Phenotypic and genetic evaluation of birth weight for F1 crossbred progeny derived from local Indonesian cattle by non-native Bos taurus and Bos indicus sires

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Abstract

The aim of this study was to estimate phenotypic and genetic parameters for birth weight using two models of crossbreds. The data included the performance of 131 F1 crossbred between Brahman sires by Peranakan Ongole dams and 83 F1 crossbred between Limousin sires by Madura dams. DNA samples were taken for 7% of the progeny. The data were analyzed using ANOVA with SPSS version 15 for phenotypic evaluation. Genetic evaluation was performed included calculating the variance component and heritability estimates using paternal half sib correlations. The similarity index of the DNA was analyzed using restriction length polymorphisms (RFLPs) and MVSP software. The least square means of birth weight was 28.58 ± 3.50 kg (Brahman x Peranakan Ongole) and 22.50 ± 3.00 kg (Limousin x Madura). The effects of crossbreed, sire and sex on birth weight were significant (P < 0.01). The heritability for birth weight was 0.63 ± 0.45 and variance component of sire was 2.14. Superiority of F1 to dam at birth weight was 12.52% (Brahman x Peranakan Ongole) and 60.71% (Limousin x Madura). The similarity index of DNA between the F1 progeny with its dam was 97.86% (Brahman x Peranakan Ongole) and 86.71% (Limousin x Madura). It was concluded that the birth weight of F1 crossbred Brahman x Peranakan Ongole progeny was significantly higher than the F1 crossbred Limousin x Madura progeny. Heritability of birth weight was considered high. The superiority F1 to dam at birth weight and similarity index with Msp I enzyme restriction of the F1 crossbred Limousin x Madura progeny tended to be higher and lower, respectively, than for F1 crossbred Brahman x Peranakan Ongole progeny.

Keywords: genetic evaluation, birth weight, crossbreeding, cattle.

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Introduction

Crossbreeding of beef cattle has been utilized widely to achieve improvements in beef production. The choice of breeds in crossbreeding should be based on additive breed and heterosis effects (Peacock et al., 1978). In Indonesia, crossbreeding of local native Peranakan Ongole and Madura cattle with non-native breeds occurs in East Java.

The crossbreeding models implemented in East Java include a cross between Limousin sires with Madura dams in Sampang Madura and between Brahman sires with Peranakan Ongole dams in the Perusda UPA Pasuruan region. Results from crossbreeding with Limousin and Brahman sires have been presented previously (Peacock et al., 1978, Franke, 1980, Massey and Benyshek, 1981, Beauchemin et al., 2006). However, data on performance of offspring resulting from crossing Brahman with Peranakan Ongole cattle and Limousin with Madura cattle are limited.

These two models of crossbreeding should be followed by phenotypic and genetic evaluations to monitor success for important characteristics of the cattle, such as birth weight, weaning weight, and yearling weight (Alejandro et al., 2008; Dawson et al., 2008). The objectives of this work were to evaluate birth weight by estimating the genetic effects, including heterosis and superiority F1 to dam, heritability, the variance components, and to analyze the DNA with restriction length polymorphisms (RFLPs) for purebred Madura and Peranakan Ongole cattle and as crosses with Limousin and Brahman.

Materials and Methods

**Birth weight.** The birth weight data used in this study were taken from UPA Perushda Pasuruan and Region of Sampang Madura, East Java. The temperatures range from 19-34° C, and the climate is considered to be tropical at these locations. In Sampang Madura, Madura cows were bred artificially to Limousin bulls. In Pasuruan, Peranakan Ongole (PO) cows were bred artificially to Brahman bulls. The order in which a cow was detected in heat determined the breed and sire to which she was bred.

**RFLP.** The DNA was extracted from Fl Brahman crossbred progeny, Brahman bulls, PO dams, F1 Limousin crossbred progeny, Limousin bulls and Madura dams. The samples included seven head for each breed. The DNA was restriction digested with Msp I. Electrophoresis was performed using horizontal gels (2 % agarose) for 90 minutes at 50 volts.

**Data analyses.** In order to equalize the effect of the dam in rating the sires and in calculating the percent to which birth weight was inheritable, the birth weights of all calves from a given dam were averaged. The inheritance studies involved all the calves from dams which produced at least one calf. Individual records for calf weight at birthing were analyzed by least square method outlined by Akesson et al. (2008) with SPSS version 15.

The variance component $\sigma^2_s$ was estimated by equating the expected mean squares to the observed mean squares. The total variance was computed as the sum the two estimates with ANOVA (Massey and Benyshek, 1981, Becker, 1992). Paternal half-sib estimate of heritability was calculated according the following formulas:

$$h^2 = \frac{4 \sigma^2_s}{\sigma^2_c + \sigma^2_s}$$

The RFLP profiles were analysed MVSP to determine the similarity index of parent to F1 crossbreed samples. Only DNA fragments (bands) with clear digest patterns were consider.
Results and Discussion

Birth weights of F1 crossbred cattle

The average of birth weight of the F1 crossbred progeny between Brahman sires with Madura dams and Limousin sires with Peranakan Ongole (PO) dams was 25.168 ± 3.502 kg with a minimum of birth weight of 20 kg and a maximum birth weight of 41 kg (Table 1). The average of the birth weight was 11.623 % higher than the average birth weight of crossbred progeny between local cattle with Friesian (22.18 kg) in Bangladesh (Islam et al., 2004).

