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THE POTENCY OF SUMBA ONGOLE (SO) CATTLE: A STUDY OF GENETIC CHARACTERIZATION AND CARCASS PRODUCTIVITY

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ABSTRAK

Telah dilakukan suatu penelitian untuk mengevaluasi keragaman genetik sapi Sumba Ongole (SO) berdasarkan DNA mikrosatelit dan mengkaji potensi sapi SO sebagai sapi potong lokal Indonesia berdasarkan kemampuan produksi karkasnya. Sebanyak 28 sampel darah sapi SO digunakan untuk melakukan karakterisasi genetik menggunakan 12 pasang primer DNA mikrosatelit yang direkomendasikan oleh FAO. Data produksi karkas dan bobot kulit berasal dari 506 ekor sapi SO yang dipotong di rumah potong hewan Karawaci, Banten, Indonesia. Nilai heterozigositas 12 lokus mikrosatelit berkisar antara 0,143 sampai dengan 1,000 (rata-rata 0,536). Nilai PIC tertinggi (0,814) ditemukan pada lokus TGLA122 sedangkan nilai terendah (0,280) ditemukan pada lokus BM1818. Sapi dengan bobot potong 351-475 kg merupakan sapi yang paling banyak dipotong pada tahun 2013 dan 2014 dengan persentase karkas antara 52,89% sampai dengan 53,43%. Persentase karkas tertinggi (56,34%) diperoleh dari sapi dengan bobot potong 626-650 kg. Sementara itu persentase karkas terendah (51,42%) diperoleh dari sapi dengan bobot potong 250-275 kg. Hasil karakterisasi genetik menunjukkan bahwa seluruh lokus mikrosatelit berada dalam kondisi beragam dan dapat digunakan untuk mendeteksi level keragaman genetik populasi sapi SO. Hasil studi produksi karkas menunjukkan bahwa sapi SO memiliki potensi yang sangat baik sebagai sapi potong bila dibandingkan dengan bangsa sapi potong lokal lain di Indonesia.

Kata kunci: karakterisasi, genetik, Sumba Ongole, karkas, potensi sapi

ABSTRACT

A study was conducted to assess the genetic characterization of the Sumba Ongole (SO) cattle based on DNA microsatellites and also to study the potency of SO cattle based on carcass productivity. Blood samples were collected from 28 individual cattle and 12 microsatellite primers as recommended by FAO were used to identify the genetic characterization of the SO cattle population. Data of carcass productivity were collected from 506 individual cattle that slaughtered in Karawaci abattoir, Banten, Indonesia. The heterozygosity values of microsatellite loci ranged from 0.143 to 1.000 (mean 0.536). The highest PIC values was 0.814 (locus TGLA122), while the lowest was 0.280 (locus BM1818). Cattle in range of 351-475 kg slaughter weight was most slaughtered in year 2013 and 2014 with carcass percentage ranged from 52.89% to 53.43%. The highest carcass percentage (56.34%) was obtained from cattle in range of 626-650 kg slaughter weight while the lowest (51.42%) was obtained from cattle in range of 250-275 kg slaughter weight. The results of genetic characterization showed that all microsatellite locus were highly polymorphic and highly informative for detecting the level of genetic diversity in the SO cattle population. The results of carcass productivity showed that the SO cattle has excellent potential as beef cattle compare with other local breeds cattle in Indonesia.

Keywords: genetic, characterization, Sumba Ongole, carcass, beef cattle potency

INTRODUCTION

Sumba Ongole (SO) cattle is one of Indonesian local breeds cattle. The existence of the SO cattle in Indonesia began since the Ongole cattle was imported from India in 1914 (Ministry of Agriculture of the Republic of Indonesia, 2014) and placed in Sumba island (East Nusa Tenggara Province) and well adapted in Indonesian climate. The Sumba island eventually set for Ongole cattle breeding center that became known as Sumba Ongole cattle (Hardjosubroto, 2004). Meat production percentage of the SO cattle was fairly high and percentage of carcass fat was low (Ngadiyono, 1995). The SO cattle can be used in fattening (feedlots), especially fattening in a relatively long period and gain a high slaughter weight. Carcass of the SO cattle are longer and wider than Brahman cross cattle (Ngadiyono, 1995).

