

Study on Relations Between Heterosis and Band J in DNA Fingerprints of Xiaoshan and SR92 Chickens in China

¹X.P. Liu, ¹K.W. Chen, ¹K.H. Wang ²J.Y. Wang, ²G.J. Dai, ¹X.Y. Zhang and ²G.B. Chang
¹Jiangsu Institute of Poultry Sciences, ²College of Animal Science and Technology,
Yangzhou University, Jiangsu, P.R. China 225009

Abstract: Xiaoshan chicken is a well-known breed in China. It has good meat quality and three yellow character. SR92A chicken and Xiaoshan chicken are parents. Sixty five offsprings were reared. DNA Fingerprint (DFP) of parental strains were conducted using one middle-repetitive DNA probe EAV (endogenous avian retroviral). Based on presence or absence of band J (3.48 kbp) in their parents, we carry out 4 mating combinations. -/- for absence of band J in both parents; +/- for absence in sire, presence in dam; +/- for presence in sire, absence in dam; ++ for presence in both parents. Quantitative traits recorded for offspring are body weight at 75 days and slaughter traits. The results show that the 75 days weight heterosis generated by -/- type is 74.1 g higher than generated by non-selected populations. We can infer that the allele may be corresponding with the different expression of genes between parents and offsprings. We find band J allele has a bearing on weight heterosis, which will lay a solid foundation for locating weight heterosis QTL.

Key words: Xiaoshan chicken, SR92 chicken, mating combination, heterosis, band J, DFP

INTRODUCTION

In China, Xiaoshan chicken is one of the famous chickens. It belongs to native breed. Its early production performance and growth rate are low. There are two ways to improve Xiaoshan chicken's growth rate. One is crossing with other breeds. The other is selective breeding of Xiaoshan chickens by modern molecular marker. SR92A chicken is a fast-gaining breed as sire.

The usage of heterosis has been major producing method in pig, chicken and rabbit etc. The overwhelming majority of important economic traits are quantitative traits. Phenotypic value is determined by the coefficient of genes and environmental factors (Zhang *et al.*, 1997). Breeding research will succeed in selection according to the genotype, but it is difficulty when it is put into practice. The linkage between genetic marker and important economic traits is a promising means to solve this problem. DNA fingerprinting is a naturally tool of this analysis. This will lay a solid foundation of source conservation and marker usage.

Efficacy of DNA fingerprint bands in marker assisted selection programs for quantitative traits in chicken is definite. DNA Fingerprint (DFP) may serve as genetic markers for loci affecting quantitative traits. An association between a DFP band and the locus coding for slaughter trait may provide selection criteria supplemental to traditional methods (Dunnington *et al.*, 1992).

A particular DFP band J had been found to be associated with 75 days weight in offspring of SR92A chicken and Xiaoshan chicken. Band J as molecular marker had a reducing effect on weight traits of chickens (Wang *et al.*, 1999).

The aim of this study is to ascertain whether presence or absence of band J in the parents influenced expression of the quantitative trait in their offspring. We will study further in locating weight heterosis QTL using band J as molecular marker.

MATERIALS AND METHODS

Materials, DNA fingerprinting: SR92A chicken and Xiaoshan chicken are parents. We detect 75 days weight heterosis in F₁. DNA fingerprinting in parental chicken refer to molecular cloning (Sambrook *et al.*, 1996). For DNA production, 10 µg samples of DNA are digested with EcoR I restriction endonuclease, electrophoresed in a 20 cm long. A 75% agarose gel at 30 V for 48 h and Southern blotted onto Amersham Hybond-N membrane. Hybridizations are conducted using EAV as the probe. Blots are hybridized at 68°C for 20 h. Stain procedure refer to Dig DNA labeling and detection kit. We determined whether presence or absence of band J in each individual.

Comparisons of slaughter traits are studied based on presence or absence of band J in their parents. There are 4 classifications of parental matings as follows: -/- for

absence of band J in both parents; -/+ for absence in sire, presence in dam; +/- for presence in sire, absence in dam; +/+ for presence in both parents.

Statistical analysis: Significance test is according to GLM procedure. The following formula is used to calculate heterosis:

$$H = \frac{\bar{F}_1 - \bar{P} = X_1 - (X_2 + X_3)}{2}$$

where,

H = Heterosis

X_1 - X_3 = Seventy five days weight in F_1 , SR92A chicken and Xiaoshan chicken

$$H\% = H / \bar{P}$$

H% = Heterosis ratio

RESULTS AND DISCUSSION

Comparison of slaughter traits for different combinations: Table 1 shows that alive weight, dressing weight, semi-eviscerated weight and eviscerated weight in offsprings from -/- parental mating are 248.7, 214.8, 192.4 and 167.9 g higher than from +/- parental mating. GLM procedure shows that mating combinations have a significant influence on slaughter traits of their offsprings ($p < 0.05$) and there are significant difference between +/- and -/-, -/+ mating combinations.

