

PRODUCTIVITY AND GENETIC DIVERSITY OF LOCAL CATTLE IN CIAMIS-WEST JAVA

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ABSTRAK

Penelitian ini bertujuan mengidentifikasi produktifitas dan keragaman genetik sapi lokal di Ciamis Jawa Barat berdasarkan DNA mikrosatelit, sebagai upaya untuk memperoleh informasi dasar untuk budidaya, konservasi dan pengembangannya. Delapan belas ekor sapi lokal dipelihara selama 58 hari dengan pakan konsentrat dan jerami padi. Parameter yang diukur adalah bobot badan yang ditimbang satu minggu sekali dan persentase karkasnya. Persentase karkas pembandingan diambil dari sapi PO, Bali dan sapi hasil persilangan sapi lokal dengan Limousin, Simental, Brahman dan Angus. Data dianalisis dengan perangkat lunak Excel dan SAS (2004). Sampel darah diambil dari dua kecamatan, yaitu Tambaksari 46 ekor dan Cijulang 52 ekor. DNA pembandingan diambil dari sapi Bali, PO, Limousin, Simmental, Brahman dan Angus. Analisis keragaman genetik dan filogenetik dilakukan dengan menggunakan 3 lokus mikrosatelit yaitu INRA35, HEL9 dan BM2113. Data genotyping dianalisis menggunakan program POPGENE.32, sedangkan pohon filogenetik dianalisis dengan program MEGA 4. Hasil penelitian menunjukkan pertambahan bobot badan harian (PBBH) sapi local Ciamis adalah $0,62 \pm 0,23$ kg/ekor/hari dengan persentase karkas $51,62 \pm 1,80\%$. Persentase karkas sapi lokal Ciamis tidak berbeda nyata ($P > 0,05$) dengan sapi Bali, PO maupun persilangan. Keragaman genetik sapi lokal Ciamis dalam kategori tinggi, keragaman genetik sapi lokal di subpopulasi Tambaksari lebih tinggi dibandingkan dengan di Cijulang. Sapi lokal Ciamis mempunyai jarak genetik lebih dekat dengan sapi PO.

Kata kunci: filogenetik, karkas, PBBH, mikrosatelit, sapi lokal Ciamis

ABSTRACT

The objectives of this study were to identify the productivity and genetic diversity of local cattle in Ciamis West Java based on DNA microsatellite, in order to provide the basic information for its rearing, conservation and development. Eighteen of local cattle were kept for 58 days by feeding concentrates and rice straw. The measured parameters were weekly body weight as well as carcass percentage. The percentage of comparing carcass was taken from PO, Bali and crossbred cattle from local cattle with Limousin, Simmental, Brahman and Angus cattle. Data were analyzed using Excel software and SAS (2004). Blood samples were taken from two subpopulations i.e., 46 and 52 samples from Tambaksari and Cijulang areas, respectively. Other DNA samples were collected from Bali, PO, Limousin, Simental, Brahman and Angus cattle. Genetic diversity and phylogenetic analysis were analyzed using 3 microsatellite loci, that were INRA35, HEL9 and BM2113. The genotyping data were analyzed using POPGENE.32 program, while phylogenetic trees were analyzed by MEGA 4. Average daily gain (ADG) of local cattle in Ciamis was 0.62 ± 0.23 kg/head/day with a carcass percentage was $51.62 \pm 1.80\%$. The carcasses percentage of local cattle in Ciamis was not significantly different from those of Bali, PO, and crossbred cattle. The genetic diversity of local cattle in Ciamis was categorized in the medium level, the diversity of local cattle in Tambaksari subpopulation was higher than in Cijulang subpopulation. Local cattle in Ciamis had a closer genetic distance with the PO cattle.

Keywords: ADG, Ciamis local cattle, carcass percentage, microsatellite, phylogenetic.

