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Selection Response, Breeding Value and Heritability of Live Weight in Ongole-Crossbred Cows

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Abstract
Breeding value and heritability, the crucial factors of economical trait inheritance, had not been studied in Ongole-crossbred cows. The objectives of this research were to identify genotypic value, breeding value and dominance deviation of live weight and to define its heritability in Ongole-crossbred cows. Total of 37 blood samples and 2 blood samples were collected from parental cows and from parental Ongole breed bulls, respectively. All blood samples were screened for the presence of growth hormone (*GH*) locus using PCR-RFLP method involving restricted enzyme *Msp1* on agarose-gel (1.2%). Data were analyzed using statistical program in Excel XP. Results showed that population mean of animal live weight were 445.41±45.95 kg. The highest selection response (Δμ) from parent generation to the progeny generation was using allele frequency ($Msp1^{+}$) of 0.50 with increasing live weight per generation of 6.14 kg. The homozygous genotype of $GH\text{-}Msp1^{+/+}$ was highly dominated by additive gene action (higher breeding value) for live weight rather than dominance gene action. However, the heterozygous genotype of $GH\text{-}Msp1^{+/-}$ was highly dominated by dominance gene action (higher dominance deviation) rather than additive gene action. The heritability of cow live weight in this study was 0.24, which were categorized as moderate heritability.

1. Introduction

The difference in the phenotypes of animals in the single locus-example is a function of the genotypic value. Parents do not pass their genotype on to their progeny but rather pass on only a random sample of one gene to each locus of the progeny. The critical question is which parental genotype will produce progeny with the highest average? The answer to the question will define an animal's breeding value.

The term breeding value is self-descriptive, referring to the value of an animal in a breeding program. Breeding value is a measure of the animal's expected progeny performance relative to the population mean. For the single locus example, the breeding value for each genotype is calculated as twice the difference of the expected progeny mean from the population mean. The reason for doubling the progeny deviation is that the progeny contain only a sample one-half of the parent's genes. The progeny deviation itself represents the transmitting ability of the parent, which is one-half the breeding value (Legates and Warwick, 1990). The breeding values are dependent on gene frequencies and thus may vary from population to population (Van Vleck et al., 1987).

The goal of animal breeders is rapid genetic improvement, for which accurate

prediction of breeding value is the most crucial factor. The breeder can rank the animals and cull those with the poorest evaluations while selecting those with the best evaluation as replacements. Accurate evaluation requires proper application of heritability and relationships to weight records of the animal and its relatives (Van Vleck et al., 1987).

In animal industry, growth traits of animals are always of primary concern during breeding for its determinant economical value. With the development of molecular biology and biotechnology, scientists are able to achieve more accurate and efficient selection goal by marker-assisted selection (MAS). In general, validating the genetic markers of growth traits is the initial and crucial step to establish a MAS system (Allan et al., 2007).

Growth hormone (GH) is an anabolic hormone synthesized and secreted by the somatotroph cells of the anterior lobe of the pituitary in a circadian and pulsatile manner, the pattern of which plays an important role in pubertal, prenatal and postnatal longitudinal growth and development, tissue growth, lactation, reproduction, as well as protein, lipid and carbohydrate metabolism (Ayuk and Sheppard, 2006). Effects of GH on growth are observed in several tissues, including bone, muscle and adipose tissue, so that GH gene, with its functional and positional potential, has been widely used for marker in several livestock species, including the cattle such as *Bos taurus* and *Bos indicus* (Beauchemin et al., 2006). It has been reported that the restriction fragment length polymorphisms (RFLP) of GH were associated with body weight in Grati dairy cows (Maylinda, 2011).

The studies of GH gene *MspI* locus have been reported in Ongole crossbred cattle (Sutarno et al., 2005), Brahman cattle (Beauchemin et al., 2006), Indian Zebu cattle (Shodi et al., 2007) and West coastal Sumatera cattle (Jakaria et al., 2007). Their studies indicated that MspI +/+ and MspI +/- genotypes can be used as the candidate genes in cattle selection for breeding program. The breeding values depend on genotypic frequencies. The breeding value represents the sum of the value of each allele in the genotype of the progeny from a parent passing on one or the other of its gene to each progeny. The difference between the genotypic value and the breeding value can be represented as the dominance deviation (Van Vleck et al., 1987). The dominance deviation is defined as the value of the gene combination in the genotype. The genotypic value is defined as the deviation of the phenotype from the average of the two homozygous phenotypes (Jain and Prabhakaran, 1992).

