

Selection Strategies for Body Weight and Reduced Ascites Susceptibility in Broilers

A. Pakdel, P. Bijma, B. J. Ducro, and H. Bovenhuis¹

*Animal Breeding and Genetics Group, Wageningen Institute of Animal Sciences,
PO Box 338, 6700 AH Wageningen, The Netherlands*

ABSTRACT Ascites syndrome is a metabolic disorder in broilers. Mortality due to ascites results in significant economic losses and has a negative impact on animal welfare. It has been shown that genetic factors play a considerable role in susceptibility of birds to ascites, which offers perspectives for selection against this syndrome. The aim of the present study was to evaluate the consequences of alternative selection strategies for BW and resistance to ascites syndrome using deterministic simulation. In addition to the consequences of current selection (i.e., selection for increased BW only) alternative selection strategies including information on different ascites-related traits measured under normal or cold conditions and the consequences of having information on the underlying genes (i.e., MAS) were quantified. Five different breeding schemes were compared based on the selec-

tion response for BW, ascites susceptibility, and the rate of inbreeding. Traits investigated in the index as indicators for ascites were hematocrit value (HCT) and ratio of right ventricle to the total ventricular weight of the heart (RV:TV). The results indicated that by ignoring ascites susceptibility in the breeding goal, the gain for BW is 130 g and the birds will become more susceptible to ascites. Testing 50% of the birds under cold temperature conditions and including information of ascites related traits (HCT and RV:TV) measured under normal and cold conditions makes it possible to achieve a relatively high gain for BW (111.4 g) while controlling the genetic level for ascites susceptibility (selection response was 0). The results of scenarios including QTL information of ascites susceptibility showed that QTL information could be used very effectively in controlling ascites susceptibility.

(Key words: broiler, ascites, breeding program, deterministic simulation, quantitative trait loci)

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INTRODUCTION

Ascites syndrome is a metabolic disorder of fast-growing meat-type chickens. It has been suggested that this syndrome is the consequence of allomorphic differences in heart and lung growth relative to the size of the animal (Siegel and Dunnington, 1997). Ascites results in significant economic losses to the broiler industry due to high mortality, especially at later ages, and has a negative impact on animal welfare. The incidence of ascites is influenced by environmental and genetic factors. The most important environmental factors causing the development of ascites in broilers are high altitudes and cold temperatures (Smith et al., 1954; Siller and Hemsley, 1966; Bendheim et al., 1992; Shlosberg et al., 1992). Several studies have shown that traits related to ascites syndrome have a relatively high heritability (Lubritz et al., 1995; Maxwell and Robertson, 1997; De Greef et al., 2001; Pakdel

et al., 2002). This indicates that genetic factors play a considerable role in susceptibility of birds to ascites, which offers perspectives for selection against this syndrome.

In practice, selection will be for a combination of production traits, such as BW and ascites susceptibility (AS). A few studies have reported genetic correlations between BW and ascites-related traits (De Greef et al., 2001; Moghadam et al., 2001; Pakdel et al., 2005a). Under normal climatic conditions, Moghadam et al. (2001) found a positive genetic correlation between ascites and BW. Under cold conditions, however, De Greef et al. (2001) and Pakdel et al. (2005a) reported a negative genetic correlation between traits related to ascites and BW. In addition Pakdel et al. (2005b) estimated a weak but positive genetic correlation among ascites-related traits measured under cold conditions and BW measured under normal conditions. These results indicate that there is considerable scope for simultaneous selection of birds for increased

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¹To whom correspondence should be addressed: henk.bovenhuis@wur.nl.

Abbreviation Key: AS = ascites susceptibility; BLUP = best linear unbiased prediction; EBV = estimated breeding value; ΔF = rate of inbreeding; HCT = hematocrit value; RV:TV = ratio of right ventricular weight to the total ventricular weight.

BW while controlling susceptibility to ascites. However, it is not obvious which selection strategy is optimal to achieve this goal.

