

Genetics of High-Value Yield in Broilers

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Summary and Implications

A genomic scan with molecular markers was used to identify regions of the broiler genome that are associated with traits of growth and carcass composition in commercial broiler chickens. Identification of markers that can be used to genetically select broiler populations for better efficiency of growth of high-value yield parts, such as white meat, will enhance the profitability of poultry production and provide consumers with more of the desired type of meat product.

Introduction

White meat is the most economically valuable part of the broiler chicken. Although the genetic correlation of white meat weight with live weight is moderately high, the genetic correlation of white meat yield (WM%) with live weight is low. This means that the traditional selection program on easily measured live weight does not increase the WM% yield in the broilers. Feed resources, therefore, may be directed towards the growth of lower valued parts of the bird. White meat yield can only be measured after harvest, and therefore is not measurable on the live birds that must be maintained for reproduction. Thus, the use of marker-assisted selection is a preferable approach to improve the trait of WM%.

Materials and methods

The experimental population was initiated by crossing two primary broiler breeder lines, which differ in

WM% by 2.7%. One F1 male was then mated with 12 unrelated F1 females to produce 201 F2 offspring that were grown under standard broiler conditions. Blood samples were collected for DNA analysis. Several important growth and composition traits were measured at 6 weeks of age (Table 1). The offspring DNA was genotyped with 50 microsatellite molecular markers. Two types of statistical analyses were conducted. Single-marker association analysis was done for chromosomes on which only one marker was typed. Interval mapping was conducted for chromosomes on which multiple markers were typed.

Results and Discussion

Four markers were found to be significant at the 10% comparison-wise level, and one of those markers was associated with several different traits (Table 2). In the interval mapping analysis, nine different chromosomal regions located on five chromosomes held significant quantitative trait loci (QTLs, Table 3). As an example, the interval mapping curve on chromosome 3 is shown in Figure 1. Each QTL generally explained 1/3 to 2/3 of the variation in the trait.

The identification of markers associated with traits of importance can be used to select broiler breeders to produce offspring that will have superior growth characteristics. Knowing the genomic regions that harbor the QTL will aid the process of identifying the specific genes that cause the physiological changes.

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TABLE 1. Phenotypic Traits Measured 6 Weeks of Age

<u>Trait</u>	<u>Mean</u>	<u>Std. Dev.</u>
Pre-Transport BW	2282 gm	295 gm
Post Transport BW	2085 gm	258 gm
Fat WT	27 gm	9 gm
Wt. of carcass without giblets	1510 gm	210 gm
Wt. of front half of carcass	854 gm	111 gm
Tender wt.	81 gm	10 gm
Fillet wt.	352 gm	56 gm
Conformation score (2-6)	4	1
White meat wt.	433 gm	65 gm
White meat percent of post trans BW (WM%)	21 %	1%

TABLE 2. Markers significant at the 10% comparison-wise level

Chromosomes tested: 5, 8, 12, 23, 24, 26, 27, 28, E47W24

<u>Chromosome</u>	<u>Marker</u>	<u>Trait</u>	<u>Sire P-val</u>	<u>Dam P-val</u>
5	MCW0193	PreBWT	NS	0.04
		PostBWT	NS	0.04
		Fat	0.01	NS
		Fillet	0.09	0.02
		FrontH	NS	0.01
		Tender	NS	0.02
		WOG	NS	0.01
		WM	0.04	0.07
		WM %	0.01	0.07
23	MCW0165	Fat	NS	0.08
26	MCW0262	PreBW	0.07	NS
		PostBW	0.07	NS
27	MCW0233	Fat	0.06	NS

TABLE 3. Significant QTL at P= 0.05 from Int. Map.

Chromosome	Pos (cM)	Trait	Substitution Effect	% of SD
2	69	Fat	7.0 g	78
2	125	BstMtYd	0.60%	60
2	247	PreBWT	117.2 g	40
3	31	PostBWT	NA	NA
3	154	PostBWT	73.0 g	28
3	154	FrontHalf	31.0 g	28
3	154	Fillet	21.4 g	38
3	154	TotalWM	24.0 g	37
3	188	Conf	0.73 units	73
7	146	Tender	4.0 g	40
13	MCW0110	PreBWT	88.3 g	30
13	MCW0110	PostBWT	73.8 g	29
13	MCW0110	WOG	52.5 g	25
13	MCW0110	FrontHalf	32.9 g	30
13	MCW0110	Fillet	18.7 g	33
13	MCW0110	WM	21.2 g	32
13	MCW0110	Conf	0.35 units	35
Z	155	WOG	52.8 g	25

Figure 1. Significant QTL at P = 0.05

