IDENTIFIKASI *SINGLE NUCLEOTIDE POLYMORPHISM* GEN *MELANOCORTIN 4 RECEPTOR* DAN *MYOGENIC FACTOR 5* SEBAGAI *MARKER* GENETIK SIFAT PERTUMBUHAN SAPI BALI DI BPTU-HPT DENPASAR

INTISARI

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Penelitian ini bertujuan untuk mengetahui keragaman genetik berdasarkan variasi *single nucleotide polymorphism* (SNP) gen *melanocortin 4 receptor* (MC4R) dan *myogenic factor 5* (MYF5) serta pengaruhnya terhadap sifat pertumbuhan sapi Bali di BPTU-HPT Denpasar. Sebanyak 43 sampel darah sapi Bali beserta data *recording* sifat pertumbuhan dikoleksi dari BPTU-HPT Denpasar. Data *recording* sifat pertumbuhan penelitian ini meliputi bobot badan lahir (BBL), bobot badan sapih (BBS), lingkar dada sapih (LDS), tinggi pundak sapih (TPS), panjang badan sapih (PBS), bobot badan *yearling* (BBY), lingkar dada *yearling* (LDY), tinggi pundak *yearling* (TPY) dan panjang badan *yearling* (PBY). Target gen MC4R (774 bp) diamplifikasi menggunakan primer *forward:* 5'-AATGAACTCTACCCAGCCCC-3' dan primer *reverse:* 5'-CAGCAGACAACAAAGACCCC-3'. Target gen MYF5 (628 bp) diamplifikasi menggunakan primer *forward:* 5'-TCCACTCCCCAACTTCATCC-3' dan primer *reverse:* 5'-CTACCTTTGATGAACGGCCC-3'. BioEdit v.7.2.5 *software* digunakan untuk mengetahui variasi SNP. Keragaman genetik dan pengaruhnya terhadap sifat pertumbuhan dianalisis menggunakan RStudio *software.* Analisis variasi SNP berhasil memperoleh empat SNP gen MC4R meliputi g.631G>T (GG, TG), g.670C>T (CC, CT), g.739G>A (GG, AG, AA) dan g.958G>A (GG, AG) serta tiga SNP gen MYF5 meliputi g.2039G>A (AA, AG), g.2242G>A (AA, AG) dan g.2288A>C (AA, AC). Populasi sapi Bali berada pada kesetimbangan *hardy-weinberg equilibrium* (HWE) dan bersifat polimorfik di mana frekuensi alel dominan (G dan C) gen MC4R dan alel dominan (A) gen MYF5 masing-masing sebesar 98%. *Single nucleotide polymorphism* g.2288A>C berpengaruh terhadap BBL sapi Bali di mana genotip AC memiliki BBL (21,20±1,80 kg) lebih tinggi dibanding genotip AA (19,12±1,50 kg) ($P<0,05$). Hal ini akibat terjadinya mutasi SNP g.2288A>C (Glutamine>Histidine). Variasi SNP gen MC4R dan MYF5 pada lokasi lainnya tidak mempengaruhi bobot badan dan ukuran tubuh sapi Bali. Bobot badan lahir sapi Bali berdasarkan tipe haplotip gen MC4R berkisar 19,00±1,81 kg-21,17±0,75 kg di mana BBL tertinggi berada pada individu dengan haplotip tipe 2 (GCAG) ($P<0,05$). Haplotip gen MYF5 berpengaruh terhadap BBL dengan kisaran BBL 18,94±1,34 kg-22,00 kg di mana individu haplotip 3 (RRA) sebagai BBL tertinggi ($P<0,05$). Analisis *linkage disequilibrium* (LD) menunjukkan hubungan yang kuat antar SNP ($r^2=1$). Hasil analisis berdasarkan variasi SNP dan tipe haplotip gen MC4R dan MYF5 tidak mempengaruhi sifat pertumbuhan sapi Bali di BPTU-HPT Denpasar sehingga keragaman genetik dalam penelitian ini tidak dapat digunakan sebagai *marker* genetik.

Kata kunci: Sapi Bali, Keragaman genetik, MC4R, MYF5, *Marker* genetik, Sifat pertumbuhan

SINGLE NUCLEOTIDE POLYMORPHISM IDENTIFICATION OF MELANOCORTIN 4 RECEPTOR AND MYOGENIC FACTOR 5 GENE AS GROWTH TRAITS GENETIC MARKERS IN BALI CATTLE AT BPTU-HPT DENPASAR

ABSTRACT

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This study aimed to determine the genetic diversity based on single nucleotide polymorphism (SNP) variation of the melanocortin 4 receptor (MC4R) and myogenic factor 5 (MYF5) genes and its effect on growth traits in Bali cattle at BPTU-HPT Denpasar. In total, 43 Bali cattle included the recording data were collected from BPTU-HPT Denpasar. The growth trait data in this study included birth weight (BBL), weaning body weight (BBS), weaning chest circumference (LDS), weaning shoulder height (TPS), weaning body length (PBS), yearling body weight (BBY), yearling chest circumference (LDY), yearling shoulder height (TPY), and yearling body length (PBY). The MC4R gene target (774 bp) was amplified using the forward primer: 5'-AATGAACTCTACCCAGCCCC-3' and the reverse primer*:* 5'-CAGCAGACAACAAAGACCCC-3'. The MYF5 gene target (628 bp) was amplified using the forward primer*:* 5'-TCCACTCCCCAACTTCATCC-3' and the reverse primer: 5'-CTACCTTTGATGAACGGCCC-3'. BioEdit v.7.2.5 software was used to identify SNP variation. Analysis of genetic diversity and its effect on growth traits were performed using RStudio software. In total, four SNPs of MC4R were succesfully identified: g.631G>T (GG, TG), g.670C>T (CC, CT), g.739G>A (GG, AG, AA), and g.958G>A (GG, AG), and also three SNPs from MYF5, namely g.2039G>A (AA, AG), g.2242G>A (AA, AG) and g.2288A>C (AA, AC). The populations of Bali cattle were fitted the hardy-weinberg equilibrium (HWE) and polymorphic with the frequency of dominant allele (G and C) of MC4R and dominant allele (A) of MYF5 were 98%. Single nucleotide polymorphism g.2288A>C affected the birth body weight (BBL) of Bali cattle, the AC genotype had a higher BBL (21.20±1.80 kg) than the AA genotype (19.12±1.50 kg) ($P<0.05$). This is due to the mutation of the SNP g.2288A>C (Glutamine>Histidine). SNP variations in the MC4R and MYF5 genes at other locations did not affect body weight or body size in Bali cattle. The BBL of Bali cattle based on the MC4R gene haplotype ranged from 19.00±1.81 kg-21.17±0.75 kg where the highest BBL was in individuals with haplotype type 2 (GCAG) ($P<0.05$). The MYF5 gene haplotype had an effect on BBL with a range of 18.94±1.34 kg-22.00 kg where individual haplotype 3 (RRA) was the highest BBL ($P<0.05$). Linkage disequilibrium (LD) analysis showed strong linkage between SNPs ($r^2=1$). The results of the analysis based on SNP variations and haplotype types of MC4R and MYF5 did not affect the growth traits of Bali cattle at BPTU-HPT Denpasar. Therefore, the genetic diversity in this study can not be used as a genetic marker.

Keywords: Bali cattle, Genetic diversity, Genetic marker, Growth traits, MC4R, MYF5