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GROWTH HORMONE GENE VARIATIONS AND MEAT PRODUCTION (GROWTH) OF INDONESIAN LOCAL CATTLE

Sutarno[1], Aris Junaidi[2], Baharudin Tappa[3]

Abstract

The objective of the study was to know the association between genetic variations at growth hormone loci and growth (meat production) of Indonesian local cattle (Madura, Bali and Ongole derived (PO) cattle). PCR-RFLPs were applied for the detection of DNA polymorphism at locus I and II of growth hormone gene, and the result indicated that polymorphisms were found at both loci using *Alu*I and *Msp*I enzymes. Association between genotype variations and growth trait was analysed using two models of Anova implemented in a program of JMP. The preliminary analysis indicated that the *Msp*I genotypes at locus II of the gene to be associated with growth (daily gain) of PO cattle, but not for locus I detected using *Alu*I.

Key words: Growth hormone gene, Polymorphism, Growth rate, Cattle

Introduction

Information on genetic diversity and genetic relationships among cattle breeds may be very useful in cattle breeding programs. Genetic diversity is the basis for livestock breeding (Buis *et al.*, 1994), because it is used as a starting point for the improvement of breeds by artificial selection. Understanding the extent and pattern of genetic variability among breeds may help in the development of more rational breeding programs and is a prerequisite to the informed conservation of genetic resources.

Genetic diversity in cattle and other livestock species is rapidly being reduced (Hall & Bradley 1995). Preference for certain breeds, because of their advantages over other breeds in specific production traits, may potentially reduce among-breed diversity. At the same time, intensive selection for the genetic improvement of production traits may also lead to reduce genetic diversity within breeds.

Advanced techniques of molecular biology have provided the opportunity to study genetic diversity within and among breeds at gene level. Candidate QTLs, such as the growth hormone gene, BoLA gene and casein gene have been

[1] Biology Department, FMIPA, Sebelas Maret University, Solo 57126, Indonesia.
[2] Faculty of Veterinary Medicine, Gadjah Mada University, Yogyakarta, Indonesia.
[3] Center of Research and Development of Biotechnology- LIPI, Cibinong, Indonesia.

Results and Discussion

Restriction Site Polymorphisms In The Growth Hormone Gene

The 223 bp fragment of locus 1 spanning intron IV and exon V of the growth hormone gene, amplified using primers GH-1 and GH-2, and the 329 bp locus 2 spanning exon III and exon IV of the growth hormone gene were amplified using primers GH5 and GH6. The cleavage pattern of restriction enzyme digestion using *MSp*I and *Alu*I restriction enzymes were shown in Figure 1 and 2.

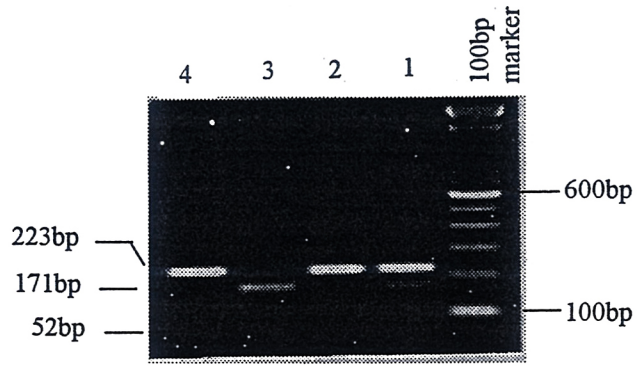

Figure 1. Gel photographs showing growth hormone gene polymorphisms detected by PCR-RFLP using *Alu*I in locus 1 fragment. Lane1 = LV, Lane 2 = VV, Lane 3 = LL, and lane 4 = Uncut.

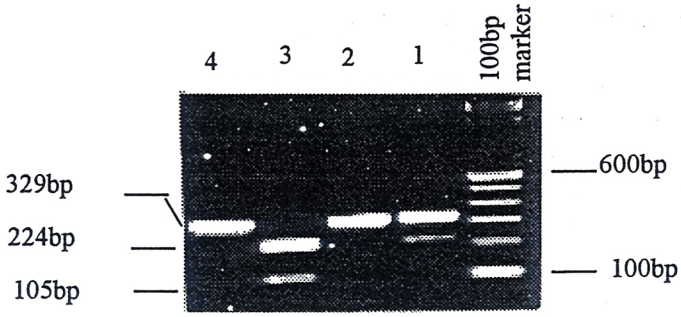

Figure 2. Gel photographs showing growth hormone gene polymorphisms detected by PCR-RFLP using *Msp*I in locus 2 fragment. Lane1 = *Msp*I (+-), Lane 2 = *Msp*I (--), Lane 3 = *Msp*I (++), and Line 4 = Uncut.

Table 1 shows the cleavage patterns from AluI digestion of the 223bp fragment and MspI digestion of the 329bp fragment of the growth hormone gene.

Table 1. Restriction sites for *Alu*I in the 223bp locus 1 (GH L1) fragment, and for *Msp*I in the 453 bp locus 2 (GH L2) fragment of the growth hormone gene

Enzyme	Allele	No of restriction sites	Fragment size (bp)
Alu I	L	1	171 , 52
	V	0	223
Msp I	Msp I +	1	224, 105
	Msp I -	0	329

Association Analysis

Preliminary analysis to the data recorded for the Ongole derived cattle, indicated that growth rate was affected by the *Msp*I polymorphism (Table 2, and Table 3).

