NUCLEOTIDE SEQUENCING AND DETECTION OF MUTATION IN CARCASS ASSOCIATED CANDIDATE GENES IN INDIGENOUS CATTLE OF BANGLADESH



A thesis by **ARJUMAN LIMA** Roll No.: 0118/01 Registration No.: 485 Session: 2018-2019 (January-June)

A thesis submitted to the Department of Genetics and Animal Breeding, Faculty of Veterinary Medicine Chattogram Veterinary and Animal Sciences University, Chattogram in the partial fulfillment of the requirements for the degree of Masters of Science in Animal Breeding and Genetics

DEPARTMENT OF GENETICS AND ANIMAL BREEDING FACULTY OF VETERINARY MEDICINE

CHATTOGRAM VETERINARY AND ANIMAL SCIENCES UNIVERSITY CHATTOGRAM-4225

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This is to certify that we have examined the above Master's thesis and have found that is complete and satisfactory in all respects, and that all revisions required by the thesis examination committee have been made

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Authorization

I, DR. Arjuman Lima assure that I have performed all works furnished here in this report. The information has been collected from books, national and international journals, websites and other references. All references have been acknowledged accordingly.

I hereby declare that I am the sole author of the thesis "Nucleotide sequencing and detection of mutation in carcass associated candidate genes in indigenous cattle of Bangladesh". I also authorize the Chattogram Veterinary and Animal Sciences University (CVASU) to lend this thesis to other institutions or individuals for the purpose of scholarly research. I further authorize the CVASU to reproduce the thesis by photocopying or by other means, in total or in part, at the request of other institutions or individuals for the purpose of scholarly research.

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The Author June, 2020

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List of Abbreviations

| А | Adenine |
|----------|--|
| ADG | Average daily gain |
| AFS | Australian friesian sahiwal |
| AI | Artificial insemination |
| Asp | Aspartic |
| BCAA | Branched-chain amino acid |
| BER | Bangladesh economic review |
| BLAST | Basic local alignment search tool |
| BONEP | Bone percentage |
| bp | Base pair |
| BTA | Bos taurus autosome |
| С | Cytosine |
| CACNA2D1 | Calcium voltage-gated channel auxiliary subunit |
| | alpha2delta 1 |
| Chr | Chromosome |
| cm | Centimeter |
| cM | Centromeric |
| CVASU | Chattogram Veterinary and Animal Sciences University |
| CWT | Carcass weight |
| Cys | Cysteine |
| dbSNP | The single nucleotide polymorphism database |
| ddATP | Dideoxyadenosine triphosphate |
| ddCTP | Dideoxycytidine triphosphate |
| ddGTP, | Dideoxyguanosine triphosphate |
| ddTTP | Dideoxythymidine triphosphate |
| DLS | Department of livestock services |
| DNA | Deoxyribonucleic acid |
| dNTPs | Deoxynucleotide triphosphates |
| dsDNA | Double stranded DNA |
| e.g. | Example |
| EDTA | Ethylene demine tetra acetic acid |

| EPD | Expected progeny differences |
|----------|---|
| FABG | Favorprep Blood Genomic |
| FAO | Food and Agricultural Organization |
| FAOSTAT | Food and Agriculture Organization Corporate Statistical |
| | Database |
| FCR | Feed conversion ratio |
| G | Guanosine |
| gDNA | Genomic DNA |
| GDP | Gross domestic product |
| Ile | Isoleucine |
| ILRI | International livestock research institute |
| kg | Kilogram |
| LMA | Longissimus muscle area |
| MAS | Marker assisted selection |
| ml | Milliliter |
| MoyD | Myogenic determination |
| mRNA | Messenger RNA |
| MTBR | Meat-to-bone ratio |
| MYF | Myogenic factor |
| MyoG | Myogenin |
| NAGRP | National animal genome research program |
| NCBI | National Center for Biotechnology information |
| ND | Non-descriptive |
| PCR | Polymerase chain reaction |
| PCR-SSCP | Polymerase chain reaction-single-strand conformation |
| | polymorphism |
| PIC | Polymorphism information content |
| PRTC | Poultry Research and Training Centre |
| QTL | Quantitative trait loci |
| RCC | Red Chittagong cattle |
| RFI | Residual feed intake |
| RFLP | Restriction fragment length polymorphism |
| RNA | Ribonucleic acid |

| SCS | Somatic cell score |
|-------|---|
| SNP | Single nucleotide polymorphism |
| Т | Thymine |
| TAE | Tris-acetate-EDTA |
| Trp | Tryptophan |
| Tyr | Tyrosine |
| UNIDO | UNIDO United Nations Industrial Development |
| | Organization |
| USA | United State of America |
| USDA | United States Department of Agriculture |
| UV | Ultraviolet |
| α-KIC | A-ketoisocaproate |
| % | Percentage |
| μl | Micro liter |

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Dedication

To my ever loving parents

Mr. Mahabubur Rahman

and

Mrs. Jarna Tara Begum

Abstract

Carcass related traits are very complex and difficult to measure phenotypically, they are not usually included in selection programs. Several studies have indicated associations between genes associated with carcass traits and the genetic polymorphisms in these genes. However, genetic research on indigenous cattle carcass traits in Bangladesh is scanty. Therefore, this study was carried out to screen polymorphisms of the CACNA2D1 gene for carcass weight, dressing percentage, meat percentage, and backfat thickness and MYF5 for live weight, loin eye height, loin eye area and water holding capacity. To identify and assess the association between polymorphisms and carcass traits a total of 80 animals were randomly selected. Genomic DNA was extracted from collected blood samples using a commercial DNA extraction kit for amplification of the fragments of exon 25 of CACNA2D1 gene and exon 2 of MYF5 gene using Polymerase Chain Reaction (PCR). PCR products were sequenced using DNA sequencing. Phylogenetic analysis was also performed to explore the genetic diversity of different cattle. This preliminary research on polymorphism of the CACNA2D1 gene exon 25 in cattle revealed C1993A, T2058A, C2068A might be helpful as genetic markers in Red Chittagong Cattle (RCC) and Crossbred (RCC \times Local) cattle. According to the score in Polyphen2, it can be confidently predicted to be deleterious. The SNP C1993A resulted in a missense mutation leading Leu (L) to 658 Ile (I) amino acid substitution, which may cause possible damage due to the less significant effect of isoleucine in protein synthesis. This detrimental effect may cause a reduction in muscle mass along with body weight. The absence of this mutation in the RCC population may have a positive effect, and carcass quality may be better in RCC than crossbreed as those mutations may negatively impact the cattle population. In case of MYF5 the mutation at the 1795C>T position, which is intronic, does not cause an amino acid substitution but several recent investigations revealed that SNPs in the intron region had significant associations with carcass and meat quality traits. Results from this study indicate that the CACNA2D1 gene and MYF5 have potential effects on carcass and meat quality traits, opening up possibilities for cattle breeding and improvement in gene-assisted selection and future research is necessary to evaluate other candidate genes. Moreover, the results for cattle carcass traits would be a scientific basis for the conservation and utilization of cattle genetic resources.

Keywords: Carcass trait, indigenous cattle, DNA sequencing, polymorphism, meat quality.