The difference between breeding values is additive gene and representing the term of heritability for certain animal economical trait such as animal live weight. Heritability (h^2) is defined as the ratio of the additive genetic variance to the phenotypic variance. Thus, h^2 is the proportion of the total variance that is due to differences among the breeding values of individuals in the population (Van Vleck et al.,1987). However, the breeding value of an individual local cow, referred to its additive genetic merit of live weight, has not been much studied. The objectives of this research were to identify the genotypic value, breeding value and dominance deviation of live weight from genotypic frequency of growth hormone (GH) *MspI* enzyme-restriction, and to define the heritability of live weight in Ongole-crossbred cows population in North Sulawesi province of Indonesia.

2. Material and Methods

2.1. Animals and Sample Collection

This study was carried out in the Sulawesi Island Northern of Indonesia using 37 cows (age ranging 4 to 5 years old) of Ongole crossbred cattle at Tumaratas Village as the artificial insemination (AI) service center of Minahasa regency, North Sulawesi province of Indonesia. All parental cows (G0) were reared under private areas belong to farmers with unknown ancestors. Progenies (G1) were born from those G0 mated by artificial insemination using germ plasmas (semen) of the two Ongole bulls called "Kirsta" and "Tunggul" from "the artificial insemination bull germ plasma center" in Singosari, East Java province, Indonesia.

Prior to blood collection, body weights of animals (G0 and G1) were determined by using a digital weighing scale when animals were standing as described in (Ozkaya and Bozkurt, 2008). The total of 37 G0 consisted of 20 superior body weight animals (cow weights heavier than at least one fifth standard deviation above the mean) and 17 inferior body weight animals (cow weights lighter than one and half standard deviation below the mean) among cow (G0) population (n = 363 heads, with body weight average of 440.20 ± 58.03 kg) were included in this study as described in (Paputungan et al., 2000).

2.2. Analysis of the Genotypic Value

DNA extraction and genotyping for GH and allele identification were done using the protocols in DNA Laboratory as described by (Sulandari and Zein, 2003; Paputungan et al., 2012). The average of two homozygous phenotypes (P_{11} and P_{22}), denoted by m, was calculated using formula (Van Vleck et al., 1987) as follows:

$$m = ½ (P_{11} + P_{22}) \quad (1)$$

The genotypic value, breeding value and dominance deviation for each genotype of the cows in this study were calculated with the formula according to Van Vleck et al., (1987) as follows:

$$\text{Genotypic value of the } P_{11} \text{ (a)} = P_{11} - m \quad (2)$$

$$\text{Genotypic value of the } P_{12} \text{ (d)} = P_{12} - m \quad (3)$$

$$\text{Genotypic value of the } P_{22} \text{ (– a)} = P_{22} - m \quad (4)$$

Because m was defined as the phenotypic mean for both homozygous genotypes, the genotypic values of each animal genotype were found as follows: *GH-Msp1*$^{+/+}$ (a) was 0.30 kg (using formula 2), *GH-Msp1*$^{+/-}$ (d) was 93.04 kg (using

formula 3), and *GH-Msp1*$^{-/-}$ (– a) was – 0.30 kg (using formula 4). These genotypic values were valuable in contribution for all phenotypic and genotypic parameters including population.

