

SCREENING AND CHARACTERIZATION OF CELLULOLYTIC BACTERIA  
ISOLATED FROM ARCTIC SOIL AND SEDIMENT SAMPLES

MUSTAPHA ABBA

UNIVERSITI TEKNOLOGI MALAYSIA

SCREENING AND CHARACTERIZATION OF CELLULOLYTIC  
BACTERIA ISOLATED FROM ARCTIC SOIL AND SEDIMENT SAMPLES

MUSTAPHA ABBA

A dissertation submitted in partial fulfillment of the  
requirements for the award of the degree of  
Master of Science (Biotechnology)

Faculty of Biosciences and Medical Engineering  
Universiti Teknologi Malaysia

JANUARY 2015

*This research work is specially dedicated to my beloved parents, and the entire Muslim.*

## ACKNOWLEDGEMENT

~In the name of ALLAH the most Gracious and the most Merciful~

First I will like to express my profound gratitude to Almighty Allah for seen me through this research and make it possible and successfully through his endless mercy. I would also like to show and express my deep appreciation to my supervisor; **Associate Prof. Dr. Zaharah Binti Ibrahim** for her tremendous and ceaseless encouragement, guidance, advice, kindness and support during my study. Thank you for sharing the knowledge and timely guidance.

Special appreciation goes to my senior colleagues in Environmental Bioengineering Research Lab. especially the efforts by I V, Mr. Lam Chi Yong, Ahmad Idi, Shehu Idris Ikara, M. Hanif Nor and those whose names were not mentioned due to limited space.

I am indebted to my parent especially my late father Alhaji Abba Abubakar, my mother Hajiya Maijidda, and the entire family and friends for their supports and prayers.

Lastly, I offer my regards and blessings to my beloved wife Aishatu Bin-Umar Barde for her caring, prayers and other issues too numerous to be mention.

I thank you all.

## ABSTRACT

The study on microorganisms living in extreme cold environment such as the arctic and antarctic regions is important for the biotechnological exploration and biodiversity. Such organisms however, could have enzymes capable of degrading complex molecules at low temperature. In this work, culturable bacteria from arctic soil and sediment samples have been isolated under low temperature (20 °C), using Antarctic Bacterium medium (ABM). A total of 40 different bacteria were isolated and screen for their ability to produce cellulase using carboxymethyl cellulose (CMC) as substrates. Cellulase producing bacteria were selected based on their hydrolytic coefficient. Molecular characterizations of the potent cellulase producing isolates were carried out using 16S rRNA gene sequence method. The effects of temperature, pH and salinity were tested on four bacterial isolates that showed high cellulase activity. However only two of the isolates (SL9 and SL 19) were able to retains their cellulolytic activity at 5%, 10%, and 15% salt concentrations. Based on the 16S rRNA gene sequence and the phylogenetic analysis, the four potential cellulolytic bacterial isolates were identified as *Massilia* sp. and *Pseudomonas* sp. The findings of this work suggested that arctic bacterial isolates such as *Massilia* and *Pseudomonas* species could serve as promising agents for the production of bacterial cellulase with various biotechnological applications; such as food supplement, animal feed supplement as well as bioremediation of pharmaceutical wastewater.

## ABSTRAK

Kajian terhadap mikroorganisma yang hidup dalam persekitaran sejuk melampau seperti kawasan artik dan antartika adalah penting untuk penerokaan bioteknologi dan biodiversiti. Walaubagaimanapun terdapat mikroorganisma yang mempunyai enzim yang mampu mengurangkan molekul kompleks pada suhu rendah. Dalam kajian ini, bakteria kultur dari tanah artik dan sedimen sampel telah diasingkan di bawah suhu rendah (20°C), dengan menggunakan bakteria Antartika sederhana (ABM). Sebanyak 40 bakteria yang berbeza telah diasingkan dan disaring untuk menghasilkan selulase menggunakan kuvboksimetil selulosa (CMC) sebagai substrat. Bakteria menghasilkan selulase dipilih berdasarkan pemalar hidrolitik mereka. Pemilihan berdasarkan kriteria molekul yang kuat menghasilkan selulase telah dijalankan menggunakan kaedah urutan gen 16S rRNA. Dari kesan suhu, pH dan kemasinan telah diuji ke atas empat isolat bakteria yang menunjukkan aktiviti selulase tinggi. Walau bagaimanapun hanya dua daripada bakteria (SL9 dan SL 19) dapat mengekalkan aktiviti cellulolytic mereka pada 5%, 10%, dan 15% kepekatan garam. Berdasarkan urutan gen 16S rRNA dan analisis filogenetik, empat bakteria cellulolytic berpotensi telah dikenal pasti sebagai *Massilia* sp. dan *Pseudomonas* sp. Cadangan daripada hasil kerja ini ialah bahawa isolat bakteria artik seperti *Massilia* dan *Peudomonas* spesis boleh dijadikan agen untuk pengeluaran enzim bakteria dengan pelbagai aplikasi bioteknologi; seperti makanan tambahan, makanan tambahan ternakan serta bioremediasi air sisa farmaseutikal.

