Selection for Bali Bull Based on Growth Traits Using Animal Model

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ABSTRACT

Bali cattle are one of the Indonesian germ plasma. The cattle have many advantages for development in the tropics. The purpose of the study was to selection for Bali cattle bulls based on animal models method. Data used comprised of 428 weaning weight, yearling weight and body weight gain derived from 28 males. Prediction of components of genetic and environment variance and co-variance, and heritability were obtained using VCE 4.2. Breeding value was estimated on the traits of production: weaning weight, yearling weight and body weight gain using PEST. The heritability of weaning weight, yearling weight and body weight gain was 0.09 ± 0.15 , 0.27 ± 0.13 , and 0.47 ± 0.15 , respectively. The AI bull coded number 4 is the best male with relative breeding value of 33.227 kg.

Keyword: Bali cattle, Animal model, Evaluation, Growth traits.

INTRODUCTION

Meat demand increased by 6-8% each year in Indonesia, especially in densely populated areas such as Java. Fulfillment of domestic meat is mostly supplied by local breed such as Bali, Ongole, Madura and some other breed. According to Indonesia livestock statistics (Anonymous 2015), population of Bali cattle occupies the highest number (26.92 percent) comparing to other population. It means that the contribution of Bali cattle in meeting the needs of the meat is very meaningful.

Growth performance of Bali breed has been a major concern, especially in the production traits (birth weight, weaning weight, yearling weight and body weight gain) and reproduction traits (service per conception, calving rate and calving interval). Some research on Bali breed showed that the service per conception of cow was 1.8 to 2.00 (Mastika, 2002), calving rate was 64-78% (Bamualim and Wirdahayati, 2002), sperm production was 2.6 x 10⁹ per day (McCool, 1992). Body weight gain of Bali breed was 0.7 kg/day (adult males) and 0.6 kg/day (adult females) when fed by good quality feeding, carcass percentage ranged from 51.5 to 59.8%, with the percentage of bone less than 1% and low-fat meat (Pane, 1991).

Those potentials encourage Indonesia government to conserve and develop genetic resources of Bali breed. On 1976 the center of Bali cattle breeding was established in Bali province aimed to improve the quality of Bali cattle and produce superior male as a source of frozen semen. Selection of Bali male is done through the performance test and progeny test.

Methods for evaluating of sire is widely available and they have been done primarily for evaluating of dairy sire which are scattered in several countries (Maltecca et al, 2004; Leclerc et al, 2005; Leclerc et al, 2006) and in one country state (Norman et al, 2005; Sun et al, 2009). For beef cattle, especially for Bali breed is very scare information available regarding the evaluation methods of sire. The purpose of this study was to evaluate the sire of Bali cattle in P3Bali using animal models.

MATERIALS AND METHODS

Data

428 data derived from 28 male were used as base data to evaluate herd of sire. The data consisted of weaning weight, yearling weight and body weight gain from weaning to yearling. Data were collected from 1994 to 2004. Calves were weaned at 186-220 days both male and female, then at 310 to 360 days the animals were weighed again as yearling weight. Body weight gain was obtained by subtracting yearling weight and weaning weight.

Management of animals

The project on the genetic improvement of growth performance of the Bali breed was started in 1976 by the Agriculture Ministry of Indonesia. In this project, bulls were selected at 1 year of age from village breeding centers (Tabanan and Karang Asem). Then, the bulls were assigned to herds in Pulukan to participate in performance test under the supervision of Bali Breeding Center. In these herds pedigree information and other information related to growth traits were collected and recorded in the database of Bali Breeding Center for the purpose of investigating the success of the Bali project. The mating period for the Bali breed was from July to December and mating was by artificial insemination (AI) and natural mating. Calving commenced from April to October of the following year. The calves were weighed and ear tagged within 12 hours of birth. The identities of the newborns and of their parents, date of birth, sex, and birth weight were recorded. The calves were outdoors together with their dams until weaning. The length of the suckling period was not the same for all calves. During the suckling period, calves were additionally fed with king grass and commercial concentrate. Most of the calves were weaned in May when they were 210±15 days of age. After weaning, the calves were separated from their dams and put in different herds. From 18 months of age, the animals were managed similarly for one year in order to evaluate their performance. All young cattle were fed the same grasses and put in the same paddock.