Up to present, almost no reports about genetic diversity of the SO cattle. Information about genetic diversity is needed to perform conservation program especially in Indonesian local cattle resources and also provide an opportunity for farmers to develop animal breeding bussiness. The development of molecular genetics analysis has made it possible to study into deoxyribonucleic acid (DNA) level. Microsatellites are almost ideal genetic markers because they are abundant, codominant, highly polymorphic, and spread across the entire euchromatic part of the genome (Bennett, 2000). Microsatellites can be used for estimating the genetic distance (Rehman and Khan, 2009), genetic diversity (Mao *et al.*, 2008), individual profiles and paternity test (Zhang *et al.*, 2010; Radko *et al.*, 2010), relationship among livestock breeds (Maretto *et al.*, 2012), and evaluating mutation drift equilibrium of animals (Kathiravan *et al.*, 2009).

Moreover, information about potency of carcass production in the SO cattle still limited. Lack of information about carcass production is one of the causes of the lack of interest of Indonesian beef industry to develop the SO cattle fattening and breeding bussiness. Therefore, continuous studies are needed to explore information about genetic diversity and potency of carcass production in the SO cattle. The objectives of this study was to evaluate genetic diversity of the SO cattle based on DNA microsatellites and also to study the potency of the SO cattle based on carcass productivity.

MATERIALS AND METHODS

Animal and Blood Samples

Blood samples were collected from 28 individual cattle belonging to PT. KAR Farm, West Java. Blood samples (3-5 ml) were taken from cattle coccigea vein using Venoject and collected in Vaccutainer tubes contained anticoagulant. The blood samples were used for obtaining DNA samples through the DNA extraction process using DNeasy® Blood & Tissue Kit (Qiagen, Germany) following the producer's method.

Productivity of the SO cattle were analysed from data of carcass and skin weight. Data of carcass and skin weight were obtained from 506 individual cattle that slaughtered in Karawaci abattoir, Banten, Indonesia from November 2013 to September 2014. Animals was slaughtered with consideration of animal welfare and "halal" way.

Primers and DNA Amplification

Twelve microsatellite labelled primers that recommended by FAO (2011) were used in Polymerase Chain Reaction (PCR) process. Primers sequen, annealing temperature, range of PCR product size, and label that used are shown in Table 1. The PCR reagent composition is as follows: KAPA2G Robust HotStart ReadyMix PCR Kit (1st BASE, Malaysia) (18 µl), forward and reverse labelled primers (2.8 µl), DW (10 µl), and DNA sample (1.4 µl). Program in the PCR machine (Eppendorf, Germany) is set as follows: 94°C; 5 min (1 cycle), 35 cycles consisting of three stages: (1) 94°C; 30 seconds, (2) 51-59°C; 30 seconds (depends on primers), and (3) 72°C; 30 seconds, followed by 1 cycle at 72°C; 5 minutes. The PCR products then visualized by electrophoresis using 2% agarose gel and followed by ethidium bromide staining. The multiplex DNA fragment analysis was used for allele identification. The multiplex DNA fragment analysis was conducted in 1st BASE Laboratorium, Malaysia.

Data Analysis

Result of the multiplex DNA fragment analysis was processed using CONVERT ver. 1.3.1 (Glaubitz, 2004), CERVUS ver. 3.0.7 (Kalinowski *et al.*, 2007), and POPGENE ver. 1:32 (Yeh and Boyle, 1997) programs. The CONVERT program was used for conversion the length of alleles which were observed for each individual sample to assure suitability for further

Table1. Information of 12 Microsatellite Primer Used in the Study Based on FAO (2011)

Locus	Sequen (5'-3')	Label	Annealing Temp.(^{o}C)	Size of PCR Product (bp)
TGLA227	F: CGAATTCCAAATCTGTTAATTTGCT	Fam	55	75-105
	R: ACAGACAGAAACTCAATGAAAAGCA			
SPS113	F: CCTCCACACAGGCTTCTCTGACTT	Hex	55	132-170*
	R: CCTAACTTGCTTGAGTTATTGCCC			
BM1824	F: GAGCAAGGTGTTTTTCCAATC	Tamra	57	176-197
	R: CATTCTCCAACTGCTTCCTTG			
ETH225	F: ATCACCTTGCCAATATTTCC	Hex	55	131-159
	R: ACATGACAGCCAGCTGCTACT			
INRA023	F: GAGTAGAGCTACAAGATAAACTTC	Tamra	55	195-225
	R: TAACTACAGGGTGTTAGATGAACTCA			
TGLA122	F: CCCTCCTCCAGGTAAATCAGC	Fam	57	136-184
	R: AATCACATGGCAAATAAGTACATAC			
CSSM66	F: ACACAAATCCTTTCTGCCAGCTGA	Hex	59	171-209
	R: AATTTAATGCACTGAGGAGCTTGG			
ILSTS006	F: TGTCTGTATTTCTGCTGTGG	Tamra	59	277-309
	R: ACACGGAAGCGATCTAAACG			
BM1818	F: AGCTGGGAATATAACCAAAGG	Tamra	59	48-278
	R: AGTGCTTTCAAGGTCCATGC			
SPS115	F: AAAGTGACACAACAGCTTCTCCAG	Fam	57	234-258
	R: AACGAGTGTCCTAGTTTGGCTGTG			
TGLA126	F: CTAATTTAGAATGAGAGAGGCTTCT	Fam	58	115-131
	R:TTGGTCTCTATTCTCTGAATATTCC			
TGLA53	F: CAGCAGACAGCTGCAAGAGTTAGC	Hex	51	143-191
	R: CTTTCAGAAATAGTTTGCATTCATGCAG			