**TABLE OF CONTENTS**

<b>CHAPTER</b>	<b>TITLE</b>	<b>PAGE</b>
	<b>DECLARATION</b>	<b>ii</b>
	<b>DEDICATION</b>	<b>iii</b>
	<b>ACKNOWLEDGEMENT</b>	<b>iv</b>
	<b>ABSTRAK</b>	<b>vi</b>
	<b>TABLE OF CONTENTS</b>	<b>vii</b>
	<b>LIST OF TABLES</b>	<b>xi</b>
	<b>LIST OF FIGURES</b>	<b>xii</b>
	<b>LIST OF ABBREVIATIONS</b>	<b>xiii</b>
	<b>LIST OF APPENDICES</b>	<b>xv</b>
<b>1</b>	<b>INTRODUCTION</b>	<b>1</b>
	1.1 Background of the study	1
	1.2 Problem statement	4
	1.3 Aims and objectives of the study	5
	1.4 Scope of the research	6
	1.5 Significance of the research	6
<b>2</b>	<b>LITERATURE REVIEW</b>	<b>7</b>
	2.1 Extreme cold environment	7
	2.1.1 Diversity of Microorganisms in Cold Environment	8
	2.1.2 Adaptation of Microorganisms in Cold Environment	9

2.2	Microbial Enzymes	11
2.2.1	Microbial Cellulases	11
2.2.2	Classification of Cellulase Enzymes	12
2.2.3	Cellulose Degradation	12
2.3	Isolation of Cellulases Producing Microorganisms	13
2.3.1	Novel Cellulase Producing Bacteria	14
2.3.2	Structure of Bacterial cellulases	14
2.4	Distribution of cellulase genes in bacteria	15
2.5	Application of Microbial Cellulases	16
2.5.1	Detergent Industry	16
2.5.2	Food Industry	17
2.5.3	Textiles Industries	17
2.5.4	Animal Feed	18
2.5.5	Bio Refining Industry	18
2.6	Improvement of Microbial Cellulases	19
2.6.1	Rational Design	19
2.6.2	Directed Evolution	20
2.7	Application of 16S rRNA for Bacterial Identification	21
<b>3</b>	<b>MATERIALS AND METHODS</b>	<b>22</b>
3.1	Source and Location of the Sample	22
3.2	Preparation of Media and Reagents	23
3.2.1	Preparation of ABM	23
3.2.2	Preparation of CMC Agar	24
3.2.3	Preparation of Glycerol Stock	24
3.2.4	Preparation of Grams Iodine	25
3.3	Isolation of Psychrotrophic Bacteria	25
3.3.1	Isolation of Pure Bacterial Culture	26



3.4	Screening of Cellulolytic Activity of the Isolates	26
3.4.1	Effect of Temperature and pH on the Bacterial Cellulolytic Activity	27
3.4.2	Effects of Salinity on Cellulolytic Activity of the Bacterial Isolates	28
3.5	Bacterial Identification	28
3.5.1	Grams Staining reaction and Microscopy	29
3.5.2	Colony Morphological characterization of the cellulolytic isolates	29
3.6	Molecular Characterization of the Isolates	29
3.6.1	Genomic DNA Extraction	30
3.6.2	Spectrophotometer Nanodrop	30
3.6.3	Agarose Gel Electrophoresis	31
3.6.4	Polymerase Chain Reaction Amplification of 16S rRNA Gene Analysis	31
3.6.5	DNA Sequence Analysis of the Samples	33
3.6.6	Multiple Sequence Alignment and Phylogenetic Tree Construction	33
3.6.7	Research Flow Chart	34
<b>4</b>	<b>RESULTS AND DISCUSSION</b>	<b>35</b>
4.1	Isolation of Psychrotrophic Bacteria	35
4.1.1	Glycerol Stock Cultures	36
4.2	Screening of Cellulolytic Activity	36
4.2.1	Effect of temperature and pH on cellulolytic activity of the bacterial isolates	38
4.2.2	Effect of Salinity on the Bacterial Cellulolytic Activity	41
4.3	Bacterial Identification	43