Data Analysis

The estimation of variance and covariance of genetics and environment, and heritability was by VCE 4.2 program package (Groeneveld, 1998). The fixed effect of weaning weight, yearling weight and body weight gain was rainfall, the age of measuring (weighing) and year of birth, while the random effect for all characters was animals.

In general statistical model for animal models is as follows: Y = Xb + Zu + ewhere: Y = vector of observations;

b = vector of fixed effects;

u = vector of random effects

X =known matrix that states fixed effect (b);

Z =known matrix that states random effect (u);

e = random vectors that can not be observed

Data were analyzed according to their respective estimates. Analysis of the data needed to estimate heritability and breeding value. Estimation of heritability for all traits

was done by using the formula heritabiltas = $\frac{\sigma_a^2}{\sigma_p^2}$ where σ_a^2 = additive genetic variance

and σ^2_P = phenotipvariance. Estimation of heritability was done using VCE 4.2 program (Groeneveld, 1998).

Breeding Value Estimation was done on the individuals themselves, sire and dam. The traits which estimated for BVE were weaning weight, yearling weight, and weight gain. Breeding value estimation was calculated by PEST program packages by

input values of genetic variance (v_g) and environmental variance (v_e) of the same traits. The values were obtained from VCE 4.2 program output.

RESULT AND DISCUSSION

Heritability estimated of weaning weight, yearling weight and body weight gain was shown in Table 1.

 Table 1. Heritability (Diagonal) and Genetic correlation (above Diagonal)

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Traits	Weaning	Yearling	Gain
	weight	weight	
Weaning weight	0.09±0.15	0.314	0.182
Yearling weight		0.27 ± 0.13	0.809
Gain			0.47 ± 0.15

High heritability indicated that there was highly correlation between phenotype and breeding value. Jan (2000) found heritability of weaning weight and yearling weight in his research using paternal half-sib method was 0.44±0.09 dan 0.23±0.02. Sukmasari et al (2002) at Pulukan station found different heritability of the same traits using VCE method was 0.10±0.05 and 0.38±0.02. For Angus breed heritability of weaning weight is very diverse, ranging from 0.20 to 0.66 (Kaps et al, 2000).

The difference in heritability is due to differences in the herd which having a heterogeneous environment, thereby there is a various heritability and gene frequencies (MacNeil et al, 2000), in addition to differences in method of analysis that lead to differences in accuracy (Kealey et al, 2006). The influence of the method of analysis will involve the genetic diversity that also analyzed, while the variety of environments experienced by an individual during his lifetime or until the individual is observed. The value of heritability depends on variance components that compose it, changes to variance components will affect the value of heritability because heritability is part of the total variation of a trait that is caused by a genetic influence (Warwick et al., 1990). Davis and Simmen (2006) stated that differences in heritability can be caused by the influence of sampling.

Heritability of weaning of this study was lower than expected even standard deviation was larger than the heritability. Animal models used could not find as expected heritability which was 0.30 to 0.55. Maternal effects were put into the model did not find good results. Some outliers discarded were also not helpful in increasing the value of heritability. The low heritability was caused by abnormal of distribution of data. The model used (animal models) requires the existence of a normal distribution of the data prior to analysis. Kealey et al (2006) stated that the low estimates of genetic variance indicate environmental effect. Other causes of low heritability were lack number of data used to estimate heritability of weaning weight (428 data). These results were consistent with Reverter et al (2000) that all genetic parameter estimates have high standard errors caused by the limited data.

Reverter (1998) compared the methods of genetic parameter estimation using simulated data with different levels of heritability and concluded that higher heritability would be followed by higher breeding value. The accuracy of breeding value for a trait with low heritability could be improved by multiple-trait model includes correlated traits that have high heritability (Sun et al, 2010).

