UNIVERSITI PUTRA MALAYSIA

BIODEGRADATION POTENTIAL OF PHENOL BY PURE AND DEFINED MIXED COLD-ADAPTED BACTERIAL CONSORTIA FROM ANTARCTICA

KAVILASNI A/P SUBRAMANIAM

FBSB 2022 1

BIODEGRADATION POTENTIAL OF PHENOL BY PURE AND DEFINED MIXED COLD-ADAPTED BACTERIAL CONSORTIA FROM ANTARCTICA

By

KAVILASNI A/P SUBRAMANIAM

Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in Fulfillment of the Requirements for the Degree of Doctor of Philosophy

November 2021

DEDICATION

This thesis is dedicated with love and grateful heart

To amma, naina, anna, ruby and my better half,

To my mentors and friends,

and

To all those good souls who wished well during this journey

Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Doctor of Philosophy

BIODEGRADATION POTENTIAL OF PHENOL BY PURE AND DEFINED MIXED COLD-ADAPTED BACTERIAL CONSORTIA FROM ANTARCTICA

By

KAVILASNI A/P SUBRAMANIAM

November 2021

Chair : Associate Professor Siti Aqlima Binti Ahmad, PhD
Faculty : Biotechnology and Biomolecular Sciences

The risk of phenol pollution from daily waste discharge and accidental oil spillage is ever-present due to increasing activities in the Antarctic continent, mainly related to the supply and operation of research stations and field expeditions, tourism, marine and air transportation. Increased levels of phenol concentration in the Antarctic environment bring significant risk to both aquatic and terrestrial biota due to its highly toxic properties and persistence. Sustainable human presence and activity in Antarctica require effective remediation technologies to be developed and their rapid application when required. The main purpose of the present study was to isolate new taxa of pure phenol-degrading bacteria from Antarctic soil and, both as a pure isolate and together with previously isolated phenol-degrading bacteria as a consortium, will be capable of rapid degradation of phenol at low temperatures (0-15°C). In addition, this study also focuses on identification of phenol-degrading pathway(s) of the pure culture, conventional and statistical optimisations of phenol degradation by both pure and mixed cultures, and the effect of heavy metals on phenol degradation by pure and mixed cultures. This thesis reports the isolation of a potential phenol-degrading bacterial strain (AQ5-15) from soil from King George Island, South Shetland Islands, Antarctica. This strain was identified as a member of the genus *Arthrobacter* based on 16S rRNA gene sequence analysis. Based on whole genome sequencing (WGS), the strain's nearest identified relative was suggested to be *Paeniglutamicibacter sulfureus* (99.38% similarity). Preliminary screening showed that strain AQ5-15 was capable of completely degrading 0.5 g/L phenol within 108 h at 10°C and it was selected for a detailed study. The genomic analysis identified the presence of genes encoding a complete pathway of aromatic compound metabolism in strain AQ5-15, consistent with the ability of the strain to utilise phenol as the sole carbon source. The genomic analysis was validated using enzyme assays of catechol 1,2-dioxygenase and catechol 2,3-dioxygenase, which confirmed the presence of the enzyme catechol 1,2-dioxygenase, consistent with the genes identified in the WGS. A study of the influence of parameters including nitrogen source, salinity, pH, and temperature

was conducted to optimise the conditions for phenol degradation using one-factor-at-a-time (OFAT) and response surface methodology (RSM). Based on the results from OFAT, strain AQ5-15 showed the highest phenol degradation at 0.5 g/L $(NH_4)_2SO_4$, 0.1 g/L NaCl, pH 7 and 20°C, proving that this strain is a psychrotolerant and prefers low salinity and near-neutral conditions. Statistical analysis of the results obtained from RSM showed that the strain could degrade phenol optimally at 0.5 g/L $(NH_4)_2SO_4$, 0.13 g/L NaCl, pH 7.25 and 15°C, with pH and temperature identified as significant factors. This strain was mixed with two other previously isolated phenol-degrading strains (AQ5-06 and AQ5-07) in different combinations to further enhance degradation efficiency. The data obtained showed that mixture of strains AQ5-06 and AQ5-15 together could completely degrade 0.5 g/L phenol within 48 h at 10°C while mixture of strains AQ5-06, AQ5-07 and AQ5-15 together could completely degrade 0.5 g/L phenol within 60 h at 10°C. RSM analysis showed that the combination of strains AQ5-06 and AQ5-15 could degrade phenol optimally at 0.4 g/L $(NH_4)_2SO_4$, 0.13 g/L NaCl, pH 7.25 and 12.5°C, with only temperature as a significant factor. RSM analysis showed that the combination of strains AQ5-06, AQ5-07 and AQ5-15 can degrade phenol optimally at 0.4 g/L $(NH_4)_2SO_4$, 0.13 g/L NaCl, pH 7.25 and 12.5°C, with ammonium sulphate concentration, sodium chloride concentration and temperature being significant factors. The tolerance levels of pure and mixed cultures towards different heavy metals that are widely present in Antarctic soils was studied by exposing strains AQ5-06, AQ5-07 and AQ5-15 individually as well as in consortia to the heavy metals Arsenic (As), Aluminum (Al), Copper (Cu), Zinc (Zn), Lead (Pb), Cobalt (Co), Cadmium (Cd), Chromium (Cr), Nickel (Ni), Silver (Ag) and Mercury (Hg) at an initial concentration of 1.0 ppm. Phenol degradation by strain AQ5-15 was inhibited when exposed to Cd, Ag and Hg while strain AQ5-06 was inhibited when exposed to Ag and Hg, and strain AQ5-07 was inhibited when exposed to Cd and Hg. Consortia containing strains AQ5-06 and AQ5-15 and all three strains were inhibited when exposed to Hg, Cd and Ag. In a nutshell, the attempt to develop highly efficient phenol-degrading bacterial consortia for significant inclusion in cold region bioremediation, specifically Antarctica was successful with a few limitations in the event of the co-occurrence of some heavy metals such as Hg, Cd, and Ag.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah Doktor Falsafah

POTENSI PENGURAIAN FENOL OLEH KULTUR BAKTERIA TULEN DAN CAMPURAN YANG SEJUK BERADAPTASI DARI ANTARTIKA

Oleh

KAVILASNI A/P SUBRAMANIAM

November 2021

Pengerusi : Profesor Madya Siti Aqlima Ahmad, PhD
Fakulti : Bioteknologi dan Sains Biomolekul

Kesan negatif akibat pencemaran fenol daripada pembuangan sampah harian dan tumpahan minyak yang tidak disengajakan selalu terjadi disebabkan oleh peningkatan aktiviti di benua Antartika, khususnya yang berkaitan dengan pembekalan dan operasi stesen penyelidikan dan ekspedisi lapangan, pelancongan dan pengangkutan laut dan udara. Peningkatan tahap kepekatan fenol di persekitaran Antartika membawa risiko yang tinggi kepada biota akuatik dan daratan kerana sifatnya yang sangat toksik dan kekekalannya. Kehadiran dan aktiviti manusia yang berterusan di Antartika memerlukan teknologi pemulihan yang berkesan untuk dikembangkan. Tujuan utama kajian ini adalah untuk mengasingkan taksa baharu bakteria tulen yang dapat menguraikan fenol daripada tanah Antartika dan, kedua-duanya sebagai bakteria tulen dan campuran bakteria pengurai fenol yang diasingkan sebelum, akan mampu menguraikan fenol dalam masa singkat pada suhu rendah (0-15°C). Di samping itu, kajian ini juga memfokuskan pada pengenalpastian laluan jalan lengkap metabolisme fenol bagi kultur tulen, pengoptimuman konvensional dan statistik penguraian fenol oleh kedua-dua kultur tulen dan campuran, dan kesan logam berat ke atas penguraian fenol oleh kultur tulen dan campuran. Tesis ini melaporkan pengasingan strain bakteria yang dapat menguraikan fenol (AQ5-15) dari tanah dari King George Island, South Shetland Islands, Antartika. Strain ini dikenal pasti sebagai genus *Arthrobacter* sp. berdasarkan analisis gen 16S rRNA. Berdasarkan penjujukan keseluruhan genom (WGS), spesis terdekat yang dikenal pasti kepada strain ini dicadangkan sebagai *Paeniglutamicibacter sulfureus* (99.38% kesamaan). Pemeriksaan awal menunjukkan bahawa strain AQ5-15 mampu menguraikan 0.5 g/L fenol sepenuhnya dalam masa 108 jam pada suhu 10°C dan dipilih untuk kajian terperinci. Analisis genomik mengenal pasti adanya gen yang mengekodkan jalan lengkap metabolisme sebatian aromatik dalam strain AQ5-15, selaras dengan kemampuan strain untuk

menggunakan fenol sebagai sumber karbon tunggal. Analisis genomik disahkan menggunakan ujian enzim catechol 1,2-dioxygenase dan catechol 2,3-dioxygenase, yang mengesahkan adanya enzim catechol 1,2-dioxygenase, selaras dengan gen yang dikenal pasti dalam WGS. Kajian mengenai pengaruh parameter termasuk sumber nitrogen, saliniti, pH dan suhu dilakukan untuk mengoptimumkan keadaan penguraian fenol dengan menggunakan satu faktor-pada-satu-waktu (OFAT) dan metodologi permukaan tindak balas (RSM). Berdasarkan hasil dari OFAT, strain AQ5-15 menunjukkan degradasi fenol tertinggi pada 0.5 g/L $(NH_4)_2SO_4$, 0.1 g/L NaCl, pH 7 dan 20°C, membuktikan bahawa strain ini boleh tahan sejuk dan lebih suka keadaan kemasinan rendah dan kondisi hampir neutral. Hasil analisis statistik yang diperoleh dari RSM menunjukkan bahawa strain ini dapat menguraikan fenol secara optimum pada 0.5 g/L $(NH_4)_2SO_4$, 0,13 g/L NaCl, pH 7.25 dan 15°C, dengan pH dan suhu dikenal pasti sebagai faktor penting. Dalam usaha untuk meningkatkan lagi kecekapan degradasi, strain ini dicampur dengan dua strain pengurai fenol yang terpencil sebelum ini (AQ5-06 dan AQ5-07) dalam kombinasi yang berbeza. Data yang diperoleh menunjukkan bahawa strain AQ5-06 dan AQ5-15 bersama-sama dapat menguraikan 0.5 g/L fenol sepenuhnya dalam masa 48 jam pada suhu 10°C sementara strain AQ5-06, AQ5-07 dan AQ5-15 bersama-sama dapat menguraikan 0.5 g/L fenol sepenuhnya dalam masa 60 jam pada suhu 10°C. Analisis RSM menunjukkan bahawa gabungan strain AQ5-06 dan AQ5-15 dapat menguraikan fenol secara optimum pada 0.4 g/L $(NH_4)_2SO_4$, 0.13 g/L NaCl, pH 7.25 dan 12.5°C, dengan hanya suhu sebagai faktor yang signifikan. Analisis RSM menunjukkan bahawa gabungan strain AQ5-06, AQ5-07 dan AQ5-15 dapat menguraikan fenol secara optimum pada kadar 0.4 g/L $(NH_4)_2SO_4$, 0.13 g/L NaCl, pH 7.25 dan 12.5°C, dengan kepekatan ammonium sulfat, kepekatan natrium klorida dan suhu menjadi faktor signifikan. Tahap toleransi kultur tulen dan campuran terhadap logam berat yang berlainan yang terdapat secara meluas di tanah Antartika dikaji dengan mendedahkan strain AQ5-06, AQ5-07 dan AQ5-15 secara individu dan juga konsortia kepada logam berat Arsenik (As), Aluminium (Al), Kuprum (Cu), Zink (Zn), Plumbum (Pb), Kobalt (Co), Kadmium (Cd), Kromium (Cr), Nikel (Ni), Perak (Ag) dan Merkuri (Hg) pada kepekatan awal 1 ppm. Degradasi fenol oleh strain AQ5-15 direncat ketika terdedah kepada Cd, Ag dan Hg sementara strain AQ5-06 direncat ketika terdedah kepada Ag dan Hg, dan strain AQ5-07 direncat ketika terdedah kepada Cd dan Hg. Konsortia yang mengandungi strain AQ5-06 dan AQ5-15 dan ketiga-tiga strain direncat apabila terdedah kepada Hg, Cd dan Ag. Ciri-ciri toleransi dan degradasi konsortia campuran menunjukkan bahawa penggunaan kultur campuran mungkin bermanfaat dalam tempat yang tercemar dengan fenol, terutamanya di persekitaran ekstrim seperti Antartika. Secara ringkasnya, usaha untuk membina konsortia bakteria yang menguraikan fenol secara pesat bagi penggunaan dalam proses bioremediasi di kawasan sejuk, khususnya Antartika berjaya dengan beberapa batasan sekiranya terdedah kepada beberapa logam berat seperti Hg, Cd, dan Ag.

ACKNOWLEDGEMENTS

'God has been there, every step of the way'

The completion of this undertaking could not have been possible without the participation and assistance of so many people whose name may not all be enumerated. Their contributions are sincerely appreciated and gratefully acknowledged.

First and foremost, my sincere appreciation to my primary supervisor, Associate Professor Dr. Siti Aqlima Ahmad for all the guidances and engagements throughout the learning process of my PhD project. I also would like to extend my sincere gratitude to my supervisory committee, Associate Professor Dr. Noor Azmi Shaharuddin, and Associate Professor Dr. Khalilah Abdul Khalil, for their help and contributions in completing this research project. Besides, I would like to acknowledge Professor Peter Convey from the British Antarctic Survey and Associate Professor Dr. Azham Zulkharnain from Shibaura Institute of Technology for all the comments, remarks, and constant support throughout this study. A special thanks to all lecturers and staffs of Faculty of Biotechnology and Biomolecular Sciences for the cooperation given on completion of this project.

