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Intervention of Genetic Flow of the Foreign Cattle toward Diversity of Phenotype Expressions of Local Cattle in the District of Banyuwangi

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ABSTRACT

The aims of the present research are two folds: to know the phenotypic diversity and to reconstruct the cross-breeding pattern of local cattle in Banyuwangi. Based on three sampling areas, it was found that there were 32 phenotypic cattle (10 in the sub districts of Rogojampi, 16 in Tegaldlimo and 6 in Glagah areas). The phenotypic varieties were caused by two factors, namely the flow of genetic intervention of the other local cattle (Bali, Ongole, and Brahman cattle) and the artificial insemination program using the semen of Limousine, Simmental, Aberdeen Angus and Santa Gertrudis cattle.

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Key words: flow of genetic intervention, local cattle, phenotypic variation.

INTRODUCTION

One of national assets in husbandry fields in Indonesia is beef cattle which has economic potentials to be developed. The existence of beef cattle can be intensified to create job opportunities, to meet national meat production, increase breeders' income and farmer prosperity, and finally it is importance source of government's income generating units. Besides that it will also reduce the dependency on meat import.

In Indonesia, Bos sp. is one kind of cattle which gives a significant contribution to national meat supplies to fulfill animal protein needs of peoples. But, the addition of cattle population is not balanced with the national needs (Putu et al. 1997). Table 1 is a list of cattle which gives the biggest contribution among five kinds of key livestock in meat supplies at a national scale. Since the economic crisis that happened in 1997, a significant decrease in the population of cattle has happened in some areas, so that the cattle population is now believed to be less than before. As a consequence, the beef cattle potential from year to year have decreased significantly. For example, in Nusa Tenggara, the case is shown at the figure of 15.92% (Sumadi 2002). If this condition is uncontrolled, there is a chance that in about 10 years later the existence of beef cattle will be drained. By then, we will have lost germplasms which are one of the national assets in the husbandry field.

This problem becomes more serious because, on one side, there has still been a lack of accurate observations in the breeding of the local cattle; and on the other side, efforts for production increase are not yet optimum. Negative selections by the breeders and the lack of observation in the breeding of local cattle cause the rest of local cattle to be the cattle with a bad quality, which let alone, commonly will serve as the cattle seed on which further cattle is to be produced. This happens because of the practice of conventional husbandry by the local people. If this case happens continuously, it is predicted that one day local cattle extinction will happen and we will lose the benefit because of losing germplasms (Hardjosubroto 2000, 2002; Mahaputra 2002). Setiadi (1997) states that a 'friendly' cross-breeding program can threaten the local cattle source which has not been renewed.

Table 1. Fluctuation of big livestock production from 1995-1998(in thousands).

Livestock	1995	1996	1997	1998
Cattle	11,534	11,816	11,938	11,663
Dairy milk	341	348	335	321
Goat	3,136	3,171	3,064	2,829
Buffalo	13,167	13,890	14,164	13,560
Sheep	7,168	7,724	7,698	7,114
(37 11 1 1	2002			

(Yudhohusodo 2003)

In the effort to conserve the pure genetic traits and the local cattle, the government makes development programs, for example to keep the purity of Bali cattle. The government has stated four areas that develop pure breeds of Bali cattle, namely Bali, South Sulawesi, West Nusa Tenggara, and East Nusa Tenggara (Pane 1991; Handiwirawan 2003).

According to statistics in the Banyuwangi district (BAPPEDA Kabupaten Banyuwangi 2007), the potential of agriculture land in Banyuwangi is in the third rank after Malang and Jember, so that Banyuwangi becomes one of food rice bran in East Java Province. Besides of the potential of agriculture fields, Banyuwangi is a place that has the potential for cattle production. The development of husbandry in this region has the same line with the history of Banyuwangi. This can be seen from the pluralism of Banyuwangi people. The majority is the Osingese, but there are Javanese and Madurese who are significant enough and there are minority Balinese and Buginese. The Osingese is the indigenous inhabitants of Banyuwangi, and they can be considered as a sub ethnic group of the Javanese. The culture from ethnic groups which are pluralistic is very colorful in the living of cattle breeding. The Osingese as a sub ethnic group of Javanese will defend their breeding culture utilizing the local Java cattle. The Balinese will defend Bali cattle. Two of major ethnic groups besides the Osingese (Javanese and Madurese), of course will influence in terms of the presence of the husbandry model in Banyuwangi. Besides, to make the government program in the cattle production development successful, in 1990s the Banyuwangi government introduced the artificial insemination (AI) with the excellence of the cattle from Australia, Switzerland and the Netherlands (Simmental, Limousine, Angus, Brahman and Ongole). The AI program which is also a genetic intervention directly will influence the genetic diversity in Banyuwangi cattle breeding practices. As a consequence of this, tracing and identification needs to be performed on phenotype diversity of the Banyuwangi cattle as a result of genetic intervention from the AI program and culture which is brought by different ethnic groups who live in this area.