Designing effective selection strategies for ascites resistance not only has to deal with the identification of good indicator traits but also the choice of the selection environment. Indicator traits, such as hematocrit value (HCT) or ratio of right ventricle to the total ventricular weight of the heart (RV:TV), differ not only with respect to their correlations to AS but also differ in that HCT can be measured on live birds, whereas RV:TV cannot. Further, measurement of birds under cold-stressed conditions is expected to reveal to a larger extent the genetic differences that exist in AS between birds as compared with the testing of birds under normal temperature conditions. New opportunities to reduce AS by means of selection will become available if genetic markers linked to AS are identified.

The aim of the present study was to evaluate the consequences of alternative selection strategies for BW and resistance to ascites syndrome using deterministic simulation. In addition to the consequences of current selection (i.e., selection for increased BW only) alternative selection strategies including information on different ascites-related traits measured under normal or cold conditions, and QTL information for AS will be quantified. Schemes will be compared based on the selection response for BW and AS as well as the rate of inbreeding.

MATERIALS AND METHODS

Population Structure

A population with discrete generations was simulated in which 50 males were randomly mated to 350 females with a mating ratio of 1 male to 7 females. Each female produced 32 progeny, 16 males and 16 females, and each male had 112 progeny of each sex. The total number of progeny of each sex was $350 \times 16 = 5,600$. Among the progeny, the best males and females were selected as parents of the next generation. In the starting situation 50 male parents out of 5,600 available males were selected (selected proportion = 0.009), and 350 females were selected out of the available 5,600 (selected proportion = 0.063). Base generation individuals were assumed to originate from a large population in Hardy-Weinberg and gametic phase equilibria.

Breeding Goal and Index

The breeding goal was a combination of 2 traits: BW and AS,

$$H = V_{BW} \times A_{BW} + V_{AS} \times A_{AS}$$

where H is a weighted sum of the true breeding values, V_{BW} is the economic value of BW, A_{BW} is the true breeding value for BW, V_{AS} is the economic value of AS, and A_{AS} is the true breeding value for AS. In practice an index I

is used to predict value for the breeding goal H of each selection candidate. The index I is the estimated breeding value (EBV) of the breeding goal:

$$I = V_{BW} \times EBV_{BW} + V_{AS} \times EBV_{AS}.$$

The breeding goal applied to normal husbandry conditions.

Two different breeding goals were used: 1) base situation in which selection was only for BW and with no emphasis on AS ($V_{AS} = 0$) and 2) the economic value for BW was fixed at 1, and the economic value of AS in the breeding goal (V_{AS}) was changed to obtain zero response in AS. In the base situation information on BW measured under normal temperature conditions was available for all birds. Selection for increased BW in this situation reflected selection based on the EBV from an animal model best linear unbiased prediction (BLUP) procedure. Alternative selection strategies considered differed with respect to the type of ascites indicator trait and the environmental conditions the traits were measured in. With respect to the type of ascites indicator trait, traits can be distinguished that can be measured on the live bird, such as HCT, and indicator traits for which the bird has to be slaughtered, such as RV:TV. It was assumed that the birds for which RV:TV was recorded were not available as selection candidates. Four different scenarios were considered:

- A-1) Measurement of BW and HCT on all birds and under normal conditions, which is indicated as [100% ($BW_N + HCT_N$)].
- A-2) Measurement of BW and HCT on all birds and measurement of RV:TV on 50% of the birds, which is indicated as [100% ($BW_N + HCT_N$) + 50% ($RV:TV_N$)]. All birds were kept under normal temperature conditions, and birds for which RV:TV was measured were not available for selection.
- A-3) 50% of the birds are tested under cold-stress conditions. In this scenario the traits BW and HCT were measured under normal and cold conditions, whereas the trait RV:TV was measured only under cold conditions. Birds for which RV:TV was measured were not available for selection [50% ($BW_N + HCT_N$) + 50% ($BW_C + HCT_C + RV:TV_C$)].
- A-4) All birds were tested under cold-stress conditions. In this scenario the traits BW and HCT were measured on all birds. Fifty percent of the birds were killed to measure the trait RV:TV [100% ($BW_C + HCT_C$) + 50% ($RV:TV_C$)].

