

# Genetic parameters for feed utilization traits in Japanese quail

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**ABSTRACT** Feed costs substantially affect the efficiency of poultry operations, justifying genetic improvement of feed utilization by selection. The current research was conducted to estimate genetic variance for the 4-wk feed conversion ratio (FCR) and its genetic correlations with BW, BW gain (WG), feed intake (FI), and residual feed intake (RFI) in Japanese quail. The data analyzed originated from a line selected for low FCR for 3 generations. In each generation, 35 sires and 70 dams were used as parents for the next generation. Body weight and WG were recorded on a total of 1,226 individuals, whereas FCR, RFI, and FI were recorded on 505 family groups. The results showed that heritability estimates ( $\pm$ SE) of BW at 28 d of age and WG between 7 and 28 d of age were  $0.22 \pm 0.05$  and  $0.28 \pm 0.06$ , respectively. For FI, FCR, and RFI, significant genetic variances were estimated. Genetic correlations of FCR between 7 and 28 d of age with WG and FI between 7 and 28 d of age were  $-0.45 \pm 0.09$

and  $0.24 \pm 0.08$ , respectively. This implies that a low FCR is genetically related to a high WG and low FI. The genetic correlation between FCR from 7 to 28 d of age and RFI from 7 to 28 d of age was  $0.26 \pm 0.08$ , indicating that the 2 alternative feed efficiency traits are genetically different traits, and that the correlated genetic response in one of them in response to selection on the other is likely to be only moderate. Genetic correlations of RFI from 7 to 28 d of age with WG and FI between 7 and 28 d of age were  $0.08 \pm 0.04$  and  $0.74 \pm 0.11$ , respectively. This reflects the fact that RFI is phenotypically independent of WG, which tends to make the genetic correlation between RFI and WG low as well. In conclusion, all the traits analyzed displayed significant genetic variance, allowing their genetic improvement by selection, yet the alternative feed utilization traits, FCR and RFI, displayed different genetic characteristics.

**Key words:** heritability, genetic correlation, feed conversion ratio, Japanese quail, residual feed intake

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## INTRODUCTION

Approximately 4 decades ago, quail were recognized as a valuable animal model for research because of their early sexual maturity, short generation interval, high rate of egg production, low maintenance cost associated with their small body size, and resistance to diseases (Yalcin et al., 1995; Oguz and Minvielle, 2001). More recently, quail have become an important source of meat and eggs for human consumption (Kayang et al., 2004). Commercially farmed Japanese quail (*Coturnix coturnix japonica*) are used mainly for meat in Europe, for eggs in Japan, and for both in other Asian countries (Minvielle, 1998). Accordingly, selective breeding for growth and feed conversion ratio (**FCR**) have been applied, with well-documented, realized genetic responses

to selection (Anthony et al., 1996; Kaur et al., 2008; Varkoohi et al., 2010).

The FCR is usually measured as the ratio of feed intake (**FI**) to BW gain (**WG**). Feed conversion is a complex, highly aggregate trait that is the net result of the interaction of many different component traits. Selection for feed conversion, and other ratio traits, influences component traits in a relatively undirected manner (Gunsett, 1984; Emmerson, 1997). For example, selection for improved FCR can either increase growth, decrease FI, or both.

Several studies on poultry species have estimated genetic parameters for FCR and its components traits in poultry species (Thomas et al., 1958; Wilson, 1969; Gill and Washburn, 1974; Pym and Nicholls, 1979; Chambers et al., 1984; Leenstra et al., 1986; Koerhuis and Hill, 1995; Gaya et al., 2006; N'Dri et al., 2006; Aggrey et al., 2010). The FCR displays moderate to high heritability, ranging from 0.2 to 0.8 (Thomas et al., 1958; Wilson, 1969; Pym and Nicholls, 1979; Chambers et

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al., 1984; Leenstra et al., 1986). Residual FI (**RFI**), defined as the observed FI minus the expected FI of each bird, has been proposed as an alternate measure of feed efficiency (Koch et al., 1963), although the number of studies available on the genetic correlation between FCR and RFI in poultry is limited (Anthony et al., 1996; Aggrey et al., 2010).