2.3. Analysis of the Population Mean

For a population in Hardy-Weinberg equilibrium, the phenotypic population mean (μ) was defined (Van Vleck et al., 1987) as follows:

$$\mu = p^2P_{11} + 2pqP_{12} + q^2P_{22}$$

An alternative computing formula for obtaining the mean is based on substituting *m* + genotypic value for each phenotype. For a population in equilibrium, the mean is computed using formula (Van Vleck et al., 1987) as follows:

$$\mu = p^2(m+a) + 2pq(m+d) + q^2(m - a)$$
$$= m(p^2 + 2pq + q^2) + a(p^2 – q^2) + 2\ pqd$$

Because $p^2 + 2pq + q^2 = 1$, and $(p^2 – q^2) = (p + q)(p – q) = (p – q)$, the mean is computed as follows:

$$\mu = m + [a(p – q) + 2\ pqd] \quad (5)$$

2.4. Analysis of the Selection Response

Because *m* is a constant, the mean of the progeny population (μ_1), is also computed using the formula as follows:

$$\mu_1 = m + [a(p_1 – q_1) + 2\ p_1q_1d] \quad (6)$$

Response to selection ($\Delta\mu$) is the change in the population mean from the parent to the progeny generation, and computed as follows:

$$\Delta\mu = \mu_1 – \mu \quad (7)$$

Because *m* is a constant, the change in the mean was a result of increasing the average genotypic value by increasing the frequency of allele *p*.

2.5. Analysis of the Breeding Value

The expected mean of the progeny of the homozygous male (μ_{11}) is the sum of the products of genotypic frequencies and corresponding phenotypic values, computed (Van Vleck et al., 1987) as follows:

$$\mu_{11} = P_{11} + P_{12} + P_{22}$$
$$= p(m + a) + q(m + d) + 0(m – a)$$
$$= m + pa + qd$$

The breeding value of the homozygous male (BV_{11}) is twice the deviation of his progeny mean from the population mean and computed using formula (Van Vleck et al., 1987) as follows:

$$BV_{11} = 2\ (\mu_{11} – \mu)$$
$$= 2[m + pa + qd – m – a(p – q) – 2pqd]$$
$$= 2(qd + qa – 2pqd)$$
$$= 2[qa + qd(1 – 2p)]$$
$$= 2q\ [a + d(q – p)] \quad (8)$$

Likewise, the breeding values of the heterozygous male (BV_{12}) and homozygous male (BV_{22}) are as follows:

$$BV_{12} = 2\ (\mu_{12} – \mu)$$
$$= (q – p)\ [a + d(q – p)] \quad (9)$$
$$BV_{22} = 2\ (\mu_{22} – \mu)$$
$$= – 2p\ [a + d(q – p)] \quad (10)$$

The Greek alpha (α) is used to represent specifically the term appearing in the breeding value of each genotype representing the term of [a + d(q – p)] referring to Van Vleck et al. (1987). Thus,

$$\alpha = [a + d(q – p)] \quad (11)$$

2.6. Analysis of the Dominance Deviation

The difference between the genotypic value (V_{ij}) and the breeding value (BV_{ij}) for each genotype can be represented by the dominance deviation using formula (Van Vleck et al., 1987) as follows:

$$V_{11} – VB_{11} = a – 2q\ \alpha$$
$$= a – 2q[a + d(q – p)]$$
$$= a – 2q[a + qd – pd]$$
$$= a – 2qa – 2q^2d + 2pqd$$
$$= a – (q + 1 – p)a – 2q^2d + 2pqd$$
$$= a – qa – a + pa – 2q^2d + 2pqd$$
$$= a(p – q) – 2q^2d + 2pqd$$
$$= a(p – q) + 2pqd – 2q^2d \quad (12)$$

$$V_{12} – VB_{12} = d – (q – p)\ \alpha$$
$$= d – (q – p)[a + d(q – p)]$$
$$= d – qa + pa + d[(q – p)(-q + p)]$$
$$= d + a(p – q) + d[-q^2 + 2pq – p^2]$$
$$= d + a(p – q) – q^2d + 2pqd – p^2d]$$
$$= d + a(p – q) + 2pqd – q^2d – p^2d]$$
$$= d + a(p – q) + 2pqd – d(p^2 + q^2)$$
$$= d + a(p – q) + 2pqd – d[p(1-q) + q(1 – p)]$$
$$= d + a(p – q) + 2pqd – d[p – pq + q – pq]$$