INTRODUCTION

Indonesian local cattle has potency to support meat self-sufficiency, that the government declared can be achieved at 2014 and its sustainability. The utilization of local cattle genetic resources with optimal management, could increase their productivity and population, and it is a good choice, to support this program. Local cattle has several advantages i.e., more resistant to disease, more resistant to extreme weather and could survive with minimal inputs, because they adapted to the local environment and the farmers culture life, however their productivity is low. The high diversity of local cattle which locally adapted, can help farmers in harsh situation such as the extreme climate at marginal areas. The local cattle genetic resources can be kept at minimum cost (input) and plays important role in the culture of rural communities (FAO, 2000).

One of the genetic resources of local cattle which the potential to utilize, is local cattle from Ciamis district which is the region with the third highest cattle population in West Java, following Tasikmalaya and Sumedang (Disnak Jabar, 2011). Ciamis local cattle has small body size with low average daily gain. However they have good body composition and efficient in their reproduction. The introgression of artificial insemination (AI) in the district of Ciamis is quite intensive, therefore local cattle genetic resources could be lost, due to crossbreeding program. Diwyanto (2005) stated that the genetic diversity of Indonesian local cattle has significance role in the development of livestock, as a resource of genetic diversity that is needed in the assembly superior breed, lead to increase their productivity.

Identification of genetic diversity can be done by using molecular technology which growing rapidly. This technology can help better exploration of genetic potential of livestock because it can be done more quickly and accurately, because directly to target genes. One of the molecular techniques that had been used widely to identify genetic diversity and phylogenetic study is microsatellite. Almeida *et al.* (2000) suggested that microsatellites or Short Tandem Repeats (STRs) are DNA markers that relatively abundant in the entire genome and have a high polymorphism, so it could potentially be used to characterize a population. By its codominant nature and have many alleles, microsatellite markers proved very efficient for

genetic diversity studies and could be a marker or genetic characterization (Khatiravan *et al.*, 2009). Until now there is no information regarding to the phenotypic characteristics of Ciamis local cattle, including productivity, as well as their genetic characteristics that could be used to analyze the population diversity and phylogenetic with other local cattle. The objectives of this study were to identify the productivity, genetic diversity and genetic distance of local cattle in Ciamis with others Indonesian local cattle.

MATERIALS AND METHODS

Materials

The nineteen of Ciamis local cattle with age ranged from 1,5-2 years were reared at faculty of Animal Science Padjadjaran University Jatinangor Sumedang. The carcass percentage were taken from 14 Ciamis local cattle, 30 crossbred, 10 Bali, and 8 PO cattle. DNA microsatellite analysis were conducted using 98 blood samples of Ciamis local cattle consist of 46 from Tambaksari and 52 from Cijulang districts. The Compared DNA were taken from 10 Bali, and 7 PO. The out grouped DNA was taken from 10 of Limousin, Simmental, Brahman and Angus, respectively

Methods

The determination of the sampling area was conducted using a purposive sampling method, with the main criteria highest cattle population at different altitudes, which were in Tambaksari and Cijulang districts. Determination of the age of cattle based on the information from the farmers and incisors removal status.

Cattle were reared in individual pen for 58 days, with 2 weeks adaptation period to the experimental feeding and environments. Feed was given restrictedly, consist of a rice straw and concentrate, based on crude fiber 2,5-3% of body weight. Blood sampling was collected using venoject vacuum tubes with EDTA on *coccygea veina* area as much as 5 ml.

Cattle weighing was done once a week, in the morning before the cattle were fed. Body weight gain was measured after 2 weeks of adaptation period, the formula was [(final body weight-initial body weight)/rearing period].

Other parameters i.e., liveweight was weight of the cattle before slaughtered, carcass weight was the weight of carcass before chilling and carcass percentage was calculated based on the ratio of carcass weight and live weight multiplied