This study was performed in Iran, where the Japanese quail is a new species farmed for meat consumption, and a breeding program has recently been established (Varkoohi et al., 2010). Genetic parameter estimates for traits can be used to assess whether genetic improvement through selection is possible, and to provide a basis for deriving selection indexes for the improvement of feed utilization traits. In this study, we first estimated genetic variance of FCR, WG, FI, and RFI and heritability of BW and WG. Second, we estimated genetic correlations of FCR with the traits WG, FI, and RFI.

## MATERIALS AND METHODS

### *Population Structure and Animal Management*

The data for the current study to estimate (co)variance components originated from a selection experiment. The selection responses have been reported by Varkoohi et al. (2010). The base population of Japanese quail was maintained at the animal research station of Tehran University in Iran. Before the beginning of the experiment, the population was not selected for any traits. To initiate the selection experiment, a total of 210 birds were randomly sampled from the base population and divided equally into 2 lines. Thereafter, the selection line (**F-line**) was selected for low FCR, measured during a 4-wk trial, and the control line (**C-line**) was a randombred control. In the current study, data from the F-line were used because pedigree was available only for the F-line. The realized selection responses after 3 generations of selection and data for the C-line have been reported by Varkoohi et al. (2010).

Quails originated from 4 generations, with 2 hatches per generation. Each generation was maintained with 70 families, produced by mating 35 sires and 70 dams, with a 1:2 (sires:dams) mating ratio. To mate the parents, each dam was placed into a floor cage, and 1 sire was mated with the dam every 2 d. In each generation, the same pair of parents was mated twice at 1-wk intervals to produce the 2 hatches of offspring. After mating, the dams were moved to special cages (24 × 25 × 20 cm) for egg laying (1 dam in each cage). Eggs were collected daily and labeled with a dam number. After 7 d, eggs were placed in a Setter incubator (Jamesway Inc., Cambridge, Ontario, Canada) for 14 d. Thereafter, eggs were transferred to cells in a Hatcher tray, and were held in the Hatcher (Jamesway Inc.) for 3 d.

When the chicks hatched, the offspring were leg-banded and each full-sib family was placed into its own cage (35 × 35 × 30 cm). When the family size was greater than 5, the family was equally divided into 2 cages. The number of birds per cage ranged from 1 to 5.

Chicks were individually weighed at weekly intervals at 7, 14, 21, and 28 d of age in each hatch. To record weekly FI, family-level observations were recorded for each week (2, 3, and 4 wk). The feed given for each family was weighed and then reweighed after 7 d of ad libitum consumption. The sex of birds was identified at 28 d of age.

To generate a next generation, birds from the dam families with the lowest family FCR until 28 d of age were used as parents. In each generation, birds from 30 families (range: 20 to 40) and on average 4 birds from each family (range: 1 to 7) were used as parents. Birds were selected across the 2 hatches after accounting for the hatch effects. Although some birds started to lay at 45 d of age, we collected eggs from 55 d onward to obtain more healthy chicks.

At the first, second, third, and fourth generations, birds were maintained between 1 and 28 d of age under 26, 26, 27, and 28% CP diets, respectively, with 2,900 kcal of ME/kg. Food and water were available ad libitum.

### *Trait Definitions*

Body weight gains were calculated as the difference between 2 successive BW records. Family FCR was calculated as the ratio of family record FI to family record WG. Residual FI was calculated as the difference between the observed and expected FI (Luiting and Urff, 1991; Kennedy et al., 1993):

$$RFI = FI - (b_1 \times MBW) - (b_2 \times WG),$$

where *FI* is the observed FI during a given time period; *MBW* is the average metabolic BW between 2 recordings ( $MBW = BW^{0.75}$ ); *WG* is the BW gain during a given period; and  $b_1$  and  $b_2$  are the regression coefficients for *BW* and *WG*. The average MBW for a cage was derived from the MBW of individual chicks at the 2 recording periods, which were then averaged for a cage. When mortality occurred, we reduced the weight of the dead bird from the total weight of birds in a cage, and reduced FI of that bird (cage average) from the total FI of birds in the cage.

