GENETIC STUDIES OF ASCITES IN A BROILER POPULATION

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INTRODUCTION

Poultry breeders have been selecting very successfully on growth related traits over the last few decades. Recently, the breeding industry has taken up new challenges and efforts are being directed to produce stock adaptable to a wide range of environments and to decrease the incidence of skeletal defects and metabolic disorders such as ascites.

Ascites is a functional hypoxia caused by the high oxygen requirement of rapid growth and the inability of the heart and lungs to deliver sufficient oxygen to the tissue. It is characterised by an increase in peritoneal lymph and can lead to sudden death. Although the incidence of this disorder in well-managed flocks is very low, it causes important economic losses to the poultry breeding industry and it is a very important issue from an animal welfare standpoint.

Ascites susceptibility is a difficult trait to measure. However, percent blood oxygen saturation (% SaO_2), which measures oxygen binding to haemoglobin, is negatively correlated with ascites susceptibility and has been shown to be a good indicator thereof (Julian and Mirsalimi, 1992). Moreover, it can be easily measured in a non-invasive fashion using an oximeter.

In this study we assess evidence for the existence of a major gene or quantitative trait locus (QTL) involved in the control of % SaO_2 and examine the effect of this putative major locus on other characters.

MATERIALS AND METHODS

Data on percent blood oxygen saturation (% SaO_2), weight at five weeks (w5w, in decagrams) and fleshing score (flesh, 1 to 5 scale) were available for a heavy meat-type chicken line that shows a slightly higher ascites-related mortality compared to other Aviagen Ltd. lines (table 1). Records on % SaO_2 were available only for male selection candidates.

Table 1. Pedigree structure

Animals with record for % SaO_2	11919
Animals with record for w5w and flesh	118782
Number of sires/paternal half-sib families	755
Number of dams	4809

Data were analysed in two steps : first genetic parameters were estimated by Restricted Maximum Likelihood (REML) in a trivariate animal model including environmental maternal effects using ASREML (Gilmour et *al.*, 2000) and secondly, a Bayesian complex segregation analysis was performed on the corrected phenotypes for % SaO_2.

A mixed inheritance model was used for the complex segregation analysis. A single major gene was modelled as an autosomal biallelic locus with an additive (*a*) and a dominant effect

(*d*). The genotypic value for birds with genotype *BB* at the major locus is *a*, *-a* for *bb* birds and *d* for *Bb* birds. The frequency of the *B* allele will be referred to as p_B. Marginal posterior distributions for the major gene parameters, population mean and polygenic and residual variances were obtained by Gibbs sampling using Markov Chain Monte Carlo (MCMC) techniques (Pong-Wong *et al.*, 1999). Individual chains were composed by 1005000 samples that were collected after allowing for a warming period of 5000 iterations, from then, 1/100 iterations were kept.
In order to investigate the effect of the putative major locus on w5w and flesh, the phenotypic values for these traits were regressed on the genotype probabilities estimated from the complex segregation analysis.

RESULTS
Descriptive statistics of the traits studied were obtained with Genstat (Genstat 5 Committee, 1993) and are shown in table 2.

Table 2. Means and standard deviations (in brackets) for weight at five weeks (w5w), fleshing score (flesh) and blood oxygen saturation (% SaO_2)

w5w (dag)	flesh	% SaO_2
216.1 (27.98)	3.10 (0.90)	81.81 (7.98)

Heritability (h^2) estimates obtained for % SaO_2, w5w and flesh were 0.15 (s.e. = 0.02), 0.32 (s.e. = 0.01), 0.19 (s.e. = 0.01) respectively. Genetic correlations (rg) between % SaO_2 and w5w and flesh are negative but not significantly different from 0 (5 % significance level).

