003).

In this study, it was aimed to determine the genetic correlations and heritabilities belonging to weekly live weights and Gompertz growth curve parameters in an unselected initial quail flock, where a breeding program to increase the live weight is going to be applied.

## MATERIALS AND METHODS

The present experiment was conducted at the Poultry Breeding Unit, Animal Science Department, Faculty of Agriculture, Akdeniz University. Data consisted of individual live weights at hatch, 7, 14, 21, 28, 35 and 42 days of age from 499 fully pedigreed Japanese quail. Full-sib and half-sib progeny belonging to 40 sires and 120 dam formed the basis of this study. One dam was placed into each cage and 3 dams for each sire were used. Both sires were mated to three individually-housed dams, with one day spent with each of these in rotation. Quail chicks were hatched, wing-banded and placed in quail battery brooders. The birds were grown in brooder cages from 1-21 days of age and were fed with starter diets of (2900 kcal ME kg<sup>-1</sup> and 28% CP) having water *ad libitum*. At 21 days of age, quail were moved to colony cages and then were fed a grower diet (2900 kcal ME kg<sup>-1</sup> and 28% CP). Water and feed were *ad libitum*. Temperature was maintained at approximately 32°C for the first week after hatching and then decreased gradually to 24°C at 21 days of age. The daily lighting period was 18 h during all of the experiments. Individual live weights of birds were recorded weekly using a digital scale ( $\pm 0.1$ ).

The Gompertz non-linear model,  $Y_t = \beta_0 \exp(-\beta_1 \exp(-\beta_2 t))$ , was used to fit the growth pattern in the study. In the model,  $Y_t$  is weight (g) at time  $t$ , which is the age of quail in days.  $\beta_0$ ,  $\beta_1$  and  $\beta_2$  are growth curve parameters.  $\beta_0$  is asymptotic weight that is the weight at time  $t = \infty$ .  $\beta_1$  is the scaling parameter (integration constant), which is related to initial values of  $Y$  and  $\beta_2$  is related to growth rate and depends on  $dy/dt$ ,  $\beta_0$  and the coordinates of point of inflection ( $I_{pw}$ ,  $I_{pt}$ ) (Akbas and Oguz, 1998).  $I_{pw} = \ln(\beta_1)/\beta_2$  represents the production at the point of inflection age ( $I_{pt} = \beta_0/e$ ) when growth rate is maximum (Akbas and Oguz, 1998). Growth curve parameters for the Gompertz model were estimated for each bird using the SAS software non-linear regression procedure (PROC NLIN) with the Levenberg-Marquardt iterative algorithm. The convergence criterion was 1.0 E-05 (SAS, 2005).

Sire, dam, environment variance components and additive genetic and environmental covariance matrix for multivariate analysis were estimated from the mixed-model

equations by SAS PROC MIXED (Fry, 2004; Holland, 2006). Procedures for estimating variance-covariance components from weekly live weights and Gompertz model parameters involved using a restricted maximum likelihood estimator and an unstructured covariance model (SAS, 2005). Genotypic correlation and heritability estimates of the traits and their approximate standard errors were obtained by the SAS Interactive Matrix Language (IML) procedure (Fry, 2004; Holland, 2006).

**RESULTS AND DISCUSSION**

Least-square means, standard errors of means, coefficients of variation and minimum and maximum observations of weekly live weights are given in Table 1. Weekly live weights were 8.67, 32.91, 75.59, 121.02, 155.04, 180.71 and 200.47 g from hatching to the slaughter age, respectively. Live weights of quails from hatching to 6 weeks of age were similar to those reported in the literature (Caron *et al.*, 1990; Toelle *et al.*, 1991; Marks, 1991; Saatci *et al.*, 2003; Sezer *et al.*, 2006). Coefficients of variation obtained at all weeks are in the range of 10.33 and 15.90%.