Table 1 Characteric of Microsatellite Loci and Primer Sequence

Loci	DNA sequences	Repeat Motive	Size (bp)	Chromosome
INRA35*	F : 5'-ATCCTTTGCAGCCTCCACATTG-3' R : 3'-TTGTGCTTTATGACACTATCCG – 5'	(CA) _n	117-141	16
HEL9**	F : 5'- CCCATTCAGTCTTCAGAGGT- 3 R : 3'- CACATCCATGTTCTCACCAC – 5'	(TG) _n	155-185	8
BM2113***	F : 5'GCTGCCTTCTACCAAATACCC 3' R : 3'CTTCCTGAGAGAAGCAACACC 5'	(CA) _n	148-172	11

by 100%

DNA Isolation and Amplification of Microsatellite

DNA isolation was performed based on Sambrook *et al.* (1989). DNA concentration was checked by NanoDrop Spectrophotometer. Microsatellites locus used was HEL9, INRA35 and BM2113 (Table 1). Each PCR reaction volume 11 µl with PCR reaction composition containing 1.1 µl thermal buffer 10x ; 0.6 µl MgCl₂ 25 mM ; 0.5 µl dNTP; 0.05 µl Taq DNA polymerase; 0.5 µl of primary F/R. PCR engine used for GeneAmp PCR System 9700 Applied Biosystem. Initial denaturized temperature was 95°C for 5 minutes, followed by 35 cycles of denaturized at 95°C for 30 seconds, 45 seconds annealing at temperature of 60°C, elongation at 72°C for 1 minute, followed with polymerase at 72°C for 5 minutes.

Visualization of PCR Products

The results of microsatellite amplification was visualized using polyacrylamide gel electrophoresis (PAGE) that were performed at 250 volts for 2 hours, continued by silver staining. Determination of genotypes was done by examining results of PAGE bands

Data Analysis

The allele frequency for particular microsatellite locus was calculated by using t Nei's formula (1987), as follow:

$$\chi_i = \frac{2n_{ii} + \sum_{j \neq i} n_{ij}}{2N}$$

Where:

χ_i = The *i*th allele frequency

n_{ii} = Number of allele homozygous individual to *i*

n_{ij} = Numbers of heterozygous individual

N = Numbers of individual sample

Heterozygosity

The degree of observed and expected heterozygosity (H_o and H_e) was calculated based on allele frequency of each microsatellite locus based on the formula of Weir (1996) and Nei (1987)

$$H_o = \sum_{i \neq j} \frac{N_{ij}}{N}$$

$$H_e = 1 - \sum_{i=1}^n p_i^2$$

Where:

H_o = Observed heterozygosity

H_e = Expected heterozygosity

N_{ij} = Number of heterozygous individual

N = The number of individuals analyzed

p_i = Allele frequency to *i* in each microsatellite locus

n = Number of allele in each microsatellite locus

The average of heterozygosity from all microsatellite was analyzed by formula :

$$\bar{H} = H_j / r$$

Where:

\bar{H} = Average of heterozygosity

H_j = Heterozygosity value to *j*

r = The number of tested loci

Data analysis of body weight and carcass

percentage was carried out using Excel program and analysis of variance for carcass percentage was conducted using SAS (2002). The result of microsatellite genotyping was analyzed using POPGENE.32 (Yeh *et al.*, 1999) while phylogenetic tree was performed based on genetic distance using UPGMA (Unweighted Pair Group Method with Arithmetic Mean) from MEGA 4 (Molecular Evolutionary Genetics Analysis) (Tamura *et al.*, 2007)

RESULTS AND DISCUSSION

Average Daily Gain

Average Daily Gain (ADG) is a reflection of the growth that can be used to assess animal productivity. The results showed that ADG of Ciamis local cattle at the age of 1.5-2 years was 0.62 ± 0.23 kg/head/day, with a ADG curve for 58 days following the linear equation $Y = 178.3 + 4.111 x$. The comparison of ADG in some Indonesian local cattle are presented in Table 2.

ADG of Ciamis local cattle which intensively reared, relatively similar to Bali, Madura, and Java cattle, but lower than Ongole breed (PO), and crossbred PO x Simental cattle (Table 2). Indonesian local cattle performance is relatively small, with low average daily gain (ADG). This condition was resulted from interaction of genotype and the environment, including management, and feeding. Quantitative traits like body weight and growth are controlled by many genes (*polygenes*) and highly influenced by the environment condition (Bourdon, 1997).