$$= d + a(p - q) + 2pqd - dp + pqd - dq + pqd$$

$$= d + a(p - q) + 2pqd + 2pqd - dp - dq$$

$$= d + a(p - q) + 2pqd + 2pqd - d(p + q)$$

$$= d + a(p - q) + 2pqd + 2pqd - dp - d(1 - p)$$

$$= d + a(p - q) + 2pqd + 2pqd - dp - d + dp$$

$$= a(p - q) + 2pqd + 2pqd \quad (13)$$

$$V_{22} - VB_{22} = - a - (- 2p\,\alpha)$$

$$= - a - (- 2p[a + d(q - p)]$$

$$= - a - (- 2pa - 2pqd + 2p^2d)$$

$$= - a + 2pa + 2pqd - 2p^2d$$

$$= - a + (p + 1 - q)a + 2pqd - 2p^2d$$

$$= - a + pa + a - qa + 2pqd - 2p^2d$$

$$= a(p - q) + 2pqd - 2p^2d \quad (14)$$

The calculation formula of genotypic value, breeding value and dominance deviation were summarized in Table 4. The phenotype of an animal (P_{ij}) may now be written as

$$P_{ij} = m + [a(p - q) + 2\,pqd] + BV_{ij} + D_{ij}$$

Because $m + [a(p - q) + 2\,pqd]$ is μ, the phenotype is represented as

$$P_{ij} = \mu + BV_{ij} + D_{ij} \quad (15)$$

Then,

$$P_{11} = \mu + BV_{11} + D_{11}$$

$$P_{12} = \mu + BV_{12} + D_{12}$$

$$P_{22} = \mu + BV_{22} + D_{22}$$

2.7. Analysis of the Heritability

Heritability is an extremely important population parameter that is used both for the estimation of breeding values for quantitative characteristics and for predicting the response expected from various selection schemes. The phenotypic variance (σ_P^2) is calculated using formula (Van Vleck et al., 1987) as follows:

$$\sigma_P^2 = 2pq\alpha^2 + (2pqd)^2 \quad (16)$$

$$\text{Standard Error} = \sqrt{\sigma_p^2} \quad (17)$$

The additive genetic variance (σ_A^2) for a single locus, is calculated using formula (Van Vleck et al., 1987) as follows:

$$\sigma_A^2 = 2pq\alpha^2 \quad (18)$$

Heritability in the narrow sense (h^2) is defined as the ratio of the additive genetic variance to the phenotypic variance (Van Vleck et al., 1987) as follows:

$$h^2 = {}^{\sigma_A^2}\!/_{\sigma_P^2} \quad (19)$$

3. Result and Discussion

3.1. Genotypic Value of Animal Live Weight

The growth hormone (GH) genotypes using restricted enzyme of *Msp1* for 37 cows were applied in this study. The PCR-RFLP data were used in establishing the observed homozygous *Msp1+/+* genotype, heterozygous *Msp1+/-* genotype and homozygous *Msp1-/-* genotype (Table 5). The 37 genotyped parental cows showed that 18 cows were detected to have homozygous genotype of the *Msp1-/-* in GH locus, 14 cows were detected to have heterozygous genotype of the *Msp1+/-* in GH locus, and 5 cows were detected to have homozygous genotype of the *Msp1+/+* in GH locus.

The number of cows and the average of the phenotypic live weight of cow population for this study were presented in Table 3. Live weight was affected by the genotype at the locus of *GH-Msp1*. The animal population was considered at the equilibrium with existing of gene frequency and phenotypic measurements as shown in Table 6.

The *GH-Msp1*$^+$ represented allele affecting animal live weight. Cow genotype represented each animal phenotype performance measured in the kg unit of cow body weight. Genotype value was defined as deviation of phenotype from the mean of both homozygous phenotypes of P_{11} and P_{22} (shown at formula 1). Mean of both homozygous genotypes of the cows (m) using formula (1) was 405.03 kg.

3.2. Population Mean and Selection Response of Animal Live Weight

Using 37 samples of the cows in this study, the allele frequency *GH-Msp1*$^+$ (p) were ${}^{24}\!/_{74}$ = 0.32. Because p = 0.32, the allele frequency of *GH-Msp1*$^-$ (q) = 0.68. Therefore, the population mean of the cows (μ), using formula (5), were 445.41 kg. Those values indicated that live weight mean of the cow population in this study would be about 445.41 kg.