Breeding value of sire evaluated based on animal model is presented in Table 2, which can be summarized as in Figure 1, Figure 2, Figure 3 and Figure 4.

Table 2. Evaluation of Sire Based on Breeding Values (BV) of Weaning Weight (WW), Yearling Weight (YW) and Body Weight Gain (BWG) Based on Animal Model

Sire		of		BV of BWG	Cumulative	Ranking
code	WW				of BV	
1	8.5	64	9.874	2.672	21.11	4
2	-11.2	35	-2.934	-5.529	-19.698	26
3	-11.7	43	9.461	5.436	3.154	12
4	1.7	28	20.748	10.751	33.227	1
5	4.7	25	-13.566	-3.708	-12.549	24
6	-2.6	35	-1.312	3.568	-0.379	15
7	3.0	29	-2.878	-3.709	-3.558	19
8	4.0	73	2.184	-0.71	5.547	9
9	-4.6	18	-0.82	1.99	-3.448	18
10	-3.6	33	2.51	2.288	1.165	13
11	7.2	42	-3.599	0.346	3.989	11
72698	-7.6	06	-4.106	-1.191	-12.903	25
73091	-3.2	51	-7.826	2.908	-8.169	22
73491	1.8	25	8.439	-0.817	9.447	7
73688		-2	-15.844	-5.618	-23.462	27
73996	12.1	64	-0.383	-0.912	10.869	6
74591	5.0	85	-1.568	-2.903	0.614	14
75994	-8.	41	9.793	6.659	8.042	8
77789	4.6	49	8.905	8.476	22.03	3
79792	8.1	51	15.68	6.303	30.134	2
105293	7.5	17	9.583	1.928	19.028	5
110296	3.5	19	0.056	0.42	3.995	10
309293	-9.0	93	3.813	2.395	-2.885	17
329293	-1.2	44	-3.02	-0.807	-5.071	21
333494	2.2	91	-12.532	1.281	-8.96	23
401899	-4.0	09	1.896	-1.825	-3.938	20
417291	0.9	51	-1.857	-0.301	-1.207	16
417292	-9.8	82	-28.319	-25.483	-63.684	28

The order of the best sires based on breeding values of WW, YW and BWG turned out to put the number of natural sires were much more than the number of AI sires. Sires code of 1-11 were frozen semen from the BIB Singosari.

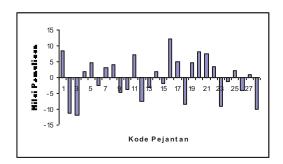


Figure 1. Breeding value of WW

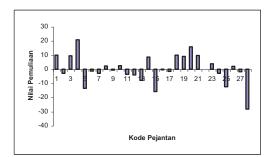
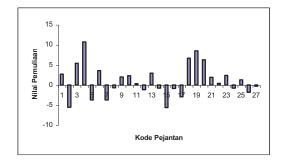


Figure 2. Breeding value of YW



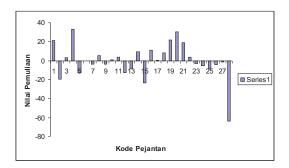


Figure 3. Breeding value of BWG

Figure 4. Breeding value of Cumulative

Figure 1 showed that from 28 tested bulls 53.57 percent had a positive breeding value and the rest had a negative breeding value. From the 28 tested bulls, 11 bulls were from BIB Singosari and only 54.54 per cent (6 bulls) that had a positive breeding value of WW.

For yearling weight, from 28 tested bulls 42.86 percent had a positive breeding value. There were 11 bulls from BIB Singosari with positive breeding value was only 18.18 percent (two bulls).

For BWG of tested bulls about 53.57 percent had a positive breeding value and from it 46.67 percent was AI bulls. The least number of AI bulls in the top ten indicated that the local bulls have been adapted well to the tropical environment so that they can express their genetic abilities. Although it is known that AI bulls were genetically superior because they have been tested previously but apparently local bulls were still better.