Table 1 summarizes the traits recorded and the number of half-sibs and full-sibs in the different breeding schemes. For BW and HCT, in addition to the average phenotypic performance of full-sibs and half-sibs, the birds own performance was available. The RV:TV trait was not available for the selection candidate.

In addition to the above indicated alternative scenarios, breeding schemes with QTL information were investi-

TABLE 1. The selected proportion per sex and the number of half-sib and full-sib birds for which phenotypic information was available under different selection strategies

Scheme	Selected proportion per sex	Normal conditions						Cold conditions					
		BW _N		HCT _N ¹		RV:TV _N		BW _C		HCT _C		RV:TV _C	
		FS ²	HS	FS	HS	FS	HS	FS	HS	FS	HS	FS	HS
Base	5,600	31	192	—	—	—	—	—	—	—	—	—	—
A-1	5,600	31	192	31	192	—	—	—	—	—	—	—	—
A-2	2,800	31	192	31	192	16	96	—	—	—	—	—	—
A-3	2,800	15	96	15	96	—	—	16	96	16	96	16	96
A-4	2,800	—	—	—	—	—	—	31	192	31	192	16	96

¹HCT = hematocrit value; RV:TV = ratio of right ventricular weight to total ventricular weight, where subscript C indicates that the trait was measured under cold conditions, and subscript N indicates that the trait was measured under normal temperature conditions.

²FS = number of full-sib birds; HS = number of half-sib birds.

gated. The QTL that were considered explained 5, 10, 20, or 50% of the genetic variance of the breeding goal trait AS. These situations will be referred to as Q05, Q10, Q20, and Q50, respectively. This fraction of the variance can be explained by one or a number of genes. The remaining genetic variation for AS results from polygenes (i.e., not marked). Details on the calculations are given in appendix 1.

Genetic Parameters

The genetic parameters used in the simulation were based on estimates from Pakdel et al. (2002, 2005a,b). Results of Pakdel et al. (2002) indicated that there is a significant maternal genetic effect for traits BW and RV:TV. Therefore, Pakdel et al. (2002) analyzed these traits using a model that accounts for a maternal genetic effect. In the current study, the estimated heritabilities for direct genetic effects were used. In the model calculations only direct genetic effects were considered, and maternal genetic effects were not included in the analyses.

For the breeding goal trait AS, no genetic parameters were available. The most apparent sign of ascites is the accumulation of fluid in the abdominal cavity of the bird. Fluid accumulation in the abdominal cavity appears in the latest stages of ascites, that is, before death occurs. In the current study the genetic parameters for AS were those that were obtained for the trait "fluid accumulation in the abdominal cavity," which was scored as 0, 1, or 2. The variation for susceptibility to ascites is only partly expressed under normal conditions. Under cold conditions, however, the trait fluid accumulation in the abdomen reflects more accurately the variation in AS. Therefore, parameters for AS were based on fluid accumulation in the abdomen under cold conditions.

The genetic correlation matrix was singular, and, therefore, a bending routine was used to make the genetic correlation matrix nonsingular. This resulted in small changes as compared with the original parameters estimated by Pakdel et al. (2002, 2005a,b). Table 2 shows the genetic parameters that were used in the simulations.

Analytical Comparison of Breeding Strategies

Predictions of the rates of genetic change and inbreeding were performed by deterministic simulation of single-stage selection schemes with discrete generation, using the program SelAction (Rutten et al., 2002). This program predicts the rate of genetic gain using multitrait pseudo-BLUP (Villanueva et al., 1993). The program accounts for reduction in variance due to selection (Bulmer, 1971) and corrects selection intensities for finite population size and for the correlation between index values of family members (Meuwissen, 1991). The program is an accurate approximation of stochastic simulation with selection on animal model BLUP, because full pedigree information is accounted for (Wray and Hill, 1989). Pedigree information consists of the EBV of the sire and dam and the mean EBV of the dams of each half-sib group. The mating structure is assumed to be hierarchical and random, and selection response is predicted for the Bulmer equilibrium situation (Rutten et al., 2002). Prediction of the rate of inbreeding was based on the long-term genetic contribution theory (Wray and Thompson, 1990).