The aims of the research are to examine the phenotypic diversity and to reconstruct the cross-breeding pattern of the local cattle in Banyuwangi and to predict factors that influence these phenotypes.

MATERIAL AND METHODS

This research is a survey which aims to examine the phenotype of the local cattle in Banyuwangi, to study the phenotype expression variation including fur color (head, body and leg), shape of horn growth, ear shape, absence of growth, hump, mouth color (Fries and Ruvinsky 2004). This research was conducted from February to April 2008, in three phases taking out samples including those located in sub district areas as Rogojampi, Tegaldlimo, and Glagah. The decision to include these three areas is based on the central husbandry development for the Banyuwangi area. Tegaldlimo sub district area serves as a central artificial insemination with local cattle Java and Bali descent; Rogojampi sub district area is a central artificial insemination with local cattle Madura cattle, Java and Bali, Ongole hybrid and Brahman. Glagah sub district functions as a central artificial insemina-tion with local cattle crossing resulting from Java and Bali cattle. Sampling was conducted by following the schedule of health services set up by husbandry department for breeder on every Wednesday.

This research is divided into two phases. The first is field research which is field data collecting in the form of phenotype data and the second is the data tabulation using the observation matrix as shown in Table 2. Table 2. Sample of field collecting data table.

Sub district area:

Sample number	Phenotype *)						
	Color (head, body, leg)	Shape/direction of horn growth	Ear shape	Hump	Mouth color		
1							
2							
3							

Note: ^{*)} this phenotype decision is based on principal characteristic cattle in Kabupaten Banyuwangi. Notice: *Body color:* Bali cattle (brown), Ongole (white), Brahman (white), Simmental (brown), Angus (black), Limousine (brown). *Shape of horn growth:* Bali cattle (no horn/very small horn), Ongole (grow long and make 45° angle with body, Brahman (grow long and make 45° angle with body, Brahman (grow long and make 45° angle with body, Simmental (grow short), Angus (grow short), Limousine (grow short). *Ear shape:* Bali cattle (grow straight parallel with horn), Ongole (hanging), Brahman (hanging), Simmental (make 90° angle with body's axis, Limousine (make angle with body's axis). *Mouth color:* Bali cattle (black), Ongole (black), Brahman (black), Simmental (white), Angus (black), Limousine (brown).

The results of analyzing the phenotype data provide evidence of the pattern of the crossbreeding of the local cattle sample which was examined. Phenotype data recording will be analyzed descriptively to decide the crossing pattern so that the ancestor of sample cattle which is researched can be traced.

RESULTS AND DISCUSSION

Based on research in three research area sampling were found 42 cows in Rogojampi area, 48 cows in Tegaldlimo area and 18 cows in Glagah area. Research finding local cattle phenotype in Rogojampi area from 42 samples investigated, it could be found 11 kinds of phenotype (variation). For cattle from Rogojampi area was given R initial, and number series was a kind of number of phenotype cattle with detail as follow: R1 (Simmental), R2 (Java-PO), R3 (Java-Limousine), R4 (Java), R5 (Madura), R6 (Java-Simmental), R7 (Java Limousine Simmental), R8 (Limousine), R9 (Brahman Angus Limousine), R10 (Simmental) (Figure 1). There were 6 cows from 18 cows that were researched in Glagah area (with "G" initial, the ordinal number is the number of cow's phenotype variety) with detail as G1 (Java-Ongole-Bali), G2 (Rambon-Limousine), G3 (Rambon Keling), G4 (Rambon-Java), G5 (Rambon-Java (Java horn) and G6 (Bali-Limousine) (Figure 2).

The result of phenotype research in Tegaldlimo area shows there are 17 kinds of phenotype (with "T" initial and the ordinal number is the number of cows' phenotype variety) with the detail as follow: T1 (Simmental), T2 (Java-Limousine), T3 (Java-Ongole), T4 (Limousine), T5 (Java-PO-Simmental), T6 (Java-PO), T7 (Java-Ongole), T8 (Rambon Keling-Ongole), T9 (Rambon Manis-Ongole), T10 (Simmental-Angus), T11 (Simmental-Limousine), T12



Figure 1. Phenotypic variation of cattle from Rogojampi (R): R1 (Simmental), R2 (Java-PO), R3 (Java-Limousine), R4 (Java), R5 (Madura), R6 (Java-Simmental), R7 (Java-Limousine-Simmental), R8 (Limousine), R9 (Brahman-Angus-Limousine), R10 (Simmental) (left to right, above to bottom).



