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Study of genetic variability of chicken growth hormone gene in broiler strain (vencobb-400) by PCR-RFLP

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Abstract

Present study to estimate the genetic variability of Chicken growth hormone gene in broiler strain (Vencobb-400). In order to study and investigate chicken growth hormone gene polymorphism, blood samples were collected from 150 individuals of broiler and Genomic DNA was extracted from whole blood using spin column method as per manufacture protocol with slight modification. The purity of extracted genomic DNA was determined by 0.8% agarose gel electrophoresis. DNA fragment with 776 bp at Chicken growth hormone gene was amplified using Polymerase Chain Reaction (PCR). The PCR product was digested with restriction enzyme *MspI* and subsequently electroforesed on 8% polyacrylamide gel with ethidium bromide. In this population, heterozygosis was estimated 0.28 and obtained genotypes frequency of *MspI* enzyme on 776 bp fragment for AA, AB and BB genotype were .22, .28, and .50, respectively. The gene frequency of A and B alleles were .39 and .61, respectively.

Keywords: Chicken growth hormone, heterozygosity, polymorphism, gene and genotype

Introduction

Poultry production is an important and diverse component of agriculture all over the world. Today, more attention has been given to poultry due to their quality of meat and sustainable production (Kaya and Yıldız, 2008) [4]. The chicken growth hormone (*cGH*) gene is one of the effective genes that influenced the chicken performance traits because it plays a crucial role in growth and metabolism (Vasilatos-Younken *et al.*, 2000; Que *et al.*, 2005) [1]. The *cGH* is a 22-kDa protein, containing 191 amino acid residues (Hrabia *et al.*, 2008) [5]. In poultry, *cGH* consists of 4,101 base pairs, having five exons and four introns (Kansaku *et al.*, 2008) [3], known as a polypeptide, hormone produced, and secreted by pituitary gland; *cGH* affects a variety of physiological functions in growth performance (Byatt *et al.*, 1993; Apa *et al.*, 1994) [6, 7]. Molecular technology has provided new opportunities to evaluate genetic variability at the DNA level (Kaya and Yildiz, 2008) [4]. The purpose of the present research was to estimate genetic variability of Chicken growth hormone gene of the broiler strain (Vencobb-400).

Material and Methods

150 unrelated birds of broiler strain (vencobb-400) were selected from poultry farm situated in the campus of Rajasthan University of Veterinary and Animal Sciences, Bikaner. Blood samples (0.25-0.5 mL) were collected from the wing vein using EDTA as an anti-coagulating agent. Blood samples were stored at -20 °C. Genomic DNA was extracted using the spin column method (Sambrook and Russell, 2001) under manufacture' protocols with slight modification through genomic DNA Isolation kit (Himedia Pvt. Ltd). The quality of the extracted DNA was checked by Agarose gel electrophoreses. Genomic DNA (2.5 µl) was amplified with 8.9 µl Nuclease Free water (NFW), 13 µl PCR master mixture and 0.3 µl of each primer in total volume of 25 µl. The PCR reaction mixture was subjected to the an initial 5 min denaturation at 95 °C, followed by 35 cycles of denaturation at 94 °C for 45 sec, annealing at 55 °C for 1 min, extension at 72 °C for 60 sec. and final extension at 72 °C for 10 min. After the addition of 5 µl of amplification product were loaded on 1.5% denaturing agarose gels. To visualize the PCR product, gels were stained with ethidium bromide. The stained gels were scanned and genotypes were scored. Then, for digestion by enzyme and determination of RFLP, 10 µl of PCR product (776 bp) was added to 1 µl of *MspI* enzyme and

2 µl 10X Buffer and final volume was 30 µl with dilution 17 µl Nuclease Free Water and digested in incubator at 37 °C overnight. Digested samples were loaded by 8% polyacrylamide gel electrophoresis at 120V for 1.5 hours. Then, stained with ethidium bromide the fragments were visualized by UV Transilluminator. Then, genotypes were scored.