In general, Ciamis local cattle as well as other Indonesian local cattle are usually reared with limited input and low quantity, and quality of

feed. Furthermore, Ciamis area is located towards the southeast of West Java Province which has tropical environment with warm temperatures and high humidity. In such condition the cattle has to be adapted with these environments, resulting in a smaller body size and low productivity, as reflected by low ADG. The individual ability to be adapted to their environments is known as *phenotypic plasticity*. It is a condition that in order to survive in a various environments, an individual or the species, should has phenotype flexibility, there is a condition which species can survive and reproduce at the various environments with phenotypic change (*plasticity*) or kept their phenotype to be constant or stable (Scheiner and Godnight, 1984).

Although Ciamis local cattle have lower ADG, as other local cattles, their reproduction is more efficient. The research of Kustiyah *et al.* (2003) demonstrated performance of calves Limousin- Madura crossbred have higher productivity than Madura cattle, but their reproductive performance is lower, was indicated by lower service per conception and higher calving rate than their crossing. Scheiner and Godnight, (1984) stated, if a species maintained one trait and sacrifice other traits is called *trade off* between the traits. In order to survive under harsh environment, the local cattle sacrifice their growth, while maintaining their reproduction traits efficiently

Carcass Percentage

The results of Ciamis local cattle carcass percentage, compared to others local cattle are presented in Table 3. Table 3 showed that the

Table 2. Comparison of ADG between Ciamis Local Cattle and Other Indonesian Local Cattle

Breed	ADG \pm Sd	Feed	Reference
Local	0.62 ± 0.23	Concentrate, rice straw	This study
Bali	0.58-0.68	Combination of forage, rice brand, bioplus Kenzymb and Laser punktur	Parwati <i>et al.</i> (1999)
PO	0.86 ± 0.18	Concentrate, forage, soybean hulls, cassava	Carvalo <i>et al.</i> (2010)
Madura	0.61	Forage, legume, coconut oilcake, bioplus	Ngadiyono <i>et al.</i> (2001)
Jawa	0.63	Concentrate, rice straw	Adiwinarti <i>et al.</i> (2011)
Crosses of PO x Simental	0.99 ± 0.20	Concentrate, forage, soybean, cassava	Carvalo <i>et al.</i> (2010)

* kg/head/day

Table 3. Average Carcass Percentage of Local Ciamis, Bali, PO and Crossbred Cattle

Breed	Number of Samples (heads)	Sex	Average Slaughtered weight (kg)	Average Carcass weight (kg)	Average Carcass (%)
Ciamis	14	Male	205.2	105.87	51.62 ^{ns} ±1.8
Bali	10	Female	178.5	89.2	49.90 ^{ns} ±0.2
Ongol	8	Male	289.88	151.13	52.09 ^{ns} ±2.4
Crossbred	30	Male	500.4	259.93	52.10 ^{ns} ±3.3

ns = non significant (P>0.05)

Table 4. Number of Allele from Genotyping Based on Microsatellite Loci

Population	INRA35		HEL9		BM2113		Average
	Size	n	Size	n	Size	n	
Tambaksari	117-137	8	155- 181	10	148- 172	10	9.3
Cijulang	117-139	8	155- 185	11	148- 172	9	9.3
Polled*	117- 139	9	155- 185	11	148- 172	10	10
Bali	121	1	163	1	152- 172	4	2.0
PO	117-125	4	163- 181	7	160- 166	3	4.7
<i>B. taurus</i>		5	171- 185	7	152- 172	10	7.3
Total Alel	117 –141	9	155 –185	14	148 -172	10	

* is polled subpopulation of Tambaksari and Cijulang; n = Sum of allele

average carcass percentage of Ciamis local cattle was not significantly different (P>0.05) from those of Bali, PO and crossbred cattle. There is indication that the proportion of carcass weight with liveweight on all breed were similar.