*Based on on Movahedin *et al.* (2010); bp = base pair

analysis by POPGENE and CERVUS program. Data of the allele frequencies, the heterozygosity, the genetic distance, and the PIC (Polymorphism Information Content) value were obtained from POPGENE ver. 1:32 and CERVUS ver. 3.0.7 analysis result.

Data of cattle productivity was calculated using MINITAB ver. 14 and analysed with descriptive analysis including mean of live weight, carcass weight, carcass percentage, skin weight, and skin percentage. Data of carcass and skin percentage was divided into sixteen category based on live weight before slaughter. Standard normality test for the data of live weight, carcass weight, and skin weight was conducted to ensure the data were normally distributed.

RESULTS AND DISCUSSION

PCR products for 12 microsatellite loci in this study were in good quality and can be used for allele identification using multiplex DNA fragment analysis. Variation of alleles was detected and followed by analysis of the allele frequency, the heterozygosity, and the PIC value. Allele frequency distribution of each primer pair

Table 2. Distribution of the Allele Frequency for 12 Microsatellite Loci in the SO Cattle Population

Locus	Allele	Allele Frequency	Locus	Allele	Allele Frequency
BM1824	181	0.214	ETH225	135	0.229
	183	0.571		139	0.042
	185	0.143		143	0.146
	189	0.018		145	0.021
	195	0.018		149	0.021
	197	0.018		151	0.042
	199	0.018		155	0.500
SPS113	131	0.161	TGLA53	135	0.816
	133	0.232		137	0.079
	135	0.036		139	0.026
	137	0.321		141	0.026
	139	0.179		161	0.053
	141	0.036	CSSM66	178	0.161
	147	0.018		180	0.054
	157	0.018		182	0.036
SPS115	242	0.161		196	0.018
	244	0.446		198	0.018
	246	0.054		220	0.714
	250	0.054	TGLA126	111	0.018
	252	0.125		117	0.143
	254	0.054		119	0.054
	258	0.018		121	0.018
	262	0.018		123	0.286
	264	0.071		125	0.304
TGLA122	136	0.192		127	0.179
	140	0.039	ILSTS006	290	0.018
	142	0.058		292	0.054
	144	0.115		294	0.482
	152	0.269		296	0.250
	154	0.115		298	0.161
	158	0.019		300	0.018
	160	0.019		302	0.018
	162	0.154	INRA023	197	0.074
	164	0.019		199	0.056
TGLA227	78	0.786		201	0.093
	80	0.036		203	0.111
	84	0.036		205	0.019
	86	0.018		209	0.056
	88	0.018		211	0.037
	92	0.036		215	0.556
	94	0.018	BM1818	262	0.214
	96	0.018		264	0.786
	100	0.036			

is presented in Table 2.

The calculation of the heterozygosity and the PIC values for all locus has been conducted (data are shown in Table 3.). The heterozygosity value ranged from 0.143 to 1.000 (mean 0.536). This value was very high (P>0.5) and indicates the number of heterozygous samples. Therefore, all the microsatellite locus in this study were highly polymorphic. The lowest heterozygosity value was 0.143 (BM1818) and the highest value was 1.000 (SPS113). The PIC value for each locus was estimated according to Botstein *et al.* (1980). The PIC value at 12 microsatellite loci that used in this study was more than 0.5 (PIC>0.5). Hence, every locus in this study was highly informative for detecting the level of genetic diversity in population.

The highest PIC value in this study was 0.814 (locus TGLA122), while the lowest value was 0.280 (locus BM1818). The low PIC and Ho values for locus BM1818 in the SO cattle in this study can be explained by several factors including null alleles, assortative mating, the Wahlund effect, selection against heterozygotes, inbreeding, or a combination of all these factors (Cervini *et al.*, 2006). Moreover, the low value of heterozygosity may indicate that a certain breeds are relatively well-conserved (Czernekova *et al.*, 2006).