The heritability estimates for hatching and weekly live weights of quails are presented in Table 2. In this study, heritability estimates for body weight of quails are ranged from 0.42-0.62. These estimates are in a good agreement with those estimated in quail by Toelle *et al.* (1991), Akbas and Yaylak (2000), El-Deen *et al.* (2005), Vali *et al.* (2005) and Resende *et al.* (2005) but are higher than those reported by Aggrey and Cheng (1994), Saatci *et al.* (2003) and (2006). Heritability estimates for body weights has been reported in a wide range by different researchers. Differences in heritability estimates can be attributed to method of estimation, strain, environmental effects and sampling error due to small data set or sample size (Mielenz *et al.*, 2006). In this study, the highest heritability (0.62) was estimated for live weight at the 2nd week of age. The second highest heritability (0.61) was found for live weight in week 6.

Heritabilities of hatching weight and live weight in weeks 1, 3, 4, 5 were 0.42 and 0.46, 0.54, 0.48, 0.52, respectively. Saatci *et al.* (2003) noticed that heritability for body weight of quails tends to increase with age. However, in this study, heritabilities for early growth traits of the quails showed no increase, rather, volatile heritability estimates were observed. The results of heritability estimates showed that the Japanese quails can be successfully selected for body weight in the early period of growth. The estimates of phenotypic and genetic correlations of hatching and weekly body weight of quails are presented in Table 2. High genetic correlations were observed among hatching and weekly weights (range from 0.60-0.98). The highest genetic correlation (0.98) was found between body weight at 5 and 6 weeks age. Sezer *et al.* (2006) found that genetic correlations 0.46-0.98 for body weight at ages from 1-42 days in an unselected flock of Japanese quail. Akbas *et al.* (2004) reported a genetic correlation between 2 and 4 week weight and for 2 and 6 week and 4 and 6 weeks as 0.84, 0.80 and 0.87, respectively. Genetic correlations between 2 and 6 weeks body weight and between 4 and 6 weeks body weight were found to be 0.76 and 0.99 by Brah *et al.* (1997). Similarly, Toelle *et al.* (1991) and Vali *et al.* (2005) reported high genetic correlations between body weight in early weeks age. The high genetic correlations were all positive, which suggested that selection for weight at an early age has a positive effect on weight at a later age (Saatci *et al.*, 2003). Heavier birds in early weeks can carry their weights into following weeks; this situation may cause a higher genetic

Table 1: Descriptive statistics of hatching and weekly live weights

Traits	Mean±SE <sup>2</sup>	CV <sup>4</sup>	Min.	Max.
HW <sup>1</sup>	8.67±0.04	10.65	6.2	11.6
BW <sup>2</sup> 1	32.91±0.23	15.90	15.5	46.8
BW 2	75.59±0.43	12.79	35.5	100.1
BW 3	121.02±0.56	10.33	77.1	158.0
BW 4	155.04±0.75	10.75	80.6	204.3
BW 5	180.71±1.00	12.42	95.3	266.1
BW 6	200.47±1.18	13.10	108.8	276.4

<sup>1</sup>Hatching weight <sup>2</sup>Body weight <sup>3</sup>Standart error <sup>4</sup>Coefficient of variation

Table 2: Heritabilities (on diagonal), genetic (below diagonal) and phenotypic correlations (above diagonal) of live weights and Gompertz model parameters

