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## Mapping of Quantitative Trait Loci Affecting Feed Efficiency in Laying Common Ducks

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**ABSTRACT:** Feed efficiency and body weight QTL in laying ducks at 39 weeks of age were detected together with body weight QTL in their mule duck sons at young age, by using a design consisting in 287 back cross female ducks and their 1202 mule ducks sons. The genetic map used consists of 102 microsatellite markers and 17 linkage groups. For laying ducks, QTL for feed intake and residual feed intake were detected at the 1% chromosome-wise threshold on linkage group 1, and 2 bodyweight QTL on linkage groups 2 and 3, were identified at the 5% threshold. For mule ducks, 3 QTL were also identified on linkage group 3 for bodyweight at different ages. This result suggests a QTL segregating in the common duck population impacting both weights of adult common ducks and of their young mule duck sons, but multi-trait analysis didn't clearly confirm a pleiotropic QTL.

Keywords: QTL, single and multi-traits, feed efficiency, bodyweight, common ducks.

### Introduction

Until now in ducks, the focus of publications on feed efficiency has mainly been on growing animals, regardless of the duck species studied (Marie-Etancelin et al., (2008)) and none concerned QTL analyses. Meanwhile, genetic research on the feed efficiency of laying hens is prolific and yields very promising results (Tixier-Boichard et al. (2002)). We present here our first QTL results on feed efficiency in laying common ducks, with a particular emphasis on bodyweight QTL when phenotypes are recorded in different generations of ducks.

### Materials and Methods

**Animals and Measurements.** The basis of the experimental design is a back-cross (BC) involving 2 INRA common duck lines: I444 (a Kaiya common duck strain) and I37 (a synthetic heavy common duck strain), in which 7 F1 common drakes were crossed to 64 I444 females to produce 287 female BC common ducks over 2 years and 3 batches per year. These BC females were in turn mated to Muskovy drakes to produce a further generation of 1202 mule duck sons in 2 years and 2 batches per year (figure 1). Hatching, breeding and measurements were carried out at the INRA waterfowl experimental farm (UEPFG, Benquet, France). All birds received an *ad libitum* starting diet from birth to 5 weeks, followed by a commercial pelleted duck feed. Animals were bred in collective pens of 50 ducks until 12 weeks of age and then transferred in individual cages

with individual feeders. Feed intake (FI) of the BC laying ducks was measured during a test period of 1 week at 39 weeks of age. To compute the feed conversion ratio (FCR) and the residual feed intake (RFI), we also recorded the egg mass laid (EML), the body weight (BW) and the BW gain ( $\Delta W$ ) during the test period. As  $\Delta W$  were measured only the second year, RFI was defined without  $\Delta W$  as the residual ( $\epsilon$ ) of the equation:

$$FI = \mu + \alpha x BW^{0.75} + \beta x EML + \epsilon$$

Basso et al. (2012) demonstrated the very low contribution of  $\Delta W$  in the RFI trait, and presented descriptions of performances and genetic parameters estimates.

The mule ducks were bred from 0 to 70 days of age in growing batches of 50 ducks and feed *ad libitum* until 42 days and then were feed-restricted until 70 days of age. Their bodyweights were recorded at 12, 28, 42 and 70 days of age (BW12d, BW28d, BW42d, and BW70d respectively). Phenotypes and genetic analyses of the bodyweights are described in Vitezica et al. (2010).

**Marker Data.** 130 microsatellite markers were genotyped on the BC female ducks, their parents and their paternal grandparents. A genetic map containing 102 markers in 17 linkage groups (LG) covering 890 cM was build using Crimap software (version 2.4). *In silico* mapping of the duck markers by sequence similarity to the chicken genome allowed the prediction of their position in the duck genome. We thus determined that the 17 linkage groups correspond to 14 different chromosomes (figure 2), with some independent duck linkage groups corresponding to a single chicken chromosome.

**Statistical analyses.** Traits for all female BC common ducks were corrected for the year and hatching batch environmental fixed effects. The mule ducks traits were corrected for the year, the hatching batch and the breeding batch fixed effects. Corrections were done using the GLM procedure in SAS (2002). Residual effects of the traits measured on female BC common ducks were directly retained as their performances for the trait. Mule duck performances were assigned to each BC female by averaging the residuals effects across its sons, taking into account the heterogeneity of the phenotypic variance due to the variation in offspring number per BC female.

