



## Canonical-correlation analysis applied to selection-index methodology in quails



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### ABSTRACT

Genetic evaluations in dual-purpose quails (*Coturnix coturnix*) have demonstrated that overall genetic gains in a breeding program are achieved not only based on a specific trait, but on several. The most common technique to use all this information is the selection index. Another alternative may be the canonical-correlation analysis applied to selection index. There is, however, a lack of studies using canonical correlation in quails. Hence, the objectives of this study were to apply canonical-correlation analysis to estimate the relationship of nine traits and to compare genetic gains obtained by this methodology to desired-gain selection index in three lines of quails. Data for three lines of layer quails consisted of body weight at 28 days (W28), egg weight (EW), age at first egg (AFE) and egg production at 30, 60, 90, 120, 150 and 180 days after onset of lay. Two sets of traits were established: the first one contained predictor variables (W28, EW and AFE) and the second one contained variables related to egg production. A selection index was constructed using the standardized coefficients of canonical covariates as weighting factors when a given canonical correlation was significant. We constructed two desired-gain selection indices: DG-SI1 and DG-SI2. The difference between them is that DG-SI2 had a desired gain for body weight set to 0. The estimated canonical correlations were as follows: 0.811, 0.058 and 0.003 for the yellow, 0.821, 0.181 and 0.076 for the red, and 0.825, 0.117 and 0.038 for the blue line. Only the first pair of canonical variates was significant ( $P < 0.05$ ). AFE and early stages of egg production were very influent and showed great importance in defining the canonical variates and, consequently, the estimated canonical correlations. All lines had, in general, similar results for the canonical analysis indicating that traits that drive management decisions in these lines would be the same. The indices under study showed differences in response to selection; however, they generally resulted in consistent favorable genetic gains. For all lines, the canonical selection index resulted in the lowest AFE and highest egg production at 30 days. The DG-SI1 showed the highest genetic gains for W28 in all lines. There was a general lower genetic gain of other traits for DG-SI1

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at the expense of the desired genetic gain for W28. Selection for AFE, according to the canonical-correlation analysis, would have a great impact on the number of eggs produced. Canonical selection index is a good alternative for a desired-gain selection index.

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## 1. Introduction

Over the years, genetic evaluations in dual-purpose quails (*Coturnix coturnix*) have demonstrated that genetic gains over all traits in a breeding program are achieved not only based on a specific trait, but on several economic traits, such as age at first egg, body weight, egg mass and egg production (Hidalgo et al., 2011; Ribeiro et al., 2012; Silva et al., 2013). The optimal combination of these several traits is needed to obtain the highest possible genetic gains for all traits selected. Therefore, records of all economic traits become necessary to understand them and how they related to each other.

The most common technique used to apply multi-trait selection is the selection index. In the selection index, all economically important traits are combined into an index, which is based on economic weights or desired gains, resulting in selection without considerable loss in any of the traits (Smith, 1936; Hazel, 1943; Pešek and Baker, 1969). This procedure, however, has some limitations clearly recognized on the difficulty to establish economic weights for the traits or to set the desired gains. Nonetheless, selection index is still widely used because, in general, it provides larger total genetic gains (Shahin et al., 2000; Martins et al., 2003; Nath et al., 2011).

Another feasible alternative may be the canonical-correlation analysis applied to a selection index. Canonical-correlation analysis is a multivariate technique that measures interrelationships between dependent and independent sets of variables, and estimates the maximum correlation and the common portion of variance between them by linear combination (Akbaş and Takma, 2005; Ventura et al., 2011).

A substantial number of studies have been reported in different areas of interest using canonical correlation in animal breeding for different species, such as pigs (Flores et al., 1988; Ventura et al., 2011), beef cattle (Piedrafita et al., 2003), dairy cattle (Meyer et al., 1989) and poultry (Akbaş and Takma, 2005; Yang et al., 2006; Mendes and Akkartal, 2007; Cankaya et al., 2008). There is, however, a lack of studies using canonical correlation in quails. Hence, the objectives of this study were to apply canonical-correlation analysis to estimate the relationship of nine traits and to compare genetic gains obtained by this methodology to desired-gain selection index in three lines of quails.

## 2. Material and methods

### 2.1. Data

Data were collected from September 2007 through April 2008 in the quail sector of the Fazenda Experimental de Iguatemi – Universidade Estadual de Maringá. Data for three lines (yellow, red and blue) of layer quails consisted of body weight in grams at 28 days (W28), egg weight in grams

(EW), age at first egg in days (AFE) and egg production in number of eggs at 30 (P30), 60 (P60), 90 (P90), 120 (P120), 150 (P150) and 180 (P180) days after onset of lay (Table 1). Egg weight consisted of a mean egg weight from two weight records at 70 and at 120 days of age. The numerator relationship matrix consisted of 356 animals for the yellow, 116 animals for the red and 256 animals for the blue line.

### 2.2. Statistical analyses

The following multi-trait animal model was applied fitting all nine traits for each line:

$$Y = \mu + a + e$$

where  $Y$  is a vector of observations of the recorded traits,  $\mu$  is the overall mean,  $a$  is a random additive genetic effect of each individual and  $e$  is the random error associated with the  $Y$  vector. There is no fixed effect because all animals

**Table 1**  
Descriptive statistics of traits under study for all quail lines.

Line	Trait	N	Mean	SD
Yellow	W28	224	92.51	7.88
	EW	175	10.47	0.78
	AFE	170	48.59	9.40
	P30	170	14.72	7.87
	P60	170	40.07	12.22
	P90	170	67.24	13.93
	P120	170	94.81	16.54
	P150	170	122.69	19.06
Red	P180	170	150.02	21.80
	W28	80	116.39	9.74
	EW	71	10.96	1.09
	AFE	60	52.48	10.12
	P30	60	13.23	8.90
	P60	60	36.72	12.25
	P90	60	62.65	13.63
	P120	60	90.18	15.32
Blue	P150	60	116.97	18.05
	P180	60	143.3	20.54
	W28	151	98.83	8.21
	EW	144	10.86	0.75
	AFE	134	51.66	10.82
	P30	134	14.13	9.03
	P60	134	38.31	13.23
	P90	134	64.57	14.30
	P120	134	92.24	15.59
	P150	134	119.20	17.70
	P180	134	146.02	20.47

W28 – body weight at 28 days (g), EW – egg weight (g), AFE – age at first egg (days), P30 – egg production at 30 days (number of eggs), P60 – egg production at 60 days (number of eggs), P90 – egg production at 90 days (number of eggs), P120 – egg production at 120 days (number of eggs), P150 – egg production at 150 days (number of eggs), P180 – egg production at 180 days (number of eggs),  $N$  – number of animals, and SD – standard deviation.

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