RESULTS

Base Situation

Table 3 gives the response for BW, AS, and the rate of inbreeding for the base and alternative scenarios. In the base situation, in which AS is ignored in the breeding goal and selection is for BW only, a selection response for BW of 130 g was observed. The correlated selection response for AS was +0.025 units. The AS is a score trait that is categorized as 0, 1, or 2. The mean of this score trait was 0.08 with a phenotypic standard deviation of 0.38. A value of 0.025 is, therefore, equal to 0.2 additive genetic standard deviation. When assuming a normal distribution for the underlying continuous variable, the percentage of birds under cold conditions with a score of 1 or 2 in the base situation was equal to 4.2%. A selection response of 0.025 corresponded to an increase of the num-

TABLE 2. The genetic parameters used in the simulation study¹

Traits	σ_p^2	Genetic parameters ²						
		BW _N	AS	HCT _N	RV:TV _N	BW _C	HCT _C	RV:TV _C
BW _N	60,000	0.20	0.18	0.55	0.46	0.46	0.27	0.37
AS	0.14	—	0.10	0.46	0.55	-0.01	0.64	0.73
HCT _N	5	-0.10	—	0.20	0.64	0.14	0.82	0.46
RV:TV _N	20	0.11	—	0.10	0.10	-0.06	0.73	0.82
BW _C	60,000	—	-0.30	—	—	0.20	-0.21	-0.25
HCT _C	15	—	0.30	—	—	-0.40	0.40	0.55
RV:TV _C	60	—	0.50	—	—	-0.30	0.50	0.25

¹AS = ascites susceptibility trait; HCT = hematocrit value; RV:TV = ratio of right ventricular weight to total ventricular weight; subscript C indicates that the trait was measured under cold conditions, subscript N indicates that the trait was measured under normal temperature conditions; σ_p^2 = phenotypic variance.

²Genetic correlations are above, phenotypic correlations are below, and heritabilities are on the diagonal.

ber of birds with score 1 or 2 to 4.8%. Therefore, under this scenario the fraction of ascites-susceptible birds will increase gradually.

Use of Ascites-Indicator Traits Measured Under Normal Temperature Conditions

When including information for a nondestructive indicator trait (HCT) for ascites measured on all the birds and these birds were kept under normal conditions (scheme A-1), the response for BW decreased 11.4% as compared with the base situation. The rate of inbreeding increased from 3% in the base situation to 4.3% per generation in the scheme A-1 (Table 3). By including information on RV:TV measured on 50% of the birds kept under normal conditions (scheme A-2), the number of selection candidates was reduced to 2,800 birds per sex. The birds on which RV:TV is measured were no longer available as selection candidates. In this scheme, selection response for BW was reduced by 17.3% as compared with the base situation. The predicted rate of inbreeding for this scheme was 2.3% per generation.

Use of Ascites-Indicator Traits Measured Under Cold Temperature Conditions

In scenarios A-3 and A-4, information on traits measured under cold conditions was used in the index. In

scheme A-3, half of the birds were kept under normal temperature conditions, and the other half were kept under cold conditions. In this scheme, information was available for BW and HCT under cold and normal conditions, and the trait RV:TV was measured only under cold conditions. The selection response achieved for BW in this scheme was higher (111.4 g) than that of scheme A-2 (Table 3). In addition, the rate of inbreeding in this scheme was reduced to 1.7% per generation, which was the lowest inbreeding rate among the different scenarios that were considered. The economic value that was required to keep AS at the same level was lower than that required for the other scenarios.

The last scenario considered was one in which all the birds were kept under cold conditions (scheme A-4). In this scheme traits BW and HCT were measured on all the birds. To measure the trait RV:TV, half of the birds were euthanized. The number of selection candidates in this scheme was equal to the number of selection candidates in the schemes A-2 and A-3. The selection response for BW in this scheme was 54.1 g (Table 3). This is clearly lower than the response under the other schemes.