Furthermore, I also owe my deepest appreciation to Universiti Putra Malaysia for providing me with the Graduate Research Fellowship in the beginning of this project. I sincerely appreciate my EcoRemTech family for always being there to support and motivate-Syazani, Nadhirah, Khadijah, Athirrah, Fareez and Syukri. Also, not to forget my other labmates and juniors who will not hesitate to lend their hands whenever I needed one.

Last but not least, my sincere gratitude to my parents, Subramaniam Perumal and Vimila Ayavoo, my brother, Kumar Subramaniam, my sister, Ruibhini Subramaniam and my fiancé, Arwenth Samson for their unrelenting support and confidence in me. Special mention to my well-wishers, Ramitha, Lim Chen Nee, and Lalitha who were there throughout this journey.

Hereby, I express my appreciation for their support, enthusiasm, and optimism.

Thank you.

Kavilasni Subramaniam, 2021

This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Doctor of Philosophy. The members of the Supervisory Committee were as follows:

Siti Aqlima binti Ahmad, PhD
Associate Professor
Faculty of Biotechnology and Biomolecular Sciences,
Universiti Putra Malaysia
(Chairperson)

Noor Azmi bin Noor Shaharuddin, PhD
Associate Professor
Faculty of Biotechnology and Biomolecular Sciences,
University Putra Malaysia
(Member)

Peter Convey, PhD
Professor
British Antarctic Survey
Natural Environment Research Council
United Kingdom
(Member)

Azham bin Zulkharnain, PhD
Associate Professor
Department of Bioscience and Engineering
College of Systems Engineering and Sciences
Shibaura Institute Technology, Japan
(Member)

Khalilah binti Abdul Khalil, PhD
Associate Professor
School of Biology
Faculty of Applied Sciences
Universiti Teknologi MARA
(Member)

_____
ZALILAH MOHD SHARIFF, PhD
Professor and Dean
School of Graduate Studies
Universiti Putra Malaysia

Date: 19 May 2022

Declaration by Graduate Student

I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
- this thesis has not been submitted previously or concurrently for any other degree at any institutions;
- intellectual property from the thesis and the copyright of the thesis are fully-owned by Universiti Putra Malaysia, as stipulated in the Universiti Putra Malaysia (Research) Rules 2012;
- written permission must be obtained from the supervisor and the office of the Deputy Vice-Chancellor (Research and innovation) before the thesis is published in any written, printed or electronic form (including books, journals, modules, proceedings, popular writings, seminar papers, manuscripts, posters, reports, lecture notes, learning modules or any other materials) as stated in the Universiti Putra Malaysia (Research) Rules 2012;
- there is no plagiarism or data falsification/fabrication in the thesis, and scholarly integrity is upheld in accordance with the Universiti Putra Malaysia (Graduate Studies) Rules 2003 (Revision 2015-2016) and the Universiti Putra Malaysia (Research) Rules 2012. The thesis has undergone plagiarism detection software

Signature: _____ Date: _____

Name and Matric No.: _____

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

$(NH_4)_2SO_4$	Ammonium sulphate
16S rRNA	16S ribosomal ribonucleic acid
2-HMS	2-hydroxymuconate semialdehyde
4-AAP	4-aminoantipyrine
AFP	Antifreeze protein
Ag	Silver
Al	Aluminium
ANI	Average nucleotide identity
ANOVA	Analysis of variance
AP	Alkylphenol
APE	Alkylphenol ethoxylate
As	Arsenic
ASMA	Antarctic Specially Managed Area
ASPA	Antarctic Specially Protected Area
ATS	Antarctic Treaty System
BDD	Boron-doped diamond
BH	Bushnell–Haas
BLAST	Basic local alignment search tool
BOD	Biochemical oxygen demand
bp	Base pair
BPA	Bisphenol A
C12O	Catechol 1,2-dioxygenase
C23O	Catechol 2,3-dioxygenase

$C_6N_6FeK_3$	Potassium ferricyanide
CCD	Central composite design
CCMA	*cis*, *cis*-muconic acid
ccs	Circular consensus sequencing
Cd	Cadmium
CDS	Protein-coding sequence
Co	Cobalt
COD	Chemical oxygen demand
COG	Clusters of orthologous groups
CP	Chlorophenol
CSP	Cold-shock protein
Cu	Copper
dH_2O	Distilled water
DMC	Defined mixed culture
DoE	Design of Experiment
dsDNA	Double-stranded deoxyribonucleic acid
EC	European Community
EC No.	Enzyme commission number
et al.	and others
FAD	Flavin adenine dinucleotide
$Fe_{2(}SO_4).H_2O$	Iron (II) sulphate monohydrate
Fe_2S_2	Iron sulphide
gDNA	Genomic deoxyribonucleic acid
H_2O_2	Hydrogen peroxide
Hg	Mercury

IC_{50}	Half maximal inhibitory concentration
IrO_2	Iridium (IV) oxide
K_2HPO_4	Dipotassium hydrogenphosphate
KH_2PO_4	Potassium dihydrogenphosphate
MEGA	Molecular Evolutionary Genetics Analysis
Mg_2SO_4	Magnesium sulphate
$MnSO_4.H_2O$	Manganese sulphate monohydrate
mPH	Multi-component phenol hydroxylase
MSM	Minimal salt medium
NA	Nutrient agar
Na_2EDTA	Ethylenediaminetetraacetic acid disodium salt
NaCl	Sodium chloride
$NaMoO_4.H_2O$	Sodium molybdate dihydrate
NaOH	Sodium hydroxide
NB	Nutrient broth
NCBI	National Centre for Biotechnology Information
NGS	Next-generation sequencing
NH_4Cl	Ammonium chloride
Ni	Nickel
NP	Nonylphenol
OD	Optical density
OFAT	One-factor-at-a-time
OGRI	Overall genome relatedness index
OP	Octylphenol
ORF	Open reading frame

PA	Phenol agar
PacBio	Pacific Biosciences
PAH	Polycyclic aromatic hydrocarbons
PB	Plackett-Burman design
Pb	Lead
PbO_2	Lead oxide
PCB	Polychlorinated biphenyl
PCR	Polymerase chain reaction
PFAS	Poly/per-fluoroalkyl substances
PGM	Personal Genome Machine
PHA	Polyhydroxyalkanoates
PM	Phenol media
POG	Pairwise orthologous groups
POP	Persistent organic pollutants
RFLP	Restriction fragment length polymorphism
ROS	Reactive oxygen species
rpm	Revolutions per minute
rRNA	Ribosomal ribonucleic acid
RSM	Response surface methodology
SD	Standard deviation
SMRT®	Single-molecule-real-time technology
SnO_2	Tin (IV) oxide
SOLiD	Sequencing by oligonucleotide ligation and detection
Taq	*Thermus aquaticus*

TCA	Tricarboxylic acid
TGS	Third-generation sequencing
tRNA	Transfer ribonucleic acid
US EPA	United States Environmental Protection Agency
VCHC	Volatile chlorinated hydrocarbons
WGS	Whole genome sequencing
Zn	Zinc

CHAPTER 1

INTRODUCTION

Phenol is an aromatic hydrocarbon commonly derived from industrial activities. It has been classified as a high-priority toxic compound by the United States Environmental Protection Agency (US EPA) due to its toxicity to living systems and recalcitrant nature. Since the Industrial Revolution, there has been a progressive increase in pollution worldwide (Jacob *et al.*, 2018). Among all pollutants, phenol contamination has been considered one of the most prevalent in the environment, requiring urgent mitigation actions. In accordance, the US EPA and European Community (EC) limited the minimum permissible level of phenol in water bodies intended for drinking to 0.1 µg/L, and to 5 µg/L for washing purposes (Salaudeen *et al*., 2019). It may cause negative impacts on biological systems as well as directly on humans (Lee *et al*., 2017; Duan *et al*., 2018).

Anthropogenic pollution is apparent even in the continent that many consider being the most pristine and isolated, Antarctica. Since the mid-Twentieth Century, the construction and operation of over 70 Antarctic research stations, increased tourism activities, shipping and air transportation as well as the rapid growth of industrial activities in distant countries in the Southern and Northern Hemispheres, have resulted in detectable pollution, including by phenol, in Antarctica (Bargagli, 2005, 2008; Mazuki *et al*., 2019). Antarctica's ecosystems and biota are susceptible to the impacts of pollution. Furthermore, the continent's extremely cold and harsh climate means that the natural processes involved in remediating pollution happen more slowly than elsewhere. As a result, the accumulation of chemical contaminants such as hydrocarbons, heavy metals and other persistent organic pollutants (POPs) has been reported to cause significant damage to Antarctica's simple ecosystems and food webs (Jara-Carrasco *et al.,* 2017). As recognised in the Environmental Protocol, the effects of such pollutants in the Antarctic environment are not considered as either "minor" or "transitory". They will continue to have significant and long-term impacts on the environment unless active remediation is applied along with changes in national operational and tourism management (Tin *et al*., 2009). The Antarctic Treaty Parties (i.e. the signatory nations to the Antarctic Treaty) and, in particular, those operating stations and other facilities on the continent must take responsibility for achieving effective clean-up of both historically polluted sites and sites subjected to new pollution events (Lee *et al*., 2018a).

Phenol can be removed from the environment by physical and chemical means (Mohammadi *et al*., 2014; Víctor-Ortega *et* al., 2016; Hernández-Francisco *et al*., 2017; Vaiano *et al*., 2018). However, biological remediation technology is preferred due to its cost-effectiveness, eco-friendly nature, applicability and usually generating non-toxic end products (Yaacob *et al.*, 2016; Ahmad *et al*., 2017a; Suárez-García *et al*., 2019). The Antarctic Treaty prohibits the importation of non-native organisms into Antarctica (Hughes *et al*., 2015) meaning that, currently, application of bioremediation approaches can only be

achieved using indigenous microorganisms. Several studies have reported the ability of native Antarctic microorganisms, primarily from the genera *Arthrobacter* and *Rhodococcus*, to degrade phenol at low temperature (Lee *et al*., 2018a; Ahmad *et al*., 2018; Zakaria *et al*., 2018; Tengku-Mazuki *et al*., 2020). However, identifying such microbes is only the first step in the development of a bioremediation process. Environmental factors and nutritional parameters such as temperature, pH, salinity, and the presence and type of nitrogen and carbon sources, exert important influences on the phenol-degrading capability and growth rate of microorganisms (Lee *et al*., 2018a; Tengku-Mazuki *et al*., 2020). Consequently, it is crucial to optimise these factors to enhance the bioremediation process at a laboratory scale before applying any process in the field environment.

With advances in statistical analysis and information technology, numerous statistical software packages have been developed as optimisation tools to aid in bioreactor design (Nawawi *et al*., 2016; Ramasamy *et al*., 2017; Titah *et al*., 2018). Amongst the best-known software in the bioremediation field (Nasr, 2018), Design-Expert® (Stat-Ease Inc.) is designed to calculate the statistical values and probability of defining the minimum run of experiments required to recognise significant cause-and-effect relationships between a given number of variables and responses. This software comprises four categories of Design of Experiment (DoE): factorial, response surface, mixture design and crossed-process mixture (Alben, 2002). Response Surface Methodology (RSM) is the most common design used for optimising multiple factors collectively, avoiding the limitations of single factor optimisation approaches like one-factor-at-a-time (OFAT) (Zhou *et al*., 2011). RSM is a sequential procedure that begins with significant factor screening using a two-level factorial design such as the Plackett-Burman design (PB) to screen for significant parameters, and then modelling and optimising the response with a three-level factorial design like Box-Behnken central composite design (CCD) (Karamba *et al*., 2016; Tengku-Mazuki *et al*., 2020).

Generally, environments polluted by aromatic compounds, including phenol, often receive discharges from non-hydrocarbon co-contaminants such as heavy metals (Ahmad *et al*., 2017a; Duraisamy *et al*., 2020). Although heavy metals also occur naturally, anthropogenic exposure plays a vital role in elevating concentrations of these metallic elements in the Antarctic environment. For instance, a study of geochemical baseline values on the Fildes Peninsula, King George Island, revealed several heavy metals in surface soils possibly due to anthropogenic sources such as sewage disposal and petroleum spillage (Lu *et al*., 2012). Similarly, a study in Solorina Valley, James Ross Island, revealed the presence of cadmium (Cd), mercury (Hg) and lead (Pb) in lichen samples, which act as biomonitors (Zvěřina *et al*., 2018). Chemical analysis of soil samples collected from various locations on King George Island confirmed areas of high concentration of various heavy metals, particularly mercury (Hg), copper (Cu) and zinc (Zn) in petroleum-contaminated soil samples (Romaniuk *et al*., 2018).

Various heavy metals are considered essential in living organisms' biochemical and physiological functions when present in trace concentrations; however, excessive exposure can lead to damage at cellular and tissue levels (Tchounwou *et al*., 2012). These metals exhibit adverse effects on bacterial cells, particularly on cellular functions and metabolism and affect cell membrane integrity and can lead to changes in function and diversity of the soil microbial community (Gao *et al*., 2010, Jiang *et al*., 2019). The presence of phenol and co-contaminant heavy metals influences intricate chemical and biological processes since their co-occurrence can trigger competitive inhibition that inhibits microbial metabolism, lowering the phenol-degrading efficiency of the microorganisms (Jiang *et al*., 2019). Therefore, it is necessary to study the phenol degrading potential of bacteria in the presence of toxic heavy metals to improve relevance to their potential for application in bioremediation processes.

In recent years, studies of mixed microbial cultures as distinct from single species have attracted research interest due to their advantages of being more effective, qualitatively, and quantitatively, than pure cultures. Synergistic interactions amongst the different taxa present result in greater metabolic capacity (Bull, 1984; Cerqueira *et al*., 2011). Consortia may also have the ability to respond more effectively to variation in local environmental conditions (Arnosti *et al*., 2016), making them better candidates to be applied in biodegradation. Phenol-degrading mixed cultures can be prepared by combining several microorganisms to form a defined mixed culture (DMC) with improved biodegradation capabilities. Attempts to evaluate the interactions between bacterial taxa that can degrade phenol have been carried out successfully (Dey and Mukherjee, 2010; Senthilvelan *et al*., 2014; Zeng *et al*., 2014; Bera *et al*., 2017; Poi *et al*., 2017; Youssef *et al*., 2019). However, phenol bioremediation using Antarctic bacterial consortia has yet to receive detailed attention.