Compared to the results from other studies that also used microsatellite which were mostly identical with our study, some differences can be observed. The differences may be on the minimum and maximum allele size, the number of observed alleles and also the PIC value. The comparison is presented in Table 4. Characteristics of microsatellite that naturally was highly polymorphic was the influential factor that caused the differences in size range of allele and the number of observed alleles. The PIC value and observed heterozygosity (Ho) value in this study for locus TGLA227 was low. This condition was same with Cervini *et al.* (2006) but contrast with Kesvulu *et al.* (2009) and Riojas-Valdes *et al.* (2009) reports that found locus TGLA227 with higher PIC and Ho values. In other hand, PIC and Ho values in locus TGLA53 in this study was low as well as other reports (Kesvulu *et al.*, 2009; Cervini *et al.*, 2006).

Data of carcass productivity was classified into sixteen groups based on the slaughter weight (Table 5). Data of the slaughter weight was ranged from 250 kg to 650 kg. Most of the SO cattle slaughtered in year 2013 and 2014 was in

Table 3. Genetic Diversity in the SO Cattle

Locus	N	na	ne	Ho	He	PIC
TGLA227	56	9	1.6033	0.357	0.383	0.368
SPS113	56	8	4.5848	1.000	0.796	0.750
BM1824	56	7	2.5372	0.286	0.617	0.560
TGLA122	52	10	6.0357	0.808	0.851	0.814
CSSM66	56	6	1.8491	0.571	0.468	0.428
BM1818	56	2	1.5077	0.143	0.343	0.280
ETH225	48	7	3.0476	0.875	0.686	0.630
INRA023	54	8	2.9160	0.593	0.670	0.635
ILSTS006	56	7	3.0806	0.321	0.688	0.629
SPS115	56	9	3.9200	0.643	0.759	0.721
TGLA126	56	7	4.3556	0.571	0.784	0.734
TGLA53	38	5	1.4795	0.263	0.333	0.310
Mean	53	7.08	3.0764	0.536	0.615	0.572
Std. Dev.		2.11	1.4265	0.268	0.186	

n_A = observed number of allele; ne = effective number of allele; Ho = observed heterozygosities; He = expected heterozygosities; PIC = polymorphism information content; s.d. = standard deviation

Table 4. Comparison of the Size Range, the Heterozygosity, and the PIC of Microsatellite Loci in the Bos indicus Cattle Study

Locus	Parameter	A	B	C	D
TGLA227	Range (bp) [n_A]	77-89 [5]	75-97 [6]	76-83 [6]	78-100 [9]
	Ho	0.739	0.368	0.7414	0.357
	PIC	0.565	0.39	0.9926	0.368
BM1824	Range (bp) [n_A]	179-197 [6]	176-196 [10]	177-192 [9]	181-199 [7]
	Ho	0.522	0.677	0.6294	0.286
	PIC	0.619	0.612	0.9998	0.56
ETH225	Range (bp) [n_A]	146-158 [4]	138-162 [10]	142-161 [8]	135-155 [7]
	Ho	0.304	0.323	0.7328	0.875
	PIC	0.308	0.6683	0.9996	0.63
INRA023	Range (bp) [n_A]	197-215 [6]	194-216 [9]		197-215 [8]
	Ho	0.609	0.541		0.593
	PIC	0.536	0.835		0.635
TGLA122	Range (bp) [n_A]	137-197 [9]	133-165 [16]	136-167 [10]	136-164 [10]
	Ho	0.826	0.661	0.790	0.808
	PIC	0.809	0.805	0.999	0.814
SPS115	Range (bp) [n_A]	245-255 [5]		140-156 [11]	242-264 [7]
	Ho	0.783		0.7155	0.643
	PIC	0.726		0.9996	0.721
TGLA126	Range (bp) [n_A]	118-130 [7]	109-127 [8]		111-127 [7]
	Ho	1.000	0.847		0.571
	PIC	0.776	0.773		0.734
TGLA53	Range (bp) [n_A]	159-179 [7]	160-190 [13]		135-161 [5]
	Ho	0.304	0.352		0.263
	PIC	0.586	0.405		0.31

n_A= observed number of alleles; bp = base pair; A = Kesvulu *et al.* (2009); B = Cervini *et al.* (2006); C = Riojas-Valdes *et al.* (2009); D = this study

range of 351-475 kg slaughter weight with carcass percentage ranging from 52.89% to 53.43%. The highest carcass weight (358.06 kg) and also highest carcass percentage (56.34%) was obtained from cattle in range of 626-650 kg slaughter weight. In other hand, the lowest carcass weight (137.4 kg) and lowest carcass percentage (51.42%) was obtained from cattle in range of 250-275 kg slaughter weight.