Effects of Proportion of Birds Euthanized

In some of the schemes considered so far, 50% of the birds were euthanized to measure the trait RV:TV. This proportion might not be optimal, and in order to investi-

TABLE 3. The effect of alternative scenarios on BW, ascites susceptibility (AS), and rate of inbreeding

Scheme	Traits in the index	Number of selection candidates	Economic value for AS ¹	Selection response for BW ²	Selection response for AS ³	ΔF^4 (%)
Base	100% (BW _N)	5,600	0	130	0.025	3.0
A-1	100% (BW _N + HCT _N)	5,600	-1,050	115.2	0	4.3
A-2	100% (BW _N + HCT _N) + 50% (RV:TV _N)	2,800	-775	107.5	0	2.3
A-3	50% (BW _N + HCT _N) + 50% (BW _C + HCT _C + RV:TV _C)	2,800	-400	111.4	0	1.7
A-4	100% (BW _C + HCT _C) + 50% (RV:TV _C)	2,800	-580	54.1	0	2.1

¹The economic value of AS in the breeding goal. The economic value of BW in each scheme was equal to 1.

²Response on BW, the unit of BW is grams. The additive genetic standard deviation (σ_a) for BW is equal to 109.5 g. Therefore 130 g = 1.2 σ_a .

³The accumulation of fluid in the abdomen is a score trait as 0, 1, or 2. The additive genetic standard deviation for AS is equal to 0.12 unit. Therefore 0.025 = 0.21 σ_a .

⁴ ΔF = rate of inbreeding per generation.

TABLE 4. The effects of the proportion of birds that is sacrificed on scenarios A-2, A-3, and A-4¹

Scheme	25%			50%			75%		
	Economic value for AS ³	Selection response for BW	ΔF^4 (%)	Economic value for AS	Selection response for BW	ΔF (F)	Economic value for AS	Selection response for BW	ΔF (%)
A-2	-825	114.6	3.2	-775	107.5	2.3	-750	92.3	1.4
A-3	-425	120.9	2.4	-400	111.4	1.7	-410	92.6	1.0
A-4	-575	58.4	2.8	-580	54.1	2.1	-580	46.5	1.2

¹For each alternative, the response for ascites susceptibility was fixed at zero.

²Scheme A-2 including traits BW_N, hematocrit value (HCT_N), and ratio of right ventricular weight to the total ventricular weight (RV:TV_N), scheme A-3 including traits BW_N, HCT_N, BW_C, HCT_C, and RV:TV_C and scheme A-4 including traits BW_C, HCT_C, and RV:TV_C. Subscripts N or C indicate that traits were measured under normal or cold temperature conditions, respectively.

³The economic value of ascites susceptibility (AS) in the breeding goal. The economic value of BW in each scheme was equal to 1.

⁴ ΔF = rate of inbreeding.

gate the effect of the proportion of birds euthanized, this proportion was changed from 50 to 25 or 75%. In each scheme, response for AS was kept constant, and responses for BW and inbreeding rate are presented in Table 4. The results indicated that by increasing the number of birds euthanized, selection response for BW decreased as well as the rate of inbreeding. In scheme A-4, in which all birds kept under cold conditions, the proportion of birds euthanized had a relatively small effect on the results.

Comparison of Schemes at Equal Rates of Inbreeding

The scheme A-1 showed higher response for BW than scheme A-3 when the proportion of euthanized birds was 50 or 75%, but the inbreeding rate in scheme A-1 was relatively high. Ideally, schemes should be compared at equal rates of inbreeding. To make scheme A-1 comparable to other schemes, the rate of inbreeding was reduced by increasing the number of selected sires (Table 5). When the number of sires increased from 50 to 90 or 140, the inbreeding rate in scheme A-1 was reduced to 2.4 and 1.7%, respectively, which was approximately equal to the rate of inbreeding in scheme A-2 (2.3%) and scheme A-3 (1.7%). At equal rates of inbreeding, the gain achieved for BW in scheme A-1 was higher than that in scheme A-2 (110.1 vs. 107.5 g) but was lower than that in scheme A-3 (105.8 vs. 111.4 g). Therefore, when comparing selection response at the same rate of inbreeding, scheme A-3 (i.e.,

including information of BW_N, HCT_N, BW_C, HCT_C, and RV:TV_C in the index) was the best among alternative breeding schemes considered. In this scheme the genetic progress of BW was reduced by around 18.4 g as compared with the base situation.