QTL detection was carried out with the QTLMap software (Elsen et al., (1999); Filangi et al., (2010)) in order to implement linkage analysis according to the interval mapping method (Lander and Botstein, (1989)). For each chromosome, the more likely phase of the F1 male founders

were first found using marker information from their progenies. Next, every 1 cM, the probabilities for the transmission of the corresponding chromosomal segments to the offspring were estimated. Then, QTL detection was carried out by within-sire linear regression. For each trait and each linkage group, 10,000 within-family permutations were performed to estimate the empirical chromosome-wide significance (CWS) level of the test statistics (Churchill and Doerge, (1994)).

In the multi-trait QTL analyses (mQTL), all combinations of the 5 BW recorded (BW12d, BW28d, BW42d, BW70d for mule ducks and BW for BC ducks) were tested, *i.e.* 10 two-traits, 10 three-traits, 5 four-traits and 1 five-traits analysis.

## Results and Discussion

**Feed efficiency.** Table 1 shows the 4 QTL significant at the CWS level for feed efficiency traits of the BC common female ducks. Two QTL for FI and RFI reached the 1% threshold on LG1. The high genetic correlation between FI and RFI (+0.89; Basso et al. (2012)) and the very close QTL location, suggests these could be the same QTL. This result is consistent with several studies in chicken - either in broiler (Van Kaam et al., (1999)), in laying hens (Wolc et al., (2013)) or in a broiler x laying hens cross (Nones et al., (2005)) - in which QTL signals on Gallus chromosome 1, reach a 5% genome-wide level in broilers and suggestive levels for the other studies. No QTL was identified for EML, FCR or  $\Delta W$ , but 2 QTL for female BW at 39 weeks, significant at 5% and 1% CWS level respectively, were detected on LG2b and LG3. On young Pekin ducks, Huang et al. (2007) also found QTL for BW on LG2 (at birth and at 1 week of age) with the same flanking microsatellite marker than us (CAUD089). Knowing that our LG3 in duck is consistent with GGA3 in chicken, our QTL is confirmed by many other QTL found in chicken. GGA3 can be considered as a very interesting chromosome for growth traits in chicken, with more than 50 QTL identified ([www.animalgenome.org](http://www.animalgenome.org); Hu et al., (2010)), for both adult and young birds. Moreover, with the same design as ours but with more animals per F1 families, Kileh-Wais et al. (2013) already found QTL for BW of young mule ducks, of which one QTL for BW28 was significant at 1% genome-wide level.

**Bodyweight QTL by generation of phenotyped ducks.** Figure 3 shows results for BW QTL identified on LG3 in single trait analyses. Significant QTL for mule duck BW appear when animals are still fed *ad libitum*, *i. e.* until 42 days of age. Thus, although the QTL for BW at 28 days comes close to the 0.1% CWS level, no QTL is detected for BW at 70 days old, when mule ducks are fed a restricted diet. For BC female ducks, the QTL for BW at 39 weeks old remained significant and reached the 1% CWS level. Note that the 3 QTL for mule ducks BW were all located between the same markers (CAUD084 and CAUD045) while the QTL for BC ducks BW was located further between the markers CAUD045 and CAUD091.

Table 2 presents significant QTL results (exceeding the 5% CWS level) in single trait and multitrait analyses. Among all the traits combinations, 3 mQTL were identified in the two-trait analyses and 4 mQTL in the three-trait analyses. Significance levels reached in single trait versus two-traits detections seem broadly comparable, and decrease for the three-traits detections, contrariwise to what was observed in Kileh-Wais et al. (2013) for results on liver quality traits. In our study, multitrait approach didn't evidence of a clear pleiotropic QTL, and didn't reduce the confidence interval of QTL (result not shown). It is interesting to note that significant mQTL always include the BW of the BC female ducks. Contrary to what we expected, combination of the 3 most correlated mule ducks traits (BW12, BW28 and BW42) or association of the 3 best single traits QTL (BW28d, BW42 and BW) didn't lead to a mQTL.

## Conclusion

To our knowledge, this paper is the first dealing with QTL detection of feed efficiency in common laying ducks. The importance of chromosome 1 is highlighted, this result is particularly interesting in Asia, which heavily on the Pekin duck for the production of consumable eggs. This work confirmed the importance of chromosome 3 for growth performance of ducks either at a young age or in adulthood. These encouraging results are based on a partial experimental design: they will be refined and extended by using a new genetic map composed of SNP, with higher marker density and a better coverage of chromosomes.