Furthermore, based on 37 samples of the progeny genetic analysis, the allele frequency *GH-Msp1*$^+$ (p_1) had changed into $[{}^{28}\!/_{74}]$ = 0.38, so the allele frequency of *GH-Msp1*$^-$ (q_1) = 0.62. Consequently, the population mean of the generation 1 (μ_1), using formula (6), were 448,69 kg. Using formula (7), the selection response (Δμ) from parent generation (G_0) to the progeny generation (G_1) were 3.38 kg.

If the samples of progeny (G_1) were selected only 20 calves from the superior live weight cows to be used for replacement, then the allele frequency of *GH-Msp1*$^+$ (p_1) changed into ${}^{20}\!/_{40} = 0.50$. Consequently, the population mean of the generation 1 (μ_1), using formula (6), were 451.55 kg. Using formula (7), the selection response (Δμ) from parent generation (G_0) to the progeny generation (G_1) using allele frequency (p_1) of 0.50 were 6.14 kg.

Based on the live weight of cows in this study, the selection response (Δμ) by mating of bull called Krista with

the genotype analysis using restricted enzyme of *Msp1* as genotype *Kr-Msp*$^{+/+}$ and bull called Tunggul with the genotype analysis using restricted enzyme of *Msp1* as genotype *Tu-Msp*$^{-/-}$ could be applied by four choices of mating system for the genotypes of cows as summarized in Table 4. In order to obtain higher selection response (Δμ) of 6.14 kg per generation, the animal mating system would be applied using the second choice involving all genotypes of cows with superior live weight mated by bulls of Krista (*Kr-Msp*$^{+/+}$) and Tunggul (*Tu-Msp*$^{-/-}$) to spread gene frequencies of *GH-Msp1*$^{+}$ (p = 0.50) and *GH-Msp*$^{-}$ (q = 0.50).

If all animals with genotypes of *GH-Msp1*$^{-/-}$ were culled in the population, then the allele frequency of *GH-Msp1*$^{+}$ (p_1) existing in the population would be $p_1 = 1/(1+q) = 2/3$. In this strategy, the ratio of animal genotypes existing in the population consisted of only 1(*GH-Msp1*$^{+/+}$) : 2(*GH-Msp1*$^{+/-}$); while 1(*GH-Msp1*$^{-/-}$) was culled and did not breed in population. Random mating of the existing animals produce progeny as presented in Table 1.

Table 1. *Genotypes of the progeny produced by random mating of the positive homozygous and heterozygous genotypes of parents*

Parental Genotypes	*Bull* (*GH-Msp1*$^{+/+}$)	*Bull* (*GH-Msp1*$^{+/-}$)
Cow (*GH-Msp1*$^{+/+}$)	*GH-Msp1*$^{+/+}$	*GH-Msp1*$^{+/+}$ and *GH-Msp1*$^{+/-}$
Cow (*GH-Msp1*$^{+/-}$)	*GH-Msp1*$^{+/+}$ and *GH-Msp1*$^{+/-}$	*GH-Msp1*$^{+/+}$; *2 GH-Msp1*$^{+/-}$ and *GH-Msp1*$^{-/-}$

Therefore, the survival genes existing were 4 (*GH-Msp1*$^{+}$) and 2(*GH-Msp1*$^{-}$), so allele proportion of *GH-Msp1*$^{+}$ (p_1) = 4/6 = 2/3, and allele proportion of *GH-Msp1*$^{-}$ (q_1) = 2/6 = 1/3. Consequently, the population mean of the generation 1 (μ_1), using formula (6), were 446.48 kg. Using formula (7), the selection response (Δμ) from parent generation (G_0) to the progeny generation (G_1) was 1.07 kg.

On the contrary; if all animals with genotypes of *GH-Msp1*$^{+/+}$ were culled in the population, then the allele frequency of *GH-Msp1*$^{+}$ (p_1) existing in the population would be $p_1 = 1/(1+q) = 2/3$. In this strategy, ratio of animal genotypes existing in the population consisted of only 1(*GH-Msp1*$^{-/-}$) : 2(*GH-Msp1*$^{+/-}$); while 1(*GH-Msp1*$^{+/+}$) was culled and did not breed in population. Random mating of the existing animals produce progeny as presented in Table 2.