Genetic Progress in Breeding Schemes Using Genetic Markers

Results of schemes with different fractions of variance explained by the QTL were compared with the base scheme and scheme A-3. The results are summarized in Table 6. By using information on QTL that describe only 5% of the genetic variance (scheme Q05) ascites could be controlled while selection response for BW was 122.3 g. This was only 6% lower than the achieved gain for BW in the base scheme (130 g) and 10% higher than the gain obtained for BW in scheme A-3. Inbreeding for the MAS schemes was at a similar level as that of the base scheme. It is good to keep in mind that in the MAS schemes, similar as in the base scheme, all the birds were available as selection candidates and they are kept under normal temperature circumstances. However, in scheme A-3 a proportion of the birds was kept under cold conditions, and they had to be euthanized to measure ascites-related traits. If the proportion of the genetic variance that was explained by the markers increased, (scheme Q10, Q20, and Q50), the gain for BW improved further. For Q50 the

TABLE 5. The effect of changing the number of sires used in scheme A-1

Number of sires	Economic value for AS ¹	Selection response for BW ²	ΔF (%) ³
50	-1,050	115.2	4.3
90	-1,075	110.1	2.4
140	-1,090	105.8	1.7

¹The economic value of ascites susceptibility (AS) in the breeding goal. The economic value of BW in each scheme was equal to 1.

²Response for BW in grams. Response for AS was fixed at zero level in each scheme.

³ ΔF = rate of inbreeding.

TABLE 6. The effect of amount of variance explained by the QTL on the breeding goal traits

Scheme	Number of selection candidates	Economic value for AS ¹	Selection response for BW	Selection response for AS	ΔF (%)
Base ²	5,600	—	130.0	0.025	3.0
A-3 ³	2,800	-400	111.4	0	1.7
Q05 ⁴	5,600	-550	122.3	0	3.0
Q10	5,600	-450	123.8	0	2.9
Q20	5,600	-320	125.9	0	2.9
Q50	5,600	-165	128.0	0	2.9

¹AS = ascites susceptibility. The economic value of BW in the breeding goal was equal to 1 in all schemes.

²Base scheme including information on BW only.

³Scheme A-3 including information of BW and hematocrit value (HCT) measured on 50% of birds under normal temperature conditions and BW, HCT, and ratio of right ventricular weight to the total ventricular weight (RV:TV) measured on the rest of birds under cold temperature conditions.

⁴Q refers to the amount of variance explained by the QTL. This value is 5, 10, 20, or 50%.

gain for BW was 128 g, which was close to the 130 g of the base scheme.

DISCUSSION

To combine selection for increased BW and resistance to AS in broilers, different schemes were compared by deterministic simulation. In the alternative schemes the traits HCT and RV:TV measured under normal and cold conditions were used as index information. It has been accepted that as an adaptation to hypoxia, HCT increases, and so direct measurement of HCT is useful in accessing ascites progression (Maxwell, 1991; Mirsalimi and Julian, 1991; Lubritz and McPherson, 1994; Shlosberg et al., 1996). Moreover, RV:TV is a pathological trait that has value as a predictive indicator of ascites (Maxwell, 1991; Enkvetchakul et al., 1995; Wideman et al., 1998). However, Shlosberg et al. (1996) showed a high nonascites mortality in experimental groups with a low hematocrit value, and, therefore, selection against HCT needs more attention and care than selection against RV:TV.