The ability of microbes to utilise toxic pollutants as sole carbon and energy sources, breaking down the complex chemical compounds to simpler substrates that can enter the tricarboxylic acid (TCA) cycle through a series of metabolic pathways, depends on the presence of critical microbial enzymes (Sridevi *et al*., 2012; Arora and Bae, 2014). The development of high-throughput sequencing methodologies contributed to revealing novel knowledge of biochemical pathways of biogeochemical and phylogenetic significance and revealing the functional diversity of microorganisms capable of phenol degradation (Hong *et al*., 2017). The genomic studies reveal information about the entire genome of the target microorganism, allowing specific genes to be explored, encoding the complete set of enzymes involved in phenol catabolic pathways (Ma and Zhai, 2012). Genomic analyses undoubtedly pave the way towards better understanding of the molecular mechanisms involved in pollutant remediation by native Antarctic bacteria, making a crucial contribution to the knowledge of microbial biodiversity and function in Antarctica. They also aid in the development of more effective remediation strategies.

Considering the hazardous effect of phenol towards the simple ecosystem of Antarctica and the challenging climate that limits natural biodegradation of this

persistent pollutant, this study focuses on developing a reliable tool to mitigate phenol pollution without causing further damage to this continent. The central premise of this study was that new taxa of pure phenol-degrading bacteria can be successfully isolated from Antarctic soil and, both as a pure isolate and together with previously isolated phenol-degrading bacteria as a consortium, will be capable of significant degradation of phenol at low temperatures (0-15°C) in a short time. This study will help explore the native microbial biodiversity of Antarctica and advance the utilisation of cold-adapted bacteria in remediating phenol-polluted sites, thereby contributing to environmental sustainability.

The main objectives of this study are:

1. To isolate, screen and identify cold-adapted phenol-degrading bacteria from Antarctic soil.
2. To identify the phenol-degrading pathway(s), phenol-degrading enzymes and their respective genes involved through bacterial whole genome sequencing and enzyme assays.
3. To determine the optimum conditions for phenol degradation by pure culture using OFAT and RSM.
4. To screen and optimise the degradation of phenol by DMCs of phenol-degrading bacteria using RSM approach.
5. To determine the effects of heavy metals on bacterial growth and phenol degradation for pure and mixed cultures.

REFERENCES

Abdel-Latif, A. and Osman, G. (2017). Comparison of three genomic DNA extraction methods to obtain high DNA quality from maize. *Plant Methods*, 13, 1. https://doi.org/10.1186/s13007-016-0152-4

Abdel-Mageed, W. M., Lehri, B., Jarmusch, S. A., Miranda, K., Al-Wahaibi, L. H., Stewart, H. A., Jamieson, A. J., Jaspars, M., and Karlyshev, A. V. (2020). Whole genome sequencing of four bacterial strains from South Shetland Trench revealing biosynthetic and environmental adaptation gene clusters. *Marine Genomics*, 54, 100782. https://doi.org/10.1016/j.margen.2020.100782

Abdel-Motaal, D. (2016). Antarctica: the battle for the seventh continent. Praeger Press, Santa Barbara, California.

Abd Manan, F., Ibrahim, Z., and Shahir, S. (2014). Plants in Antarctica: current and future phytoremediation potential. *Jurnal Teknologi*, 69, 59-65. https://doi.org/10.11113/jt.v69.2413

Abdulrasheed, M., Roslee, A. F., Zakaria, N. N., Zulkharnain, A., Lee, G. L. Y., Convey, P., Napis, S. and Ahmad, S. A. (2020). Effects of heavy metals on diesel metabolism of psychrotolerant strains of *Arthrobacter* sp. from Antarctica. *Journal of Environmental Biology*, 41, 966-972. http://doi.org/10.22438/jeb/41/5/MRN-1319

Abdulrasheed, M., Zakaria, N. N., Roslee, A. F. A., Shukor, M. Y., Zulkharnain, A., Napis, S., Convey, P., Alias, S. A., Gonzalez-Rocha, G., and Ahmad, S. A. (2020). Biodegradation of diesel oil by cold-adapted bacterial strains of *Arthrobacter* spp. from Antarctica. *Antarctic Science*, 32, 341-353. https://doi.org/10.1017/S0954102020000206

Abussaud, B., Asmaly, H. A., Saleh, T. A., Gupta, V. K., and Atieh, M. A. (2016). Sorption of phenol from waters on activated carbon impregnated with iron oxide, aluminum oxide and titanium oxide. *Journal of Molecular Liquids*, 213, 351-359. https://doi.org/10.1016/j.molliq.2015.08.044

Acosta, C. A., Pasquali, C. L., Paniagua, G., Garcinuño, R. M., and Hernando, P. F. (2018). Evaluation of total phenol pollution in water of San Martin Canal from Santiago del Estero, Argentina. *Environmental Pollution*, 236, 265-272. https://doi.org/10.1016/j.envpol.2018.01.062

Adams, G. O., Fufeyin, P. T., Okoro, S. E., and Ehinomen, I. (2015). Bioremediation, biostimulation and bioaugmention: a review. *International Journal of Environmental Bioremediation and Biodegradation*, 3, 28-39. https://doi.org/10.12691/ijebb-3-1-5

Afzal, M., Iqbal, S., Rauf, S., and Khalid, Z. M. (2007). Characteristics of phenol biodegradation in saline solutions by monocultures of *Pseudomonas*

aeruginosa and *Pseudomonas pseudomallei. Journal of Hazardous Materials*, 149, 60-66. https://doi.org/10.1016/j.jhazmat.2007.03.046

Agnello, A. C., Bagard, M., van Hullebusch, E. D., Esposito, G., and Huguenot, D. (2016). Comparative bioremediation of heavy metals and petroleum hydrocarbons co-contaminated soil by natural attenuation, phytoremediation, bioaugmentation and bioaugmentation-assisted phytoremediation. *Science of the Total Environment*, 563, 693-703. https://doi.org/10.1016/j.scitotenv.2015.10.061

Ahmad, S. A., Asokan, G., Yasid, N. A., Nawawi, N. M., Subramaniam, K., Zakaria, N. N., and Shukor, M. Y. (2018). Effect of heavy metals on biodegradation of phenol by Antarctic bacterium: *Arthrobacter bambusae* strain AQ5-003. *Malaysian Journal of Biochemistry and Molecular Biology*, 21, 47-51.

Ahmad, S. A., Shamaan, N. A., Syed, M. A., Dahalan, F. A., Abdul Khalil, K., Rahman, N. A., and Shukor, M. Y. (2017a). Phenol degradation by *Acinetobacter* sp. in the presence of heavy metals. *Journal of the National Science Foundation of Sri Lanka*, 45, 247-253. https://oarep.usim.edu.my/jspui/handle/123456789/3483

Ahmad, S. A., Shamaan, N. A., Syed, M. A., Khalid, A., Ab Rahman, N. A., Khalil, K. A., Dahalan, F. A., and Shukor, M. Y. (2017b). Meta-cleavage pathway of phenol degradation by *Acinetobacter* sp. strain AQ5NOL 1. *Rendiconti Lincei*, 28, 1-9. https://doi.org/10.1007/s12210-016-0554-2

Ahmad, S. A., Syed, M. A., Mat Arif, N., Abd. Shukor, M. Y., and Shamaan, N. A. (2011). Isolation, identification and characterization of elevated phenol degrading *Acinetobacter* sp. strain AQ5NOL 1. *Australian Journal of Basic and Applied Sciences*, 5, 1035-1045. https://oarep.usim.edu.my/jspui/handle/123456789/2558

Ahmed, F., Fakhruddin, A. N. M., and Kabir, M. M. (2018). Degradation of diesel and phenol using bacteria isolated from petroleum hydrocarbon contaminated soil. *Bangladesh Journal of Scientific and Industrial Research*, 53, 53-62. https://doi.org/10.3329/bjsir.v53i1.35911

Aisami, A., Yasid, N. A., Johari, W. L. W., and Shukor, M. Y. (2017). Estimation of the Q10 value; the temperature coefficient for the growth of *Pseudomonas* sp. aq5-04 on phenol. *Bioremediation Science and Technology Research*, 5, 24-26.

Aislabie, J. M., Chhour, K. L., Saul, D. J., Miyauchi, S., Ayton, J., Paetzold, R. F., and Balks, M. R. (2006). Dominant bacteria in soils of Marble point and Wright valley, Victoria land, Antarctica. *Soil Biology and Biochemistry*, 38, 3041-3056. https://doi.org/10.1016/j.soilbio.2006.02.018

Alben K. T. (2002). Design, analyze, and optimize with Design-Expert. *Analytical Chemistry*, 74, 222-223. https://doi.org/10.1021/ac0219703

Alegbeleye, O. O., Opeolu, B. O., and Jackson, V. A. (2017). Polycyclic aromatic hydrocarbons: a critical review of environmental occurrence and bioremediation. *Environmental Management*, 60, 758-783. https://doi.org/10.1007/s00267-017-0896-2

Al-Beshari, K. A. Y., Abdullah, T., and Safirah, A. (2018). The impact of diluted detergents on *Escherichia coli* K12 (JM109). *International Journal of Sciences: Basic and Applied Research*, 39, 184-193.

Al-Chalabi, M. (2017). The final frontier? An expedition to Antarctica and implications for the future. *Critical Arts*, 31, 110-118. https://doi.org/10.1080/02560046.2017.1318156

Al-Defiery, M. E. and Reddy, G. (2014). Influence of metal ions concentration on phenol degradation by *Rhodococcus pyridinivorans* GM3. *Mesopotamia Environmental Journal*, 1, 30-38.

Alexieva, Z., Yemendzhiev, H., Tossi, S., Krumova, E., Angelova, M., Terziyska, A., Peneva, N., and Gerginova, M. (2012). Growth of fungal strains isolated from Livingston Island on phenolic compounds - biodegradation potential. *In Microbes in Applied Research* (pp. 131-134). World Scientific Publishing, Singapore. https://doi.org/10.1142/9789814405041_0026

Al-Khalid, T. and El-Naas, M. H. (2012). Aerobic biodegradation of phenols: a comprehensive review. *Critical Reviews in Environmental Science and Technology*, 42, 1631-1690. https://doi.org/10.1080/10643389.2011.569872

Al-Said, H. M. and Ashgar, S. S. (2020). A comparison of antibacterial efficacy of some household detergents available in Makkah, Saudi Arabia, against 16 ATCC bacterial strains and clinical isolates. *African Journal of Microbiology Research*, 14, 388-394. https://doi.org/10.5897/AJMR2020.9281

Al-Saleh, E. S. and Obuekwe, C. (2005). Inhibition of hydrocarbon bioremediation by lead in a crude oil-contaminated soil. *International Biodeterioration and Biodegradation*, 56, 1-7. https://doi.org/10.1016/j.ibiod.2004.11.003

Alshehrei, F. (2017). Effect of physicochemical factors on the biodegradation of phenol by *Pseudomonas putida* ATCC 12842 and *Pseudomonas fluorescens* ATCC 948. *African Journal of Biotechnology*, 16, 1962-1968. https://doi.org/10.5897/AJB2017.16172

Al-Talib, H., Alkhateeb, A., Ruzuki, A. S. A., Zulkifli, N. F., Hamizi, S., Muhammad, N. S., and Abd Karim, A. F. (2019). Effectiveness of commonly used antiseptics on bacteria causing nosocomial infections in tertiary hospital in Malaysia. *African Journal of Microbiology Research*, 13, 188-194. https://doi.org/10.5897/AJMR2019.9058

Amaro, E., Padeiro, A., de Ferro, A. M., Mota, A. M., Leppe, M., Verkulich, S., Hughes, K. A., Peter, H. U., and Canário, J. (2015). Assessing trace element contamination in Fildes peninsula (king George Island) and Ardley Island, Antarctic. *Marine Pollution Bulletin*, 97, 523-527. https://doi.org/10.1016/j.marpolbul.2015.05.018

An, T., Huang, Y., Li, G., He, Z., Chen, J., and Zhang, C. (2014). Pollution profiles and health risk assessment of VOCs emitted during e-waste dismantling processes associated with different dismantling methods. *Environment international*, 73, 186-194. https://doi.org/10.1016/j.envint.2014.07.019

Annadurai, G., and Lee, J. F. (2007). Application of artificial neural network model for the development of optimized complex medium for phenol degradation using *Pseudomonas pictorum* (NICM 2074). *Biodegradation*, 18, 383-392. https://doi.org/10.1007/s10532-006-9072-8

Annadurai, G., Ling, L. Y., and Lee, J. F. (2008). Statistical optimization of medium components and growth conditions by response surface methodology to enhance phenol degradation by *Pseudomonas putida*. *Journal of Hazardous Materials*, 151, 171-178. https://doi.org/10.1016/j.jhazmat.2007.05.061

APHA (American Public Health Association). (2005). Standard method for the examination of water and wastewater, 20th edn., (pp. 540-544), Washington DC, USA.