Factors	HW <sup>3</sup>	BW <sup>1</sup>	BW 2	BW 3	BW 4	BW 5	BW 6	β <sub>0</sub>	β <sub>1</sub>	β <sub>2</sub>	Ipw	Ipt
HW	0.42 (0.15) <sup>1</sup>	0.52	0.44	0.45	0.45	0.39	0.40	0.33	-0.30	-0.21	0.33	0.05
BW 1	0.74 (0.12)	0.46 (0.18)	0.76	0.66	0.49	0.42	0.41	0.28	-0.56	-0.13	0.28	-0.20
BW 2	0.74 (0.12)	O.E. <sup>2</sup>	0.62 (0.27)	0.74	0.53	0.48	0.45	0.28	-0.36	-0.02	0.28	-0.24
BW 3	0.70 (0.32)	0.89 (0.06)	0.88 (0.06)	0.54 (0.23)	0.61	0.55	0.50	0.28	-0.10	0.07	0.28	-0.25
BW 4	0.56 (0.46)	0.42 (0.23)	0.94 (0.03)	0.89 (0.05)	0.48 (0.18)	0.83	0.75	0.60	-0.01	-0.17	0.60	0.13
BW 5	0.68 (0.35)	0.67 (0.15)	0.86 (0.07)	O.E.	0.92 (0.04)	0.52 (0.20)	0.88	0.78	-0.04	-0.41	0.78	0.35
BW 6	0.82 (0.21)	0.57 (0.18)	O.E.	0.89 (0.05)	0.93 (0.03)	0.97 (0.01)	0.60 (0.23)	0.92	-0.16	-0.58	0.92	0.50
β <sub>0</sub>	0.92 (0.03)	0.92 (0.02)	0.82 (0.07)	0.90 (0.03)	0.92 (0.03)	0.97 (0.01)	0.99 (0.01)	0.42 (0.15)	-0.55	-0.89	1.00	0.70
β <sub>1</sub>	-0.70 (0.10)	-0.99 (0.01)	-0.86 (0.06)	-0.59 (0.14)	-0.29 (0.19)	-0.37 (0.18)	-0.86 (0.05)	-0.42 (0.24)	0.21 (0.10)	0.82	-0.18	-0.02
β <sub>2</sub>	-0.55 (0.12)	-0.58 (0.12)	-0.38 (0.17)	-0.33 (0.17)	-0.32 (0.17)	-0.55 (0.13)	-0.58 (0.12)	-0.92 (0.03)	0.51 (0.22)	0.40 (0.15)	-0.43	-0.62
IPt	0.79 (0.08)	0.93 (0.03)	0.83 (0.07)	0.87 (0.06)	0.91 (0.04)	0.97 (0.01)	0.99 (0.01)	0.93 (0.07)	-0.88 (0.07)	-0.83 (0.09)	0.36 (0.18)	0.70
IPw	0.39 (0.18)	0.43 (0.19)	0.24 (0.23)	0.42 (0.19)	0.42 (0.19)	0.92 (0.03)	0.74 (0.10)	0.97 (0.02)	-0.43 (0.29)	-0.84 (0.18)	0.51 (0.27)	0.08 (0.04)

<sup>1</sup>Standard error, <sup>2</sup>Overestimated, <sup>3</sup>Hatching weight, <sup>4</sup>Body weight

correlation between the week weights (Saatci *et al.*, 2003). On the other hand, some genetic correlation coefficients were not estimated, while other estimates of genetic correlations were overestimated. These unexpected estimates of genetic correlations between the studied traits may be due to sampling errors and some missing observations (El-Deen *et al.*, 2008; Baylan *et al.*, 2009).

The highest phenotypic correlation was detected between 5 and 6 weeks weight (0.88). The phenotypic correlation between hatching weight and 5 weeks age was the lowest estimate (0.39). Similarly, Sezer and Tarhan (2005) reported a weak phenotypic correlation (0.25) between the hatching weight and the 5 weeks weight of Japanese quail. The phenotypic correlations between body weights at different ages were in a good agreement with those reported by Saatci *et al.* (2003) and Sezer *et al.* (2006). The results showed that coefficients of phenotypic correlation for body weight of quails tend to decrease with larger age intervals. Genetic correlations were higher than phenotypic correlations as expected and reported by Brah *et al.* (1997) and Saatci *et al.* (2003) for all weeks' live weights of Japanese quail. Because of high heritability for body weights and genetic correlations between them and weight recorded at later ages, selection on the basis of early body weights is feasible.