4.3.1 Grams Staining Reaction	43
4.3.2 Colony and Cellular Morphology of the cellulolytic isolates	43
4.4 Molecular Characterization	44
4.4.1 Genomic DNA Extraction	44
4.4.2 Polymerase Chain Reaction (PCR)	45
4.4.3 Analysis of the 16S rRNA Gene Sequence	47
4.4.4 BLAST Result and -Phylogenetic Tree Construction	47
<b>5 CONCLUSION AND RECOMMENDATION</b>	<b>52</b>
5.1 Conclusion	52
5.2 Recommendation for future work	53
REFERENCES	54
APPENDICES	64

**LIST OF TABLES**

<b>TABLE NO.</b>	<b>TITLE</b>	<b>PAGE</b>
3.1	chemical composition of ABM	23
3.2	Chemical Composition of Carboxymethyl Cellulose (CMC) agar	24
3.3	composition of reaction mix for PCR	32
3.4	properties of universal primers used	32
3.5	PCR thermal cycling profile	33
4.1	Summarized Results for Cellulolytic Activity of the Bacterial Isolates	37
4.2	Effect of temperature and pH on cellulolytic activity of the bacterial isolates	39
4.3	Effect of salinity on cellulolytic activity of the bacterial isolates	41
4.4	Colony Morphological Characterization of the Isolates	44
4.5	DNA Quantitative analysis (Nanodrop)	45

**LIST OF FIGURES**

<b>FIGURE NO.</b>	<b>TITLE</b>	<b>PAGE</b>
3.1	Sample location	22
3.2	Serial Dilution Method	25
3.3	Flow Chart	34
4.1	Bacterial Cellulose Activity on CMC Agar Plates	37
4.2	Cellulolytic Bacterial Activity 10% and 15% Salt Concentrations (a) and (a) respectively.	42
4.4	Agarose Gel Electrophoresis of PCR Products	46
4.5	Phylogenetic trees showing the relationships between the isolates with their related species	50

**LIST OF ABBREVIATIONS**

CMC	-	Carboxymethyl Cellulose
ABM	-	Antarctic Bacterium Medium
DNA	-	Deoxyribonucleic Acid
RNA	-	Ribonucleic Acid
<i>et al.</i>	-	And others
cm	-	centimeter
g	-	grams
ml	-	Milliliter
nm	-	Nanometer
L	-	Liter
pH	-	Hydrogen ion concentration
rpm	-	Rotation per minute
v/v	-	Volume by volume
w/v	-	Weight by volume
%	-	percent
°C	-	Degree Celsius
PCR	-	Polymerase Chain Reaction
rRNA	-	Ribosomal ribonucleic acid
BLAST	-	Basic Local Alignment search Tool
NCBI	-	National Centre for Biotechnology information
sp.	-	species
β	-	Beta
H <sub>c</sub>	-	Hydrolytic coefficient

$\mu\text{l}$	-	Microlitre
EtBr	-	Ethidium Bromide
UV	-	Ultra violet

**LIST OF APPENDICES**

<b>APPENDIX</b>	<b>TITLE</b>	<b>PAGE</b>
A	Grams Staining steps and Results	64
B	Multiple Sequence Alignment Results (BLAST)	66
C	Results of the Sequences	69
D	Genomic DNA Extraction	72

## CHAPTER 1

### INTRODUCTION

#### 1.1 Background of the study

Cold environment are the most abundant environment on the planet surface which has been successfully colonizes by a vast number of microorganisms. Bacteria, Fungi, Unicellular Algae, and Yeast are the most diverse group due to their closed internal temperature, when it is not identical to their surrounding environment. In spite of the durable negative consequence of low temperatures on biological reactions, these organisms sort, grow and change at rates comparable to those attained by closely related class existing in temperate surroundings. They have consequently developed numerous adaptations in the form of wonderfully adjusted organizational changes at their cellular level, for example, their membranes, constitutive proteins and enzymes, enabling them to compensate for the deleterious effects of low temperature (Gerday *et al.*, 2000).