Table 2. *Genotypes of the progeny produced by random mating of the negative homozygous and heterozygous genotypes of parents*

Parental Genotypes	***Bull* (*GH-Msp1*$^{-/-}$)**	***Bull* (*GH-Msp1*$^{+/-}$)**
Cow (*GH-Msp1*$^{-/-}$)	*GH-Msp1*$^{-/-}$	*GH-Msp1*$^{-/-}$ and *GH-Msp1*$^{+/-}$
Cow (*GH-Msp1*$^{+/-}$)	*GH-Msp1*$^{-/-}$ and *GH-Msp1*$^{+/-}$	*GH-Msp1*$^{+/+}$; *2 GH-Msp1*$^{+/-}$ and *GH-Msp1*$^{-/-}$

Therefore, the survival genes existing were 4 (*GH-Msp1*$^{-}$) and 2(*GH-Msp1*$^{+}$), so allele proportion of *GH-Msp1*$^{-}$ (p_1) = 4/6 = 2/3, and allele proportion of *GH-Msp1*$^{+}$ (q_1) = 2/6 = 1/3. Consequently, the population mean of the generation 1 (μ_1), using formula (6), were 446.28 kg. Using formula (7), the selection response (Δμ) from parent generation (G_0) to the progeny generation (G_1) was 0.87 kg.

3.3. Breeding Value and Dominance Deviation of Animal Live Weight

The term of *[a + d(q – p)]*, in the calculation of breeding value at each animal genotype denoted by α (alpha), was used as the average effect of gene substitution. Breeding value was a function of gene frequency and genotype values. Gene frequency could differ from one generation to the next generation; likewise, the breeding value was depended on the gene frequency.

Live weight of cows (G_0) in this study, the allele frequency of *GH-Mspl*$^{+}$ ($p = {}^{24}/_{74}$) was 0,32. Thus, the genotype frequency of the animals in the population would be 0.10 for genotype *GH-Msp1*$^{+/+}$, 0.44 for genotype of *GH-Msp1*$^{+/-}$, and 0.46 for genotype of *GH-Msp1*$^{-/-}$. Using formula (8), (9), and (10), the breeding value of homozygous genotype of *GH-Msp1*$^{+/+}$ was 45.96 kg, that of heterozygous genotype of *GH-Msp1*$^{+/-}$ was 12.17 kg, and that of homozygous genotype of *GH-Msp1*$^{-/-}$ was –21.63 kg. Using formula (11), the average effect of gene subtitution in term of α (alpha) was 33.79 kg.

Furthermore, using formula (12), (13), and (14), the dominance deviation of homozygous genotype of *GH-Msp1*$^{+/+}$ was – 86.04 kg, that of heterozygous genotype of *GH-Msp1*$^{+/-}$ was 40.49 kg, and that of homozygous genotype of *GH-Msp1*$^{-/-}$ was – 19.05 kg. The breeding values and dominance deviations were considered at the equilibrium with existing of genotype frequency and phenotypic measurements as summarized in Table 8.

Using formula (15), $P_{ij} = \mu + BV_{ij} + D_{ij}$, the phenotypes are represented as follows:

$$P_{11} = \mu + BV_{11} + D_{11}$$
$$= 445.41 \text{ kg} + 45.96 \text{ kg} + (-86.04 \text{ kg})$$
$$= 405.33 \text{ kg}$$
$$P_{12} = \mu + BV_{12} + D_{12}$$
$$= 445.41 \text{ kg} + 12.17 \text{ kg} + 40.49 \text{ kg}$$
$$= 498.07 \text{ kg}$$
$$P_{22} = \mu + BV_{22} + D_{22}$$
$$= 445.41 + (-21.63 \text{ kg}) + (-19.05 \text{ kg})$$
$$= 404.73 \text{ kg}$$

The products of calculation using those phenotypic formulas were presented in Table 3.