Figure 2. Phenotypic variation of cattle from Glagah (G): G1 (Java-Ongole-Bali), G2 (Rambon-Limousine), G3 (Rambon Keling), G4 (Rambon-Java), G5 (Rambon-Java/Java horn) and G6 (Bali-Limousine) (left to right, above to bottom).



Figure 3. Phenotypic variation of cattle from Tegaldlimo (T): T1 (Simmental), T2 (Java-Limousine), T3 (Java-Ongole), T4 (Limousine), T5 (Java-PO-Simmental), T6 (Java-PO), T7 (Java-Ongole), T8 (Rambon Keling-Ongole), T9 (Rambon Manis-Ongole), T10 (Simmental-Angus), T11 (Simmental-Limousine), T12 (Simmental), T13 (Limousine-Brahman-Angus), T14 (Ongole-Limousine), T15 (Ongole), T16 (Bali-Limousine) (left to right, above to bottom).

(Simmental), T13 (Limousine-Brahman-Angus), T14 (Ongole-Limousine), T15 (Ongole), T16 (Bali-Limousine) (Figure 3). Based on observation, there were 31 phenotype variations, namely the color of fur (head, body, leg), the shape of the horn growth, the shape of ear, the humps, the

color of mouth. Banyuwangi cattle history background is explained below (Figure 5).

In the beginning of the Banyuwangi cattle development, many people breeded the local Java and Bali cows according to the people's social conditions. In the Dutch

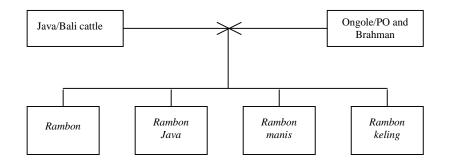


Figure 4. The pattern of Rambon cow varieties.

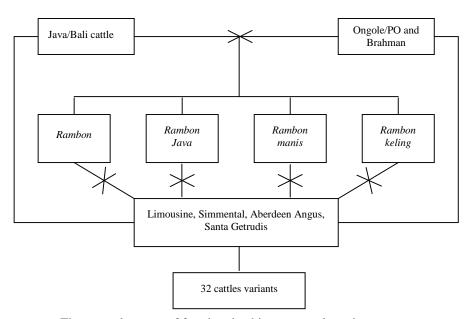


Figure 5. The general pattern of forming the thirty two cattle variants

Colonial era, they imported a lot of Ongole and Brahman cows. This gave an opportunity for the three kinds of cows to mingle and as a result, a new phenotype variant was born (produced). This represents the characteristic of the three kinds of cows, the local Java cow, the Bali cow, Ongole characteristics (including PO or Ongole breed) and the Brahman cow.

The crossbreeding of local Java and Bali cow is called Rambon cattle. It can be finding in Osing people's area (Glagah sub-district). Rambon is the breed of Java and Bali; it has phenotype expression of them (Java and Bali cattle). Rambon divided into many kinds of variety; they are Rambon, Rambon Java, Rambon Manis and Rambon Keling. Rambon Java ("Java" describes the characteristic of Bali cattle especially the pinkish fur and white leg (Banyuwangi people call it "sock", it is not characteristic of local Java cattle cow. But this cattle shows the Java cattle's horn that grows same way as the body. Bali cattle show the same characteristic with local Java cattle. Rambon Manis has brown furs as Bali cattle and it does not have white legs (socks). The other is Rambon Keling. It has brighter fur and legs, but it has the same type of horn with local Java cattle. Based on the characteristic, the appearance of the Rambon is explained as follow: Rambon Java is a crossbreed of Bali and Ongole cattle. The offspring (F1) is crossed by Bali cattle. Rambon Manis is a crossbreed of Bali and Brahman cattle (no horn) and Rambon Keling is a crossbreed of Rambon Manis and Bali cattle and Keling cattle (Ongole or PO (Ongole breed). Rambon is a crossbreed Rambon Manis and Bali cattle.

A lot of Rambon cattle breeder by Osing people practiced according to this cattle quality or ability to help the farmer in the This practiced can field. be understood because of the whole life of Osing people is farmer. Rambon cattle known to has a strong slim leg that help farmer to cultivate plant in the field. The formed pattern of Rambon cow varieties is shown in Figure 4.