The extreme cold environment have been found to contain several habitats such as sea water , ice, and permafrost, which can serve as the region potentially used for isolation of bacteria with biotechnological abilities (Reddy *et al.*, 2009). The cold regions have become a model system for global warming and are regarded



as key European sites for biodiversity monitoring (Reddy *et al.*, 2009). The extreme cold region such as arctic and antarctica have been found to constitute more than 14% of the biosphere and are the most coldest and most arid environment on earth (Møller *et al.*, 2011). The structure and function of arctic soil microbial communities with the various numbers of glaciers contained by arctic, little is known about the diversity of bacteria in the glaciers (Reddy *et al.*, 2009).

Various range of microbes have been revealed to be found in cold environment and comprises of representatives of the bacteria, eukaryotes and Achaea (Cavicchioli, *et al.*, 2002). Microorganisms found to adapt low - temperature for their optimal growth condition under natural and artificial condition are divided into psychrophiles which are capable of growing at temperature above 20°C and psychrotrophs those that can grow optimally at temperature between 15°C and 30°C (Kato, *et al.*, 2001). The psychrotrophic microorganisms that have the potential in natural bioremediation of certain organic compounds such as hydrocarbons in the soil, water, and marine environment are cold adapted and metabolically poorly understood, despite their importance in bioremediation (Kato *et al.*, 2001)

The survival of microorganisms to harsh environmental conditions has made them very promising source for bio prospecting. These environmental conditions are extensively described as drivers for several processes in existing organisms; this contributes to microbial selection for differential enzymatic activity. Stressing factors have been divided into physical (pressure, temperature, and radiation), and geochemical (pH and salinity) which are the contributing factors for microbial diversity (Van Den Burg, 2003). Soil microorganisms, has been found to play an important role in bioconversion and degradation of organic matter. Soil bacteria has the ability to decomposed cellulose- based materials (Soares *et al.*, 2012). The resistance to extreme temperatures, pH and pressure by the microorganisms and synthesis of particular enzymes are necessary for their adaptive response (Clarke, 2003). The microbial presence in such condition are of enormous importance for the exploration of biodiversity in biotechnology (Soares *et al.*, 2012)

Cellulases as the term refer to the group of enzymes that can catalyze the hydrolysis of cellulose into sugars. Therefore cellulolytic microorganisms plays and important role in the biosphere by recycling cellulose, which is the most abundant carbohydrate produced by plant (Kasana *et al.*, 2008). Microorganisms with cellulolytic enzymes have many potential biotechnological as well as industrial applications; it is therefore required in a large quantities due to their industrial applications, such as; detergent, animal feed, textile biofuel, paper and pulp, waste management and pharmaceuticals (Kasana *et al.*, 2008).

The study of cultivable cold adaptive cellulases producing bacteria are of metabolically important owing to their potential in biodegradation, these group of bacteria have been found to contain various enzymes with bioremediation and industrial applications (Rashid *et al.*, 1999). The enzymes with thermo stable activity are of great importance for industries (Rashid *et al.*, 1999). However enzymes with little stability at elevated temperature are favourable for some purposes especially in certain reaction which can only be activated at low temperature. Sources such as arctic and antarctica are expected to contain microorganisms that can produce cold adapted enzymes (Rashid *et al.*, 1999). The properties of cold-active enzymes may be responsible for various industrial applications, though, specific properties may be enhanced through enzymes engineering (Cavicchioli *et al.*, 2002).

The 16S rDNA sequence is the most widely used to study bacterial phylogenetic relationship due to its presence in almost all bacteria existing as a multi genic family or their operons (Janda and Abbott, 2007). The gene sequencing of the 16S rDNA in the laboratory has been considered to be reliable method for identification of unidentified bacteria biochemically by providing reference from the strain of related species (Janda and Abbott, 2007). The 16S rDNA sequence has an intensifying role in the proof of identity of bacteria, but it is not fool proof and relevant in each and every situation (Janda and Abbott, 2007). It is imprecise, however, whether the outcomes from laboratory investigation with these categories of bacteria can be generalized to the extreme cold environment, since the bacteria originated from the arctic and other cold region remain only remotely associated to

the *gamma-proteobacteria* (*Escherichia .coli* and *vibrio*) and other cultured bacteria inspected in the laboratory experimentations conducted to date (Kirchman *et al.*, 2005).