Table 3. *Average live weight as the products of population average, breeding value and dominance deviation of each genotype*

Genotype Frequency	Average of Phenotype (Live Weight, kg)
p^2	P_{11} = 405,33
2pq	P_{12} = 498,07
q^2	P_{22} = 404,73

The phenotype values of P_{11}, P_{12}, and P_{22} were the averages of phenotype values of live weight as shown in the Table 6. The genotype frequencies of the progeny defined the selection response ($\Delta\mu$) using four animal mating choices involving Ongole-crossbred cows and bulls of Krista (Kr-Msp$^{+/+}$) and Tunggul (Tu-Msp$^{-/-}$) as presented in Table 7.

These values indicated that the homozygous genotype of *GH-Msp1*$^{+/+}$ was more dominated by additive gene action for live weight rather than dominance gene action. However, the heterozygous genotype of *GH-Msp1*$^{+/-}$ was more dominated by the dominance gene action rather than the additive gene action. Breeding value of an individual is referred to its additive genetic merit and the difference between breeding values is additive and representing in term of heritability for certain animal economical trait such as animal live weight (Van Vleck et al., 1987). The breeding values of cows in this study varied from –21,63 to 45,96 kg, while those in temperate beef cows varied from –15,0 to 22,0 kg (Legates and Warwick, 1990). These values indicated that local Ongole-crossbred cows were more various in the breeding values compared with those of the temperate cows.

3.4. Variance and Heritability of Animal Live Weight

The population mean is the phenotype average. The real observation varied in term of mean. Variation of observation for mean could be calculated in term of variance. In this study, the variance is denoted (σ^2_p) to represent phenotype variance. Using formula (16), the value of phenotype variance (σ^2_p) in this study were 2109.34. Thus, using formula (17), the standard error value of phenotype (σ_p) in this study were 45.93 kg. The eatimation average population of animal live weight in this study were 445.41 ± 45.95 kg.

Using formula (18), the additive genetic variance (σ^2_A) in a single locus was 496.90. Therefore, the heritability of cow live weight as calculated using formula (19) in this study was 0.24. This heritability value of cow live weight would be categorized as moderate value (Van Vleck et al., 1987). For breeding program, the heritability (h^2) in narrow sense using the additive genetic variance (σ^2_A) was applicably more accurate in the improvement prediction for animal economically traits, including animal live weight, due to the representation and expression of the quantitative gene action involved. The accuracy of this heritability value of 0.24 based on individual records was about 55 percents (Legates and Warwick, 1990).

4. Conclusion

1 The eatimation average population of animal live weight in this study were 445.41 ± 45.95 kg. The highest selection response ($\Delta\mu$) from parent generation (G_0) to the progeny generation (G_1) was using allele frequency (p_1) of 0.50 with increasing live weight per generation of 6.14 kg.

2 Measurements of animal live weight in this study indicated that the breeding value of homozygous genotype of *GH-Msp1*$^{+/+}$ was 45.95 kg, that of heterozygous genotype of *GH-Msp1*$^{+/-}$ was 12.16 kg, and that of homozygous genotype of *GH-Msp1*$^{-/-}$ was – 21.63 kg. Furthermore, the dominance deviation of homozygous genotype of *GH-Msp1*$^{+/+}$ was – 86.04 kg, that of heterozygous genotype of *GH-Msp1*$^{+/-}$ was 40.49 kg, and that of homozygous genotype of *GH-Msp1*$^{-/-}$ was – 19.05 kg. These values indicated that the homozygous genotype of *GH-Msp1*$^{+/+}$ was highly dominated by additive gene action for live weight rather than dominance gene action. However, the heterozygous genotype of *GH-Msp1*$^{+/-}$ was highly dominated by the dominance gene action rather than the additive gene action.

3 The heritability of cow live weight in this study was 0.24. This heritability value of cow live weight would be categorized as moderate value.

