شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكروفيلم

شبكة المعلومات الجامعية

التوثيق الالكتروني والميكروفيلم

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MONA MAGHRABY

شبكة المعلومات الجامعية
التوثيق الإلكتروني والميكروفيلم

جامعة عين شمس

التوثيق الإلكتروني والميكروفيلم

قسم

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MONA MAGHRABY

DETECTION OF CANDIDATE GENES ASSOCIATED WITH MILK PRODUCTION TRAITS IN EGYPTIAN BUFFALO

By

MOHAMED ATTIA AHMED AWAD
B.Sc. Agric. Sci. (Animal Production), Fac. Agric., Cairo Univ., Egypt, 2008
M.Sc. Agric. Sci. (Animal Production), Fac. Agric., Cairo Univ., Egypt, 2014

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APPROVAL SHEET

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SUPERVISION SHEET

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ABSTRACT

The aim of this study was to perform a genome-wide association study (GWAS) to identify genomic loci and detect potentially candidate genes associated with seven milk production traits; daily milk yield (DMY), fat percentage (FP), fat yield (FY), protein percentage (PP), protein yield (PY), lactose percentage (LP) and lactose yield (LY) in Egyptian buffalo. The phenotypic dataset included 161,479 daily milk records from 1,670 animals and 60,318 monthly measures for other traits from 1481 animals. Adjustment for non-genetic effects has been made using univariate animal model by BLUPF90. A total number of 114 animals with high and low deviated performance were selected for genotyping with Axiom Buffalo Genotyping 90K Array. Adjusted phenotypes were used for GWAS in the way of SNP-by-SNP using a single marker regression. With 5% Bonferroni genome-wide threshold, 55 significant and 33 suggestive SNPs were detected for association with the tested traits and were distributed over 25 buffalo chromosomes (BBU). The 88 SNPs were two for DMY, three for FP, seven for FY, 21 for PP, 14 for PY, 39 for LP and two for LY. The identified genomic regions were coincided with previously reported QTL in buffalo and cattle populations. In addition, novel genomic loci were suggested. The identified SNPs are placed within or close to many promising candidate genes with biological roles associated with milk production traits, for example:, TPD52, ZBTB10, RALYL, and SNX16 on BBU15; ADGRD1 on BBU17; ESRRG on BBU5; and GRIP1 on BBU4. This is the first GWAS for milk quality traits in Egyptian buffalo. The consistence of the identified genomic regions with known QTL and candidate genes provide further evidence for the importance of such loci for the variation in milk production traits. The current findings provide the basis to uncover the key markers and genes affecting milk production traits in Egyptian buffalo which may play a role to increase the rate of genetic improvement in Egyptian buffalo using genomic approaches.

Key words: Egyptian buffalo, milk traits, GWAS, SNP, candidate genes.

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LIST OF ABBREVIATIONS

A	Adenine
ARMS	Amplification Refractory Mutation System
BBU	Buffalo Chromosome
bp	Base Bair
BTA	*Bos taurus* Autosome
C	Cytosine
cM	Centimorgan
CV	Coefficient of Variation
D	Disequilibrium Coefficient
DGGE	Denaturing Gradient Gel Electrophoresis
FDR	False Discovery Rate
G	Guanine
GC	Genomic Control
GEBV	Genomic Estimated Breeding Value
GS	Genomic Selection
GWAS	Genome Wide Association Study
h^2	Heritability
HWE	Hardy-Weinberg Equilibrium
IBS	Identity-By-State
kb	Kilo Base
kJ	Kilojoule
LD	Linkage Disequilibrium
LE	Linkage Equilibrium
MA	Minor Allele
MAF	Minor Allele Frequency
MAS	Marker Assisted Selection
Mb	Mega Base
MDS	Multidimensional Scaling
ng	Nanogram
nm	Nanometer
PCA	Principal Component Analysis
PPC	Pairwise Population Concordance
Q-Q	Quantile-Quantile