Descriptive statistics of estimated growth curve parameters and inflection point age (Ipa) and weight (Ipw) are given in Table 3. Estimated weekly body weights and residuals by Gompertz equation are shown in Table 4. The growth curve was plotted in Fig. 1. Observed and estimated values of the quail growth pattern using the Gompertz model, as well as values of model error measurements and determined residuals are shown in Table 4. The results show that the Gompertz model provides a powerful fit to quail growth data (mean square error 2.8039, coefficient of determination 0.9999, adjusted coefficient of determination 0.9998). The estimates of the Gompertz model parameters were 227.57, 3.44 and 0.084, respectively for  $\beta_0$  representing the mature weight,  $\beta_1$  constant of integration and  $\beta_2$  the relative rate of growth. Asymptotic weight and integration constant parameters were similar to previous literature values reported by different researchers.  $\beta_0$  and  $\beta_1$  parameters were estimated as 208.3 and 3.894, 244.7 and 3.399, 214 and 3.95 by Akbas and Oguz (1998), Akbas and Yaylak (2000) and Balcioglu *et al.* (2005), respectively.  $\beta_2$  parameter value (0.084) was in good agreement with those estimated as 0.087 and 0.073 in quail by Du Preez and Sales (1997) and Aggrey *et al.* (2003). The relative growth rate parameter was higher than the values 0.069, 0.055 reported by Akbas and Oguz (1998) and Akbas and Yaylak (2000). A high  $\beta_2$  parameter indicates early maturing and smaller

Table 3: Descriptive statistics of Gompertz model parameters and inflection point

Traits	Mean±SE	CV <sup>1</sup>	Min.	Max.
$\beta_0$	227.57±1.760	17.30	112.660	307.500
$\beta_1$	3.44±0.020	13.13	2.360	8.030
$\beta_2$	0.084±0.00	19.38	0.040	0.124
IP <sub>w</sub>	83.72±0.650	17.31	36.660	142.550
IP <sub>i</sub>	15.23±0.130	19.38	7.870	29.920

<sup>1</sup>Coefficient of variation

Table 4: Observed and estimated values with residuals for hatching and weekly live weights

Traits	Observed	Estimated	Residual
HW	8.67	10.12	-1.45
BW 1	32.91	32.96	-0.05
BW 2	75.59	74.94	0.65
BW 3	121.02	119.75	1.27
BW 4	155.04	156.47	-1.43
BW 5	180.71	182.27	-1.55
BW 6	200.47	198.85	1.62

<sup>1</sup>Hatching weight, <sup>2</sup> Body weight

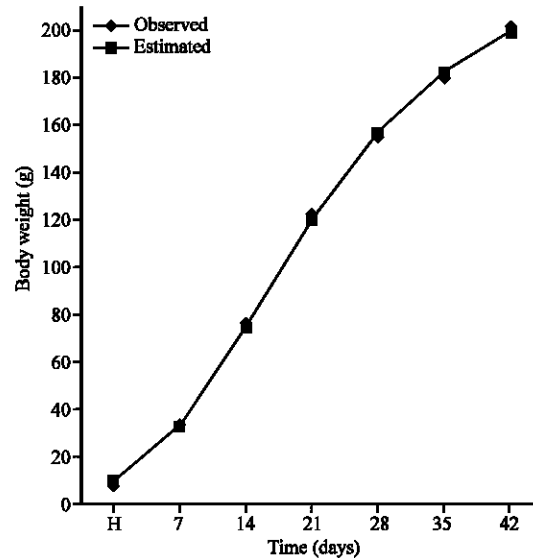


Fig. 1: Gompertz growth curve of Japanese quails

mature weights (Akbas and Yaylak, 2000). Age and weight at point of inflection were day 15, 23 day and 83, 71, respectively. The IIPT value was in a good agreement with those calculated as day 13.4-16.4 and 15.8-17.9 for male-female in control line reported by Du Preez and Sales (1997) and Hyankova *et al.* (2001). However, the value of age at inflection point for unselected quails found in this study was smaller than those reported by Akbas and Oguz (1998) and Akbas and Yaylak (2000) for the control line (day 20.2) and the unselected line (day 22.7).