The results of the current study indicated that by using information of ascites-related traits measured under normal conditions AS can be controlled. However, control of AS comes at a cost (i.e., a reduction in selection response for BW). This reduction in BW was higher in scheme A-2, in which RV:TV was measured on a proportion of the birds kept under normal temperature conditions. However, when ascites-related traits were measured on a proportion of the birds kept under cold conditions (scheme A-3), the gain achieved for BW was higher. This finding also holds when results are compared at the same level of inbreeding. If all information was collected for birds kept under cold conditions (scheme A-4), the selection response for BW was reduced considerably. This finding can be ascribed to the low genetic correlation between BW measured under cold and normal conditions (0.49). It has to be realized that the breeding goal is defined at normal temperature conditions. Therefore, in case no marker information on AS is available, the best scheme for improving BW while controlling AS is scheme A-3 in which ascites-related traits are measured under cold and normal conditions.

Inbreeding

It has been generally recommended that the rate of inbreeding in broiler lines should be kept at a level lower than 1% (Morris and Pollott, 1997). In all the simulations in the current study the rate of inbreeding (ΔF) was greater than this critical level. SelAction calculates the rate of inbreeding for a Bulmer equilibrium situation accounting for the effect of selection (Rutten et al., 2002). Prediction of the rate of inbreeding is based on the long-term genetic contribution theory (Wray and Thompson, 1990; Woolliams and Bijma, 2000). In the current simulation it was assumed that selection is for BW and AS only. However, in a practical poultry breeding program selection will be for several other traits. Therefore, in practice the number of selection candidates will be lower than what has been assumed in the current study. If the number of available selection candidates was reduced by 50%, to allow for selection on other traits not correlated to the breeding goal traits, on average ΔF was reduced by about 40% in each scheme (e.g., in the base scheme ΔF reduced from 3 to 1.9% or in scheme A-3 ΔF reduced from 1.7 to 1.1%).

In addition to the number of parents, there are other mechanisms that affect ΔF . For instance, more sib information in the index increases the probability of co-selection of relatives, which in turn increases ΔF . By changing the number of sires used in scheme A-1, the ΔF of that scheme was made equal to that of schemes A-2 and A-3. The results indicated that at equal rate of inbreeding the gain achieved for BW in this scheme was lower than the gain achieved for BW in scheme A-3.

There are, however, more efficient ways of maximizing gain while restricting inbreeding (i.e., by using stochastic simulation rather than deterministic simulation). Meuwissen (1997) introduced a dynamic selection tool to maximize genetic gain while restricting the rate of inbreeding. In this method the number of parents and the number of offspring per parent may vary, depending on the candidates available in a particular generation, which results in a dynamic breeding program. Dynamic selection tools are likely to reduce the variance of the rate of inbreeding as well (Meuwissen, 1997).

MAS

The use of MAS can be especially useful for traits that have a low heritability or are difficult to measure (Dekkers and Hospital, 2002). Both of these characteristics apply to AS, and, therefore, it is expected that MAS can make an important contribution. Rabie (2004) performed a whole genome scan aimed at the mapping of QTL for ascites. Three significant QTL affecting ascites-related traits were detected, whereas 2 QTL reached the genome-wide suggestive threshold.

The results of present study showed that QTL information could be used very effectively in controlling AS. Even if the QTL explained only 5% of the genetic variance, the reduction in gain for BW was limited as compared with a scheme in which selection was for BW only (base). By using QTL, information no longer requires that some of the birds are euthanized (e.g., in scheme A-3 a proportion of birds have to be euthanized to measure the trait RV:TV). This illustrates that MAS can make an important contribution in selection of birds that are resistant to ascites. Whether implementation of MAS in a breeding scheme is economically beneficial will depend upon the cost and the benefits from increased genetic progress.

Literature

The results of current study showed that selection for increased BW and resistance to ascites syndrome was possible in broilers. This result was in agreement with the previous results obtained by Wideman and French (2000), Anthony et al. (2001), Balog et al. (2001), and McMillan and Quinton (2002). In a theoretical study, McMillan and Quinton (2002) investigated the effects of selecting for a production trait, such as growth rate, on a fitness trait, such as ascites, using stochastic simulation. They reported that the use of sib information and an indicator trait for ascites reduces the genetic level for AS.