In the beginning of 70's, the Government of the Republic of Indonesia introduced a program to increase cattle quality through an artificial insemination program. The program invited imported semen from the best quality of abroad, cattle from namely Simmental Limousine. and Aberdeen cattle. This program enriched the number of phenotype of the local cattle. The structure of the phenotype variation is shown in Figure 2. A study conducted by

MacHugh et al. (1999) studied five extant Nordic and Irish cattle breeds and suggested that the cattle used by the Vikings of the early medieval Dublin were similar to the modern cattle population found in the northern Europe. The medieval population displayed similar levels of mtDNA diversity to the modern European breeds.

In general, the appearances of the phenotype variations are seen in the hair of body color. Based on research result, it is shown that there is a variation of the body color (as a color parameter) signed by 31 kinds of cattle. For Indonesia as a tropical area, the adaptive color for the cattle to obtain the fitness is a bright color with a pigmented darker skin. The basis of the coat color and cattle and all mammals is the presence of melanin in the hair (Searle 1968). Melanin is found in the melanosomes of the cytoplasm of the melanocytes. These melanosomes are transferred to the hair as it grows through a process exocytosis. The melanocytes migrate from the neural crest during embryonic development and only areas of the body in which they are found are pigmented. White spotting occurs in the area where the skin or hair lacks melanocytes. The expression of the observed pigmentation in the cattle is caused by pigmentation that is controlled by genes. The *Extension* (E) locus is responsible for most of the variation in the cattle coat color. Three alleles present at this locus include: E^{D} , dominant black, E^{+} responsible for most combination of red or reddish brown and black, and *e*, recessive, red (Olson 2004). Based on the observation there is the color change from normal which is gene mutation expression. The normal color is red and darker black (brown black) and the modification in the three basic colors is brown, black and red. Here genes that control hair color in the cattle breed reflect on the variety of the cattle that is discovered in Banyuwangi.

The extension locus encodes the melanocytestimulating hormone receptor (MSHR; also known as MC1R1). This receptor controls the level of tyrosinase within melanocytes. Tyrosinase is the limiting enzyme involved in synthesis of melanin: high levels of tyrosinase result in the production of eumelanin (dark color, e.g. brown or black) while low levels result in the production of phaeomelanin (light color, e.g. red or yellow). When melanocyte-stimulating hormone binds to its receptor, the level of tyrosinase is increased, leading to production of eumelanin. The wild-type allele at the extension locus corresponds to a functional MSHR, and hence to dark pigmentation in the presence MSH. The wild-type allele (E^{+}) encodes the normal functional receptor for MSH. The E^{D} allele contains a mis-sense mutation, changing the 99th amino acid from leucine to proline. The *e* allele contains a single base deletion (a frame-shift mutation), which gives rise to a non-functional receptor, and hence to low levels of tyrosinase, resulting in production of phaeomelanin (red coat color) (Nicholas 2004).

Of the cattle body gen controlling the color of body furs identified by Olson (2004), the variety of cattle body color in Banyuwangi is controlled by gene on all the alleles except E^{D} . It can be understood because black is rare to be found in all observed population. The rest of black color is caused by the crossbreeding between the local and the Angus cattle at the beginning of 70's in which a program to increase the cattle quality by government through artificial insemination program was introduced.

Genetic variation that is discussed is a general characteristic in population among individuals. Appearance of variation is caused by some variables, e.g. migration, mutation, natural selection process and breeding (Drent 1995). Breeding has a purpose to enrich the genetic variation of population. The gene frequency from one generation to the next generation is defended. The condition without changing gene frequency is called genetic balance. It means the number of variety is constant. It seems in big population which has random breeding (Caughiey and Gunn 1996). Individual breed with family member (relationship population member) in a small population is called inbreeding. If it happens continuously, an increase in the number of homozygote individual in that population will take place (Klug and Cummings 2002). Some researches about inbreeding on fish showed the phenotype production decreasing, e.g. growth, immunity and abnormality (Tave 1993; Tamarin 2002).

CONCLUSION

There are 32 kinds of phenotypes in Banyuwangi based on the color of furs (head, body, and leg), the shape of the horn growth, shape of ear, the humps and the color of mouth. The pattern of breeding which causes the phenotype variation of cattle in Banyuwangi can be stated as follows: there are interactions between Java cattle, Bali cattle, Ongole cattle and Brahman cattle. This result is supported by an artificial insemination program with Limousine, Simmental, Aberden Angus and Santa Gertrudis cattle sperms. So, the research on genotype is suggested to explore the genetic variation and it will be useful in the conservation and the genetic tracing of population of cattle in Banyuwangi.

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