The heritability estimates of the Gompertz growth model parameters and IPt, IPw traits are given in Table 2. Heritabilities of  $\beta_0$ ,  $\beta_1$ ,  $\beta_2$ , IPw and IPt were 0.42, 0.21, 0.41, 0.36 and 0.08, respectively. The heritability estimate for asymptotic weight parameter was in close agreement with

heritability of mature body weight and that was related with the heritabilities of last weeks live weight. In the present study, heritabilities of weekly live weights were higher than the heritability estimate of asymptotic weight parameter. The similar result reported by Akbas and Yaylak (2000).

They found a heritability estimate of  $\beta_0$  (0.176) smaller than the heritabilities of body weight at 4-6 weeks of age (0.586, 0.690, 0.567, respectively). In the present study, the heritability estimate of  $\beta_1$  was smaller than the value (0.328) reported by Akbas and Yaylak (2000) and it was higher than the value (0.058) reported by Akbas and Oguz (1998). The heritability estimate of  $\beta_0$  was higher than values (0.383 and 0.322) reported by Akbas and Oguz (1998) and Akbas and Yaylak (2000). Akbas and Yaylak (2000) found that the heritabilities of IPT and IPw were 0.319 and 0.176, respectively.

Estimates of genetic and phenotypic correlations between Gompertz growth curve parameters, Ipt, IPw, hatching and weekly body weights were given in Table 2. Genetic and phenotypic correlations between the parameter  $\beta_0$  and body weights were positive and moderate to high. Genetic correlations were higher than phenotypic correlations among the traits. The highest genetic (0.99) and phenotypic (0.92) correlation estimates among the traits were found between  $\beta_0$  with final weight. Akbas and Yaylak (2000) also reported the highest correlations between parameter  $\beta_0$  and final weight. These high correlations show that the parameter  $\beta_0$  is a reflection of final weight (Akbas and Oguz, 1998; Akbas and Yaylak, 2000).

All phenotypic and genetic correlations between parameter  $\beta_1$  and weekly body weights were negative. Most of these phenotypic correlations were low to moderate. Genetic correlations of  $\beta_1$  with body weights were moderate to high, generally. The genetic and phenotypic correlations of  $\beta_1$ -hatching weight,  $\beta_1$ -1-weeks weight and  $\beta_1$ -2-weeks weight were higher than other coefficients of correlation, except for the genetic correlation of  $\beta_1$ -final weight. These high correlations between  $\beta_1$  and live weights at younger ages show that the parameter  $\beta_1$  is a reflection of initial weight (Akbas and Oguz, 1998; Akbas and Yaylak, 2000).

The genetic and phenotypic correlation estimates of parameter  $\beta_2$  with weekly body weights were generally negative except for the  $\beta_2$ -3-week weight. Genetic and phenotypic correlations between the growth curve parameters were relatively high and negative with one exception. The only positive correlation was between  $\beta_1$  and  $\beta_2$ . A negative correlation between  $\beta_0$  and  $\beta_2$  has been commonly reported by different researchers (Du Preez and Sales, 1997; Hyankova *et al.*, 2001; Akbas and Oguz, 1998;

Akbas and Yaylak, 2000; Balcioglu *et al.*, 2005). The negative correlations between  $\beta_0$  and  $\beta_2$  indicates that if selection is used to increase mature weight, then there will be negative indirect selection on growth rate and growth rate tends to decrease (Koivula *et al.*, 2008).

## CONCLUSION

Modern selection methods are not applied equally in all commercial meat type quail lines. Selection studies have focused mostly on live weight at a fixed age. Heritability estimates of the Gompertz growth curve parameters and their correlations with weekly body weights suggest that the growth rate parameter may be useful in selecting animals that have rapidly growth at early ages.

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