Individual records of BW and WG, and family records of FI, FCR, and RFI in each hatch were calculated separately for wk 2, 3, and 4, and across the whole 3-wk trial. The timing of trait recording is indicated by subscripts to the trait abbreviations (7 = 7 d of age, 14 = 14 d of age, 21 = 21 d of age, 28 = 28 d of age, 7–14 = between 7 and 14 d of age, 14–21 = between 14 and 21 d of age, 21–28 = between 21 and 28 d of age, and

7–28 = between 7 and 28 d of age). Trait means and sample sizes are shown in Table 1.

## Statistical Analysis

For the calculation of (co)variance components and heritability for BW and WG, we used individual records, and for FCR, FI, and RFI, we used family records. For family records, it was not possible to calculate heritabilities because using the family means reduced residual variance, giving upwardly biased heritability estimates. Similarly, phenotypic correlations for the traits recorded at the family level are not reported.

Genetic parameters were estimated using ASReml (Gilmour et al., 2000). For the traits with individual-level data (BW and WG), the model used was

$$y_{ijkl} = \mu + \text{bird}_i + \text{dam}_j + \text{hatch}_k + \text{generation}_l + e_{ijkl}$$

where  $y_{ijkl}$  refers to the observations for a trait;  $i$  is the  $i$ th bird,  $j$  is the  $j$ th dam,  $k$  is the  $k$ th hatch,  $l$  is the  $l$ th generation,  $\mu$  is the overall trait mean;  $\text{bird}_i$  is the random genetic effect of the  $i$ th animal;  $\text{dam}_j$  is the random effect of the  $j$ th dam without a pedigree;  $\text{hatch}_k$  is the fixed effect of the  $k$ th hatch;  $\text{generation}_l$  is the fixed effect of the  $l$ th generation; and  $e_{ijkl}$  is the random error term. The maternal environmental variances were nonsignificant except for BW<sub>7</sub>, BW<sub>14</sub>, WG<sub>7–14</sub>, and WG<sub>14–21</sub>. When it was nonsignificant, the dam effect was excluded from the model. Variance components

larger than their SE and correlations higher than  $1.96 \times \text{SE}$  were considered significant.

For traits with family-level data (FCR, FI, and RFI), the bird effect was replaced with the random genetic family effect for the  $m$ th family with a pedigree, and the dam effect was excluded from a model. The family variance represents broad-sense genetic variance. The genetic parameters were obtained from a multitrait model with 2 traits each time, yet keeping always FCR as a trait in the model to account for selection bias.

It should be noted that although chicks were weighed individually, FI was collected by cage. Although each family was replicated over 2 hatches, it is possible that with this design, full-sib family and cages were confounded with any variation in social behaviors (e.g., feeding behavior) intrinsic to a cage. Dam was fitted as a random maternal environmental effect, which would define variation among both dam families and cages.

## RESULTS AND DISCUSSION

### Genetic Variance and Heritability

The results showed that heritability estimates ( $\pm \text{SE}$ ) for BW<sub>28</sub> and WG<sub>7–28</sub> were  $0.22 \pm 0.05$  and  $0.28 \pm 0.06$ , respectively. Heritability estimates for BW and WG were different in different weeks, with BW<sub>14</sub> and WG<sub>7–14</sub> having the highest heritability estimates (Table 2).

Michalska (1994) reported that heritability estimates for 4-wk BW in quail have ranged from 0.25 to 0.38.