Arahal, D. R. (2014). Whole-genome analyses: average nucleotide identity. *Methods in Microbiology*, 41, 103-122. https://doi.org/10.1016/bs.mim.2014.07.002

Arif, N. M., Ahmad, S. A., Syed, M. A., and Shukor, M. Y. (2013). Isolation and characterization of a phenol-degrading *Rhodococcus* sp. strain AQ5NOL 2 KCTC 11961BP. *Journal of Basic Microbiology*, 53, 9-19. https://doi.org/10.1002/jobm.201100120

Arnosti, C., Ziervogel, K., Yang, T., and Teske, A. (2016). Oil-derived marine aggregates – hot spots of polysaccharide degradation by specialized bacterial communities. *Deep Sea Research Part II: Topical Studies in Oceanography*, 129, 179-186. https://doi.org/10.1016/j.dsr2.2014.12.008

Arora, P. K. and Bae, H. (2014). Integration of bioinformatics to biodegradation. *Biological Procedures Online*, 16, 8. https://doi.org/10.1186/1480-9222-16-8

Arrhenius, S. (1889). Quantitative relationship between the rate a reaction proceed and its temperature. *Journal of Physical Chemistry*, 4, 226-248. https://doi.org/10.1016/B978-0-08-012344-8.50005-2

Aryal, M. and Liakopoulou-Kyriakides, M. (2015). Phenol degradation in aqueous solutions by *Pseudomonas* sp. isolated from contaminated soil of mining

industry. *Journal of Water Sustainability*, 5, 45-37. https://doi.org/10.11912/jws.2015.5.2.45-57

Azarbaijani, R., Yeganeh, L. P., Blom, J., Younesi, H., Fazeli, S. A. S., Tabatabaei, M., and Salekdeh, G. H. (2016). Comparative genome analysis of *Oceanimonas* sp. GK1, a halotolerant bacterium with considerable xenobiotics degradation potentials. *Annals of Microbiology*, 66, 703-716. https://doi.org/10.1007/s13213-015-1156-4

Aziz, R. K., Bartels, D., Best, A. A., DeJongh, M., Disz, T., Edwards, R. A., Formsma, K., Gerdes, S., Glass, E. M., Kubal, M., and Meyer, F. (2008). The RAST Server: rapid annotations using subsystems technology. *BMC Genomics*, 9, 1-15. https://doi.org/10.1186/1471-2164-9-75

Bai, X., Nie, M., Diwu, Z., Nie, H., and Wang, Y. (2021). Enhanced degradation and mineralization of phenol by combining two highly efficient strains with divergent ring-cleavage pathways. *Journal of Water Process Engineering*, 39, Article ID 101743. https://doi.org/10.1016/j.jwpe.2020.101743

Bajaj, S. and Singh, D. K. (2015). Biodegradation of persistent organic pollutants in soil, water and pristine sites by cold-adapted microorganisms: mini review. *International Biodeterioration and Biodegradation*, 100, 98-105. https://doi.org/10.1016/j.ibiod.2015.02.023

Bak, F. and Widdel, F. (1986). Anaerobic degradation of phenol and phenol derivatives by *Desulfobacterium phenolicum* sp. nov. *Archives of Microbiology*, 146, 177-180. https://doi.org/10.1007/BF00402347

Banerjee, A. and Ghoshal, A. K. (2011). Phenol degradation performance by isolated *Bacillus cereus* immobilized in alginate. *International Biodeterioration and Biodegradation*, 65, 1052-1060. https://doi.org/10.1016/j.ibiod.2011.04.011

Banerjee, A. and Ghoshal, A. K. (2016). Biodegradation of real petroleum wastewater by immobilized hyper phenol-tolerant strains of *Bacillus cereus* in a fluidized bed bioreactor. *3 Biotech*, 6, 1-4. https://doi.org/10.1007/s13205-016-0447-1

Barathi, S. and Vasudevan, N. (2001). Utilization of petroleum hydrocarbons by *Pseudomonas fluorescens* isolated from a petroleum-contaminated soil. *Environment International*, 26, 413-416. https://doi.org/10.1016/S0160-4120(01)00021-6

Bargagli, R. (2005). Antarctic ecosystems: environmental contamination, climate change, and human impact (Vol. 175). Springer, Berlin.

Bargagli, R. (2008). Environmental contamination in Antarctic ecosystems. *Science of The Total Environment*, 400, 212-226. https://doi.org/10.1016/j.scitotenv.2008.06.062

Barrett, J. R. (2010). Opening the Window to Cancer: Potential Mechanism behind Increased Susceptibility in Rats Exposed Prenatally to BPA. *Environmental Health Perspectives*, 118, A490-A491. https://doi.org/10.1289/ehp.118-a490b

Barrientos-Díaz, L., Gidekel, M., and Gutiérrez-Moraga, A. (2008). Characterization of rhizospheric bacteria isolated from *Deschampsia antarctica* Desv. *World Journal of Microbiology and Biotechnology*, 24, 2289-2296. https://doi.org/10.1007/s11274-008-9743-1

Basha, K. M., Rajendran, A., and Thangavelu, V. (2010). Recent advances in the Biodegradation of Phenol: A review. *Asian Journal of Experimental Biological Sciences*, 1, 219-234.

Behera, S. K., Meena, H., Chakraborty, S., and Meikap, B. C. (2018). Application of response surface methodology (RSM) for optimization of leaching parameters for ash reduction from low-grade coal. *International Journal of Mining Science and Technology*, 28, 621-629. https://doi.org/10.1016/j.ijmst.2018.04.014

Bento, F. M., de Oliveira Camargo, F. A., Okeke, B. C., and Frankenberger Jr, W. T. (2005). Diversity of biosurfactant producing microorganisms isolated from soils contaminated with diesel oil. *Microbiological Research*, 160, 249-255. https://doi.org/10.1016/j.micres.2004.08.005

Bera, S., Roy, A. S., and Mohanty, K. (2017). Biodegradation of phenol by a native mixed bacterial culture isolated from crude oil contaminated site. *International Biodeterioration and Biodegradation*, 121, 107-113. https://doi.org/10.1016/j.ibiod.2017.04.002

Bergauer, P., Fonteyne, P. A., Nolard, N., Schinner, F., and Margesin, R. (2005). Biodegradation of phenol and phenol-related compounds by psychrophilic and cold-tolerant alpine yeasts. *Chemosphere*, 59, 909-918. https://doi.org/10.1016/j.chemosphere.2004.11.011

Beveridge, T. J. (2001). Use of the Gram stain in microbiology. *Biotechnic and Histochemistry*, 76, 111-118. https://doi.org/10.1080/bih.76.3.111.118

Bharti, P. K., Sharma, B., Singh, R. K., and Tyagi, A. K. (2016). Waste generation and management in Antarctica. *Procedia Environmental Sciences*, 35, 40-50. https://doi.org/10.1016/j.proenv.2016.07.004

Bhasin, M. and Raghava, G. P. S. (2006). Computational methods in genome research. *In Applied Mycology and Biotechnology* (pp. 179-207). Elsevier. https://doi.org/10.1016/S1874-5334(06)80011-0

Bhatia, S. K., Bhatia, R. K., Choi, Y. K., Kan, E., Kim, Y. G., and Yang, Y. H. (2018). Biotechnological potential of microbial consortia and future perspectives. *Critical Reviews in Biotechnology*, 38, 1209-1229. https://doi.org/10.1080/07388551.2018.1471445

Bhattacharya, M., Guchhait, S., Biswas, D., and Datta, S. (2015). Waste lubricating oil removal in a batch reactor by mixed bacterial consortium: a kinetic study. *Bioprocess and Biosystems Engineering*, 38, 2095-2106. https://doi.org/10.1007/s00449-015-1449-9

Biselli, E., Schink, S. J., and Gerland, U. (2021). Slower growth of *Escherichia coli* leads to longer survival in carbon starvation due to a decrease in the maintenance rate. *Molecular Systems Biology*, 17, Article ID e10070. https://doi.org/10.15252/msb.20209478

Block, W., Lewis Smith, R. I., and Kennedy, A. D. (2009). Strategies of survival and resource exploitation in the Antarctic fellfield ecosystem. *Biological Reviews*, 84, 449-484. https://doi.org/10.1111/j.1469-185X.2009.00084.x

Bockheim J. G. (2014) Antarctic Soil Properties and Soilscapes. In: Cowan D. (eds) *Antarctic Terrestrial Microbiology*. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-642-45213-0_16

Bokhorst, S., Convey, P., and Aerts, R. (2019). Nitrogen inputs by marine vertebrates drive abundance and richness in Antarctic terrestrial ecosystems. *Current Biology*, 29, 1721-1727. https://doi.org/10.1016/j.cub.2019.04.038

Bramley-Alves, J., King, D. H., Robinson, S. A., and Miller, R. E. (2014). Dominating the Antarctic Environment: Bryophytes in a Time of Change. *In Photosynthesis in Bryophytes and Early Land Plants* (pp. 309–324). Springer, Dordrecht.

Braun, C., Hertel, F., Mustafa, O., Nordt, A., Pfeiffer, S., and Peter, H. U. (2014) Environmental Assessment and Management Challenges of the Fildes Peninsula Region. In: Tin T., Liggett D., Maher P., Lamers M. (eds.) *Antarctic Futures*. Springer, Dordrecht. https://doi.org/10.1007/978-94-007-6582-5_7

Braun, C., Mustafa, O., Nordt, A., Pfeiffer, S., and Peter, H. U. (2012). Environmental monitoring and management proposals for the Fildes region, King George Island, Antarctica. *Polar Research*, 31, Article ID 18206. https://doi.org/10.3402/polar.v31i0.18206

Brinkrolf, K., Brune, I., and Tauch, A. (2006). Transcriptional regulation of catabolic pathways for aromatic compounds in *Corynebacterium glutamicum*. *Genetics and Molecular Research*, 5, 773-789.

British Antarctic Territory. (2019). Two hundred years since the discovery of the South Shetland Islands - British Antarctic Territory. [online] Available at: <https://britishantarcticterritory.org.uk/two-hundred-years-since-the-discovery-of-the-south-shetland-islands/> [Accessed 15 January 2021].

Britto-Costa, P. H. and Ruotolo, L. A. M. (2012). Phenol removal from wastewaters by electrochemical oxidation using boron doped diamond (BDD) and Ti/Ti0. 7Ru0. 3O2 DSA® electrodes. *Brazilian Journal of*

Chemical Engineering, 29, 763-773. https://doi.org/10.1590/S0104-66322012000400008

Brown, D. M., Camenzuli, L., Redman, A. D., Hughes, C., Wang, N., Vaiopoulou, E., Saunders, D., Villalobos, A. and Linington, S. (2020). Is the Arrhenius-correction of biodegradation rates, as recommended through REACH guidance, fit for environmentally relevant conditions? An example from petroleum biodegradation in environmental systems. *Science of the Total Environment*, 732, 139293. https://doi.org/10.1016/j.scitotenv.2020.139293

Brown, K. E., King, C. K., and Harrison, P. L. (2017). Lethal and behavioral impacts of diesel and fuel oil on the Antarctic amphipod *Paramoera walkeri*. *Environmental Toxicology and Chemistry*, 36, 2444-2455. https://doi.org/10.1002/etc.3778

Bruins, M. R., Kapil, S., and Oehme, F. W. (2000). Microbial resistance to metals in the environment. *Ecotoxicology and Environmental Safety*, 45, 198-207. https://doi.org/10.1006/eesa.1999.1860

Brzeszcz, J. and Kaszycki, P. (2018). Aerobic bacteria degrading both n-alkanes and aromatic hydrocarbons: an undervalued strategy for metabolic diversity and flexibility. *Biodegradation*, 29, 359-407. https://doi.org/10.1007/s10532-018-9837-x

Buermans, H. P. J. and Den Dunnen, J. T. (2014). Next generation sequencing technology: advances and applications. *Biochimica et Biophysica Acta (BBA)-Molecular Basis of Disease*, 1842, 1932-1941. https://doi.org/10.1016/j.bbadis.2014.06.015

Bull, A. T. (1984). Mixed microbial culture technology. *Biochemical Society Transactions*, 12, 1137-1138. https://doi.org/10.1042/BST0121137

Busca, G., Berardinelli, S., Resini, C., and Arrighi, L. (2008). Technologies for the removal of phenol from fluid streams: a short review of recent developments. *Journal of Hazardous Materials*, 160, 265-288. https://doi.org/10.1016/j.jhazmat.2008.03.045

Bushnell, L. D. and Haas, H. F. (1941). The utilization of certain hydrocarbons by microorganisms. *Journal of Bacteriology*, 41, 653-673.

Busse, H. J. (2016). Review of the taxonomy of the genus *Arthrobacter*, emendation of the genus *Arthrobacter sensu lato*, proposal to reclassify selected species of the genus *Arthrobacter* in the novel genera *Glutamicibacte*r gen. nov., *Paeniglutamicibacter* gen. nov., *Pseudoglutamicibacter* gen. nov., *Paenarthrobacter* gen. nov. and *Pseudarthrobacter* gen. nov., and emended description of *Arthrobacter roseus*. *International Journal of Systematic and Evolutionary Microbiology*, 66, 9-37. https://doi.org/10.1099/ijsem.0.000702

Cabrerizo, A., Tejedo, P., Dachs, J., and Benayas, J. (2016). Anthropogenic and biogenic hydrocarbons in soils and vegetation from the South Shetland

Islands (Antarctica). *Science of The Total Environment*, 569-570, 1500-1509. https://doi.org/10.1016/j.scitotenv.2016.06.240

Camenzuli, D. and Freidman, B. L. (2015). On-site and in situ remediation technologies applicable to petroleum hydrocarbon contaminated sites in the Antarctic and Arctic. *Polar Research*, 34, Article ID 24492. https://doi.org/10.3402/polar.v34.24492

Cao, B., Geng, A., and Loh, K. C. (2008). Induction of ortho-and meta-cleavage pathways in *Pseudomonas* in biodegradation of high benzoate concentration: MS identification of catabolic enzymes. *Applied Microbiology and Biotechnology*, 81, 99-107. https://doi.org/10.1007/s00253-008-1728-3

Cao, Y., Fanning, S., Proos, S., Jordan, K., and Srikumar, S. (2017). A review on the applications of next generation sequencing technologies as applied to food-related microbiome studies. *Frontiers in Microbiology*, 8, Article ID 1829. https://doi.org/10.3389/fmicb.2017.01829

Carlos Guimaraes, L., Benevides de Jesus, L., Vinicius Canario Viana, M., Silva, A., Thiago Juca Ramos, R., de Castro Soares, S., and Azevedo, V. (2015). Inside the pan-genome-methods and software overview. *Current Genomics*, 16, 245-252. https://doi.org/10.2174/1389202916666150423002311.