The affecting factors of carcass percentage are body conformation, feed, age and live weight. Sex does not affect the percentage of carcasses, but affect the composition of the carcass. Tonbesi *et al.* (2009) stated that the carcasses percentage of female and male Bali cattle at similar age > 2-3 years, were not different, 53.56 ± 3.21% and 53.94 ± 4.57% respectively. Sex affects carcass composition, it is due to the hormonal system, the male hormone, androgen stimulates bone growth better than the female and steer, and increases protein synthesis in muscle, while the female hormone estrogen related to fat deposition. The different breeds have an impact on the large proportion of fat compared to meat and bone during fattening (Aberle *et al.*, 2001). Therefore,

it can be argued that meat (muscle) which a prime part that can be consumed, either Ciamis local cattle, Bali, PO or their crosses is similar.

Genetic Diversity of Local Cattle in Ciamis

Allele Frequency

The results showed that all of loci were polymorphic. The number of alleles in a population, which can be detect by three of microsatellite loci was ranged from 8-11 alleles, with an average was 9.3 alleles. INRA35, HEL9 and BM2113 loci in the local cattle population at Ciamis had 9, 11 and 10 alleles respectively (Table 4).

It is in line, with research of Abdullah *et al.* (2008) in Aceh cattle in which these loci was polymorphic, it had 10, 13, and 10 alleles respectively. INRA35 and HEL9 loci in Bali cattle are monomorphic, there was only one allele, which was consistent with other studies, that

Table 5. Distribution of Highest and Lowest Allele Frequencies at Different Breed and Cattle Population

Population	INRA35		HEL9		BM2113	
	Highest Frequency	Lowest Frequency	Highest Frequency	Lowest Frequency	Highest Frequency	Lowest Frequency
Tambaksari						
Allele	C	F, G	B	K	G	F
Frequency	0.43	0.02	0.24	0.013	0.28	0.01
Cijulang						
Allele	C	D	C	M	G, I	K
Frequency	0.42	0.01	0.43	0.012	0.22	0.01
Polled *						
Allele	C	G	C	M	G	F
Frequency	0.42	0.01	0.42	0.006	0.25	0.005
Bali						
Allele	C	-	C	-	G	K, H
Frequency	1	-	1	-	0.78	0.056
Ongol Grade						
Allele	C	A, B	H	D, F	I	F
Frequency	0.5	0.14	0.75	0.083	0.5	0.14

* Polled population as a merge populations between Tambaksari and Cijulang subpopulation

showed those locus were monomorphic. Therefore, those locus may be a specific locus in Bali cattle (Winaya *et al.*, 2007; Handiwirawan *et al.*, 2003; Abdullah *et al.*, 2008).

When compared to the results of other studies on the Indonesian local cattle, the number of alleles of Ciamis cattle was lower than Katingan cattle, that was 13.6 alleles (Utomo *et al.*, 2011) and Coastal cattle was 11.7 alleles (Sarbaini, 2004) and similar to the Aceh cattle that was 9.25 alleles (Abdullah *et al.*, 2008). The amount of alleles that can be detected depends on the number of samples, the type and the amount of loci that are used. Meanwhile the study of Ginja *et al.* (2009) on the local cattle in Portugal, using 39 microsatellite loci, showed the average amount of allele was of 8.3 ± 2.5 alleles. The study of Winaya *et al.* (2007) by using 16 loci showed that the average number of alleles in Bali, Madura, Ongole cattle were 1.94, 2.19 and 2.63 alleles respectively. These indicated that the pure cattle had lower number of alleles.

The high number of alleles at the local cattle in Ciamis, maybe due to the mutations in these loci or there was introgression of other genes into the population. The three microsatellite loci used,

had two nucleotide repeat motifs (*dinucleotide*). Mutation rate of microsatellite loci was high, because the sequence of these loci was short (short tandem repeats), therefore it was quite high polymorphic (Almida *et al.*, 2000). DNA microsatellite has a high rate of changed nucleotide, due to a change in the number of repeats its sequence can reach 10^{-3} /gamet/generation. The rate of change is influenced by microsatellite motif. Microsatellites with dinucleotide motifs have 1.5-2 times mutation rates faster than the tetra-nucleotide motif (Muladno, 2006).