The order of the best cumulative breeding value was a bull code number 4 with a relative breeding value of 33.227, it meant that if the bull mated by random dam then the average weaning weight their offspring would demonstrate excellence around 16.6135 of the herd, due to the excellence bull would be transferred half of breeding value to the offspring (Hardjosubroto, 1994).

Animal models had been well tested to evaluate sires, especially for dairy cattle. Study of Sun et al (2009) who compared the method of sire models and of animal models concluded that animal models were much better in the genetic evaluation of fertility traits in a herd of Danish Holstein. Reliability of breeding value of animal model (0.27) was also better than sire models (0.21) (Sun et al, 2009). However currently sire models were used for genetic evaluation of fertility traits in many countries (Interbull, 2009).

Utilization of sire models was based on the advantages of this method which was much simpler in calculation and they had a good prediction under the condition there was no genetic relationship between the sires and dam, dam and dam, and mating occurs randomly (Schaeffer, 1983). One of the advantage of animal models was the model allows the use of cows records directly to predict breeding value while for sire model cows records were only used as progeny records and the breeding value was obtained from the sibling (Sun et al, 2009).

Sire evaluation using a lot of information from the progeny will improve accuracy. Powell et al (2000) indicated that additional information from female offspring who located in other countries improved the ability of sire to predict the next offspring.

A sire when used as a naturally bull has limitations because of age. In addition when ages as consideration all sires that fall within the top ten were old. Utilization of bull naturally in the top ten should be thought again preferably all the sires were utilized for the purpose of AI.

CONCLUSION

Metode *animal model* dapat digunakan sebagai salah satu cara untuk mengevaluasi pejantan sapi Bali berdasarkan nilai pemuliaan dari karakter bobot sapih, bobot setahun dan pertambahan bobot badan. Berdasarkan hasil evaluasi, pejantan IB masih merupakan pejantan terbaik walaupun dalam urutan 10 besar pejantan alami juga masuk dalam kategori baik.

Animal models can be used as one method to evaluate the sire of Bali cattle based on breeding value of weaning weight, yearling weight and body weight gain. Based on the evaluation, AI bulls was the best bull although from the top ten naturally bulls also fit in a goo category.

REFERENCES

- Anonimous, 2009. BPS Peternakan. Direktorat Jenderal Bina Produksi Peternakan. Jakarta.
- Bamualim, A. dan R.B. Wirdahayati, 2002. Nutrition and management strategies to improve Bali cattle productivity in Nusa Tenggara. Working Papers: Bali Cattle Workshop. Bali, 4-7 February 2002.
- Davis, M.E and R.C.M. Simmen, 2006. Genetic parameter estimates for serum insulin-like growth factor I concentrations, and body weight and weight gains in Angus beef cattle divergently selected for serum insulin-like growth factor I concentration. *J. Anim. Sci.* 84: 2299-2308.
- Groeneveld, E. 1998. VCE 4.2 Programme, User's Guide and Manual Version 1.1. Institut furr Tierzuch und Tierverhalten, FAL, Mariensee.
- Hardjosubroto, W., 1994. Aplikasi pemuliabiakan ternak di lapangan. PT. Gramedia Widiasarana Indonesia, Jakarta.
- Interbull, 2009. National GES Information. http://www-interbull.slu.se/national ges info2/framesida-ges.htm. Akses 22 Januari 2009.
- Jan, R. 2000. Penampilan sapi Bali di wilayah proyek pembibitan dan pengembangan sapi Bali di daerah tingkat I Bali. Tesis PPS-UGM, Yogyakarta.
- Kaps, M., W.O. Herring and W.R. Lamberson, 2000. Genetic and environmental parameter for traits derived from the Brody growth curve and their relationships with weaning weight in Angus cattle. *J. Anim. Sci.* 78: 1436-1442.
- Kealey, C.G., M.D. MacNeil, M.W. Tess, T.W. Geary and R.A. Bellows, 2006. Genetic parameter estimates for scrotal circumference and semen characteristics of Line 1 Hereford bulls. *J. Anim. Sci.* 84: 283-290.
- Leclerc, H., W.F. Fikse, and V. Ducrocq, 2005. Principal components and factorial approaches for estimating genetic correlations in international sire evaluation. *J. Dairy Sci.* 88: 3306-3315.
- Leclerc, H., S. Minery, I. Delaunay, T. Druet, W.F. Fikse and V. Ducrocq, 2006. Estimation of genetic correlations among countries in international dairy sire evaluations with structural models. *J. Dairy Sci.* 89: 1792-1803.
- MacNeil M.D., J.J. Urick and G. Decoudu, 2000. Characteristics of Line 1 Hereford females resulting from selection by independent culling levels for below-average