Carlson, H. K., Price, M. N., Callaghan, M., Aaring, A., Chakraborty, R., Liu, H., Kuehl, J. V., Arkin, A. P., and Deutschbauer, A. M. (2019). The selective pressures on the microbial community in a metal-contaminated aquifer. *The ISME Journal*, 13, 937-949. https://doi.org/10.1038/s41396-018-0328-1

Cavicchioli, R., Siddiqui, K. S., Andrews, D., and Sowers, K. R. (2002). Low-temperature extremophiles and their applications. *Current Opinion in Biotechnology*, 13, 253-261. https://doi.org/10.1016/S0958-1669(02)00317-8

Centurion, V. B., Lacerda-Júnior, G. V., Duarte, A. W. F., Silva, T. R., Silva, L. J., Rosa, L. H., and Oliveira, V. M. (2021). Dynamics of microbial stress responses driven by abiotic changes along a temporal gradient in Deception Island, Maritime Antarctica. *Science of The Total Environment*, 758, Article ID 143671. https://doi.org/10.1016/j.scitotenv.2020.143671

Cerqueira, V. S., Hollenbach, E. B., Maboni, F., Vainstein, M. H., Camargo, F. A. O., Peralba, M. do C. R., and Bento, F. M. (2011). Biodegradation potential of oily sludge by pure and mixed bacterial cultures. *Bioresource Technology*, 102, 11003-11010. https://doi.org/10.1016/j.biortech.2011.09.074

Chae, Y., Kim, L., Kim, D., Cui, R., Lee, J., and An, Y. J. (2020). Deriving hazardous concentrations of phenol in soil ecosystems using a species sensitivity distribution approach. *Journal of Hazardous Materials*, 399, Article ID 123036. https://doi.org/10.1016/j.jhazmat.2020.123036

Chakraborty, S., Bhattacharya, T., Patel, T. N., and Tiwari, K. K. (2010). Biodegradation of phenol by native microorganisms isolated from coke processing wastewater. *Journal of Environmental Biology*, 31, 293-296.

Chakraborty, S., Gogoi, M., and Chakravortty, D. (2015). Lactoylglutathione lyase, a critical enzyme in methylglyoxal detoxification, contributes to survival of *Salmonella* in the nutrient rich environment. *Virulence*, 6, 50-65. https://doi.org/10.4161/21505594.2014.983791

Chattopadhyay, M. K. (2006). Mechanism of bacterial adaptation to low temperature. *Journal of Biosciences*, 31, 157-165. https://doi.org/10.1007/BF02705244

Chavali, A. K. and Rhee, S. Y. (2018). Bioinformatics tools for the identification of gene clusters that biosynthesize specialized metabolites. *Briefings in Bioinformatics*, 19, 1022-1034. https://doi.org/10.1093/bib/bbx020

Chen, X., Chen, M., Xu, B., Tang, R., Han, X., Qin, Y., Xu, B., Hang, B., Mao, Z., Huo, W., and Xia, Y. (2013). Parental phenols exposure and spontaneous abortion in Chinese population residing in the middle and lower reaches of the Yangtze River. *Chemosphere*, 93, 217-222. https://doi.org/10.1016/j.chemosphere.2013.04.067

Chen, Y., He, H., Liu, H., Li, H., Zeng, G., Xia, X., and Yang, C. (2018). Effect of salinity on removal performance and activated sludge characteristics in sequencing batch reactors. *Bioresource Technology*, 249, 890-899. https://doi.org/10.1016/j.biortech.2017.10.092

Chiale, M. C., Fernández, P. E., Gimeno, E. J., Barbeito, C., and Montalti, D. (2014). Morphology and histology of the uropygial gland in Antarctic birds: relationship with their contact with the aquatic environment? *Australian Journal of Zoology*, 62, 157-165. https://doi.org/10.1071/ZO13103

Chu, W. L., Dang, N. L., Kok, Y. Y., Yap, K. S. I., Phang, S. M., and Convey, P. (2018). Heavy metal pollution in Antarctica and its potential impacts on algae. *Polar Science*, 20, 75-83. https://doi.org/10.1016/j.polar.2018.10.004

Chun, J., Grim, C. J., Hasan, N. A., Lee, J. H., Choi, S. Y., Haley, B. J., Taviani, E., Jeon, Y. S., Kim, D. W., Lee, J. H., and Brettin, T. S. (2009). Comparative genomics reveals mechanism for short-term and long-term clonal transitions in pandemic *Vibrio cholerae*. *Proceedings of the National Academy of Sciences*, 106, 15442-15447. https://doi.org/10.1073/pnas.0907787106

Chun, J., Lee, J. H., Jung, Y., Kim, M., Kim, S., Kim, B. K., and Lim, Y. W. (2007). EzTaxon: a web-based tool for the identification of prokaryotes based on 16S ribosomal RNA gene sequences. *International Journal of Systematic and Evolutionary Microbiology*, 57, 2259-2261. https://doi.org/10.1099/ijs.0.64915-0

Cipro, C. V., Colabuono, F. I., Taniguchi, S., and Montone, R. C. (2013). Persistent organic pollutants in bird, fish and invertebrate samples from King George Island, Antarctica. *Antarctic Science*, 25, 545-552. https://doi.org/10.1017/S0954102012001149

Committee on Environmental Protection (CEP). (2017). Status of Antarctic Specially Protected Area and Antarctic Specially Managed Area Management Plans.

Convey, P. (2017). Antarctic ecosystems. In *Reference Module in Life Sciences* (pp. 179-188). Elsevier Inc. https://doi.org/10.1016/B978-0-12-809633-8.02182-8

Convey, P. and Peck, L. S. (2019). Antarctic environmental change and biological responses. *Science Advances*, 5, eaaz0888. https://doi.org/10.1126/sciadv.aaz0888

Convey, P., Chown, S. L., Clarke, A., Barnes, D. K., Bokhorst, S., Cummings, V., Ducklow, H. W., Frati, F., Green, T. A., Gordon, S., and Griffiths, H. J. (2014). The spatial structure of Antarctic biodiversity. *Ecological Monographs*, 84, 203-244. https://doi.org/10.1890/12-2216.1

Convey, P., Coulson, S. J., Worland, M. R., and Sjöblom, A. (2018). The importance of understanding annual and shorter-term temperature patterns and variation in the surface levels of polar soils for terrestrial biota. *Polar Biology*, 41, 1587-1605. https://doi.org/10.1007/s00300-018-2299-0

Croll, D. and McDonald, B. A. (2012). The accessory genome as a cradle for adaptive evolution in pathogens. *PLoS Pathog*, 8, Article ID e1002608. https://doi.org/10.1371/journal.ppat.1002608

Cutts, T. A., Ijaz, M. K., Nims, R. W., Rubino, J. R., and Theriault, S. S. (2019). Effectiveness of dettol antiseptic liquid for inactivation of Ebola virus in suspension. *Scientific Reports*, 9, 1-8. https://doi.org/10.1038/s41598-019-42386-5

Dalal, S., Pandey, R. R., and Dubey, R. C. (2012). Bacterial degradation of phenol and cyanide from industrial wastewater. In D.K. Maheshwari and R.C. Dubey (Eds.), *Bioremediation of Pollutants* (pp. 1-23). IK International Pub. Com, New Delhi, India.

Das, N. and Chandran, P. (2011). Microbial degradation of petroleum hydrocarbon contaminants: an overview. *Biotechnology Research International*, Article ID 941810. https://doi.org/10.4061/2011/941810.

De Broyer, C., Koubbi, P., Griffiths, H. J., Raymond, B., Udekem d'Acoz, C. d', Van de Putte, A. P., Danis, B., David, B., Grant, S., Gutt, J., Held, C., Hosie, G., Huettmann, F., Post, A., and Ropert-Coudert, Y. (eds.) (2014). Biogeographic atlas of the Southern Ocean (p. 498). Scientific Committee on Antarctic Research, Cambridge.

de Lourdes Moreno, M., Sánchez-Porro, C., Piubeli, F., Frias, L., García, M. T., and Mellado, E. (2011). Cloning, characterization and analysis of cat and ben genes from the phenol degrading halophilic bacterium *Halomonas organivorans*. *PloS One*, 6, Article ID e21049. https://doi.org/10.1371/journal.pone.0021049

de Renzy-Martin, K. T., Frederiksen, H., Christensen, J. S., Kyhl, H. B., Andersson, A. M., Husby, S., Barington, T., Main, K. M., and Jensen, T. K. (2014). Current exposure of 200 pregnant Danish women to phthalates, parabens and phenols. *Reproduction*, 147, 443-453. https://doi.org/10.1530/REP-13-0461

Dehghani, M., Nasseri, S., and Hashemi, H. (2013). Study of the bioremediation of atrazine under variable carbon and nitrogen sources by mixed bacterial consortium isolated from corn field soil in Fars Province of Iran. *Journal of Environmental and Public Health*, Article ID 973165, https://doi.org/10.1155/2013/973165

Deppe, U., Richnow, H. H., Michaelis, W., and Antranikian, G. (2005). Degradation of crude oil by an arctic microbial consortium. *Extremophiles*, 9, 461-470. https://doi.org/10.1007/s00792-005-0463-2

Desjardins, P. and Conklin, D. (2010). NanoDrop microvolume quantitation of nucleic acids. *Journal of Visualized Experiments*, 45, Article ID e2565. https://doi.org/10.3791/2565

Dey, S. and Mukherjee, S. (2010). Performance and kinetic evaluation of phenol biodegradation by mixed microbial culture in a batch reactor. International *Journal of Water Resources and Environmental Engineering*, 2, 40-49. https://doi.org/10.5897/IJWREE.9000043

Dobslaw, D. and Engesser, K. H. (2015). Degradation of toluene by ortho cleavage enzymes in *Burkholderia fungorum* FLU 100. *Microbial Biotechnology*, 8, 143-154. https://doi.org/10.1111/1751-7915.12147

Drancourt, M. and Raoult, D. (2005). Sequence-based identification of new bacteria: a proposition for creation of an orphan bacterium repository. *Journal of Clinical Microbiology*, 43, 4311-4315. https://doi.org/10.1128/JCM.43.9.4311-4315.2005

Dresen, C., Lin, L. Y. C., D'Angelo, I., Tocheva, E. I., Strynadka, N., and Eltis, L. D. (2010). A flavin-dependent monooxygenase from *Mycobacterium tuberculosis* involved in cholesterol catabolism. *Journal of Biological Chemistry*, 285, 22264-22275. https://doi.org/10.1074/jbc.M109.099028

Dsouza, M., Taylor, M. W., Turner, S. J., and Aislabie, J. (2015). Genomic and phenotypic insights into the ecology of Arthrobacter from Antarctic soils. *BMC Genomics*, 16, 1-18. https://doi.org/10.1186/s12864-015-1220-2

Duan, W., Meng, F., Cui, H., Lin, Y., Wang, G., and Wu, J. (2018). Ecotoxicity of phenol and cresols to aquatic organisms: a review. *Ecotoxicology and*

Environmental Safety, 157, 441-456. https://doi.org/10.1016/j.ecoenv.2018.03.089

Duraisamy, P., Sekar, J., Arunkumar, A. D., and Ramalingam, P. V. (2020). Kinetics of phenol biodegradation by heavy metal tolerant rhizobacteria *Glutamicibacter nicotianae* MSSRFPD35 from distillery effluent contaminated soils. *Frontiers in Microbiology*, 11, Article ID 1573. https://doi.org/10.3389/fmicb.2020.01573

Dziewit, L. and Drewniak, L. (2016). Heavy metals resistance, metabolism and transformation-genomic, metagenomic and metatranscriptomic studies. In *Microbial biodegradation: from omics to function and application*. Caister Academic Press, Poole, 13-26. https://doi.org/10.21775/9781910190456.02

e Silva, A. A. D. L., Pereira, M. P., Silva Filho, R. G., and Hofer, E. (2007). Utilization of phenol in the presence of heavy metals by metal-tolerant non-fermentative Gram-negative bacteria isolated from wastewater. *Revista Latinoamericana de Microbiologia*, 49, 68-73.

Edgar, R. C. (2010). Search and clustering orders of magnitude faster than BLAST. *Bioinformatics*, 26, 2460-2461. https://doi.org/10.1093/bioinformatics/btq461

El Mahmood, A. M., and Doughari, J. H. (2008). Effect of Dettol® on viability of some microorganisms associated with nosocomial infections. *African Journal of Biotechnology*, 7, 1554-1562.