Table 2. Least square mean of growth rate in Bali, PO and Madura cattle with different MspI genotypes

Growth rate for cattle breed	Genotype		
	MspI (+/+)	MspI (+/-)	MspI (-/-)
Bali cattle	0.86 ± 0.02	0.89 ± 0.02	0.89 ± 0.04
PO cattle	0.98 ± 0.02	1.07 ± 0.03	1.02 ± 0.03
Madura cattle	0.91 ± 0.02	0.93 ± 0.03	0.94 ± 0.02

Table 3. Probability of observing the differences in means between genotypes under ANOVA of growth rate of Bali, PO and Madura cattle.

Growth rate of cattle breed	P values
Bali cattle	0.28
PO cattle	0.05
Madura cattle	0.20

A number of major genes that have large effects on economic traits, especially in animals used for meat production, have been identified; e.g. the double muscling gene (mh gene) in cattle (Hanset & Michaux, 1985), the acid meat gene (RN) involved in pig meat quality (Le Roy *et al.*, 1990) and the Boorola gene that affects ovulation rate and litter size in sheep (Piper, Bindon & Davis, 1985). However, the traits of greatest economic importance in livestock are quantitative in nature and

controlled by a large number of quantitative trait loci (QTLs), each of small effect. QTLs are much more difficult to detect with genetic markers.

Genetic variation within breeds is important and its study has become a subject of interest in livestock species, as it has many applications in animal breeding and genetics, such as the identification of animals and parentage testing, gene mapping and identifying markers for performance traits. Since all phenotypic characters are influenced by the genetic information carried by DNA, DNA variation may be correlated with variation in performance traits. This idea is the basis for marker-assisted selection (MAS), which has aroused much interest in recent years (Schwerin *et al.*, 1995; Soller 1994). Genetic variation, measured at the DNA level, can also be used as a check on the level of genetic variation in quantitative traits maintained within breeds.

The *Alu*I and *Msp*I restriction site polymorphisms in the locus 1 and locus 2 fragments of the growth hormone gene found in the study have also been previously reported in dairy cattle (Hoj *et al.*, 1993; Lucy *et al.*, 1993), Indian cattle (Mitra *et al.*, 1995) and Hereford and composite cattle (Sutarno 1998). Preliminary analysis in this study indicated that the *Msp*I genotypes at locus II of the gene was significantly correlated with growth (daily gain), but not for locus I detected using *Alu*I. The final analysis will be done after complete genotyping of about 300 samples. It seems likely from this and previous studies, that polymorphism in the growth hormone gene affects milk production and growth traits in cattle. The mechanism by which these effects are generated is not known. Kazmer *et al.* (1986) and Klemetsdal *et al.* (1991) demonstrated an elevated growth hormone level in cows selected for high milk yield in contrast to animals selected for low milk yield or control animals. Indeed, the galactopoietic effect of GH is currently well established, and it can be generalized that the growth hormone treatment increases milk production and productive efficiency (Armstrong *et al.*, 1995; Burton *et al.*, 1994).

Many recent studies have investigated the hypothesis that different growth hormone genotypes are associated with production parameters. In laboratory animals, Winkelmann *et al.* (1992; 1990) for example, found that RFLPs of the growth hormone gene were significantly correlated with 42-day weight and post weaning growth rate in F2 populations of mice selected for high 42-day weight. However, in other experiments to show the interaction between genetic backgrounds and exogenous growth hormone, Hastings *et al.* (1993) demonstrated that disruption of endogenous growth hormone or addition of exogenous growth hormone had similar effects on body weight. This suggests that sensitivity to growth hormone has not been altered during the course of selection, and also implied that the sensitivity or possibly the numbers of the hormone receptors remain unchanged in mice.

It has long been proposed that growth hormone effects on growth rate and protein accretion are mediated via IGF-I action. Indeed, the increases of IGF-I following GH treatment have been demonstrated in cattle, sheep and pigs (Armstrong *et al.*, 1995; Crooker *et al.*, 1990), and increases in the circulating IGF-I

are dependent on the dose of the administered GH (Etherton *et al.*, 1987). This indirect effect of growth hormone via IGF-I may be the most probable action of growth hormone leading to growth promotion (Ballard *et al.*, 1993).

Bali cattle (*Bos javanicus*), more popularly called Banteng, have been domesticated largely in Indonesia, especially in Bali, Lombok and Borneo. The wild type of Banteng currently occurs in Burma, Thailand, Kampuchea and Indonesia (Baker & Manwell 1991). Cattle of this type superficially resemble Zebu, as they possess a hump, but the bone structure of the head is quite different. Copland (Copland 1996) suggested that Bali cattle are more similar to ancestral cattle than other modern types. According to the assessment done by AWCSG (Asian Wild Cattle Specialist Group) in 1995, *Bos javanicus* has been categorized as endangered, due to disease, hunting, hybridisation or trade (Heinen & Srikosamatara 1996). Indeed, the introduction of modern cattle to Indonesia in the last few decades has partly caused a reduction in the diversity of Bali cattle. This is unfortunate because they are considered an original species with several economic advantages such as high fertility rate, adaptability and carcass percentage (Wiryosuhanto 1996).

Conclusion

Polymorphisms of growth hormone gene were found in all breeds of Bali, PO and Madura cattle, and the preliminary analysis shown that the variation in PO cattle affected the growth rate.

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