<table>
<thead>
<tr>
<th>F1 Crossbred progeny</th>
<th>BW (kg)</th>
<th>SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brahman x Peranakan Ongole</td>
<td>28.58b</td>
<td>3.50</td>
</tr>
<tr>
<td>Limousin x Madura</td>
<td>22.50a</td>
<td>3.00</td>
</tr>
</tbody>
</table>

The average birth weight of F1 crossbred progeny between Brahman with Peranakan Ongole (28.58 kg) was higher than the average birth weight of 25.4 kg purebred Peranakan Ongole cattle (Talib and Siregar, 1998 in Astuti, 2004), and the birth weight of purebred Brahman in Thailand (27.78 ± 3.52 kg) (Suwanmojo, 2008), but lower than the average birth weight of purebred Brahman in the United States (28.8 kg) (Franke, 1980).

The average birth weights of the F1 progeny from the Brahman bulls were significantly different in some instances (P < 0.05 for sire D versus sires B and A) but not in other instances (P> 0.05 for sires B and C). These results showed that the birth weight of the Brahman bull D was superior compared with sires A, B and C. The average birth weight of Brahman bull D was higher 9.48 % - 1.92 % compared with sires A, B and C. Difference of birth weight of F1 between Brahman bulls was due to the genomic variation of individuals in a breed that causes additive gene action to vary. The additive genetic variation is caused by multiple genes and multiple alleles which results in phenotypic variation within one population or the progeny of one individual parent (Lasley, 1987).

<table>
<thead>
<tr>
<th>F1 crossbred</th>
<th>Brahman sire</th>
<th>A</th>
<th>D</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>Brahman x PO</td>
<td></td>
<td>28.21a</td>
<td>30.32b</td>
<td>29.17ab</td>
</tr>
</tbody>
</table>

Superiority of F1 progeny to Dam

It is assumed that average birth weight of Peranakan Ongole (PO) cows is 25.4 kg (Astitu, 2003) and Madura cows is 14 kg based on previous results (Gunawan, 1993). Given this assumption, it was calculated that the superiority of the F1 crossbred progeny between Brahman bulls with PO cows to their dams was 11.13%, and the superiority of the F1 crossbred progeny between Limousin bulls with Madura cows to their dams was 60.71 %. Thus, the F1 crossbred progeny from Limousin and Madura cattle were more superior to their dams than the F1 crossbred progeny from Brahman and PO cattle.

Heritability and Variance Component of Birth Weight

Heritability was only estimated for the birth weight of F1 crossbred progeny from Brahman sires and PO dams because the data from the the F1 crossbred progeny from the Limousin sires and Madura dams did not fulfill the required data structure for the estimates. Heritability estimates were based on sire half-sib relationships and did not use any component from the dams.
Table 3. Heritability and Variance Component of Birth Weight

<table>
<thead>
<tr>
<th>Quantitative Character</th>
<th>h²</th>
<th>VG</th>
<th>VP</th>
<th>Variance Component of sires</th>
<th>Variance component between progeny within sires</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth Weight</td>
<td>0.630 ± 0.450</td>
<td>7,809</td>
<td>12,403</td>
<td>2,140</td>
<td>11,457</td>
</tr>
</tbody>
</table>

The heritability of birth weight for the F1 Brahman x PO progeny was 0.630 (Table 6). This means that the inheritance of birth weight of 63% was influenced by genetic variation, while 37% was influenced by environmental variation. The heritability of birth weight is high, which means that birth weight can be used as the basis of selection for sires or the F1 progeny.

According to Lasley (1978), selection is very effective on characters that have a high heritability value, because the success of selection is directly proportional to the value of heritability. The genetic and phenotypic variance (VG and VP) are also important components in genetic evaluation and livestock breeding. If the VG has a low value, then the opportunity to perform genetic evaluation and breed livestock is also difficult as VG is a component of heritability, and heritability is associated positively with the success of selection. Moreover, if the genetic variance in the population is high, this diversity increases the opportunity to improve the genetic quality through selection.

DNA Index similarity in F1 Crossbreed progeny

The DNA profile as a result of RFLP electrophoresis was analysed with MVSP. Only DNA fragments (bands) that had a clear pattern of digestion were included in the calculations (Liu and Tsunekawi (1991) and Parejo et al. (2002).

Table 4. Similarity index of F1 crossbreed

<table>
<thead>
<tr>
<th>Parent</th>
<th>Similarity index (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>F1 crossbred between Brahman with PO</td>
</tr>
<tr>
<td>Dam</td>
<td>97.86</td>
</tr>
<tr>
<td>Sire</td>
<td>79.00</td>
</tr>
</tbody>
</table>

The similarity index of DNA profiles of F1 crossbred Brahman x PO progeny compared with the PO dams was 97.86% and with the Brahman sires was 79% (Table 4). The similarity index of DNA profiles of F1 crossbred Limousin x Madura progeny compared with the Madura dams was 86.71% and with the Limousin sires was 75.43%. These results showed that the DNA profile of F1 crossbred progeny tended to be more similar to the local dams than the sires. In addition, the similarity index of F1 crossbred progeny from Brahman and PO cattle was higher with the parental breeds than the F1 crossbred progeny from Limousin with Madura cattle.

Conclusions

The birth weight of the F1 crossbred progeny from Brahman x Peranakan Ongole cattle was significantly higher than the F1 crossbred Limousin x Madura progeny. The heritability estimate of birth weight was high. The superiority of the F1 crossbred progeny from Limousin x Madura to the dam for birth weight tended to be higher than for the F1 crossbred progeny from Brahman x Peranakan Ongole cattle. The similarity index of F1 crossbreds with the dams was lower between the Limousin x Madura progeny than the Brahman x Peranakan Ongole progeny.
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References


