IDENTIFICATION OF BACTERIAL COMMUNITY IN MILK OF MASTITIC WATER BUFFALO IN SELECTED COOPERATIVES OF THE NATIONAL IMPACT ZONE USING PCR AND DGGE METHOD

NIÑA RICA A. PAGADUAN

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ACCEPTANCE SHEET

This undergraduate thesis entitled "**IDENTIFICATION OF BACTERIAL COMMUNITY IN MILK OF MASTITIC WATER BUFFALO IN SELECTED COOPERATIVES OF THE NATIONAL IMPACT ZONE USING PCR AND DGGE METHOD**" prepared and submitted by **NIÑA RICA A. PAGADUAN**, in partial fulfillment of the requirements for the degree of **BACHELOR OF SCIENCE IN BIOLOGY (MICROBIOLOGY)**, is hereby accepted.

JERWIN R. UNDAN, Ph.D.
Adviser

06/13/18
Date Signed

CLARO N. MINGALA, Ph.D.
Co-Adviser

06/13/18
Date Signed

ANGELES M. DE LEON, Ph.D.
Critic

06/13/18
Date Signed

RICH MILTON R. DULAY, M.Sc.
Department Research Coordinator

06/13/18
Date Signed

Accepted as partial fulfillment of the requirements for the degree of **BACHELOR OF SCIENCE IN BIOLOGY (MICROBIOLOGY)**

ANGELES M. DE LEON, Ph.D.
Chair, Department of Biological Sciences

06/13/18
Date Signed

RICH MILTON R. DULAY, M.Sc.
College Research Coordinator

6/13/18
Date Signed

EVARISTO A. ABELLA, Ph.D.
Dean, College of Arts and Sciences

06/13/18
Date Signed

BIOGRAPHICAL SKETCH

The author's name is Niña Rica Anselmo Pagaduan, she is a 20 years old from Ibona, Dingalan, Aurora. She was born on October 29, 1997 in Cabanatuan City and her religion is Pentecost. Her father's name is Arnold P. Pagaduan and her mother's name is Francisca A. Pagaduan. She used to live in Bagong Sikat, Taylan's Residence while studying in Central Luzon State University.

She finished her primary education at Ibona Elementary School from school year 2004-2010, and her secondary at Ibona National High School in Ibona, Dingalan, Aurora from school year 2010-2014. She obtained her tertiary education pursuing Bachelor of Science in Biology major in Microbiology at the Department of Biological Sciences, College of Arts and Sciences, Central Luzon State University, in Science City of Munoz and she completed her on the job training in the Ramon Magsaysay- Center for Agricultural Resources and Environmental Studies (RM-CARES) in Science City of Muñoz.

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ABSTRACT

PAGADUAN, NIÑA RICA A., Department of Biological Sciences, College of Arts and Sciences, Central Luzon State University, Science City of Munoz, Nueva Ecija, Philippines, **JUNE 2018, IDENTIFICATION OF BACTERIAL COMMUNITY IN MILK OF MASTITIC WATER BUFFALO IN SELECTED COOPERATIVES OF THE NATIONAL IMPACT ZONE USING PCR AND DGGE METHOD**

Adviser: JERWIN R. UNDAN, Ph. D.

This study was conducted to determine and identify the presence of bacteria in mastitic milk of water buffalo in selected cooperatives of NIZ using PCR and DGGE method. The milk samples collected from selected cooperatives wherein PCC was conducting the regular milk testing and only those samples which were positive in CMT were used prior to the extraction of DNA. Milk extraction of DNA was done and 16S bacterial primers were used to amplify the target region of 16S rRNA. The amplified PCR products were resolve in DGGE and the bands were excised prior to sequencing in order to identify the bacteria present in the samples.

The identified bacteria in BLAST were all gram-positive bacteria. Among these identified strains of bacteria genus of *Bacillus* was most dominant, genus of *Staphylococcus* and *Kurthia* were second most dominant. These bacteria were commonly found in soil and caused infections. The prevalence of these bacteria could be associated with the handling practices conducted in every cooperative. The identification of the presence of these bacteria can lead to development of drugs used for aiding mastitic in water buffalo and can be used in assessing the proper sanitation and handling practices in any dairy farms. The used of DGGE method was very useful in rapid detection of

bacterial communities in a sample, however it has limitations to be considered as a molecular technique.

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