El-Naas, M. H., Alhaija, M. A., and Al-Zuhair, S. (2014). Evaluation of a three-step process for the treatment of petroleum refinery wastewater. *Journal of Environmental Chemical Engineering*, 2, 56-62. https://doi.org/10.1016/j.jece.2013.11.024

Emerson, E. (1943). The condensation of aminoantipyrine. II. A new color test for phenolic compounds. *The Journal of Organic Chemistry*, 8, 417-428. https://doi.org/10.1021/jo01193a004

Emerson, E. and Kelly, K. (1948). The condensation of aminoantipyrine. VI. A study of the effect of excess base on the reaction of amino-antipyrine with phenolic compounds in the presence of oxidizing agents. *The Journal of Organic Chemistry*, 13, 532-534. https://doi.org/10.1021/jo01162a008

Emnet, P., Gaw, S., Northcott, G., Storey, B., and Graham, L. (2015). Personal care products and steroid hormones in the Antarctic coastal environment associated with two Antarctic research stations, McMurdo Station and Scott Base. *Environmental Research*, 136, 331-342. https://doi.org/10.1016/j.envres.2014.10.019

Enache, A. T., Fatibello-Filho, O., and Oliveira-Brett, M. A. (2010). Electrochemical behavior of triflusal, aspirin and their metabolites at glassy carbon and boron doped diamond electrodes. *Combinatorial Chemistry and*

High Throughput Screening, 13, 569-577. https://doi.org/10.2174/138620710791601314

Ereqat, S. I., Abdelkader, A. A., Nasereddin, A. F., Al-Jawabreh, A. O., Zaid, T. M., Letnik, I., and Abdeen, Z. A. (2018). Isolation and characterization of phenol degrading bacterium strain *Bacillus thuringiensis* J20 from olive waste in Palestine. *Journal of Environmental Science and Health*, Part A, 53, 39-45. https://doi.org/10.1080/10934529.2017.1368300

Fernández, P. M., Martorell, M. M., Blaser, M. G., Ruberto, L. A. M., de Figueroa, L. I. C., and Mac Cormack, W. P. (2017). Phenol degradation and heavy metal tolerance of Antarctic yeasts. *Extremophiles*, 21, 445-457. https://doi.org/10.1007/s00792-017-0915-5

Festa, S., Coppotelli, B. M., and Morelli, I. S. (2013). Bacterial diversity and functional interactions between bacterial strains from a phenanthrene-degrading consortium obtained from a chronically contaminated-soil. *International Biodeterioration and Biodegradation*, 85, 42-51. https://doi.org/10.1016/j.ibiod.2013.06.006

Fichot, E. B. and Norman, R. S. (2013). Microbial phylogenetic profiling with the Pacific Biosciences sequencing platform. *Microbiome*, 1, 10. https://doi.org/10.1186/2049-2618-1-10

Filipowicz, N., Momotko, M., Boczkaj, G., Pawlikowski, T., Wanarska, M., and Cieśliński, H. (2017). Isolation and characterization of phenol-degrading psychrotolerant yeasts. *Water, Air, and Soil Pollution*, 228, 210. https://doi.org/10.1007/s11270-017-3391-8

Flynn, E. E., Bjelde, B. E., Miller, N. A., and Todgham, A. E. (2015). Ocean acidification exerts negative effects during warming conditions in a developing Antarctic fish. *Conservation Physiology*, 3, Article ID cov033. https://doi.org/10.1093/conphys/cov033

Foong, C. P., Ling, C. M. W. V., and González, M. (2010). Metagenomic analyses of the dominant bacterial community in the Fildes Peninsula, King George Island (South Shetland Islands). *Polar Science*, 4, 263-273. https://doi.org/10.1016/j.polar.2010.05.010

Fulekar, M. H. and Pathak, B. (2019). Bioremediation Technology: Hazardous Waste Management. In P. Hirpara, and N. Bhatt (eds.) *Bacterial biodegradation of phenolics and derivatives of phenolics* (pp. 127-144), Taylor and Francis Group, Boca Raton, Florida.

Gami, A. A., Shukor, M. Y., Khalil, A. K., Dahalan, F. A., Khalid, A., and Ahmad, S. A. (2014). Phenol and its toxicity. *Journal of Environmental Microbiology and Toxicology*, 2, 11-24.

Gao, C. H., Cao, H., Cai, P., and Sørensen, S. J. (2021a). The initial inoculation ratio regulates bacterial coculture interactions and metabolic capacity. *The ISME Journal*, 15, 29-40. https://doi.org/10.1038/s41396-020-00751-7

Gao, Y., Li, R., Gao, H., Hou, C., Jin, S., Ye, J., and Na, G. (2021b). Spatial distribution of cumulative impact on terrestrial ecosystem of the Fildes Peninsula, Antarctica. *Journal of Environmental Management*, 279, Article ID 111735. https://doi.org/10.1016/j.jenvman.2020.111735

Gao, Y., Zhou, P., Mao, L., Zhi, Y. E., and Shi, W. J. (2010). Assessment of effects of heavy metals combined pollution on soil enzyme activities and microbial community structure: modified ecological dose–response model and PCR-RAPD. *Environmental Earth Sciences*, 60, 603-612. https://doi.org/10.1007/s12665-009-0200-8

Garneau, M. È., Michel, C., Meisterhans, G., Fortin, N., King, T. L., Greer, C. W., and Lee, K. (2016). Hydrocarbon biodegradation by Arctic sea-ice and sub-ice microbial communities during microcosm experiments, Northwest Passage (Nunavut, Canada). *FEMS Microbiology Ecology*, 92, fiw130. https://doi.org/10.1093/femsec/fiw130

Gavrilescu, M., Demnerová, K., Aamand, J., Agathos, S., and Fava, F. (2015). Emerging pollutants in the environment: present and future challenges in biomonitoring, ecological risks and bioremediation. *New biotechnology*, 32, 147-156. https://doi.org/10.1016/j.nbt.2014.01.001

George, S. F., Fierer, N., Levy, J. S., and Adams, B. (2021). Antarctic water tracks: Microbial community responses to variation in soil moisture, pH, and salinity. *Frontiers in Microbiology*, 12, Article ID 616730. https://doi.org/10.3389/fmicb.2021.616730

Gérecová, G., Neboháčová, M., Zeman, I., Pryszcz, L. P., Tomáška, Ľ., Gabaldón, T., and Nosek, J. (2015). Metabolic gene clusters encoding the enzymes of two branches of the 3-oxoadipate pathway in the pathogenic yeast *Candida albicans*. *FEMS Yeast Research*, 15, Article ID fov006. https://doi.org/10.1093/femsyr/fov006

Gerginova, M., Manasiev, J., Yemendzhiev, H., Terziyska, A., Peneva, N., and Alexieva, Z. (2013). Biodegradation of phenol by Antarctic strains of *Aspergillus fumigatus*. *Zeitschrift für Naturforschung C*, 68, 384-393. https://doi.org/10.1515/znc-2013-9-1006

Ghosh, M. and Singh, S. P. (2005). A review on phytoremediation of heavy metals and utilization of its by products. *Asian Journal on Energy and Environment,* 3, 1-18. http://dx.doi.org/10.15666/aeer/0301_001018

Gong, Y., Ding, P., Xu, M. J., Zhang, C. M., Xing, K., and Qin, S. (2021). Biodegradation of phenol by a halotolerant versatile yeast *Candida tropicalis* SDP-1 in wastewater and soil under high salinity conditions. *Journal of Environmental Management*, 289, 112525. https://doi.org/10.1016/j.jenvman.2021.112525

González, P. S., Capozucca, C. E., Tigier, H. A., Milrad, S. R., and Agostini, E. (2006). Phytoremediation of phenol from wastewater, by peroxidases of

tomato hairy root cultures. *Enzyme and Microbial Technology*, 39, 647-653. https://doi.org/10.1016/j.enzmictec.2005.11.014

González-Alonso, S., Merino, L. M., Esteban, S., López de Alda, M., Barceló, D., Durán, J. J., López-Martínez, J., Aceña, J., Pérez, S., Mastroianni, N., Silva, A., Catalá, M., and Valcárcel, Y. (2017). Occurrence of pharmaceutical, recreational and psychotropic drug residues in surface water on the northern Antarctic Peninsula region. *Environmental Pollution*, 229, 241-254. https://doi.org/10.1016/j.envpol.2017.05.060

Goodson, A., Robin, H., Summerfield, W., and Cooper, I. (2004). Migration of bisphenol A from can coatings—effects of damage, storage conditions and heating. *Food Additives and Contaminants*, 21, 1015-1026. https://doi.org/10.1080/02652030400011387

Google maps (2015). Dery, M. X. Base Presidente Eduardo Frei Montalva, Antarctica. Retrieved from https://www.google.com/maps/place/62%C2%B011'47.7%22S+58%C2%B058'11.5%22W/@-62.1965833,-58.9698611,17z/data=!3m1!4b1!4m5!3m4!1s0x0:0x0!8m2!3d-62.1965681!4d-58.9698569

Gran-Scheuch, A., Fuentes, E., Bravo, D. M., Jiménez, J. C., and Pérez-Donoso, J. M. (2017). Isolation and characterization of phenanthrene degrading bacteria from diesel fuel-contaminated Antarctic soils. *Frontiers in Microbiology*, 8, Article ID 1634. https://doi.org/10.3389/fmicb.2017.01634

Gröndahl, F., Sidenmark, J., and Thomsen1, A. (2009). Survey of waste water disposal practices at Antarctic research stations. Polar Research, 28, 298–306. https://doi.org/10.1111/j.1751-8369.2008.00056.x

Gu, Q., Wu, Q., Zhang, J., Guo, W., Wu, H., and Sun, M. (2017). *Acinetobacter* sp. DW-1 immobilized on polyhedron hollow polypropylene balls and analysis of transcriptome and proteome of the bacterium during phenol biodegradation process. *Scientific Reports*, 7, 1-18. https://doi.org/10.1038/s41598-017-04187-6

Guerra, M. B., Amarasiriwardena, D., Schaefer, C. E., Pereira, C. D., Spielmann, A. A., Nobrega, J. A., and Pereira-Filho, E. R. (2011). Biomonitoring of lead in Antarctic lichens using laser ablation inductively coupled plasma mass spectrometry. *Journal of Analytical Atomic Spectrometry*, 26, 2238-2246. DOI https://doi.org/10.1039/C1JA10198F

Habib, S., Ahmad, S. A., Johari, W. L. W., Abd Shukor, M. Y., Alias, S. A., Khalil, K. A., and Yasid, N. A. (2018). Evaluation of conventional and response surface level optimisation of n-dodecane (n-C12) mineralisation by psychrotolerant strains isolated from pristine soil at Southern Victoria Island, Antarctica. *Microbial cell factories*, 17, 1-21. https://doi.org/10.1186/s12934-018-0889-8

Hallsworth, J. E., Yakimov, M. M., Golyshin, P. N., Gillion, J. L., D'Auria, G., de Lima Alves, F., La Cono, V., Genovese, M., McKew, B. A., Hayes, S. L., and Harris, G. (2007). Limits of life in $MgCl_2$-containing environments: chaotropicity defines the window. *Environmental Microbiology*, 9, 801-813. https://doi.org/10.1111/j.1462-2920.2006.01212.x

Hamzah, R. Y. and Al-Baharna, B. S. (1994). Catechol ring-cleavage in *Pseudomonas cepacia*: the simultaneous induction of ortho and meta pathways. *Applied Microbiology and Biotechnology*, 41, 250-256. https://doi.org/10.1007/BF00186968

Hamitouche, A., Amrane, A., Bendjama, Z., and Kaouah, F. (2010). Effect of the ammonium chloride concentration on the mineral medium composition - Biodegradation of phenol by a microbial consortium. *International Journal of Environmental Research*, 4, 849-854. https://doi.org/10.22059/ijer.2010.271

Harley, K. G., Berger, K. P., Kogut, K., Parra, K., Lustig, R. H., Greenspan, L. C., Calafat, A. M., Ye, X., and Eskenazi, B. (2019). Association of phthalates, parabens and phenols found in personal care products with pubertal timing in girls and boys. *Human Reproduction*, 34, 109-117. https://doi.org/10.1093/humrep/dey337

Harris, J. K., Kelley, S. T., Spiegelman, G. B., and Pace, N. R. (2003). The genetic core of the universal ancestor. *Genome Research*, 13, 407-412. https://doi.org/10.1101/gr.652803

Hasan, S. A. and Jabeen, S. (2015). Degradation kinetics and pathway of phenol by *Pseudomonas* and *Bacillus species*. *Biotechnology and Biotechnological Equipment*, 29, 45-53. https://doi.org/10.1080/13102818.2014.991638

He, P., Li, L., Liu, J., Bai, Y., and Fang, X. (2016). Diversity and distribution of catechol 2, 3-dioxygenase genes in surface sediments of the Bohai Sea. *FEMS Microbiology Letters*, 363, Article ID fnw086. https://doi.org/10.1093/femsle/fnw086

Heine, T., Van Berkel, W. J., Gassner, G., Van Pée, K. H., and Tischler, D. (2018). Two-component FAD-dependent monooxygenases: current knowledge and biotechnological opportunities. *Biology*, 7, 42. https://doi.org/10.3390/biology7030042

Hengge, R. (2011). Stationary-Phase Gene Regulation in Escherichia coli §. *EcoSal Plus*, 4(2). https://doi.org/10.1128/ecosalplus.5.6.3

Henry, N. D. and Fair, P. A. (2013). Comparison of in vitro cytotoxicity, estrogenicity and anti-estrogenicity of triclosan, perfluorooctane sulfonate and perfluorooctanoic acid. *Journal of Applied Toxicology,* 33, 265-272. https://doi.org/10.1002/jat.1736

Hernández-Francisco, E., Peral, J., and Blanco-Jerez, L. M. (2017). Removal of phenolic compounds from oil refinery wastewater by electrocoagulation and

Fenton/photo-Fenton processes. *Journal of Water Process Engineering*, 19, 96-100. https://doi.org/10.1016/j.jwpe.2017.07.010

Hoffelder, M., Raasch, K., van Ooyen, J., and Eggeling, L. (2010). The E2 domain of OdhA of *Corynebacterium glutamicum* has succinyltransferase activity dependent on lipoyl residues of the acetyltransferase AceF. *Journal of Bacteriology*, 192, 5203-5211. https://doi.org/10.1128/JB.00597-10

Hong, Y. H., Ye, C. C., Zhou, Q. Z., Wu, X. Y., Yuan, J. P., Peng, J., Deng, H., and Wang, J. H. (2017). Genome sequencing reveals the potential of *Achromobacter* sp. HZ01 for bioremediation. *Frontiers in Microbiology*, 8, Article ID 1507. https://doi.org/10.3389/fmicb.2017.01507

Horváthová, H., Lászlová, K., and Dercová, K. (2018). Bioremediation of PCB-contaminated shallow river sediments: the efficacy of biodegradation using individual bacterial strains and their consortia. *Chemosphere*, 193, 270-277. https://doi.org/10.1016/j.chemosphere.2017.11.012

Hossain, M. M. and Nakamoto, H. (2003). Role for the cyanobacterial HtpG in protection from oxidative stress. *Current Microbiology*, 46, 70-76. https://doi.org/10.1007/s00284-002-3831-5

Hrbáček, F., Nývlt, D., and Láska, K. (2017). Active layer thermal dynamics at two lithologically different sites on James Ross Island, Eastern Antarctic Peninsula. *Catena*, 149, 592-602. https://doi.org/10.1016/j.catena.2016.06.020

Hrynkiewicz, K. and Baum, C. (2014). Application of Microorganisms in Bioremediation of Environment from Heavy Metals. In: Malik, A., Grohmann, E., Akhtar, R. (eds.) *Environmental Deterioration and Human Health* (pp. 215-227). Springer, Dordrecht. https://doi.org/10.1007/978-94-007-7890-0_9

Hughes, K. A. (2010). How committed are we to monitoring human impacts in Antarctica?. *Environmental Research Letters*, 5, Article ID 041001.