**Table 1.** Descriptive statistics for different traits

Trait <sup>1</sup>	No. of observations	Mean	SD	CV (%)
BW (g)				
BW <sub>7</sub>	1,226	27.9	4.2	15.2
BW <sub>14</sub>	1,226	74.3	8.3	11.2
BW <sub>21</sub>	1,226	131.5	13.9	10.6
BW <sub>28</sub>	1,226	181.7	16.9	9.3
WG (g)				
WG <sub>7–14</sub>	1,226	46.5	6.4	13.8
WG <sub>14–21</sub>	1,226	57.2	11	19.3
WG <sub>21–28</sub>	1,226	51.9	12.5	24.1
WG <sub>7–28</sub>	1,226	155.6	16.8	10.8
FI (g)				
FI <sub>7–14</sub>	505	101	11	10.9
FI <sub>14–21</sub>	505	137	16.8	12.3
FI <sub>21–28</sub>	505	140	19.6	14
FI <sub>7–28</sub>	505	378	35	9.3
FCR				
FCR <sub>7–14</sub>	505	2.19	0.23	10.1
FCR <sub>14–21</sub>	505	2.43	0.25	10.3
FCR <sub>21–28</sub>	505	2.77	0.27	9.7
FCR <sub>7–28</sub>	505	2.47	0.26	10.5
RFI				
RFI <sub>7–14</sub>	505	−0.15	0.54	—
RFI <sub>14–21</sub>	505	−0.47	0.64	—
RFI <sub>21–28</sub>	505	−0.57	0.75	—
RFI <sub>7–28</sub>	505	−0.93	0.73	—

<sup>1</sup>BW = individual BW in different days (7, 14, 21, or 28 d); WG = individual BW gain between different days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28); FI = family feed intake between different days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28); FCR = family feed conversion ratio between different days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28); RFI = family residual feed intake between different days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28).

**Table 2.** Estimates of genetic ( $\sigma_a^2$ ), environmental ( $\sigma_e^2$ ), dam ( $\sigma_{dam}^2$ ), and phenotypic variances ( $\sigma_p^2$ ), and heritabilities and their SE ( $h_{(SE)}^2$ ) for traits with individual records

Trait <sup>1</sup>	$\sigma_a^2$	$\sigma_e^2$	$\sigma_{dam}^2$	$\sigma_p^2$	$h_{(SE)}^2$
<b>BW</b>					
BW <sub>7</sub>	2.6	9.1	6.2	17.9	0.15 <sub>(0.05)</sub>
BW <sub>14</sub>	20.3	32.2	17.2	69.7	0.29 <sub>(0.06)</sub>
BW <sub>21</sub>	34.9	159.0	—	193.9	0.18 <sub>(0.05)</sub>
BW <sub>28</sub>	63.9	223.9	—	287.8	0.22 <sub>(0.05)</sub>
<b>WG</b>					
WG <sub>7-14</sub>	9.6	19.2	12.3	41.1	0.23 <sub>(0.05)</sub>
WG <sub>14-21</sub>	18.4	77.3	26.9	122.6	0.15 <sub>(0.04)</sub>
WG <sub>21-28</sub>	29.8	127.0	—	156.8	0.19 <sub>(0.03)</sub>
WG <sub>7-28</sub>	80.5	202.9	—	283.4	0.28 <sub>(0.06)</sub>

<sup>1</sup>BW = individual BW in days (7, 14, 21, or 28 d); WG = individual BW gain between days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28).

Mielenz et al. (1994) reported that the heritability estimate for BW was 0.62 in hens. Schuler et al. (1998) estimated heritabilities of 0.44 to 0.47 for 4-wk BW in quail. Our BW and WG heritability estimates were at the lower range of the previous estimates.