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Table 4. *A summary of formula for the different values for each genotype of the cows*

Genotype (G_{ij})	Genotypic Value (V_{ij})	Breeding Value (BV_{ij})	Dominance Deviation (D_{ij})
GH-Msp1$^{+/+}$	$V_{11} = P_{11} – m = a$	$2q\ \alpha$	$– 2q^2d$
GH-Mspl$^{+/-}$	$V_{12} = P_{12} – m = d$	$(q –p)\ \alpha$	$2pqd$
GH-Msp1$^{-/-}$	$V_{22} = P_{22} – m = – a$	$–2p\ \alpha$	$– 2p^2d$

V_{ij} values were derived from formula (2), (3), and (4);
BV_{ij} values were derived from formula (8), (9), and (10);
$\alpha = [a + d(q – p)]$ as shown at the formula (11);
D_{ij} values were derived from formula (12), (13), and (14).

Table 5. *Band of the fragment after Msp1 enzyme restriction*

Length of DNA band (bp)	Identified allele	Genotype
224	Normal allel (Msp1 +)*	Msp1 +/+
103		
327	Msp1 + and Msp1 –	Msp1 +/–
224		
103		
323	Mutant allel (Msp1 –)**	Msp1 –/–

*) Cut by *Msp1* enzyme; **) Uncut by *Msp1* enzyme.

Table 6. *Average of live weight and genotypic value for each genotype GH restriction enzyme Msp1 in Ongole-crossbred cows*

Genotype of Cows	Number of Cows (n)	Genotype Frequency	Average of Phenotype (Live Weight, kg)	Genotypic Value (V_{ij})
GH-Msp1$^{+/+}$	8	p^2	P_{11} = 405,33	a = 0,30 kg
GH-Msp1$^{+/-}$	14	2pq	P_{12} = 498,07	d = 93,04 kg
GH-Msp1$^{-/-}$	15	q^2	P_{22} = 404,73	– a = – 0,30 kg

Table 7. *Summary of selection response (Δμ) by four animal mating choices involving Ongole-crossbred cows and bulls of Krista (Kr-Msp*$^{+/+}$*) and Tunggul (Tu-Msp*$^{-/-}$*)*

Genotypes of Mated Cows	Genotypes of Mated Bulls	Genotype Frequencies of Progeny (G_1)	Selection Response (Δμ) of Live Weight in G_1 (kg)
First Choice:			
GH-Msp1$^{+/+}$	*Kr-Msp*$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/+}$ = 0,38	3,38
GH-Msp1$^{+/-}$	*Kr-Msp*$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/-}$ = 0,47	
GH-Msp1$^{-/-}$	*Kr-Msp*$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{-/-}$ = 0,15	
Second Choice:			
	Kr-Msp$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/+}$ = 0,25	6,14
	Kr-Msp$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/-}$ = 0,50	
	Kr-Msp$^{+/+}$ & *Tu-Msp*$^{-/-}$	*GH-Msp1*$^{-/-}$ = 0,25	
Third Choice:			
GH-Msp1$^{+/+}$	*Kr-Msp*$^{+/+}$	*GH-Msp1*$^{+/+}$ =4/9	1,07
GH-Msp1$^{+/-}$	*Kr-Msp*$^{+/+}$	*GH-Msp1*$^{+/-}$ =4/9	
		GH-Msp1$^{-/-}$ = 1/9	
Forth Choice:			
GH-Msp1$^{+/-}$	*Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/+}$ =1/9	0,87
GH-Msp1$^{-/-}$	*Tu-Msp*$^{-/-}$	*GH-Msp1*$^{+/-}$ =4/9	
		GH-Msp1$^{-/-}$ = 4/9	

Table 8. *A summary of the genotypic value, breeding value and dominance deviation for each genotype of the cows*

Genotype of Cows (Enzyme *GH-Msp1*)	Genotypic Value (V_{ij}), kg	Breeding Value (BV_{ij}), kg	Dominance Deviation (D_{ij}), kg
GH-Msp1$^{+/+}$, p^2	a = 0,30	2q α = 45,96	$-2q^2d$ = – 86,04
GH-Mspl$^{+/-}$, 2pq	d = 93,04	(q–p)α = 12,17	$2pqd$ = 40,49
GH-Msp1$^{-/-}$, q^2	– a = – 0,30	– 2p α = –21,63	$-2p^2d$ = – 19,05

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