Genetic Parameters Of Fatty Liver And Breast Muscle Composition Predicted By Near-Infrared Spectroscopy

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Introduction

In France, over 95% of the duck fatty liver production comes from overfed male mule ducks, an intergeneric hybrid resulting from the mating between male Muscovy ducks (*Cairina moschata*) and female common ducks (*Anas platyrhynchos*). As mule ducks are sterile, the selection has to be carried out in the parental lines. Genetic parameters for overfed mule duck traits had previously been estimated either in the Pekin line (Poujardieu et al. 1994) or in both parental lines (Chapuis and Larzul, 2006; Marie-Etancelin et al., 2009). Until now, as the composition of fatty liver and fattened breast muscle are difficult to record in large numbers, no genetic parameters were available to describe such quality traits in mule duck. In the frame of a research project (GENECAN, Marie-Etancelin et al., 2008), various equipments and methods to record NIRS spectra were tested in order to optimize the meat and liver composition predictions. The present study aims at presenting genetic parameters of composition traits from mule ducks products predicted by NIRS in both parental lines, using the model of Lo et al. (1997).

Material and methods

Animals. During 2 years, 1,600 male mule ducks were hatched in 2 pedigree batches at the INRA experimental unit of Artiguères (UEPFG, France). These mule ducks were hybrids between 2 experimental populations: the female ducks were 382 back-cross (BC) common ducks and the male ducks were 56 Muscovy drakes. At 12 weeks of age, ducks were bred for 12 days in collective cages of 4 or 5 individuals and were overfed twice a day, in two successive series of 200 animals with 2 different crammers. At the end of the overfeeding period, animals were slaughtered after electronarcosis, at 93 days of age. They were bled, plucked, and eviscerated: liver, breast muscle (*Pectoralis major*), legs and abdominal fat were extracted from the carcasses.

Measurements. Fatty liver (N=1476) were weighed. The technological properties of fatty liver were measured by the liver melting rate (percentage of fat releases after sterilisation of 60 g of liver). On each breast and liver, two samples (about 20 g per sample) were removed and grounded. Samples were stored at -20°C for further spectrometric and chemical analyses.

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Two types of spectrometric measurement were done in reflectance. A first spectrometric measurement was done immediately after slaughter directly on the breast muscle and on fatty liver with an ASD Labspec Pro (350-2500 nm) portable spectrometer. A second measurement was done in the laboratory with a FOSS NIRSystem 6500 (400-2500 nm) spectrometer on ground breast muscle and liver and presented in quartz cells. The FOSS values were used for the later calibration. A total of 198 muscle samples and 195 liver samples were selected in order to represent the spectral variability of the 1476 ground samples measured with FOSS spectrometer. The samples were analyzed with the reference laboratory methods: lipid extraction (Folch *et al.*, 1957); moisture (oven at 104°C); dry matter (JOCE, 1971a); ash content (JOCE, 1971b) and protein content (Verdouw et al., 1977). The calibration equations were obtained by Partial Least Square (PLS) regression. The calibrating performances were described by their determination coefficient (R^2), and their residual standard error for calibration (SEC) or cross validation (SECV).

Statistical analysis. Genetic parameters were estimated by combining pedigree information from both parental population (common and Muscovy) and from mule duck performances (Lo et al., 1997). The model included two random effects, corresponding to the additive genetic values of sires and dams in the 2 parental populations, and a fixed effect corresponding to the combination of year, batch and crammer effects (12 levels). Pedigrees were traced back up to 5 generations of ancestors on both parental lines and consisted on 596 animals in the common line and 201 animals in the Muscovy line. Genetic parameters computations with a multitraits approach were performed by REML and confirmed by Gibbs sampling using respectively "remlf90" and "gibbsf90" programs (Misztal, 1999). A total chain length of 100,000 iterations was run and 20,000 samples were discarded as burn-in.

Results and discussion

Biochemical prediction. With the FOSS spectrometer (Table 1), the coefficient of determination (R^2) ranged from 0.46 for ash to 0.94 for DM, lipid contents in the liver and in the breast muscle having also high R^2 (0.93 and 0.89, respectively). The R^2 value for the meat intramuscular fat was similar to Tejerina et al. (2009) estimates (0.96) in guinea fowl. For the fatty liver, R^2 values were all higher than those obtained by Molette et al. (2001) on goose (0.151; 0.255; 0.805 and 0.908 respectively for ash, protein and lipid contents, and dry matter). The low prediction for ash in the liver was expected since minerals do not absorb radiation in near infrared, and was confirmed by Berzaghi et al. (2005) and Prieto et al. (2006). With the ASD spectrometer, R^2 values were between 0.01 to 0.08 points lower than with the FOSS spectrometer, except for liver ash which dramatically falls (from 0.46 to 0.28). Nevertheless, the direct measurements with the ASD spectrometer allowed a rather good prediction of the composition of products. Predictions obtained by Bastianelli et al. (2009) on muscle composition with the first year samples were higher. The addition of the second year NIRS samples seemed to reduce the prediction precision even if references measurements were added.