Hughes, K. A., Ireland, L. C., Convey, P., and Fleming, A. H. (2016). Assessing the effectiveness of specially protected areas for conservation of Antarctica's botanical diversity. *Conservation Biology*, 30, 113-120. https://doi.org/10.1111/cobi.12592

Hughes, K. A., Pertierra, L. R., Molina-Montenegro, M. A., and Convey, P. (2015). Biological invasions in terrestrial Antarctica: what is the current status, and can we respond? *Biodiversity and Conservation*, 24, 1031-1055. https://doi.org/10.1007/s10531-015-0896-6

Hui-Peng, L., Jian, S., Hua, Z., Li, Z., and Yu-tai, Q. (2009). Effects of Phenols on the Stability of FCC Diesel Fuel. *Petroleum Science and Technology*, 27, 486-497. https://doi.org/10.1080/10916460802097269

Hupert-Kocurek, K., Guzik, U., and Wojcieszyńska, D. (2012). Characterization of catechol 2, 3-dioxygenase from *Planococcus* sp. strain S5 induced by high phenol concentration. *Acta Biochimica Polonica*, 59, 345-351. https://doi.org/10.18388/abp.2012_2119

Hupert-Kocurek, K., Wojcieszyńska, D., and Guzik, U. (2014). Activity of a carboxyl-terminal truncated form of catechol 2, 3-dioxygenase from *Planococcus* sp. S5. *The Scientific World Journal*, Article ID 598518. https://doi.org/10.1155/2014/598518

Hurtado, L., Amado-Piña, D., Roa-Morales, G., Peralta-Reyes, E., Martin del Campo, E., and Natividad, R. (2016). Comparison of AOPs efficiencies on phenolic compounds degradation. *Journal of Chemistry*, Article ID 4108587. https://doi.org/10.1155/2016/4108587

Hyatt, D., Chen, G. L., LoCascio, P. F., Land, M. L., Larimer, F. W., and Hauser, L. J. (2010). Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics*, 11, 1-11. https://doi.org/10.1186/1471-2105-11-119

Ibáñez, S. G., Alderete, L. G. S., Medina, M. I., and Agostini, E. (2012). Phytoremediation of phenol using *Vicia sativa* L. plants and its antioxidative response. *Environmental Science and Pollution Research*, 19, 1555-1562. https://doi.org/10.1007/s11356-011-0664-4

Ibrahim, S., Abdul Khalil, K., Zahri, K. N. M., Gomez-Fuentes, C., Convey, P., Zulkarnain, A., Sabri, S., Alias, S. A., González-Rocha, G., and Ahmad, S. A. (2020b). Biosurfactant production and growth kinetics studies of the waste canola oil-degrading bacterium *Rhodococcus erythropolis* AQ5-07 from Antarctica. *Molecules*, 25, Article ID 3878. https://doi.org/10.3390/molecules25173878

Ibrahim, S., Shukor, M. Y., Khalil, K. A., Halmi, M. I. E., Syed, M. A., and Ahmad, S. A. (2015). Application of response surface methodology for optimising caffeine-degrading parameters by *Leifsonia* sp. strain SIU. *Journal of Environmental Biology*, 36, Article ID 1215.

Ibrahim, S., Zahri, K. N. M., Convey, P., Khalil, K. A., Gomez-Fuentes, C., Zulkarnain, A., Alias, S. A., González-Rocha, G., and Ahmad, S.A. (2020a). Optimisation of biodegradation conditions for waste canola oil by cold-adapted *Rhodococcus* sp. AQ5-07 from Antarctica. *Electronic Journal of Biotechnology*, 48, 1-12. https://doi.org/10.1016/j.ejbt.2020.07.005

Ibrahim, S., Zulkharnain, A., Zahri, K. N. M., Lee, G. L. Y., Convey, P., Gomez Fuentes, C., Sabri, S., Khalil, K. A., Alias, S. A., Gonzales-Rocha, G. and Ahmad, A. (2020). Effect of heavy metals and other xenobiotics on biodegradation of waste canola oil by cold-adapted *Rhodococcus* sp. AQ5-07. *Revista Mexicana de Ingeniería Química*, 19, 1041-1052. https://doi.org/10.24275/rmiq/Bio917

Igbinosa, E. O., Ibhazukor, M. A., Eribo, O. A., and Ogofure, A. G. (2015). Efficacy of household cleaning agents against some selected pathogenic bacteria. *African Journal of Clinical and Experimental Microbiology*, 16, 73-78. https://doi.org/10.4314/ajcem.v16i2.5

Igiri, B. E., Okoduwa, S. I., Idoko, G. O., Akabuogu, E. P., Adeyi, A. O., and Ejiogu, I. K. (2018). Toxicity and bioremediation of heavy metals contaminated ecosystem from tannery wastewater: a review. *Journal of Toxicology*, Article ID 2568038. https://doi.org/10.1155/2018/2568038.

Issazadeh, K., Jahanpour, N., Pourghorbanali, F., Raeisi, G., and Faekhondeh, J. (2013). Heavy metals resistance by bacterial strains. *Annals of Biological Research*, 4, 60-63.

Jabeen, H., Iqbal, S., Anwar, S., and Parales, R. E. (2015). Optimization of profenofos degradation by a novel bacterial consortium PBAC using response surface methodology. *International Biodeterioration and Biodegradation*, 100, 89-97. https://doi.org/10.1016/j.ibiod.2015.02.022

Jackman, J. (2012). The Microbe: The Basics of Structure, Morphology, and Physiology as They Relate to Microbial Characterization and Attribution. In: Cliff J., Kreuzer H., Ehrhardt C., Wunschel D. (eds) *Chemical and Physical Signatures for Microbial Forensics. Infectious Disease* (pp. 13-34). Springer, New York, NY. https://doi.org/10.1007/978-1-60327-219-3_2

Jacob, J. M., Karthik, C., Saratale, R. G., Kumar, S. S., Prabakar, D., Kadirvelu, K., and Pugazhendhi, A. (2018). Biological approaches to tackle heavy metal pollution: a survey of literature. *Journal of Environmental Management*, 217, 56-70. https://doi.org/10.1016/j.jenvman.2018.03.077

Jain, C., Rodriguez-R, L. M., Phillippy, A. M., Konstantinidis, K. T., and Aluru, S. (2018). High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *Nature Communications*, 9, 1-8. https://doi.org/10.1038/s41467-018-07641-9

Jara-Carrasco, S., Barra, R., Espejo, W., Celis, J. E., González-Acuña, D., Chiang, G., and Sánchez-Hernández, J. (2017). Persistent organic pollutants and porphyrin levels in excreta of penguin colonies from the Antarctic Peninsula area. *Polar Record*, 53, 79-87. https://doi.org/10.1017/S0032247416000607

Jian, C., Yang, Z., Su, Y., Han, F. X., and Monts, D. L. (2011). Phytoremediation of heavy metal/metalloid-contaminated soils. In: *Contaminated Soils: Environmental Impact, Disposal and Treatment.,* Ed: Robert V. Steinberg (pp. 181-206). Nova Science publisher, Inc.

Jiang, B., Adebayo, A., Jia, J., Xing, Y., Deng, S., Guo, L., Liang, Y., and Zhang, D. (2019). Impacts of heavy metals and soil properties at a Nigerian e-waste site on soil microbial community. *Journal of Hazardous Materials*, 362, 187-195. https://doi.org/10.1016/j.jhazmat.2018.08.060

Jiang, B., Zhou, Z., Dong, Y., Tao, W., Wang, B., Jiang, J., and Guan, X. (2015). Biodegradation of benzene, toluene, ethylbenzene, and o-, m-, and p-xylenes by the newly isolated bacterium *Comamonas* sp. JB. *Applied Biochemistry and Biotechnology*, 176, 1700-1708. https://doi.org/10.1007/s12010-015-1671-6

Jiang, C., Cheng, Y., Zang, H., Chen, X., Wang, Y., Zhang, Y., Wang, J., Shen, X., and Li, C. (2020). Biodegradation of lignin and the associated degradation pathway by psychrotrophic *Arthrobacter* sp. C2 from the cold region of China. *Cellulose*, 27, 1423-1440. https://doi.org/10.1007/s10570-019-02858-3

Jin, D. F., Hu, H., Liu, D. F., Ding, H. T., Jia, X. M., and Zhao, Y. H. (2012). Optimisation of a bacterial consortium for nitrobenzene degradation. *Water Science and Technology*, 65, 795-801. https://doi.org/10.2166/wst.2012.692

Joutey, N. T., Bahafid, W., Sayel, H., and El Ghachtouli, N. (2013). Biodegradation: involved microorganisms and genetically engineered microorganisms. In: *Biodegradation-life of science* (pp. 289-320). InTech, Croatia.

Jung, W. K., Koo, H. C., Kim, K. W., Shin, S., Kim, S. H., and Park, Y. H. (2008). Antibacterial activity and mechanism of action of the silver ion in *Staphylococcus aureus* and *Escherichia coli*. *Applied and Environmental Microbiology*, 74, 2171-2178. https://doi.org/10.1128/AEM.02001-07

Kanematsu, H. and Barry, D. M. (2015). Environmental Problems: Soil and Underground Water Treatment and Bioremediation. In: Kanematsu H., Barry D. (eds) *Biofilm and Materials Science*. Springer, Cham. https://doi.org/10.1007/978-3-319-14565-5_14

Kang, C. H., Kwon, Y. J., and So, J. S. (2016). Bioremediation of heavy metals by using bacterial mixtures. *Ecological Engineering*, 89, 64-69. https://doi.org/10.1016/j.ecoleng.2016.01.023

Karamba, K. I., Ahmad, S. A., Zulkharnain, A., Syed, M. A., Khalil, K. A., Shamaan, N. A., Dahalan, F. A., and Shukor, M. Y. (2016). Optimisation of biodegradation conditions for cyanide removal by *Serratia marcescens* strain AQ07 using one-factor-at-a-time technique and response surface methodology. *Rendiconti Lincei*, 27, 533-545. https://doi.org/10.1007/s12210-016-0516-8

Karigar, C., Mahesh, A., Nagenahalli, M., and Yun, D. J. (2006). Phenol degradation by immobilized cells of *Arthrobacter citreus*. *Biodegradation*, 17, 47-55. https://doi.org/10.1007/s10532-005-3048-y

Karimi, M. and Hassanshahian, M. (2016). Isolation and characterization of phenol degrading yeasts from wastewater in the coking plant of Zarand, *Kerman. Brazilian Journal of Microbiology*, 47, 18-24. https://doi.org/10.1016/j.bjm.2015.11.032

Kauppi, S., Sinkkonen, A., and Romantschuk, M. (2011). Enhancing bioremediation of diesel-fuel-contaminated soil in a boreal climate: comparison of biostimulation and bioaugmentation. *International Biodeterioration and Biodegradation*, 65, 359-368. https://doi.org/10.1016/j.ibiod.2010.10.011

Kebede, G., Tafese, T., Abda, E. M., Kamaraj, M., and Assefa, F. (2021). Factors influencing the bacterial bioremediation of hydrocarbon contaminants in the soil: mechanisms and impacts. *Journal of Chemistry*, Article ID 9823362. https://doi.org/10.1155/2021/9823362

Keeling, P. J., and Palmer, J. D. (2008). Horizontal gene transfer in eukaryotic evolution. *Nature Reviews Genetics*, 9, 605-618. https://doi.org/10.1038/nrg2386

Kennicutt II, M. C., Klein, A., Montagna, P., Sweet, S., Wade, T., Palmer, T., Sericano, J., and Denoux, G. (2010). Temporal and spatial patterns of anthropogenic disturbance at McMurdo Station, Antarctica. *Environmental Research Letters*, 5, Article ID 034010. https://doi.org/10.1088/1748-9326/5/3/034010

Kennicutt, M. C., Sweet, S. T., Fraser, W. R., Stockton, W. L., and Culver, M. (1991). Grounding of the Bahia Paraiso at Arthur Harbor, Antarctica. 1. Distribution and fate of oil spill related hydrocarbons. *Environmental Science and Technology*, 25, 509-518. https://doi.org/10.1021/es00015a020

Kim, H., Vinueza, N. R., Kelley, S. S., and Park, S. (2018). Correlation between solubility parameters and recovery of phenolic compounds from fast pyrolysis bio-oil by diesel extraction. *Carbon Resources Conversion*, 1, 238-244. https://doi.org/10.1016/j.crcon.2018.08.004

Kim, K. K., Lee, K. C., Oh, H. M., Kim, M. J., Eom, M. K., and Lee, J. S. (2008). *Arthrobacter defluvii* sp. nov., 4-chlorophenol-degrading bacteria isolated from sewage. *International Journal of Systematic and Evolutionary Microbiology*, 58, 1916-1921. https://doi.org/10.1099/ijs.0.65550-0

King, A. and Cole, B. (2008). Antarctica Map - Antarctica Satellite Image. [online] Geology.com. Available at: <https://geology.com/world/antarctica-satellite-image.shtml> [Accessed 15 January 2021].

