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## **S138 Genetic parameters and QTL detection of social behaviors, fear behaviors and production traits in Japanese Quail.**

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### **Abbreviated Title: Genetic parameters and QTL detection in the Quail**

**ABSTRACT:** The social behavior of animals, which is partly controlled by genetics, is involved in their adaptation to large breeding groups. Genetic analysis (i.e. genetic parameters estimation and QTL detection) of several social behaviors, fear behaviors and production traits were estimated in a second generation cross between two lines of Japanese Quail divergently selected for their social reinstatement behavior. A strong genetic correlation (0.90) existed between sexual and aggressive behaviors, both being significantly correlated to the response to the novel object test (0.89 and 0.63, respectively). Strong genetic correlations between behaviors and productions were highlighted. Higher weights at 17 and 65 days were genetically associated with increased emotional reactivity estimated through the duration of tonic immobility (0.76 and 0.79, respectively). The onset of egg lay was earlier in birds with high social reinstatement behavior (-0.71) but delayed in case of higher emotional reactivity (0.74). A higher egg number was genetically associated with a lower emotional reactivity toward a novel object but with higher sexual and aggressive behaviors. QTL detection was performed after genotyping the F0, F1 and F2 birds with a total of 2145 SNP markers. A genetic map was built in which 1479 markers were positioned on a total of 29 different linkage groups. Linkage analyses allowed identifying 8 chromosome-wide significant QTL linked to the social motivation.

**Keywords:** Sociability - Fear - Genetic parameters - QTL - Selection - Quail

### **Introduction**

In modern farms, the birds live mostly in large breeding groups of animals from the same age and sometimes the same sex. These particular conditions may favor the expression of deleterious behaviors (such as aggression, feather pecking, and cannibalism in the most severe cases) or stress-related pathologies that affect both productivity and animal welfare (Mignon-Grasteau and Faure, 2002). In addition to optimized rearing practices, adaptability of animals is of major importance to prevent welfare problems. The aim of our study was to investigate the genetic control of different social behaviors (social motivation, sexual motivation, aggressiveness) and fear behaviors (tonic immobility, reaction to an unknown object), and their relationships with production traits (weight and egg). The analysis focused on individuals from a second generation cross (F2) between two lines of quail divergently selected on their social reinstatement behavior (Mills and Faure, 1991).

## Materials and Methods

The experimental design, the housing conditions, the behavioral and production measurements are detailed in Recoquillay *et al.* (2013).

**Behavior and production variables.** DistSR (Social motivation, distance traveled during the treadmill test), DistIso (Social motivation, distance traveled during the social isolation test), TI (Emotional reactivity, duration of the tonic immobility after a physical restraint), HeadNO (Emotional reactivity, reaction to a novel object), Mount (Sexual motivation, number of mounts during the sexual motivation test), AgrP (Aggressiveness, number of aggressive pecks during the aggressiveness test), GentleP (Number of gentle pecks during the aggressiveness test), W17 and W65 (body weight at 17 and 65 days respectively), AFEgg (Age at the first egg laid), NEgg (Number of eggs laid).

**Genetic parameters estimation.** More details can be found in Recoquillay *et al.* (2013). The heritability ( $h^2$ ) and genetic correlations ( $r_g$ ) were estimated for each combination of two traits using TM software (Legarra *et al.*, 2011) which can process continuous and categorical traits. Genetic parameters were estimated by Gibbs sampling. A total of 100,000 iterations were realized, from which the first 20,000 iterations were discarded and one estimation every 20 iterations was saved to have a final set of 4000 useful estimations. The model used included the fixed effects of hatch and sex, the additive genetic effect of animal, and the maternal permanent environmental effect for body weights and age at first egg.

**QTL detection.** QTL were detected by linkage analyses using the version 0.9.6 of QTLMAP software (<http://www.inra.fr/qtlmap>). Two different models were used: the first one estimating only the “Sires” QTL effects and the second one the “Sires plus Dams” effects, for parents with at least 20 offsprings. The likelihood ratio test between the hypothesis of the existence of a QTL ( $H_1$ ) and the hypothesis of the absence of QTL ( $H_0$ ) was calculated on a given chromosome at each position every 0.5 cM. The rejection threshold of the test was estimated by 10,000 simulations under the  $H_0$  hypothesis with a polygenic model using the heritabilities in Table 1. QTL were deemed chromosome-wide significant if  $P < 0.05$ . The effect of the QTL corresponded to the average of the significant sires and dams ( $P < 0.05$ ).

## Results

**Heritability estimates:** Heritability coefficients for behavioral traits were moderate (from 0.19 to 0.36 for DistSR, DistIso, TI and HeadNO) to high (from 0.39 to 0.49 for Mount, AgrP and GentleP). For production traits,  $h^2$  was moderate for AFEgg (0.30) and higher for W17, W65 and NEgg (from 0.39 to 0.49) (Table 1).

**Genetic correlation estimates:** As shown in Table 1, quite a high positive genetic correlation (0.90) was found between Mount and AgrP. Moreover, the two traits were positively correlated with HeadNO, highly for Mount (0.89) and more moderately for AgrP (0.63). GentleP was positively correlated to HeadNO (0.63) and Mount (0.73), while it was not significantly genetically correlated to AgrP (0.20). As expected, W17 and W65 exhibited a strong positive genetic correlation (0.72), and AFEgg and NEgg a strong negative genetic correlation (-0.88). In addition, significant genetic correlations were found between behavioral and production traits. This was the case between TI and W17 (0.76) as well as W65 (0.79). NEgg was positively genetically correlated with Mount (0.82) and AgrP (0.58), as well as with GentleP (0.72) and

HeadNO (0.61). AFEgg was negatively correlated with GentleP (-0.81), DistSR (-0.71) and Mount (-0.68), but positively correlated with TI (0.74).