The results of this study showed that the SO cattle has excellent potential as beef cattle according to the ability of the SO cattle to gain a fairly higher carcass percentage (51.42% - 56.34%) compare with other local breed cattle in Indonesia. Several studies of the SO cattle in Indonesia was reported and it can be summarized that the lowest carcass percentage of the SO cattle ever reported was 46.8% (Sumadi and Siliwolu, 2004) while the highest carcass percentage ever reported was 53.89% (Ngadiyono, 1995). Data of

Table 5. Distribution of the Carcass Weight and the Skin Weight of the SO Cattle

Weight Range (kg)	Slaughter Weight (kg)	Carcass Weight (kg)	Carcass Percentage	Skin Weight (kg)	Skin Percentage	n
			(Mean ± s.d.)			
250 - 275	267.80 ± 8.00	137.40 ± 9.85	51.42 ± 2.27	18.33 ± 0.58	6.87 ± 0.29	3
276 - 300	284.18 ± 7.35	148.81 ± 8.46	52.37 ± 2.81	20.36 ± 2.58	7.16 ± 0.78	11
301 - 325	313.80 ± 6.33	167.13 ± 6.35	53.27 ± 2.10	23.87 ± 5.42	7.60 ± 1.68	15
326 - 350	339.19 ± 8.21	179.34 ± 7.15	52.88 ± 1.94	26.00 ± 3.72	7.67 ± 1.11	21
351 - 375	366.53 ± 6.63	194.56 ± 7.22	53.09 ± 1.81	27.47 ± 3.15	7.50 ± 0.87	57
376 - 400	386.38 ± 6.99	204.57 ± 7.99	52.95 ± 1.87	28.63 ± 3.55	7.41 ± 0.91	64
401 - 425	413.49 ± 6.95	218.73 ± 9.15	52.89 ± 1.89	30.70 ± 3.43	7.42 ± 0.81	77
426 - 450	436.27 ± 7.13	230.98 ± 9.12	52.94 ± 1.75	32.20 ± 2.57	7.38 ± 0.59	70
451 - 475	463.08 ± 7.59	247.45 ± 10.74	53.43 ± 2.08	33.59 ± 4.02	7.26 ± 0.88	64
476 - 500	486.92 ± 7.83	264.06 ± 14.72	54.23 ± 2.85	35.61 ± 4.80	7.32 ± 1.00	36
501 - 525	511.26 ± 6.45	279.43 ± 13.28	54.65 ± 2.36	36.56 ± 4.58	7.15 ± 0.90	27
526 - 550	539.24 ± 6.86	289.90 ± 12.67	53.76 ± 2.11	37.00 ± 3.21	6.86 ± 0.60	21
551 - 575	561.90 ± 7.29	306.20 ± 17.82	54.48 ± 2.83	37.60 ± 4.43	6.69 ± 0.77	20
576 - 600	582.75 ± 8.21	317.25 ± 5.44	54.45 ± 1.43	39.13 ± 3.83	6.71 ± 0.66	8
601 - 625	610.25 ± 8.22	333.50 ± 5.80	54.66 ± 1.06	40.50 ± 2.38	6.64 ± 0.41	4
626 - 650	635.50 ± 6.91	358.06 ± 15.35	56.34 ± 2.24	44.38 ± 4.98	6.98 ± 0.75	8

Total number of animal; 506; s.d.= standard deviation; n=number of animal

carcass percentage for another local breed cattle in Indonesia was also reported. Carvalho *et al.* (2010) have reported that the carcass percentage of the Ongole Grade (PO) cattle was 49.4% while the SimPO (crossing result from the Simmental and the PO cattle) was 51.18%. Ngadiyono (1995) reported that the carcass percentage of the Brahman cross cattle was 54.18%. In addition, Muthalib (2003) reported that the carcass percentage of the Bali cattle was 50.19%. According to average daily gain values, Ngadiyono (1995) reported that the SO cattle can gain 0.85 kg/day in feedlots condition while the PO cattle can gain 0.86 kg/day (Carvalho *et al.*, 2010).

CONCLUSION

The results of genetic characterization showed that all the microsatellite locus in this study were highly polymorphic and highly informative for detecting the level of genetic diversity in the SO cattle population. The results of carcass productivity study showed that the SO cattle has excellent potential as beef cattle according to the ability to gain higher carcass percentage (51.42% - 56.34%) compare with other local breeds cattle in Indonesia.

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