Results and discussion

DNA extraction and quality determination with electrophoresis and UV Transilluminator was done obtained result was acceptable (fig.1). The PCR amplification carried out using the forward and reverse primers were 5'ATCCCCAGGCAACATCCTC3' and 5'CCTCGACATCCAGGTCACAT3' respectively. The PCR products with 776 bp length which run on 1.5% agarose gel were presented in Figure 2. With electroforesing of digested samples, 3 types of genotype were diagnosed. In AA genotype 235 and 541 bp band were registered. In AB genotype 126, 148, 235 and 267 bp bands were registered and BB genotype 148, 235, and 393 bp bands were determined. In total, 43 samples have AA genotype, 32 samples have AB genotype and 75 samples shown BB genotype (fig.3). These restriction patterns were in concurrence with the observations made earlier by Kaur *et al.* (2008) [8] in Panjabi broiler and Singh *et al.* (2008) [9] in Rhode Island red and White Leghorn layer (Figure 2). The genotype and gene frequency in population is shown in Table 1. Calculations were done with standard formula (Falconer and Mackay, 1996) [10]. The observed heterozygosity was 0.28 in this study.

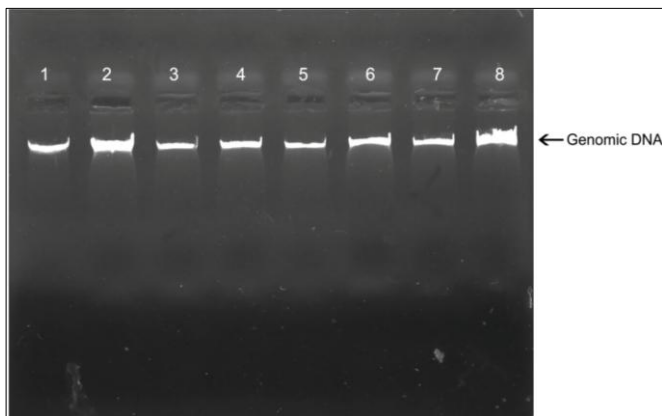


Fig 1: DNA extracted samples

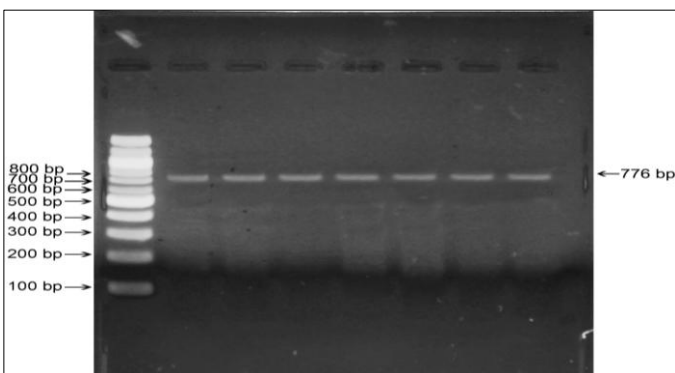


Fig 2: Electrophoresed PCR product on agarose gel; Marker 100 bp

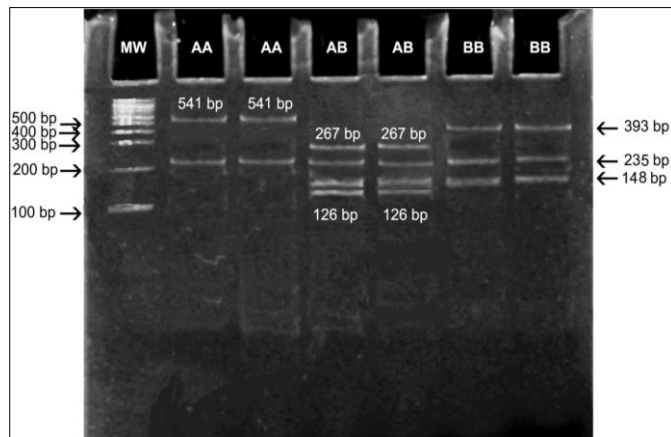


Fig 3: Electroforesing digested product on polyacrylamide gel: Marker 100 bp

Table 1: Obtained genotype and gene frequency of MspI enzyme on 776 bp fragment.

Genotype	Number	Frequency
AA	43	0.22
AB	32	0.28
BB	75	0.50
Allele		
A	118	.39
B	182	.61

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