## 1.2 Problem statement

Microbial life have proved not limited to specific environments, as microorganisms can be found in the most diverse area with extreme conditions, such as temperature, salinity , pH, and pressure. Extremophiles produced functional biocatalyst under extreme condition; the unique properties of this biocatalyst have impacts on industrial processes (Van Den Burg, 2003). The presence of microorganisms living in extreme cold environment such as arctic and antarctic regions is important for the biotechnological exploration as well as biodiversity. From a biotechnological perspective, it might be useful to study organisms found in harsh environments. Such organisms could have enzymes that can reduce complex molecules, like cellulose, which is the most ample renewable energy source on Earth (Soares *et al.*, 2012). However, the complete degradation of cellulose requires the action of various enzymes, cooperatively called cellulases, due to its complex assembly.

The screening of cellulolytic bacterial community isolated from cold environment is of immense importance owing to their biotechnological potentials, which may lead to the enzymes discovery and the improvement of their biotechnological applications. This group of microorganisms are anticipated to produce several numbers of cold adapted enzymes such as cellulases and other hydrolases. Though, there have been limited number of reports on the screening and characterization of bacteria with cellulolytic activity from extreme cold environment, which may be found to have the potential to play a significant role in bioremediation as well as industrial applications. Therefore, it is in the light of the above; that this

research is designed with the aim of isolating psychotropic bacteria with cellulolytic activity from the arctic soil and sediment samples. There is a need to further the study and characterize bacteria from such environments. This research will further explore in the search for cellulolytic enzymes to be used in bioenergy industries. At present-day, only a slight portion of the microorganisms on Earth have been exploited.

### **1.3 Objectives of the study**

This research was aimed at isolating psychotropic bacteria with cellulolytic activity from the arctic soil and sediment samples and test the effects of growth parameters for their activity. The main objectives of the study are;

1. To isolate and screen for bacteria with cellulolytic activity from arctic soil and sediment samples
2. To test the effect of pH, temperature and salinity on the bacterial cellulolytic activity
3. To identify bacteria with high cellulolytic activity using the 16S rRNA gene sequencing method

#### **1.4 Scope of the research**

This research was focused on the isolation, screening, characterization and identification of cellulolytic bacteria associated with extreme cold environment (arctic region) , the bacteria with the high cellulolytic activity among test isolates were identified further using 16S rDNA characterizations methods, The bacteria identified were further subjected to different temperature condition, pH and salinity to observe the effects of the physical parameters on the cellulolytic activity of the isolates.

#### **1.5 Significance of the research**

The extreme cold environment has been identified as major source of new natural products and also serves as the source for bio-prospecting of bacteria with cellulolytic activity. It harbours many bacteria that survive under different low temperature. This study when completed will give an insight to the understanding of the role of bacteria isolated from cold environment as well as their ability to produce cellulolytic enzymes under low temperature. This study will serve as starting point to further the research on enzymes produced by bacteria that can be used for biotransformation at low temperature and further promote the industrial applications of cellulase in the production of animal feeds, textiles, detergents and food processing industries as well as bioenergy industries.

## REFERENCES

- Abascal, F. and Valecia, A (2002). Clustering of Proximal Sequence Space for the Identification of Protein Families. *Bioinformatics*, 18(7), 908-921.
- Agematu, H., Suzuki, K., and Tsuya, H. (2011). *Massilia* sp. BS-1, a novel violacein-producing bacterium isolated from soil. *Bioscience, Biotechnology, and Biochemistry*, 75(10), 2008-2010.
- Armstrong, G. A., Alberti, M., Leach, F., and Hearst, J. E. (1989). Nucleotide sequence, organization, and nature of the protein products of the carotenoid biosynthesis gene cluster of *Rhodobacter capsulatus*. *Molecular and General Genetics MGG*, 216(2-3), 254-268.
- BEguin, P. and Aubert, J.P. (1994). The biological degradation of cellulose. *FEMS Microbiology Reviews*, 13(1), 25-58.
- Bhat, M. (2000). Cellulases and related enzymes in biotechnology. *Biotechnology Advances*, 18(5), 355-383.
- Bhat, M., and Bhat, S. (1997). Cellulose degrading enzymes and their potential industrial applications. *Biotechnology Advances*, 15(3), 583-620.