Genetic variances for FI, FCR, and RFI were significantly different from zero, as shown by the SE values smaller than the genetic variance estimates (Table 3). The results from our selection experiment (Varkoohi et al., 2010) using the same data as used here illustrate the implications of this genetic variation. Varkoohi et al. (2010) compared the F-selection line for improved FCR with the randombred C-line. They reported that realized heritability for FCR after 3 generations of selection was 0.67. This represents a 6.1% improvement in FCR per generation. The realized heritability estimate of Varkoohi et al. (2010) was higher than the FCR heritability estimates published previously (Mielenz et al., 1994; N'Dri et al., 2006; Aggrey et al., 2010). In chickens, heritability estimates for individually recorded FI, FCR, and RFI in wk 5 were 0.48, 0.49, and 0.45,

respectively, and in wk 6 were 0.46, 0.41, and 0.42, respectively (Aggrey et al., 2010). N'Dri et al. (2006) found that the heritability of RFI in chickens was moderate to high, 0.38 to 0.45. Mielenz et al. (1994) estimated a heritability of 0.22 for RFI in hens.

Varkoohi et al. (2010), selecting on reduced FCR, also demonstrated correlated genetic responses of a 5.5% increase per generation for BW, a 5.7% increase per generation for WG, a -1.6% decrease for FI, and a -11.6 g decrease per generation for RFI. Overall, these results indicate that BW, WG, FI, FCR, and RFI all exhibited genetic variation, thus allowing their improvement by selection.

### Genetic Correlations

The results showed that the genetic correlation between FCR<sub>7-28</sub> and WG<sub>7-28</sub> was -0.45 (Table 4). Similarly, genetic correlations between FCR and WG in different weeks ranged from -0.12 to -0.44 (Table 5). This means that increasing WG is genetically related to an improved FCR. Our results are in line with previous studies. Koerhuis and Hill (1995) reported a genetic correlation of -0.20 between FCR and BW in broilers. Wilson (1969) reported that the average realized genetic correlation between WG and FCR from 1 generation of selection in 2 lines of broilers was -0.51. N'Dri et al. (2006) found that the genetic correlation between FCR and WG was -0.55 in chickens. These results imply that selection for WG only (or FCR only) should improve FCR (or WG) as a correlated genetic response. This result was consistent with that reported from a selection experiment for reduced FCR in Japanese quail (Varkoohi et al., 2010). In our study, the genetic correlation between FCR<sub>7-28</sub> and FI<sub>7-28</sub> was 0.24 (Table 4), showing that a low FCR was genetically related to a low FI. Likewise, genetic correlations between FCR and FI in different weeks ranged from 0.12 to 0.25 (Table 6). N'Dri et al. (2006) found that the genetic correlation between FCR and FI from 8 to 10 wk of age was 0.01 in chickens. Aggrey et al. (2010) reported that genetic correlations between FCR and FI in chickens at wk 5 and 6 of age were 0.45 and 0.54, re-

**Table 3.** Estimates of genetic ( $\sigma_a^2 \pm SE$ ), environmental ( $\sigma_e^2$ ), and phenotypic variances ( $\sigma_p^2$ ) for traits with family-level records

Trait <sup>1</sup>	$\sigma_a^2 \pm SE$	$\sigma_e^2$	$\sigma_p^2$
<b>FI</b>			
FI <sub>7-14</sub>	107.2 ± 82.6	14.0	121.2
FI <sub>14-21</sub>	228.1 ± 155.8	55.8	283.9
FI <sub>21-28</sub>	268.4 ± 164.3	113.8	382.2
FI <sub>7-28</sub>	1,115.7 ± 948.1	112.8	1,228.5
<b>FCR</b>			
FCR <sub>7-14</sub>	0.04 ± 0.02	0.01	0.05
FCR <sub>14-21</sub>	0.06 ± 0.03	0.01	0.06
FCR <sub>21-28</sub>	0.06 ± 0.04	0.01	0.07
FCR <sub>7-28</sub>	0.05 ± 0.03	0.01	0.07
<b>RFI</b>			
RFI <sub>7-14</sub>	0.22 ± 0.15	0.08	0.29
RFI <sub>14-21</sub>	0.26 ± 0.18	0.15	0.41
RFI <sub>21-28</sub>	0.34 ± 0.23	0.23	0.57
RFI <sub>7-28</sub>	0.38 ± 0.31	0.15	0.53

<sup>1</sup>FI = family feed intake between days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28); FCR = family feed conversion ratio between days (d 7 to 14, d 14 to 21, d 21 to 28, or d 7 to 28); RFI = family residual feed intake between days (d 7 to 14, d 14 to 21, d 21 to 28, d 7 to 28).