Table 1: Comparison of calibration equations between FOSS and ASD spectrometers

Reference	FOSS	ASD

	N	Mean	SD	SEC	R^2	SECV	SEC	R^2	SEC
Fatty liver									
DM	198	64.2	4.9	1.20	0.94	1.3	1.45	0.91	1.62
AC	198	0.41	0.09	0.07	0.46	0.07	0.08	0.28	0.09
LipC	198	51.0	6.5	1.70	0.93	1.8	2.07	0.89	2.24
ProtC	198	8.1	1.4	0.65	0.78	0.73	0.66	0.79	0.72
Breast muscle									
MC	195	71.7	1.2	0.55	0.77	0.60	0.58	0.73	0.60
LipC	195	4.9	1.1	0.35	0.89	0.41	0.47	0.81	0.54

DM: dry matter; AC: ash content; LipC: lipid content; ProtC: protein content; MC: moisture content

Heritabilities. Considering the confidence intervals, heritabilities estimated on the FOSS and ASD spectrometers were not significantly different on both parental lines (Table 2). The smallest heritability estimates were obtained on liver dry matter and liver ash contents. The breast muscle traits have the highest heritabilities, in particular the muscle lipid contents, but in comparison liver lipid contents were lower. This difference of genetic determinism between meat and liver was already shown by Marie-Etancelin et al. (2009) in common line where fatty liver weight and breast muscle weight heritabilities were respectively of 0.16 and 0.32. On duck populations from breeders, Chapuis and Larzul (2006) also obtained the highest heritability value for breast muscle weight in the Pekin line (0.23). Noticeably, the melting rate had a heritability comparable to lipid and protein contents ones (0.17 on the maternal line versus 0.09 on the paternal one; Marie-Etancelin et al., 2009). Conversely, the meat cooking losses had very low heritability values (0.03 on both lines, Marie-Etancelin et al., 2009) while meat composition predicted by NIRS had high heritability values. Overall, heritability values tended to be lower in the Muscovy line than in the common line, as already outlined by Chapuis and Larzul (2006).

Table 2: Heritabilities (st. dev.) of composition traits for both lines and spectrometers

	Fatty Liver				Breast muscle	
	DM	AC	LipC	ProtC	MC	LipC
Common line (CL)						
FOSS	0.139±0.034	0.118±0.030	0.154±0.033	0.170±0.032	0.183±0.033	0.249±0.035
ASD	0.151±0.032	0.144±0.032	0.148±0.031	0.126±0.028	0.191±0.033	0.211±0.033
Muscovy line (ML)						
FOSS	0.088±0.030	0.104±0.032	0.097±0.033	0.127±0.038	0.141±0.043	0.153±0.044
ASD	0.102±0.032	0.101±0.032	0.103±0.033	0.114±0.035	0.218±0.051	0.227±0.052

Genetic correlations. On the common line, correlations between a trait predicted with FOSS spectrometer and the same trait predicted with the ASD spectrometer (Table 3) ranged from 0.92 to 0.94 for liver and were about 0.95 for muscle. On the Muscovy line, estimates were more variable and less accurate but quite high, varying from 0.83 (for liver ash content) to 0.97 (for muscle lipid content). Except for the ash content, we can assert that composition traits predicted either with the FOSS spectrometer on ground samples or with the ASD spectrometer on the surface of products were genetically the same trait. We confirmed the

strong genetic correlation between fatty liver weight and its melting rate (+0.80 in both lines), as already shown by Poujardieu *et al*. (1994). Nevertheless, the melting rate appeared to be even more correlated with the liver lipid and protein contents predicted by the ASD spectrometer, with values about +0.87 and -0.91 respectively, in both lines. Using selection index theory, we estimated that the genetic correlation between melting rate and its prediction knowing the liver weight, and the lipid and protein contents was +0.924 in the common line and +0.913 on the Muscovy line. So the prediction of the liver composition with the ASD spectrometer added to the liver weight allowed to enface an indirect selection on liver melting.

Table 3: Genetic correlations (st. dev.) between FOSS and ASD spectrometers

	Fatty Liver				Breast muscle	
	DM	AC	LipC	ProtC	MC	LipC
CL	0.945±0.025	0.920±0.050	0.923±0.030	0.927±0.031	0.959±0.034	0.956±0.017
ML	0.952±0.032	0.829±0.083	0.923±0.046	0.897±0.053	0.895±0.056	0.968±0.023

Conclusion

This study aimed at proposing new genetic parameter estimates for the selection of overfed mule ducks on product quality traits in both common and Muscovy lines. A selection on the liver or meat composition predicted with an ASD spectrometer on the undamaged product will be equivalent to that carried out with a FOSS spectrometer on ground sample. Moreover, a selection index combining the liver weight, the liver lipid and protein contents predicted by NIRS would be effective to improve the liver melting rate.

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