Table 3. Point estimates and standard deviations (in brackets) of additive (*a*) and dominant effect (*d*) and frequency (p_B) of the major gene, polygenic (V_A), major gene (V_{MG}) and residual (V_E) variances, variance ratios and dominance deviance (*d/a)*

a	6.46 (0.21)	
d	6.60 (0.32)	
p_B	0.65 (0.02)	
d/a*	1.02 (0.06)	
V_{MG}*	18.24 (1.82)	$V_{MG} = 2p_B p_b [a+d(p_b-p_B)]^2 + [2p_B p_b d]^2$
V_A	3.93 (0.62)	
V_E	32.67 (0.85)	
V_T*	54.85 (1.84)	$V_T = V_{MG} + V_A + V_E$
h^2_T*	0.40 (0.02)	$h^2_T = (V_{MG} + V_A)/ V_T$
h^2_{MG}*	0.33 (0.02)	$h^2_{MG} = V_{MG} / V_T$

Means of the posterior distributions of the major gene parameters, population mean and polygenic and residual variances obtained from the complex segregation analysis were similar across the five chains run. The posterior distributions of these parameters were also similar in shape and approached normality, so the samples (10000/chain) were pooled across chains and

the posterior means of the pooled distributions of the parameters sampled have been used as point estimates. The sample autocorrelation for the major gene parameters estimated was calculated using Genstat's CORRELATE directive (Genstat 5 Committee, 1993) and ranged from 0.10 to 0.26 for all the chains. The following table shows the point estimates of the parameters sampled or derived from the sampled parameters (indicated by *).
The regression of trait values on the estimated genotype probabilities revealed that the putative major locus would be overdominant for w5w and flesh : while there would be no difference between *BB* and *bb* birds in weight at five weeks or fleshing score, *Bb* birds would be around 60 grams heavier than homozygous birds and would have a fleshing score 0.25 units higher.

DISCUSSION

The results obtained for the heritabilities and genetic correlations from the REML analyses are not substantially different to the ones obtained for other lines (results not shown). The heritabilities obtained for body weight are similar to the ones reported in the literature (Dunnington and Siegel, 1996 ; Koerhuis and Thompson, 1997). For % SaO_2, the heritabilities reported are different across studies : Druyan *et al.* (1999) obtained estimates around 0.5-0.6 but De Greef *et al*. (2001b) estimated an heritability for 'arterial oxygen pressure' (directly related with oxygen saturation level) of 0.13 and a genetic correlation between this trait and weight at 35 days of -0.33. However, the studies by Druyan *et al.* and De Greef *et al*. (2001b) were carried out on animals exposed to ascites-inducing conditions whilst our populations were reared in standard commercial conditions and Knap and Bishop (2000) pointed out by referring to the study by De Greef *et al*. (2001b) how environmental sensitivity may have important effects on genetic parameter estimation.
We have found suggestive evidence of a locus with large effect on % SaO_2 segregating in the population studied. Other studies suggest as well that ascites susceptibility could have a simple genetic control (Druyan *et al.*, 2001) and that the gene or genes involved are dominant (Wideman and French, 2000).
Complex segregation analysis is the most powerful marker-free method for major gene/QTL detection but it is sensitive to deviations from normality, and the distribution of the data analysed was skewed (skewness coefficient = -0.75). A QTL mapping study is a necessary further step that would confirm or refute our findings. Such a study would allow the identification of markers closely linked to a region or regions of the poultry genome that affect blood oxygen carrying capacity.
Our results also suggest that the putative major locus involved in the genetic control of % SaO_2 could also have an effect on body weight and fleshing score at five weeks, and that it would act in an overdominant fashion. This could explain that the frequency in the population is intermediate, and would make it difficult to manipulate allele frequencies at the putative major locus without the help of molecular tools.
The ability to directly manipulate allele frequencies at this putative major locus would allow the deleterious allele to be eliminated and hence allow broiler health to be improved, a result that could not readily be obtained by selection on oximeter values alone. Based on our results, a power study was carried out which led us to conclude that a mapping population consisting on 20 sires with around 100 offspring each would allow us to identify regions of/ markers in the poultry genome associated with blood oxygen carrying capacity.

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