**Table 4.** Estimates of genetic correlations ( $\pm$ SE) between traits recorded during the whole 3-wk period<sup>1</sup>

Trait	FI <sub>7-28</sub>	FCR <sub>7-28</sub>	RFI <sub>7-28</sub>
WG <sub>7-28</sub>	0.61(0.10)	-0.45(0.09)	0.08(0.04)
FI <sub>7-28</sub>		0.24(0.08)	0.74(0.11)
FCR <sub>7-28</sub>			0.26(0.08)

<sup>1</sup>FI<sub>7-28</sub> = feed intake between 7 and 28 d of age; FCR<sub>7-28</sub> = feed conversion ratio between 7 and 28 d of age; RFI<sub>7-28</sub> = residual feed intake between 7 and 28 d of age; WG<sub>7-28</sub> = BW gain between 7 and 28 d of age.

spectively. Thus, selection for FCR is expected to lead to reduced FI or to no response in FI. Varkoohi et al. (2010) showed a small decrease in FI in response to selection for reduced FCR.

The genetic correlation between FCR<sub>7-28</sub> and RFI<sub>7-28</sub> was 0.26 (Table 4). Genetic correlations of FCR with RFI in different weeks ranged from 0.11 to 0.28 (Table 7). Accordingly, selection for improved FCR will improve RFI as a correlated response, as also shown by Varkoohi et al. (2010) in a selection experiment. However, the estimated genetic correlation was far from unity, implying that the 2 traits clearly are genetically different traits. Aggrey et al. (2010) reported that genetic correlations between FCR and RFI in chickens at wk 5 and 6 of age were 0.31 and 0.84, respectively. The result further showed that the genetic correlation between WG<sub>7-28</sub> and FI<sub>7-28</sub> was 0.61 (Table 4), indicating that with increasing growth, FI increases. In a selection experiment for increased BW in Japanese quail, increasing BW was accompanied by increasing FI and decreasing FCR (Marks, 1993). Our results are in line with this study. The results also showed that the genetic correlation between WG<sub>7-28</sub> and RFI<sub>7-28</sub> was 0.08 and that between FI<sub>7-28</sub> and RFI<sub>7-28</sub> was 0.74 (Table 4). Residual FI is phenotypically independent of WG, which tends to make the genetic correlation between RFI and WG low, yet it does not need to be zero (Kennedy et al., 1993). N'Dri et al. (2006) estimated a genetic correlation of 0.25 between WG and RFI and of 0.73 between FI and RFI in hens. Aggrey et al. (2010) reported that genetic correlations between WG and RFI in chickens at wk 5 and 6 of age were 0.34 and 0.06, respectively, and that genetic correlations between FI and RFI at wk 5 and 6 of age were 0.56 and 0.33, respectively.

**Table 5.** Estimates of genetic correlations ( $\pm$ SE in subscript) of feed conversion ratio (FCR) with BW gain (WG) in different weeks<sup>1</sup>

Trait	WG <sub>7-14</sub>	WG <sub>14-21</sub>	WG <sub>21-28</sub>
FCR <sub>7-14</sub>	-0.42(0.02)	-0.26(0.09)	-0.12(0.08)
FCR <sub>14-21</sub>	-0.23(0.04)	-0.34(0.08)	-0.28(0.10)
FCR <sub>21-28</sub>	-0.21(0.10)	-0.36(0.10)	-0.44(0.08)

<sup>1</sup>WG = BW gain between days (d 7 to 14, d 14 to 21, or d 21 to 28); FCR = feed conversion ratio between days (d 7 to 14, d 14 to 21, or d 21 to 28).

