Association between Cholecystokinin Type A Receptor Gene Haplotypes and Growth Traits in Hinai-dori Chicken Cross

Kazuhiro Rikimaru[1,2] , Megumi Komatsu[1] , Keiichi Suzuki [2] , Yoshinobu Uemoto [3] , Hisato Takeda[4] , Hideaki Takahashi[4]

[1]Livestock Experiment Station, Akita Prefectural Agriculture, Forestry, and Fisheries Research Center, [2]Graduate School of Agricultural Science, Tohoku University, [3]National Livestock Breeding Center, [4]National Institute of Livestock and Grassland Science

INTRODUCTION

The Hinai-dori is a breed of chicken native to Akita Prefecture, Japan. To identify QTLs associated with growth traits in the Hinai-dori breed, an F_2 resource population produced by crossing low- and high-growth lines of the breed was analyzed. We identified quantitative trait loci (QTL) for body weight (BW) at 10 and 14wk and average daily gain (ADG) between 4 and 10wk and between 10 and 14wk in a common region on chromosome 4. We focused on the cholecystokinin type A receptor (*CCKAR*, chr 4: 75.6Mb) because it has also been identified as a candidate gene for human obesity. In this study, we genotyped polymorphisms of the *CCKAR* gene and investigated its association with growth traits in a Hinai-dori F_2 intercross population.

MATERIALS AND METODS

Hinai-dori breed

High-growth line Low-growth line

Hinai-dori population and phenotype

F_1 chickens were produced by crossing three cocks from a low-growth line with nine hens from a high-growth line. Body weight was measured at 4 weeks (BW-4wk), 10 weeks (BW-10wk), and 14 weeks(BW-14wk) of age. Average daily gain between 0 and 4 weeks of age (ADG 0–4wk), between 4 and 10 weeks of age (ADG 4–10wk), between 10 and 14 weeks of age (ADG 10–14wk), and 0 and 14 weeks of age (ADG 0–14wk) was calculated from BW at each week of age.

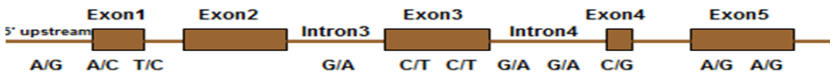
Identification of *CCKAR* haplotypes

The nucleotide sequences of the five exons of *CCKAR* in the parent individuals were determined by PCR amplification followed by direct sequencing to determine nucleotide variance of the gene in the resource family. Five PCR primers were designed to amplify the five exons of *CCKAR* and the PCRs were performed. The *CCKAR* gene haplotypes in the F_2 intercross population were then identified.

Statistical analysis

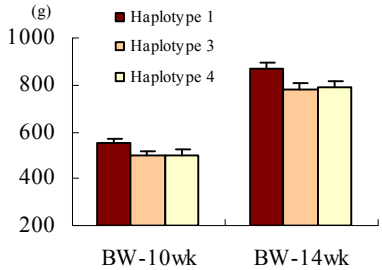
To examine the effects of CCKAR gene, a mixed-inheritance animal model was used to evaluate the effects of CCKAR haplotypes by using QxPak software (Perez-Enciso and Misztal, 2004).

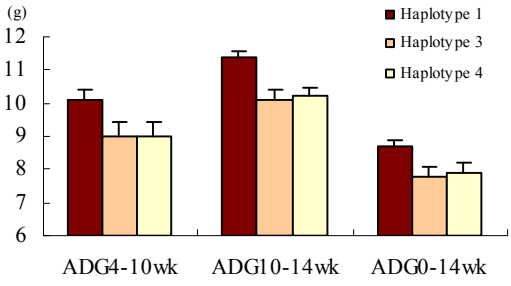
SNPs of *CCKAR* gene and haplotypes



A total of 11 SNPs in the region and five *CCKAR* haplotypes (Haplotypes 1–5) were identified in the population.

Effects of *CCKAR* haplotypes on the growth traits





Phenotypic values of growth traits and effects of *CCKAR* haplotypes

Trait	*n*	Phenotypic values Mean ± SD	LRT	*P*-value	Haplotype 1 Mean ± SE	Haplotype 3 Mean ± SE	Haplotype 4 Mean ± SE
BW-4wk (g)	417	231.1 ± 38.3	1.5	n.s.			
BW-10wk (g)	418	960.6 ± 163.5	36.6	5.7×10^{-8}	548 ± 17.0	497 ± 18.2	502.7 ± 18.9
BW-14wk (g)	418	1467 ± 260.7	57.7	1.9×10^{-12}	867 ± 23.2	779 ± 24.8	790.0 ± 25.7
ADG0-4wk (g/day)	417	5.2 ± 1.0	1.5	n.s.			
ADG4-10wk (g/day)	417	17.4 ± 3.3	46.5	4.4×10^{-10}	10.1 ± 0.3	9.0 ± 0.4	6.8 ± 0.4
ADG10-14wk (g/day)	418	18.1 ± 4.4	50.1	7.5×10^{-11}	11.4 ± 0.2	10.1 ± 0.3	7.1 ± 0.3
ADG0-14wk (g/day)	418	14.6 ± 2.7	57.5	2.2×10^{-12}	8.7 ± 0.2	7.8 ± 0.3	3.3 ± 0.3

No individuals with Haplotypes 2 were detected in the F_2 population.

CONCLUSIONS

A highly significant association was found between *CCKAR* haplotypes (Haplotype 1, 3, and 4) and growth traits (BW-10wk, BW-14wk, ADG4-10wk, ADG0-14wk, and ADG0-14wk).

CCKAR is a useful marker of growth traits and could be used to develop strategies for improving growth traits in the Hinai-dori breed.