

**ANALISIS POTENSI GENETIK SAPI MADURA
DI KABUPATEN PAMEKASAN DAN
LOKA PENELITIAN SAPI POTONG
JAWA TIMUR**

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INTISARI

Penelitian ini bertujuan untuk mengetahui potensi populasi, parameter genetik, polimorfisme gen MC4R, dan keterkaitan gen MC4R terhadap sifat pertumbuhan sapi Madura. Lokasi penelitian di Kabupaten Pamekasan dan Lolitsapi, Jawa Timur. Waktu penelitian 7 Desember 2016 sampai dengan 30 Desember 2017. Materi tahap I adalah 2.594 peternak dan 5.035 ekor sapi Madura di Kabupaten Pamekasan; Tahap II, 366 *data* sapi Madura di kedua lokasi. Tahap III berupa 268 sampel darah sapi Madura di kedua lokasi. Metode tahap I, II dan III berturut-turut adalah survey dan wawancara, pengukuran ternak dan analisis DNA. Hasil tahap I menunjukkan bahwa nilai NI 61,94%, NRR jantan 662,23% dan betina 266,83%, *output* 60,45%. Hasil estimasi parameter genetik (tahap II) berkisar antara sedang sampai dengan tinggi. Heritabilitas tertinggi TG lahir ($0,76 \pm 0,44$; Lolitsapi) dan LD setahun ($0,71 \pm 0,67$; Kabupaten Pamekasan), sedangkan terendah PB lahir ($0,35 \pm 0,29$; Lolitsapi) dan TG lahir ($0,26 \pm 0,24$; Kabupaten Pamekasan). Selanjutnya untuk riptabilitas terendah diperoleh pada pada TG dan LD lahir ($0,14 \pm 0,19$; Lolitsapi dan $0,23 \pm 0,36$; Kabupaten Pamekasan). Riptabilitas tertinggi dicapai pada LD setahun ($0,60 \pm 0,27$; Lolitsapi) dan TG setahun ($0,66 \pm 0,36$; Kabupaten Pamekasan). Korelasi genetik tertinggi adalah antara BB 205 hari dengan TG setahun ($0,58 \pm 0,23$; Lolitsapi), dan BB lahir dengan LD lahir ($0,68 \pm 0,16$; Kabupaten Pamekasan). Sedangkan korelasi terendah terjadi antara BB 205 hari dengan BB 365 hari sebesar $0,14 \pm 0,50$ (Lolitsapi) dan $0,17 \pm 0,56$ (Kabupaten Pamekasan). Hasil tahap III berdasarkan SNP g. 1133 C>G gen MC4R ditemukan dua alel (C dan G) dan tiga genotip (CC = 17, CG = 112 dan GG = 139). SNP g.1133C>G berkaitan secara signifikan terhadap LD lahir ($P < 0,041$) dan BB sapih ($P < 0,020$) di Lolitsapi, dan TG setahun ($P < 0,008$) di Kabupaten Pamekasan. Ternak bergenotip GG memiliki LD ($61,18 \pm 4,36$) lebih tinggi daripada CG ($58,60 \pm 3,03$) dan CC ($60,33 \pm 4,31$) di Lolitsapi. Sedangkan di Kabupaten Pamekasan, ternak bergenotip GG memiliki TG setahun ($110,35 \pm 6,40$) lebih tinggi dibandingkan CG ($105,96 \pm 6,23$) dan CC ($102,00 \pm 8,00$). Kesimpulannya, Kabupaten Pamekasan, Provinsi Jawa Timur merupakan sumber bibit dan produsen sapi Madura. Nilai parameter genetik di Kabupaten Pamekasan dan Lolitsapi adalah sedang sampai dengan tinggi. Gen MC4R pada *exon* 1 bersifat polimorfik dan terdapat keterkaitan antara polimorfisme gen MC4R dengan kinerja pertumbuhan (LD, BB dan TG) sapi Madura umur lahir, sapih dan satu tahun.

Kata kunci: Potensi Populasi, Parameter Genetik, Genetika Molekuler dan Sapi Madura.

**ANALYSIS OF GENETIC POTENCY IN MADURA CATTLE REARED IN
PAMEKASAN REGENCY AND BEEF CATTLE RESEARCH STATION,
EAST JAVA PROVINCE**

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ABSTRACT

The objective of this study was to determine the population potency, genetic parameter for growth traits, and association between melanocortin-4 receptor (MC4R) gene polymorphism and growth traits in Madura cattle. This study was conducted over a period of one year, from December 2016 to December 2017, in Pamekasan regency (PKS) and Beef Cattle Research Station (BCRS) of East Java province. A total of 2594 breeders and 5035 heads of Madura cattle in PKS (Phase I), 366 heads of Madura cattle in both locations (Phase II) and 268 blood samples collected from both locations (Phase III) were used. Survey and interview, determination of body weights and body measurements and DNA analysis were consecutively carried out in Phase I, Phase II and Phase III, respectively. The results showed that indicators for population potency (Phase I) were obtained to be 61.94% (NI), 662.23% (female NRR), 266.83% (male NRR), and 60.45% (output). Estimates of genetic parameters for growth traits (Phase II) were categorized in medium to high magnitude. The highest heritability was found for SH at birth (0.76 ± 0.44 ; BCRS) and CC at yearling (0.71 ± 0.67 ; PKS), while the lowest heritability was obtained for BL (0.35 ± 0.29 ; BCRS) and SH (0.26 ± 0.24 ; PKS) at birth. The lowest repeatability was identified for SH (0.14 ± 0.19 ; BCRS) and CC (0.23 ± 0.36 ; PKS) at birth, while the highest repeatability was indicated for CC (0.60 ± 0.27 ; BCRS) and SH (0.66 ± 0.36 ; PKS) at yearling. For genetic correlation, the highest value was found between BW at 205 days and SH at yearling (0.58 ± 0.23 ; BCRS) and between BW at birth and CC at birth (0.68 ± 0.16 ; PKS), while the lowest value was found between BW at 205 days and BW 365 days (0.14 ± 0.50 ; BCRS and 0.17 ± 0.56 ; PKS). Based on SNP g.1133C>G of MC4R gene (Phase III), 2 alleles (C and G) and 3 genotypes (CC = 17, CG = 12 and GG = 139) were identified. The SNP was significantly associated with CC at birth ($P < 0.041$) and BW at weaning ($P < 0.020$) in BCRS, and SH at yearling ($P < 0.008$) in PKS. Animals having GG genotype had a higher CC (61.18 ± 4.36) than those having CG (58.60 ± 3.03) and CC (60.33 ± 4.31) genotypes in BCRS. Similarly, animals having GG genotype had a higher SH (110.35 ± 6.40) than those having CG (105.96 ± 6.23) and CC (102.00 ± 8.00) genotypes. In conclusion, Pamekasan regency can be considered as a breeding region and producer of Madura cattle. Estimates of genetic parameters in PKS and BCRS are identified to be moderate to high magnitude. Moreover, MC4R gene in exon 1 is found to be polymorphic and there is an association between MC4R gene polymorphism and growth traits (BW, CC and SH) at birth, weaning and yearling.

Keywords: Population Potency, Genetic Parameters, Molecular Genetics and Madura Cattle