**Table 6.** Estimates of genetic correlations ( $\pm$ SE in subscript) of feed conversion ratio (FCR) with feed intake (FI) in different weeks<sup>1</sup>

Trait	FI <sub>7-14</sub>	FI <sub>14-21</sub>	FI <sub>21-28</sub>
FCR <sub>7-14</sub>	0.22(0.04)	0.15(0.04)	0.12(0.10)
FCR <sub>14-21</sub>	0.14(0.05)	0.18(0.04)	0.16(0.10)
FCR <sub>21-28</sub>	0.13(0.06)	0.17(0.06)	0.25(0.08)

<sup>1</sup>FI = feed intake between days (d 7 to 14, d 14 to 21, or d 21 to 28); FCR = feed conversion ratio between days (d 7 to 14, d 14 to 21, or d 21 to 28).

Together, the results imply that the strategies for genetic improvement of FCR and RFI are different. For instance, FCR can be improved indirectly by selecting for WG. Selection for WG increases WG as a direct response, and although FI is increased as a correlated genetic response, FI increases at a lower rate than WG, leading to genetic improvement in FCR. Improvement of feed utilization in farm animals has been attributed to decreased maintenance energy requirements and reduced thermogenesis, physical activity, and protein turnover rates (Luiting et al., 1991; Luiting, 1999; McDonagh et al., 2001; McPhee et al., 2001). Direct selection for FCR will be more effective than indirect selection, but it requires FI recording, which is laborious. In contrast to FCR, RFI is not expected to be affected by sole selection for WG. Thus, indirect improvement of RFI via growth selection is more challenging than that of FCR. Body weight gain is among the first traits to be selected in newly established low-cost quail breeding programs, whereas recording of FI is a challenge.

Both FCR and RFI are composite traits influenced by underlying growth and FI traits. Sole selection for composite traits, such as ratios, may lead to unwanted changes in the underlying component traits (Gunsett, 1984). However, selection for FCR can be combined with selection for BW and WG, ensuring that the growth traits are improved and FI is reduced. Moreover, FCR and RFI can be improved simply by selecting for (metabolic) BW and WG and against FI with appropriate selection index weights (Kennedy et al., 1993; Kause et al., 2006; Quinton et al., 2007).

In the present study, RFI was calculated using phenotypic regressions of FI with metabolic BW and WG, in which case genetic correlations of RFI with MBW and WG do not need to be zero. To make the traits genetically independent, genetic regressions could have been used (Kennedy et al., 1993). Yet again, selection

**Table 7.** Estimated of genetic correlations ( $\pm$ SE in subscript) of FCR with RFI in different weeks<sup>1</sup>

Trait	RFI <sub>7-14</sub>	RFI <sub>14-21</sub>	RFI <sub>21-28</sub>
FCR <sub>7-14</sub>	0.18(0.05)	0.16(0.05)	0.13(0.08)
FCR <sub>14-21</sub>	0.15(0.04)	0.21(0.05)	0.18(0.10)
FCR <sub>21-28</sub>	0.11(0.08)	0.16(0.06)	0.28(0.05)

<sup>1</sup>RFI = residual feed intake between days (d 7 to 14, d 14 to 21, or d 21 to 28); FCR = feed conversion ratio between days (d 7 to 14, d 14 to 21, or d 21 to 28).

for RFI based on genetic regressions is equivalent to selection on an index for FI, WG, and MBW, restricted to holding WG and BW constant (Kennedy et al., 1993). Although phenotypic and genetic parameters of FCR and RFI can be sufficiently described by the analysis of their constituent traits, BW, WG, and FI, the genetic parameters of FCR and RFI are illustrative to describe their genetic potential and relationships with other traits.

In conclusion, all traits analyzed displayed significant genetic variance, allowing their genetic improvement by selection. Improved FCR was genetically related to increased WG and reduced FI. Residual FI is expected to display low to moderate correlated genetic change in response to selection for FCR.

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