Heterosis generated by -/- combination type: From Table 2, we can seen the 75 days weight heterosis generated by -/- type is 74.1 g higher than generated by non-selected populations. The average heterosis value of +/-, -/+ and +/- is 311.2 g and the average heterosis ratio is 25.3%.

Xiaoshan chicken is one of the most famous breeds in Chinese native breeds. It has many excellent properties. In Xiaoshan chicken, SR92A chicken and F_1 chicken, we all find the individuals with absence or presence of specific band J. People are attaching more and more importance to Chinese native breed with band J as molecular marker.

Genes coding chicken weight and DNA fingerprint bands are randomly disseminate in the whole genome (Yancovich, 1996). Some DNA fingerprint alleles and genes that coding weight traits are site in the same region of chromosome. Although, the probes they used were 33.6, Jeffreys *et al.* (1985) and R18.1, Haberfeld and Hillel (1991), their distribution in genome are similar with EAV.

The site band J and the gene coding weight traits may be located in the same area in one chromosome. There are significantly different between -/+ and +/- combination, but as far as long economic benefits are concerned, we should select the -/- combination. Uniformity is guaranteed in this way. Study proves that band J as molecular marker has a reducing effect on weight traits of chickens and reveal that -/- combination has important applied prospect. All these lay a foundation for band J as genetic marker.

Heterosis is of practical importance in the poultry industry (Haberfeld *et al.*, 1996). The level of heterosis depends on different expression between parents and offsprings (Jiang and Deng, 2001). At present, construction of molecular genetic map make estimating heterosis based on molecular marker possible. Analysis was maken for a pig family (0-5 generations) by genomic scanning (Wu, 2000). The aim is to probe the possibility of locating heterosis QTL. They found five chromosome regions, which had a significant effect on heterosis. Depending on this one marker, we can't find the heterosis QTL, but from this, we can infer that band J allele may be correlated with the gene that has different expression in

Table 1: Comparisons of slaughter traits between SR92A x Xiaoshan mating combination unit (g)

Mating combination	Sex	n	Weights ($\bar{X} \pm S$)			
			Alive	Dressing	Semi-eviscerated	Eviscerated
-/-	♂	12	1710.2±319.5	1503.5±281.9	1356.3±264.9	1136.6±238.3
	♀	3	1316.6±283.3	1186.3±257.0	1055.0±224.4	877.3±236.3
	♂ + ♀	15	1631.5±343.8 ^a	1440.1±298.5 ^a	1296.1±279.1 ^a	1085.0±252.8 ^a
+/-	♂	11	1480.8±408.7	1319.1±358.9	1197.0±338.3	990.3±301.3
	♀	8	1248.1±297.3	1096.3±283.9	975.5±263.8	816.5±236.7
	♂ + ♀	19	1382.8±375.6 ^b	1225.3±340.1 ^b	1103.7±321.3 ^b	917.1±282.8 ^b
-/+	♂	14	1735.7±144.6	1551.1±125.2	1402.4±128.5	1164.8±114.0
	♀	4	1442.7±64.40	1270.7±65.80	1158.5±67.70	963.2±58.200
	♂ + ♀	18	1671.1±179.5 ^a	1488.8±164.7 ^a	1348.2±156.1 ^a	1120.0±134.1 ^a
+/-	♂	10	1662.7±392.7	1434.0±344.8	1297.1±312.2	1082.6±280.0
	♀	3	1394.6±168.1	1240.3±158.6	1121.0±125.3	939.7±102.4
	♂ + ♀	13	1570.1±361.1 ^{ab}	1390.7±316.9 ^{ab}	1256.5±285.8 ^{ab}	1049.6±253.9 ^{ab}

^{a,b}means within a column with no common superscripts are significantly different ($p < 0.05$)

Table 2: Heterosis generated from different band J combinations

Mating combination	Heterosis value (g)	Heterosis ratio (%)
Non-selected	327.3	26.6
-/-	401.4	32.6
+/+	152.7	12.4
-/+	441.0	35.8
+/-	340.0	27.6
Average value	311.2	25.3

parents and offsprings. There are three types of the different expression, crossing distinctive expression, crossing surpass expression, crossing silence express (Zhong and Chen, 1999). At present, we can't determine the direct correlations between different expression of gene and F_1 phenotype. But it is definite that the level of heterosis is correlated with crossing gene.

A key link of heterosis usage is choosing outstanding cross combination. Selecting the band J-absence will make profits. To quantitative traits, weight trait is under the control of polygene, then they affect its expression. In poultry industry, it has great potential value searching for the genetic marker linked with major gene or QTL. On the one hand, once we have this genetic marker, it's easy to manipulate and control major gene; on the other hand, this marker will supply a way to separate the gene, which is linked with molecular marker. If there are 100 molecular markers, we have 70% possibility to find a marker linked with QTL (Haley, 1991). In this study, we find band J allele has a bearing on weight heterosis, which will lay a solid foundation for locating weight heterosis QTL.

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