In experimental studies several researchers have chosen a strategy to test an animal's ability to withstand severe stress and not succumb to ascites (Wideman and French, 2000; Anthony et al., 2001; Balog et al., 2001). Wideman and French, (2000) demonstrated improvement in ascites resistance of progeny from broiler breeders that, for 2 consecutive generations, had survived the rigorous selection pressure imposed by unilateral pulmonary artery occlusion. Chronic unilateral pulmonary artery occlusion triggers a pathophysiological progression that terminates with a high incidence of mortality diagnosed as ascites. Wideman and French (2000) concluded that by using this technique, genetic selection for ascites resistance could be accomplished. However the final BW in nonascitic broilers in one experiment was less than for nonascitic base population birds, but in the second experiment there was no difference for final BW among nonascitic birds. Anthony et al. (2001) made sire-family selections from siblings in broilers based on mortality data obtained in a hypobaric chamber. They reported success at selecting an ascites-resistant and an ascites-

susceptible population of broilers. Balog et al. (2001) reported that the selection for ascites resistance or susceptibility did not affect weight gain.

In conclusion, alternative selection schemes were considered for simultaneous selection on BW as well as reduction of AS in the present study. The alternative selection strategies indicated that by selection for increased BW only and ignoring AS in the breeding goal, the AS of the birds increased. Inclusion of information on ascites-related traits (HCT and RV:TV) measured under normal and cold conditions made it possible to achieve relatively high gain for BW (111.4 g) while keeping the AS level constant (no genetic change). The results of using QTL information indicated that MAS could be used very effectively in the breeding scheme for ascites resistance even if the QTL explains only 5% of the genetic variance of the AS.

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APPENDIX 1

Heritability of BW was 0.2, and the phenotypic variance was 60,000. The heritability of AS was 0.10, and phenotypic variance was 0.14. The economic value of BW was set equal to 1, and the economic value of AS was changed to obtain zero response for AS. The information source for the genetic evaluation of BW was the animal's record, pedigree information, average phenotypic performance of full-sibs, and average phenotypic performance of half-sibs. The information sources for the genetic evaluation of AS were the QTL information. All birds were kept under normal conditions, and no birds were killed. The QTL considered explained 5, 10, 20, or 50% of the genetic variance of AS. These situations are referred to as Q05, Q10, Q20, and Q50, respectively. Variance could be explained by one or number of genes. The remaining genetic variation for AS resulted from polygenes (i.e., not marked). The QTL information was modeled as a trait that was correlated to AS in the breeding goal and had a heritability of 1. It was assumed that the QTL had no pleiotropic effects on BW, and, therefore, the genetic correlation between the QTL and BW was zero. Further, it was assumed that the correlation between the QTL and the polygenic component was 0 in the base generation. (i.e., prior to selection). The correlation between the QTL and the breeding goal trait AS depended on the amount of variation that was explained by the QTL.

The genetic correlations of AS with the QTL and the polygenic component are $\sqrt{q}$ and $\sqrt{1 - q}$, respectively, and the phenotypic correlation of AS with QTL and polygenic component are $\sqrt{q \times h_{AS}^2}$ and $\sqrt{(1 - q) \times h_{AS}^2}$, respectively, where q is the fraction of the genetic variance in AS trait explained by the QTL. The genetic correlation between polygenic component and BW is equal to $\frac{r_{AS,BW}}{\sqrt{1 - q}}$ so that

for any q , the total genetic correlation of BW and AS is equal to 0.18. The heritability of the polygenic component is $\frac{1 - q}{h_{AS}^2 - q}$. The phenotypic variance of QTL is equal to additive genetic variance of QTL, which is equal to $q \times \sigma_{A_{AS}}^2$, and the phenotypic variance of polygenic component is equal to $\sigma_{P_{AS}}^2 - \sigma_{QTL}^2$.