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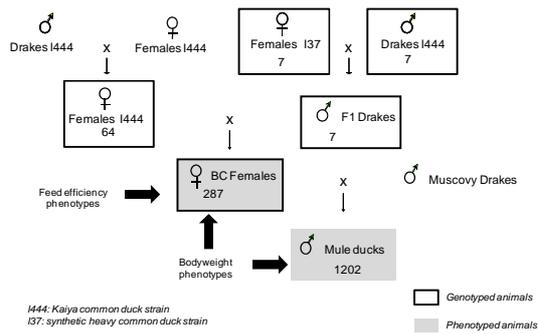


Figure 1: Experimental back cross design

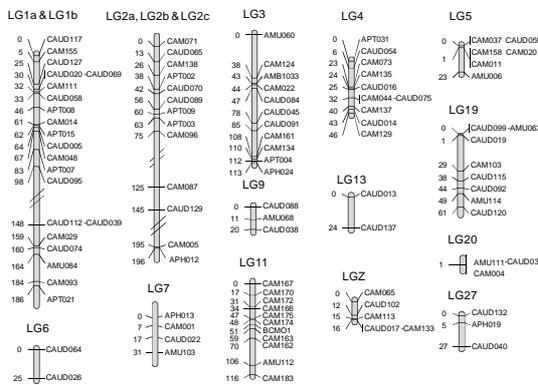
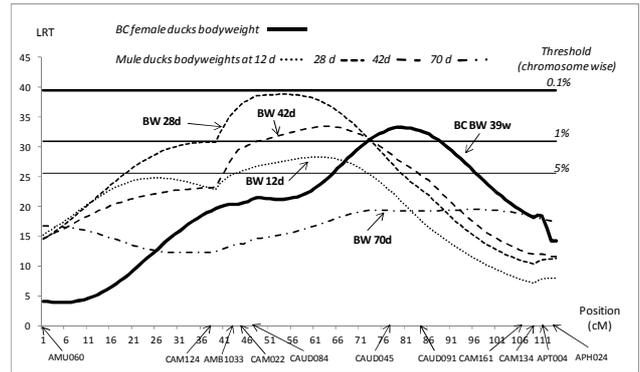


Figure 2: microsatellites map of common ducks

Table 1: QTLs related to feed efficiency traits recorded on BC female ducks – single trait analysis on all linkage groups

LG	Traits	Flanking markers	QTL Location (cM)	LRT	Threshold	Confidence interval (cM)
1b	FI	CAUD039	148	26.6	••	0 – 5
1b	RFI	CAUD039-CAM029	151	26.6	••	0 – 11
2a	BW	CAUD070-CAUD089	46	24.9	•	35 – 54
3	BW	CAUD045	78	33.3	••	69 – 90

LG: Linkage group; BW: body weights; FI: feed intake; RFI: residual feed intake. All measured at 39 weeks of age; LRT: Maximum likelihood ratio. Level of chromosome-wide significance of P-value: • 0.01 > P > 0.005 and •• 0.005 > P > 0.001



Positions of markers (in centiMorgan) on LG3 are shown on the x-axis.

Figure 3: Global likelihood ratio test profile for bodyweight traits recorded on mule ducks and on BC female ducks – single trait analysis on LG3

Table 2: Significant QTLs related to bodyweights of mule and BC ducks – comparison of single and multitraits analysis (n=287)

1 Trait	BW28d	BW42d	BW	BW12d
QTL Location	0.53	0.62	0.78	0.61
LRT	38.83	33.42	33.30	38.31
Threshold	••	••	••	•
	0.12%	0.44%	0.47%	2.02%
2 Traits	BW12d-BW		BW28d-BW	
QTL Location	0.67		0.61	
LRT	42.43		42.41	
Threshold	••		••	
	0.87%		0.90%	
3 Traits	BW12d-BW42d-BW		BW12d-BW28d-BW	
QTL Location	0.67		0.66	
LRT	50.57		48.30	
Threshold	•		•	
	2.22%		3.67%	
3 Traits	BW12d-BW28d-BW		BW28d-BW70d-BW	
QTL Location	0.67		0.61	
LRT	50.57		48.17	
Threshold	•		•	
	2.22%		3.95%	

LRT: Maximum likelihood ratio. BW12: mule ducks bodyweights at 12 days old. BW28: mule ducks bodyweights at 28 days old. BW42: mule ducks bodyweights at 42 days old. BW: BC female ducks bodyweights at 39 weeks old. Level of chromosome-wide significance of P-value: • 0.01 > P > 0.005 and •• 0.005 > P > 0.001