**QTL detection:** As shown in Table 2, 8 chromosome-wide significant QTL linked to the social motivation (DistSR) were detected by the 'Sires' or 'Sires plus Dams' models. Two close QTL were found by the two models on CJA2 (at 155 and 149 cM, for Sires and Sires plus Dams models, respectively) and on CJA9 (at 55 and 42 cM, respectively). The other chromosome-wide significant QTL were observed on CJA1 (281 cM), CJA11 (47 cM), CJA13 (70 cM) and CJA26 (21 cM).

## Discussion

Despite several factors affecting the level of heritability of our behavioral traits such as the age of the birds, the environmental conditions (housing in group or individually), our heritabilities seems consistent with previous studies. Moreover, even if our genetic parameters were estimated in a F2 cross and thus part of the heritability could be due to heterosis, results for the DistSR and TI traits were consistent with previous study (Mills and Faure, 1991).

Several significant genetic correlations were found between behavioral and production traits. Unfavorable genetic correlations were observed between the level of emotional reactivity estimated by the duration of tonic immobility and the weight at 17 or 65 days. In the same way, a genetic correlation between AgrP and the number of eggs laid (NEgg) was observed. In the same time, favorable genetic relationships between the sociability (estimated by DistSR) and the emotional reactivity (estimated by HeadNO) and the egg production traits were also observed.. Indeed, HeadNO was positively genetically correlated with NEgg while DistSR was negatively correlated with the age at the first egg laid (AFEgg). This indicated that less fearful or more sociable birds would lay earlier and/or more abundantly. Consistently, in the study by Marin *et al.* (2002) in which social motivation was assessed by the time to rejoin conspecifics in a T-Maze, the most socially motivated individuals also showed earlier puberty and laid more eggs per day.

Several QTL for DistSR were detected for the first time in quail. Some of them co-localized with QTL previously identified on the homologous regions in the Chicken. It is noticeable that DistSR QTL found on CJA1, CJA2 and CJA13 were close to QTL identified for AFEgg on GGA1 (Goraga *et al.*, 2012), GGA2 and GGA13 (Podisi *et al.*, 2011) in the chicken.

## Conclusion

Our study pointed out a possible negative impact of selection for production traits on the emotional reactivity and the social behaviors of the birds. In the same time, it suggested that improving sociability and fear-related traits could have a positive impact on performance. QTL detection will allow bringing new insights on the genetic control of these traits and, at term, contribute to develop new tools for an efficient and sustainable selection.

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**Table 1. Heritabilities (on diagonal) and genetic correlations (above the diagonal) between behavioral and production traits.**

Trait	DistSR	DistIso	TI	HeadNO	Mount	AgrP	GentleP	W17	W65	AFEgg	NEgg
DistSR	<b>0.19</b> <sup>1</sup>	0.16	-0.35	0.37	0.32	0.05	0.29	0.14	0.03	<b>-0.71</b>	0.32
DistIso	-	<b>0.34</b>	-0.33	-0.08	0.00	0.35	0.45	-0.33	-0.44	-0.21	0.04
TI	-	-	<b>0.21</b>	0.24	-0.22	0.01	-0.24	<b>0.76</b>	<b>0.79</b>	<b>0.74</b>	-0.35
HeadNO	-	-	-	<b>0.36</b>	<b>0.89</b>	<b>0.63</b>	<b>0.63</b>	0.49	0.44	-0.55	<b>0.61</b>
Mount	-	-	-	-	<b>0.49</b>	<b>0.90</b>	<b>0.73</b>	0.18	0.36	<b>-0.68</b>	<b>0.82</b>
AgrP	-	-	-	-	-	<b>0.42</b>	0.20	-0.29	0.00	-0.38	<b>0.58</b>
GentleP	-	-	-	-	-	-	<b>0.39</b>	0.45	0.28	<b>-0.81</b>	<b>0.72</b>
W17	-	-	-	-	-	-	-	<b>0.48</b>	<b>0.72</b>	0.48	-0.06
W65	-	-	-	-	-	-	-	-	<b>0.49</b>	0.11	-0.21
AFEgg	-	-	-	-	-	-	-	-	-	<b>0.30</b>	<b>-0.88</b>
NEgg	-	-	-	-	-	-	-	-	-	-	<b>0.39</b>

<sup>1</sup> Significant parameters are indicated in bold.

**Table 2. QTL detected for the DistSR trait.**

Chromosome	Position (cM)	Nearest Markers	Model*	Level of significance	QTL Effect*	Sires*	Dams*
CJA1	281	snp_soc_4666-snp_soc_2881	S+D	P=0.037	0.31	3	9
CJA2	149	snp_soc_1978-snp_soc_3824	S+D	P=0.043	0.36	3	6
	155	snp_soc_4405-snp_soc_3819	S	P=0.024	0.22	4	-
CJA9	42	snp_soc_1270-snp_soc_0268	S+D	P<0.01	0.43	3	7
	55	snp_soc_2491-snp_soc_0558	S	P=0.016	0.28	2	-
CJA11	47	snp_soc_1642-snp_soc_1220	S	P=0.023	0.21	4	-
CJA13	70	snp_FSIEL0M02D43ZD_185-snp_soc_0855	S	P=0.031	0.21	4	-
CJA26	21	snp_FQU5R7M02I6ZE8-0_225-snp_soc_1180	S	P=0.025	0.30	3	-

\*Model: S = "Sires" model and S+D = "Sires plus Dams" model; QTL effect: the average effect of the QTL expressed in phenotypic standard deviation.; Sires: number of significant Sires; Dams: number of significant Dams.