- birth weight and high yearling weight or by mass selection fpr high yearling weight. *J. Anim. Sci.* 78: 2292-2298.
- Maltecca, C., A. Bagnato and K.A. Weigel, 2004. Comparison of international dairy sire evaluations from meta-analysis of national estimated breeding values and direct analysis of individual animal performance records. *J. Dairy Sci.* 87: 2599-2605.
- Mastika, I.M., 2002. Feeding strategies to improve the production performance and meat quality of Bali cattle (*Bos sondaicus*). Working Papers: Bali Cattle Workshop. Bali, 4-7 February 2002.
- McCool, C., 1992. Buffalo and Bali cattle-exploiting their reproductive behaviour and physiology. *Tropic. Anim. Health and Prod.* 24, 165-172.
- Norman, H.D, P.M. VanRaden, R.L. Powell, J.R. Wright and W.R. VerBoort, 2005. Effectiveness of national and regional sire evaluations in predicting future-daughter milk yield. *J. Dairy Sci.* 88: 812-826.
- Pane, I., 1991. Produktivitas dan breeding sapi Bali. Proceeding Seminar Nasional Sapi Bali. Ujung Pandang, 2-3 September 1991. Ujung Pandang: Fakultas Peternakan Universitas Hasanuddin, p. 50-69.
- Powell, R.L., H.D. Norman and G. Banos, 2000. Improving prediction of national evaluations by use of data from other countries. *J. Dairy Sci.* 83: 368.
- Reverter, A., D.J. Johnston, H.U. Graser, M.L. Wolcott, and W.H. Upton, 2000. Genetic analyses of live-animal ultrasound and abattoir carcass traits in Australian Angus and Hereford cattle. *J. Anim. Sci.* 78: 1786-1795.
- Reverter, A. 1998. Empirical evidence of the optimality of method R estimates. In Book of Abstract, Proc. 6th World Congr. Genet. Appl. Livest. Prod., Armidale, Australia. Commun. No. 25533.
- Schaeffer, L.R., 1983. Effectiveness of model for cow evaluation intraherd. *J. Dairy Sci.* 66: 874-880.
- Sukmasari, A.H., R.R. Noor, H. Martojo, dan C. Talib, 2002. Pendugaan nilai pemuliaan dan kecenderungan genetika bobot badan sapi Bali di Proyek Pembibitan dan Pengembangan Sapi Bali. *Hayati*, Vol. 9, No.4. Desember, 2002. hal. 109-113.
- Sun, C., P. Madsen, U.S. Nielsen, Y. Zhang, M.S. Lund, and G. Su, 2009. Comparison between a sire model and an animal model for genetic evaluation of fertility traits in Danish Holstein population. *J. Dairy Sci.* 92: 4063-4071.
- Sun, C., P. Madsen, M.S. Lund, Y. Zhang, U.S. Nielsen, and G. Su, 2010. Improvement in genetic evaluation of female fertility in dairy cattle using multiple-trait models including milk production traits. *J. Anim. Sci.* 88: 871-878.
- Warwick, E.J., J.M. Astuti dan W. Hardjosubroto, 1990. Pemuliaan Ternak. Gadjah Mada University Press, Yogyakarta.