The highest allele frequency on INRA35 loci is C allele with 121 bp size (Table 5). The highest frequency of microsatellite BM2113 in the research population and Bali cattle were G allele which has 162 bp. At Cijulang subpopulation, I allele (166 bp) was the highest allele and similar with PO cattle. Allel of HEL9 loci that had a highest frequency in the two subpopulations was different, but the highest allele in polled population was the C allele (159 bp), It was similar to Cijulang population. Based on these result, it can be concluded that the Ciamis cattle were genetically closed with Bali and PO cattle.

Table 6. Distribution of Specific Genotype of Local Cattle in Ciamis

Loci	Number of Genotype	Specific Genotype in Subpopulation				Number of Same Genotype in Subpopulasi
		Tambaksari		Cijulang		
		Amount	%	Amount	%	
INRA35	21	10	47.62	7	33.33	4
HEL09	27	7	25.93	9	33.33	11
BM2113	26	7	26.92	4	15.38	15

Table 7. The Observed and Expected Heterozygosity Value of Three Microsatellite Loci

Population	INRA35		HEL9		BM2113		Average	
	Ho	He	Ho	He	Ho	He	Ho	He
Tambaksari	0.48	0.76	0.39	0.83	0.48	0.83	0.45	0.81
Cijulang	0.26	0.66	0.37	0.78	0.48	0.83	0.37	0.76
Polled*	0.36	0.72	0.38	0.86	0.48	0.84	0.41	0.81
Bali	0	0	0	0	0.33	0.38	0.11	0.13
PO	0.43	0.66	1	0.83	0.71	0.6	0.71	0.70
Simental	0	0	0.7	0.8	0.6	0.67	0.43	0.49
Limousin	0.1	0.19	0.3	0.72	0.6	0.79	0.33	0.57
Brahman	0.5	0.64	0.44	0.76	0.55	0.76	0.50	0.72
Angus	0	0	0.25	0.78	0.4	0.76	0.22	0.51

Ho = Observation Heterozygosity ; He = Expected Heterozygosity ; *a merge populations between Tambaksari and Cijulang

The highest distinctive genotype of local cattle in Ciamis was INRA35 loci that was 47.62% in Tambaksari subpopulation, and the lowest genotype frequency was BM2113 in Cijulang subpopulation that is 15.38% (Table 6). Sarbaini (2004) suggested that increasing of distinctive genotype in a population could be used as a diagnostic loci between subpopulations.

Heterozygosity

Heterozygosity value is the most accurate parameter to evaluate genetic diversity in a population. The results of analysis heterozygosity value in this study are presented in Table 7.

The observed and expected heterozygosity (Ho and He) values in Tambaksari subpopulation was higher than in Cijulang population and both

were also higher than Bali cattle. Based on the previous studies, the INRA35 and HEL9 were a specific loci at Bali cattle (Handiwirawan *et al.*, 2003; Winaya *et al.*, 2007). Whereas heterozygosity of PO cattle was high. The heterozygosity value of Tambaksari subpopulation was higher than in Cijulang subpopulation, These indicated that the cattle in Cijulang more homogen. The distribution of cattle in Cijulang was limited. The farmer collected the heifers, just in the south coastal areas in West Java, whereas in the Tambaksari, cattle distribution was wider, from the south coastal to the north area, also covering Cirebon and Kuningan district, consequently, their genetic in these area was more diverse.

The average of expected heterozygosity in

Table 8. Matrix of Genetic Distance

Population	Tambaksari Local	Cijulang Local	Bali	PO	Simental	Limousin	Brahman	Angus
T.sari	0							
Cijulang	0.2869	0						
Bali	0.5224	0.2921	0					
PO	0.3081	0.2682	0.4371	0				
Simental	1.0094	0.6036	2.4873	1.4192	0			
Limosin	0.9335	0.5576	1.7565	0.8812	0.1027	0		
Brahman	0.6177	0.5031	1.0901	0.8401	0.3702	0.1952	0	
Angus	1.0254	0.6424	2.8352	1.5508	0.0918	0.1139	0.4340	0

