Identification of Growth Hormone (Gh) Gene MspI and AluI Loci Polymorphism in Beef Cattles

Jakaria[1], R.R. Noor[1], H. Martojo[1], D. Duryadi[2] and B. Tappa[3]
[1]Fakultas Peternakan, Institut Pertanian Bogor Indonesia
[2]Fakultas Matermatika dan Ilmu Pengetahuan Alam, Institut Pertanaian Bogor, Indonesia
[3]Lembaga Ilmu Pengetahuan Indonesia, Cibinong, Indonesia
email: jakaria@ipb.ac.id

ABSTRACT

The research was conducted in order to identify the polymorphism of MspI and AluI locus of the growth hormone (GH) gene in Bali, Limousine and Simmental cattle. Total blood samples of 87 cattle were taken from population of Bali cattle were collected from Balai Pembibitan Ternak Unggul Sapi Bali in Bali island, whereas Limousine and Simmental cattle blood samples were collected from Balai Inseminasi Buatan (BIB) Singosari-Malang, West Java. PCR-RFLP and sequencing methods used to detect the polymorphism and mutation at MspI and AluI loci of GH gene. The results showed that at MspI locus, the Bali, Limousine and Simmental cattle had one genotype (-/-), three genotypes(+/+, +/- , -/-) and two genotypes (+/+, +/-), respectively whereas for AluI locus, the Bali, Limousine and Simmental cattles had one genotype (LL), two genotypes (LL, LV) and three genotypes (LL, LV, VV), respectively. The allele frequencies of + and – alleles in Bali, Limousine and Simmental cattle were 0.000 and 1.000; 0.636 and 0.364; 0.889 and 0.111 respectively, whereas the frequencies of L and V alleles in Bali, Limousine and Simmental cattle were 0.000 and 0.000; 0.818 and 0.182; 0.694 and 0.306 respectively. Based on polymorphic informative content (PIC) value, it can be concluded that MspI and AluI loci in Bali cattle are monomorphic, while in Limousine and Simmental cattle is polymorphic. Based on the sequencing results, the MspI (+/+ and -/- genotypes) and AluI (LL and VV genotypes) loci showed a occurrences of nucleotide base mutation from cytosine (C) to thymine (T) and cytosine (C) to guanine (G), respectively.

Key words: Indonesian cattle, growth hormone gene, PCR-RFLP, sequence, polymorphism

INTRODUCTION

Indonesia has some animal genetic resources that need more attentions to be utilized and developed sustainable. The Bali breed is one of the four existing indigenous cattle breeds (Aceh, Pesisir, Madura and Bali) in Indonesia. Although no official historical records exists, it is generally accepted that the Bali cattle is the domesticated direct descendant of the wild Banteng still surviving as an endangered species in three National Wild Reservation Parks (Ujung Kulon, Baluran and Blambangan) in Java (Martojo, 2003).

Some molecular genetic studies have been reported in Indonesian cattle breeds using microsatellite DNA (nuclear genome) and mitochondrial genome markers (Handiwirawan et al., 2003; Nijman et al., 2003; Abdullah, 2008; Uggla 2008; Mohamad et al., 2009). However, molecular genetic marker based on coding sequence or candidate gene approach is limited and still needs more in depth study of its existence in Indonesian cattle breeds.

Molecular genetic markers in animal breeding programs could make selection more precise and efficient. Some of these markers are called candidate genes, e.g. the growth hormone genes, which are usually selected because of their biological significance on the quantitative traits of interest. Growth hormone has wide physiological activities, which include the regulation of growth, lactation and mammary gland development, gluconeogenesis, the activation of lipolysis, and the enhancement of amino acid incorporation into muscle protein (Burton et al., 1994). There is also evidence that growth hormone may be involved in the pubertal development and testicular function (Lin, 1996). Because of these important relationships, GH is a candidate gene for marker-assisted selection programs in cattle.

The GH gene is considered as an attractive candidate gene to be used as a marker due to its