



METAGENOMIC SOURCE TRACKING OF MICROBIAL CONTAMINANTS FROM MANURE TO LETTUCE

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**FOOD TECHNOLOGY STUDY PROGRAM
FACULTY OF ENGINEERING AND TECHNOLOGY
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ABSTRACT

AMMARA LATIFA PUTI HASCARYOTOMO. Metagenomic Source Tracking of Microbial Contaminants from Manure to Lettuce. Supervised by SITI NURJANAH and INAS SUCI RAHMAWATI.

Raw lettuce consumption poses food safety risks when its cultivated using animal manure, which serves as a reservoir for enteric microorganisms. This study used shotgun metagenomic sequencing to profile microbial communities in lettuce, chicken manure, and goat manure and identify potential contamination pathways along with its associated food safety risks. Shotgun metagenomic sequencing was conducted, followed by quality control and host DNA depletion, then directly to taxonomic classification. Lettuce showed lower bacterial diversity (Shannon 1.59) compared to chicken manure (Shannon 4.59) and goat manure (Shannon 5.07). Based on the classified reads, lettuce is dominated by phyla Pseudomonadota (87.91%) while manure samples are dominated by phyla Actinomycetota (58%). Spoilage-associated microorganisms predominated on lettuce, led by the genera *Pseudomonas* (31.39%) and *Pectobacterium* (25.81%). Furthermore, indicator microorganisms such as Enterobacteriaceae, *Enterobacter*, *Klebsiella*, *Enterococcus*, as well as foodborne pathogens *Escherichia coli* and *Salmonella enterica* are shared between lettuce and manure samples. These shared microorganisms highlight the potential microbial contamination pathway associated with animal manure fertilizer application in vegetables cultivation.

Keywords: food safety, lettuce, manure, metagenomics, microbial contaminants



ABSTRAK

AMMARA LATIFA PUTI HASCARYOTOMO. Metagenomic Source Tracking of Microbial Contaminants from Manure to Lettuce. Dibimbing oleh SITI NURJANAH dan INAS SUCI RAHMAWATI.

Konsumsi selada segar menimbulkan risiko keamanan pangan ketika dibudidayakan menggunakan pupuk kandang yang berpotensi menjadi sumber mikroorganisme enterik. Penelitian ini menggunakan *shotgun metagenomic sequencing* untuk memprofil komunitas mikroba dan mengidentifikasi potensi jalur kontaminasi beserta risiko keamanan pangan pada sampel selada, pupuk kandang ayam, dan pupuk kandang kambing. *Shotgun metagenomic sequencing* dilakukan, diikuti oleh kontrol kualitas dan penghilangan DNA inang, dilanjutkan dengan klasifikasi taksonomi. Selada menunjukkan keanekaragaman bakteri yang lebih rendah (Shannon 1,59) dibandingkan dengan pupuk kandang ayam (Shannon 4,59) dan pupuk kandang kambing (Shannon 5,07). Berdasarkan pembacaan yang terklasifikasi, selada didominasi oleh filum Pseudomonadota (87,91%), sedangkan sampel pupuk kandang didominasi oleh filum Actinomycetota (58%). Mikroorganisme yang berkaitan dengan pembusukan mendominasi pada selada, khususnya genera *Pseudomonas* (31,39%) dan *Pectobacterium* (25,81%). Selain itu, mikroba indikator seperti *Enterobacteriaceae*, *Enterobacter*, *Klebsiella*, *Enterococcus*, serta bakteri patogen *Escherichia coli* dan *Salmonella enterica* ditemukan pada kedua sampel selada dan pupuk kandang. Keberadaan mikroorganisme yang terdeteksi ini menyoroti potensi jalur kontaminasi mikroba yang berkaitan dengan aplikasi pupuk kandang dalam budidaya sayuran.

Keywords: cemaran mikroba, keamanan pangan, metagenomik, pupuk kandang, selada

METAGENOMIC SOURCE TRACKING OF MICROBIAL CONTAMINANTS FROM MANURE TO LETTUCE

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Undegraduate Thesis
as a requirement for obtaining
Bachelor's degree in Food Technology

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PREFACE

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LIST OF CONTENTS

LIST OF TABLES	iii
LIST OF FIGURES	iii
APPENDIX LIST	iii
I INTRODUCTION	1
1.1 Background	1
1.2 Problem Formulation	2
1.3 Objective	2
1.4 Benefit	2
1.5 Scope	2
II LITERATURE REVIEW	3
2.1 Lettuce	3
2.2 Manure Microbial Diversity	4
2.3 Shotgun Metagenomics	5
2.4 Microbial Contaminants in Fresh Produce	7
III METHOD	9
3.1 Time and Place	9
3.2 Tools and Materials	9
3.3 Work Procedures	9
IV RESULTS AND DISCUSSIONS	13
4.1 Metagenomic Data Sequencing and Pre-processing	13
4.2 Taxonomic Classification	15
4.3 Alpha Diversity Analysis	19
4.4 Target Microbial Contaminants	20
4.5 Microbial Source Analysis	28
4.6 Implications about Food Safety	30
4.7 Limitations	30
V CONCLUSION AND RECCOMENDATION	32
5.1 Conclusion	32
5.2 Reccomendation	32
BIBLIOGRAPHY	33
APPENDIX	42
BIOGRAPHY	77

LIST OF TABLES

1	Table 1 Lettuce, chicken manure, and goat manure raw sequencing data	13
2	Table 2 Quality control and sequence trimming result of samples sequencing dataset	13
3	Table 3 Host DNA removal result of all samples sequencing dataset	14
4	Table 4 Relative abundance of classified target microbial contaminants on chicken manure, goat manure, and lettuce	21

LIST OF FIGURES

1	Figure 1 Workflow of metagenomics	6
2	Figure 2 Research work procedure flowchart	9
3	Figure 3 Krona chart showing dominant taxa and overall taxonomic composition in lettuce sample	13
4	Figure 4 Krona chart showing dominant taxa and overall taxonomic composition in chicken manure sample	15
5	Figure 5 Krona chart showing dominant taxa and overall taxonomic composition in chicken manure sample	15
6	Figure 6 Phylum-level relative abundance of classified microbial reads across lettuce and animal manure samples	16
7	Figure 7 Alpha diversity metrics of lettuce, chicken manure, and goat manure samples	19
8	Figure 8 Shared microbial taxa between lettuce and manure samples	27
9	Figure 9 Stages of pathogen contamination on leaves	29

APPENDIX LIST

1	Appendix 1 Relative abundance of dominant classified microbial reads across lettuce and animal manure samples at genus-level	43
2	Appendix 2 Alpha diversity metrics (Observed Richness, Shannon, Simpson, Inverse Simpson) of lettuce, chicken manure, and goat manure	44
3	Appendix 3 NanoDrop DNA extraction purity and concentration of all samples	45
4	Appendix 4 Kraken2 taxonomic classification of lettuce metagenomic dataset	46
5	Appendix 5 Kraken2 taxonomic classification of chicken manure metagenomic dataset	51
6	Appendix 6 Kraken2 taxonomic classification of chicken manure metagenomic dataset	63