- Boesenberg-Smith, K. A., Pessarakli, M. M., and Wolk, D. M. (2012). Assessment of DNA yield and purity: an overlooked detail of PCR troubleshooting. *Clinical Microbiology Newsletter*, 34(1), 1-6.
- Cavicchioli, R., Siddiqui, K. S., Andrews, D., and Sowers, K. R. (2002). Low-temperature extremophiles and their applications. *Current Opinion in Biotechnology*, 13(3), 253-261.
- Clarke, A. (2003). Evolution, adaptation and diversity: global ecology in an Antarctic context.
- Davies, G., and Henrissat, B. (1995). Structures and mechanisms of glycosyl hydrolases. *Structure*, 3(9), 853-859.
- de Pascale, D., De Santi, C., Fu, J., and Landfald, B. (2012). The microbial diversity of Polar environments is a fertile ground for bioprospecting. *Mararine Genomics*, 8, 15-22. doi: 10.1016/j.margen.2012.04.004
- Deming, J. (2010). Extremophiles: cold environments. *Desk Encyclopedia of Microbiology*, 483.
- Doi, R. (2008). Cellulases of mesophilic microorganisms. *Annals of the New York Academy of Sciences*, 1125(1), 267.
- Fagade, O., and Bamigboye, O. (2012). Effect of cultural conditions on the cellulase activity of bacteria species isolated from degrading corn cob. *Archives of Applied Science Research*, 4(6).

Frank, J. A., Reich, C. I., Sharma, S., Weisbaum, J. S., Wilson, B. A., and Olsen, G. J. (2008). Critical evaluation of two primers commonly used for amplification of bacterial 16S rRNA genes. *Applied Environmental Microbiology*, 74(8), 2461-2470.

Friedmann, E. I., and Thistle, A. B. (1993). Antarctic microbiology.

Gerday, C., Aittaleb, M., Bentahir, M., Chessa, J.P., Claverie, P., Collins, T., Georgette, D. (2000). Cold-adapted enzymes: from fundamentals to biotechnology. *Trends in Biotechnology*, 18(3), 103-107.

Hankin, L., and Anagnostakis, S. L. (1977). Solid media containing carboxymethylcellulose to detect Cx cellulase activity of micro-organisms. *Journal of General Microbiology*, 98(1), 109-115.

Hazlewood, G., Laurie, J., Ferreira, L., and Gilbert, H. (1992). *Pseudomonas fluorescens* subsp. cellulosa: an alternative model for bacterial cellulase. *Journal of Applied Bacteriology*, 72(3), 244-251.

Henrissat, B., Teeri, T., and Warren, R. (1998). A scheme for designating enzymes that hydrolyse the polysaccharides in the cell walls of plants. *FEBS Letters*, 425(2), 352-354.

Horneck, G. (2000). The microbial world and the case for Mars. *Planetary and Space Science*, 48(11), 1053-1063.



- Hugenholtz, P., Goebel, B. M., and Pace, N. R. (1998). Impact of culture-independent studies on the emerging phylogenetic view of bacterial diversity. *Journal of bacteriology*, 180(18), 4765-4774.
- Ibrahim, A. S. S., and El-diwany, A. I. (2007). Isolation and identification of new cellulases producing thermophilic bacteria from an Egyptian hot spring and some properties of the crude enzyme. *Australian Journal of Basic and Applied Sciences*, 1(4), 473-478.
- Janda, J. M., and Abbott, S. L. (2007). 16S rRNA gene sequencing for bacterial identification in the diagnostic laboratory: pluses, perils, and pitfalls. *Journal of Clinical Microbiology*, 45(9), 2761-2764.
- Jeon, J. H., Kim, J.-T., Kang, S. G., Lee, J.-H., and Kim, S.-J. (2009). Characterization and its potential application of two esterases derived from the arctic sediment metagenome. *Marine Biotechnology (NY)*, 11(3), 307-316.
- Juturu, V., and Wu, J. C. (2014). Microbial cellulases: Engineering, production and applications. *Renewable and Sustainable Energy Reviews*, 33, 188-203.
- Kasana, R. C., Salwan, R., Dhar, H., Dutt, S., and Gulati, A. (2008). A rapid and easy method for the detection of microbial cellulases on agar plates using Gram's iodine. *Current Microbiology*, 57(5), 503-507.
- Kato, T., Haruki, M., Imanaka, T., Morikawa, M., and Kanaya, S. (2001). Isolation and characterization of psychrotrophic bacteria from oil-reservoir water and

oil sands. *Applied Microbiology and Biotechnology*, 55(6), 794-800. doi: 10.1007/s002530000556

Kim, J. (2014). *Massilia kyonggiensis* sp. nov., isolated from forest soil in Korea. *Journal of Microbiology*, 52(5), 378-383.