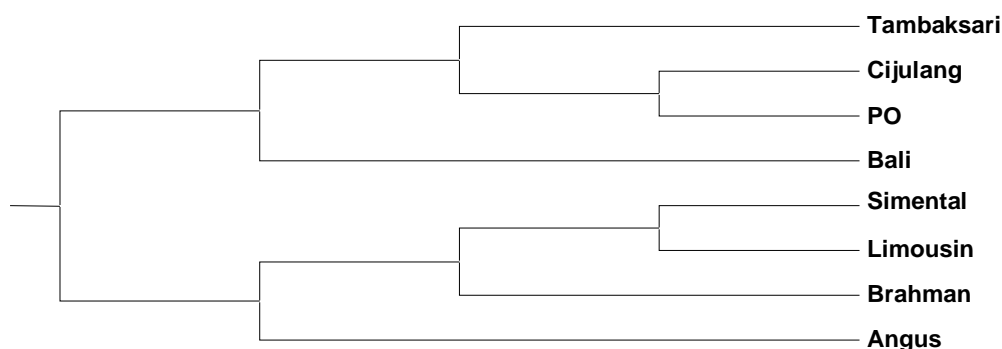


Figure 1. Phylogenetic Tree of Local Cattle in Ciamis Compared to the Outgrouped

Ciamis local cattle was 0.81, it was higher than in Aceh cattle was 0.62 (Abdullah *et al.*, 2008) and Katingan cattle in Central Kalimantan was 0.49 (Utomo *et al.*, 2011). The heterozygosity value depends on the sample size, the type and number of used microsatellites. However heterozygosity of pure cattle population was relatively low, as heterozygosity value of Bali cattle was 0.13, similar to the research of Winaya *et al.* (2007) using 16 microsatellite loci, heterozygosity value of Bali and Madura cattle were 0.33 and 0.31, respectively

In both subpopulations, the farmers usually sell a male juvenile after weaning off, due to unprofitable. Introduction of artificial insemination (AI) in two subpopulation research was intensive, therefore the farmers reared dam to produce crossbred calves, that can be sold in

highly prices. Generally, the farmers looking for dam from broker or other farmers in surrounding areas, where natural mating is still practiced. Therefore, it is possible that expected heterozygosity were high in both subpopulations.

There was a difference value, between observed, and expected heterozygosity. Significant difference between observed ((Ho) and expected heterozygosity (He) was indicated imbalance population genotypes. Subsequently Machado *et al.* (2003) stated that if Ho value was lower than He value, its indicated a high level of endogamy, as a result of intensive selection in the population.

Genetic Distances

The genetic distance of Cijulang subpopulation was closed to PO cattle, as well as

cattle in Tambaksari was closed to Cijulang subpopulation, followed by PO cattle (Tabel 8; Figure 1) . Population in Cijulang was closer to Bali than cattle in Tambaksari. The Ciamis local cattle, PO, and Bali cattle were in the same cluster, while the Simental, Limousin, Brahman and Angus cattle were in a separate cluster.

Based on 16 of microsatellite loci, Aceh cattle was in the same cluster with PO cattle and perform a branch of phylogeny tree with Coastal and Madura cattle (Abdullah *et al.*, 2008). Further, the research of Katingan cattle, using fifteen microsatellite loci showed that their heterozygosity quite high (0.49) and was in the same cluster with PO cattle (Utomo *et al.*, 2011). Generally, these conditions indicated, Indonesian local cattle closed to PO cattle, despite having different phenotypes. Genetic diversity analysis of Hariana and Hisar cattle in Pakistan, using 30 microsatellite indicated that although both types of those cattle were derived from a common ancestor but, genetically can be distinguished into different breed (Rehman and Khan, 2009).

CONCLUSION

Average daily gain of Ciamis local cattle was 0.62 ± 0.23 kg/head/day, and the carcass percentage was $51.62 \pm 1.80\%$. The carcasses percentage of Ciamis local cattle was not different from Bali, PO and crossbred cattle. The genetic diversity of local cattle between and within Ciamis subpopulation was high category. Genetic diversity of Tambaksari subpopulation was higher than Cijulang subpopulation. Genetic distance of local cattle in Ciamis closed to PO cattle. Its was within one cluster with PO cattle.

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