Kirchman, D. L., Malmstrom, R. R., and Cottrell, M. T. (2005). Control of bacterial growth by temperature and organic matter in the Western Arctic. *Deep Sea Research Part II: Topical Studies in Oceanography*, 52(24), 3386-3395.

Kramer, M. F., and Coen, D. M. (2001). Enzymatic amplification of DNA by PCR: Standard procedures and optimization. *Current Protocols in Toxicology*, A. 3C. 1-A. 3C. 14.

Krumbein, W. E. (1996). Geophysiology and Parahistology of the Interactions of Organisms with the Environment. *Marine Ecology*, 17(1-3), 1-21.

La Scola, B., Birtles, R. J., Mallet, M.-N., and Raoult, D. (1998). *Massilia timonae* gen. nov., sp. nov., isolated from blood of an immunocompromised patient with cerebellar lesions. *Journal of Clinical Microbiology*, 36(10), 2847-2852.

Maki, M., Leung, K. T., and Qin, W. (2009). The prospects of cellulase-producing bacteria for the bioconversion of lignocellulosic biomass. *International Journal of Biological Sciences*, 5(5), 500.

Maki, M. L., Broere, M., Leung, K. T., and Qin, W. (2011). Characterization of some efficient cellulase producing bacteria isolated from paper mill sludges

and organic fertilizers. *International journal of Biochemistry and Molecular Biology*, 2(2), 146.

Margesin, R., and Miteva, V. (2011). Diversity and ecology of psychrophilic microorganisms. *Research Microbiol*, 162(3), 346-361.

Margesin, R., and Miteva, V. (2011). Diversity and ecology of psychrophilic microorganisms. *Research Microbiology*, 162(3), 346-361. doi: 10.1016/j.resmic.2010.12.004

Medie, F. M., Davies, G. J., Drancourt, M., and Henrissat, B. (2012). Genome analyses highlight the different biological roles of cellulases. *Nature Reviews Microbiology*, 10(3), 227-234.

Møller, A. K., Barkay, T., Al-Soud, W. A., Sørensen, S. J., Skov, H., and Kroer, N. (2011). Diversity and characterization of mercury-resistant bacteria in snow, freshwater and sea-ice brine from the High Arctic. *FEMS Microbiology Ecology*, 75(3), 390-401.

Muyzer, G., De Waal, E. C., and Uitterlinden, A. G. (1993). Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. *Applied Environmental Microbiology*, 59(3), 695-700.

Newman, M. M., Feminella, J. W., and Liles, M. R. (2010). Purification of genomic DNA extracted from environmental sources for use in a polymerase chain reaction. *Cold Spring Harbor Protocols*, 2010(2), pdb. prot5383-pdb. prot5383.

- Niehaus, F., Bertoldo, C., Kähler, M., and Antranikian, G. (1999). Extremophiles as a source of novel enzymes for industrial application. *Applied Microbiology and Biotechnology*, 51(6), 711-729.
- Percival Zhang, Y.-H., Himmel, M. E., and Mielenz, J. R. (2006). Outlook for cellulase improvement: screening and selection strategies. *Biotechnology Advances*, 24(5), 452-481.
- Prakash, O., Nimonkar, Y., and Shouche, Y. S. (2013). Practice and prospects of microbial preservation. *FEMS Microbiol Letter*, 339(1), 1-9.
- Rashid, N., Kikuchi, H., Ezaki, S., Atomi, H., and Imanaka, T. (1999). Isolation and characterization of psychrotrophs from subterranean environments. *Journal of Bioscience and Bioengineering*, 87(6), 746-751.
- Rastogi, G., Muppidi, G. L., Gurram, R. N., Adhikari, A., Bischoff, K. M., Hughes, S. R., Sani, R. K. (2009). Isolation and characterization of cellulose-degrading bacteria from the deep subsurface of the Homestake gold mine, Lead, South Dakota, USA. *Journal of Industrial Microbiology and Biotechnology*, 36(4), 585-598.
- Rohban, R., Amoozegar, M. A., and Ventosa, A. (2009). Screening and isolation of halophilic bacteria producing extracellular hydrolyses from Howz Soltan Lake, Iran. *Journal of industrial microbiology and biotechnology*, 36(3), 333-340.
- Rolfe, M. D., Rice, C. J., Lucchini, S., Pin, C., Thompson, A., Cameron, A. D., Baranyi, J. (2012). Lag phase is a distinct growth phase that prepares bacteria

for exponential growth and involves transient metal accumulation. *Journal of Bacteriology*, 194(3), 686-701.

Sato, M., Beppu, T., and Arima, K. (1983). Studies on antibiotics produced at high alkaline pH. *Agricultural and Biological Chemistry*, 47(9), 2019-2027.

Sethi, S., Datta, A., Gupta, B. L., and Gupta, S. (2013). Optimization of cellulase production from bacteria isolated from soil. *International Scholarly Research Notices*, 2013.

Smith, J. J., Tow, L. A., Stafford, W., Cary, C., and Cowan, D. A. (2006). Bacterial diversity in three different Antarctic Cold Desert mineral soils. *Microbial Ecology*, 51(4), 413-421. doi: 10.1007/s00248-006-9022-3

Soares Jr, F. L., Melo, I. S., Dias, A. C. F., and Andreote, F. D. (2012). Cellulolytic bacteria from soils in harsh environments. *World Journal of Microbiology and Biotechnology*, 28(5), 2195-2203.

Stackebrandt, E., Liesack, W., and Witt, D. (1992). Ribosomal RNA and rDNA sequence analyses. *Gene*, 115(1), 255-260.

Tamura, K., Stecher, G., Peterson, D., Filipinski, A., and Kumar, S. (2013). MEGA6: molecular evolutionary genetics analysis version 6.0. *Molecular biology and evolution*, 30(12), 2725-2729.

Ueda, M., Goto, T., Nakazawa, M., Miyatake, K., Sakaguchi, M., and Inouye, K. (2010). A novel cold-adapted cellulase complex from *Eisenia foetida*. Characterization of a multi enzyme complex with carboxymethylcellulase,  $\beta$ -

glucosidase,  $\beta$ -1, 3 glucanase, and  $\beta$ -xylosidase. *Comparative Biochemistry and Physiology Part B: Biochemistry and Molecular Biology*, 157(1), 26-32.

V Wintzingerode, F., Göbel, U. B., and Stackebrandt, E. (1997). Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. *FEMS Microbiology Reviews*, 21(3), 213-229.

Van Den Burg, B. (2003). Extremophiles as a source for novel enzymes. *Current Opinion in Microbiology*, 6(3), 213-218.

Vardhan Reddy, P. V., Shiva Nageswara Rao, S. S., Pratibha, M. S., Sailaja, B., Kavya, B., Manorama, R. R., Shivaji, S. (2009). Bacterial diversity and bioprospecting for cold-active enzymes from culturable bacteria associated with sediment from a melt water stream of Midtre Lovénbreen glacier, an arctic glacier. *Research Microbiology*, 160(8), 538-546. doi: 10.1016/j.resmic.2009.08.008

Venkatachalam, S., Sivaprakash, M., Gowdaman, V., and Prabakaran, S. R. (2014). Bioprospecting of Cellulase Producing Extremophilic Bacterial Isolates from India. *British Microbiology Research Journal*, 4(2), 142-154.

Wang, J., Zhang, J., Pang, H., Zhang, Y., Li, Y., and Fan, J. (2012). *Massilia flava* sp. nov., isolated from soil. *International Journal of Systematic and Evolutionary Microbiology*, 62(Pt 3), 580-585.

Wang, L., and Stegemann, J. P. (2010). Extraction of high quality RNA from polysaccharide matrices using cetyltrimethylammonium bromide. *Biomaterials*, 31(7), 1612-1618.

- Weisburg, W. G., Barns, S. M., Pelletier, D. A., and Lane, D. J. (1991). 16S ribosomal DNA amplification for phylogenetic study. *Journal of Bacteriology*, 173(2), 697-703.
- Zahran, H. (1997). Diversity, adaptation and activity of the bacterial flora in saline environments. *Biology and Fertility of Soils*, 25(3), 211-223.
- Zhang, N., Suen, W. C., Windsor, W., Xiao, L., Madison, V., and Zaks, A. (2003). Improving tolerance of *Candida antarctica* lipase B towards irreversible thermal inactivation through directed evolution. *Protein Engineering*, 16(8), 599-605.
- Zhang, Y.Q., Li, W.-J., Zhang, K.Y., Tian, X.-P., Jiang, Y., Xu, L.H., . . . Lai, R. (2006). *Massilia dura* sp. nov., *Massilia albidiflava* sp. nov., *Massilia plicata* sp. nov. and *Massilia lutea* sp. nov., isolated from soils in China. *International Journal of Systematic and Evolutionary Microbiology*, 56(2), 459-463.