Kotresha, D. and Vidyasagar, G. M. (2008). Isolation and characterisation of phenol-degrading *Pseudomonas aeruginosa* MTCC 4996. *World Journal of Microbiology and Biotechnology*, 24, 541-547. https://doi.org/10.1007/s11274-007-9508-2

Krallish, I., Gonta, S., Savenkova, L., Bergauer, P., and Margesin, R. (2006). Phenol degradation by immobilized cold-adapted yeast strains of *Cryptococcus terreus* and *Rhodotorula creatinivora*. *Extremophiles*, 10, 441-449. https://doi.org/10.1007/s00792-006-0517-0

Krastanov, A., Alexieva, Z., and Yemendzhiev, H. (2013). Microbial degradation of phenol and phenolic derivatives. *Engineering in Life Sciences*, 13, 76-87. https://doi.org/10.1002/elsc.201100227

Krause, M., Klit, A., Blomberg, J. M., Soeborg, T., Frederiksen, H., Schlumpf, M., Lichtensteiger, W., Skakkebaek, N. E., and Drzewiecki, K. T. (2012). Sunscreens: are they beneficial for health? An overview of endocrine disrupting properties of UV-filters. *International Journal of Andrology,* 35, 217-222. https://doi.org/10.1111/j.1365-2605.2012.01280.x

Kulecka, M., Waker, E., Ambrozkiewicz, F., Paziewska, A., Skubisz, K., Cybula, P., Targoński, Ł., Mikula, M., Walewski, J., and Ostrowski, J. (2021). Higher genome variability within metabolism genes associates with recurrent *Clostridium* difficile infection. *BMC Microbiology*, 21, 1-10. https://doi.org/10.1186/s12866-021-02090-9

Kulkarni, P. R., King, D. C., McHugh, T. E., Adamson, D. T., and Newell, C. J. (2017). Impact of temperature on groundwater source attenuation rates at hydrocarbon sites. *Groundwater Monitoring and Remediation*, 37, 82-93. https://doi.org/10.1111/gwmr.12226

Kumar Bhar, P. and Niyogi, U. K. (2015). Assessment of Pollution in a Freshwater Lake at Fisher Island, Larsemann Hills over East Antarctica. *Science International*, 3, 25-30. https://doi.org/10.5567/sciintl.2015.25.30

Kumar, S., Stecher, G., and Tamura, K. (2016). MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution*, 33, 1870-1874. https://doi.org/10.1093/molbev/msw054

Kumavath, R. N. and Deverapalli, P. (2013). Scientific swift in bioremediation: an overview. *International Journal of Pharmacy and Pharmaceutical Sciences*, 4, 375-388. https://doi.org/10.5772/56409

Kweon, O. J., Lim, Y. K., Kim, H. R., Kim, T. H., Ha, S. M., and Lee, M. K. (2020). Isolation of a novel species in the genus *Cupriavidus* from a patient with sepsis using whole genome sequencing. *PloS One*, 15, Article ID e0232850. https://doi.org/10.1371/journal.pone.0232850

Ladomersky, E. and Petris, M. J. (2015). Copper tolerance and virulence in bacteria. *Metallomics*, 7, 957-964. https://doi.org/10.1039/c4mt00327f

Láska, K., Barták, M., Hájek, J., Prošek, P., and Bohuslavová, O. (2011). Climatic and ecological characteristics of deglaciated area of James Ross Island, Antarctica, with a special respect to vegetation cover. *Czech Polar Reports*, 1, 49-62.

Leal, T. W., Lourenço, L. A., Brandão, H. de L., da Silva, A., de Souza, S. M. A. G. U., and de Souza, A. A. U. (2018). Low-cost iron-doped catalyst for phenol degradation by heterogeneous Fenton. *Journal of Hazardous Materials*, 359, 96-103. https://doi.org/10.1016/j.jhazmat.2018.07.018

Lebedev, A. T., Mazur, D. M., Polyakova, O. V., and Hänninen, O. (2015). Snow Samples as Markers of Air Pollution in Mass Spectrometry Analysis. In: R. H. Armon and O. Hänninen (Eds.), *Environmental Indicators* (pp. 515-541). Dordrecht: Springer Netherlands.

Lee, G. L. Y. (2018b). Biodegradation of phenol by cold-adapted bacteria isolated from Antarctic soils (Doctoral dissertation). Universiti Putra Malaysia, Selangor.

Lee, G. L. Y., Ahmad, S. A., Yasid, N. A., Zulkharnain, A., Convey, P., Wan Johari, W.L., and Shukor, M.Y. (2018a). Biodegradation of phenol by cold-adapted bacteria from Antarctic soils. *Polar Biology*, 41, 553-562. https://doi.org/10.1007/s00300-017-2216-y

Lee, G. L. Y., Zakaria, N. N., Convey, P., Futamata, H., Zulkharnain, A., Suzuki, K., Abdul Khalil, K., Shaharuddin, N. A., Alias, S. A., González-Rocha, G., and Ahmad, S. A. (2020). Statistical optimisation of phenol degradation and pathway identification through whole genome sequencing of the cold-adapted Antarctic bacterium, *Rhodococcus* sp. strain AQ5-07. *International Journal of Molecular Sciences*, 21, Article ID 9363. https://doi.org/10.3390/ijms21249363

Lee, I., Kim, Y. O., Park, S. C., and Chun, J. (2016). OrthoANI: an improved algorithm and software for calculating average nucleotide identity. *International Journal of Systematic and Evolutionary Microbiology*, 66, 1100-1103. https://doi.org/10.1099/ijsem.0.000760

Lee, S. Y., Ahmad, S. A., Mustapha, V., and Ong-Abdullah, J. (2017). Ability of *Ipomoea aquatica* Forssk. to remediate phenol in water and effects of phenol on the plant's growth. *Pertanika Journal of Science and Technology*, 25, 441-452.

Li, D., Yan, Y., Ping, S., Chen, M., Zhang, W., Li, L., Lin, W., Geng, L., Liu, W., Lu, W., and Lin, M. (2010a). Genome-wide investigation and functional characterization of the β-ketoadipate pathway in the nitrogen-fixing and root-associated bacterium *Pseudomonas stutzeri* A1501. *BMC Microbiology*, 10, 1-14. https://doi.org/10.1186/1471-2180-10-36

Li, H., Meng, F., Duan, W., Lin, Y., and Zheng, Y. (2019). Biodegradation of phenol in saline or hypersaline environments by bacteria: A review. *Ecotoxicology and Environmental Safety*, 184, 109658. https://doi.org/10.1016/j.ecoenv.2019.109658

Li, Y., Li, J., Wang, C., and Wang, P. (2010b). Growth kinetics and phenol biodegradation of psychrotrophic *Pseudomonas putida* LY1. *Bioresource Technology*, 101, 6740-6744. https://doi.org/10.1016/j.biortech.2010.03.083

Liang, C. Y., Yang, C. H., Lai, C. H., Huang, Y. H., and Lin, J. N. (2019). Genomic features, comparative genomic analysis, and antimicrobial susceptibility

patterns of *Chryseobacterium arthrosphaerae* strain ED882-96 isolated in Taiwan. *Genes*, 10, 309. https://doi.org/10.3390/genes10040309

Lischka, A., Bustamante, P., Braid, H., Piatkowski, U., and Lacoue-Labarthe, T. (2021). Trophic ecology drives trace element concentrations in the Antarctic octopod community. *Science of the Total Environment*, 768, Article ID 144373. https://doi.org/10.1016/j.scitotenv.2020.144373

Liu, H., Yang, C., Tian, Y., Lin, G., and Zheng, T. (2010). Screening of PAH-degrading bacteria in a mangrove swamp using PCR–RFLP. *Marine Pollution Bulletin*, 60, 2056-2061. https://doi.org/10.1016/j.marpolbul.2010.07.013

Liu, N. and Wu, Z. (2018). Growth and antioxidant response in *Ceratophyllum demersum* L. under sodium dodecyl sulfate (SDS), phenol and joint stress. *Ecotoxicology and Environmental Safety*, 163, 188-195. https://doi.org/10.1016/j.ecoenv.2018.07.074

Liu, Z., Xie, W., Li, D., Peng, Y., Li, Z., and Liu, S. (2016). Biodegradation of phenol by bacteria strain *Acinetobacter calcoaceticus* PA isolated from phenolic wastewater. *International Journal of Environmental Research and Public health,* 13, 300. https://doi.org/10.3390/ijerph13030300

Livingstone, P. G., Morphew, R. M., and Whitworth, D. E. (2018). Genome sequencing and pan-genome analysis of 23 *Corallococcus* spp. strains reveal unexpected diversity, with particular plasticity of predatory gene sets. *Frontiers in Microbiology*, 9, Article ID 3187. https://doi.org/10.3389/fmicb.2018.03187

Lu, Q., Zou, X., Liu, J., Liang, Z., Shim, H., Qiu, R., and Wang, S. (2020). Inhibitory effects of metal ions on reductive dechlorination of polychlorinated biphenyls and perchloroethene in distinct organohalide-respiring bacteria. *Environment International*, 135, Article ID 105373. https://doi.org/10.1016/j.envint.2019.105373

Lu, Z., Cai, M., Wang, J., Yang, H., and He, J. (2012). Baseline values for metals in soils on Fildes Peninsula, King George Island, Antarctica: the extent of anthropogenic pollution. *Environmental Monitoring and Assessment*, 184, 7013-7021. https://doi.org/10.1007/s10661-011-2476-x

Lupachev, A. V., Abakumov, E. V., Goryachkin, S. V., and Veremeeva, A. A. (2020). Soil cover of the Fildes Peninsula (King George Island, West Antarctica). *Catena*, 193, Article ID 104613. https://doi.org/10.1016/j.catena.2020.104613

Ma, J. and Zhai, G. (2012). Microbial bioremediation in omics era: opportunities and challenges. *Journal of Bioremediation and Biodegradation*, 3, e120. http://dx.doi.org/10.4172/2155-6199.1000e120

Machovina, M. M., Usselman, R. J., and DuBois, J. L. (2016). Monooxygenase substrates mimic flavin to catalyze cofactorless oxygenations. *Journal of*

Biological Chemistry, 291, 17816-17828. https://doi.org/10.1074/jbc.M116.730051

Magnin, J. P., Gondrexon, N., and Willison, J. C. (2014). Zinc biosorption by the purple non-sulfur bacterium *Rhodobacter capsulatus*. *Canadian Journal of Microbiology*, 60, 829-837. https://doi.org/10.1139/cjm-2014-0231

Mahiudddin, M. and Fakhruddin, A. N. M. (2012). Degradation of phenol via meta cleavage pathway by *Pseudomonas fluorescens* PU1. *International Scholarly Research Notices*, Article ID 741820. https://doi.org/10.5402/2012/741820

Maji, J., Mukhopadhyay, B. C., Mitra, S., and Biswas, S. R. (2018). Molecular characterization of Yeasts and Bacteria isolated from Handia, an Indian traditional rice fermented alcoholic beverage. *American Journal of Current Microbiology*, 6, 1-12.

Majumder, A. and Jha, S. (2012). Hairy Roots: A Promising Tool for Phytoremediation. In: Satyanarayana, T., Johri, B., Anil Prakash, (eds.) *Microorganisms in Environmental Management*. Springer, Dordrecht. https://doi.org/10.1007/978-94-007-2229-3_27

Mamou, G., Mohan, G. B. M., Rouvinski, A., Rosenberg, A., and Ben-Yehuda, S. (2016). Early developmental program shapes colony morphology in bacteria. *Cell Reports*, 14, 1850-1857. https://doi.org/10.1016/j.celrep.2016.01.071.

Manan, F., Ibrahim, Z., and Shahir, S. (2014). Plants in Antarctica: Current and Future Phytoremediation Potential. *Jurnal Teknologi*, 69, 59-65. https://doi.org/10.11113/jt.v69.2413

Mandal, S., Bhunia, B., Kumar, A., Dasgupta, D., Mandal, T., Datta, S., and Bhattacharya, P. (2013). A statistical approach for optimization of media components for phenol degradation by *Alcaligenes faecalis* using Plackett–Burman and response surface methodology. *Desalination and Water treatment*, 51, 6058-6069. https://doi.org/10.1080/19443994.2013.769746

Manogaran, M., Shukor, M. Y., Yasid, N. A., Khalil, K. A., and Ahmad, S. A. (2018). Optimisation of culture composition for glyphosate degradation by *Burkholderia vietnamiensis* strain AQ5-12. *3 Biotech*, 8, 1-13. https://doi.org/10.1007/s13205-018-1123-4

Margesin, R., Fonteyne, P. A., and Redl, B. (2005). Low-temperature biodegradation of high amounts of phenol by *Rhodococcus* spp. and basidiomycetous yeasts. *Research in Microbiology*, 156, 68-75. https://doi.org/10.1016/j.resmic.2004.08.002

Margesin, R., Moertelmaier, C., and Mair, J. (2013). Low-temperature biodegradation of petroleum hydrocarbons (n-alkanes, phenol, anthracene, pyrene) by four actinobacterial strains. *International Biodeterioration and Biodegradation*, 84, 185-191. https://doi.org/10.1016/j.ibiod.2012.05.004

Margesin, R., Neuner, G., and Storey, K. B. (2007). Cold-loving microbes, plants, and animals-fundamental and applied aspects. *Naturwissenschaften*, 94, 77-99. https://doi.org/10.1007/s00114-006-0162-6

Margesin, R., Schumann, P., Spröer, C., and Gounot, A. M. (2004). *Arthrobacter psychrophenolicus* sp. nov., isolated from an Alpine ice cave. *International Journal of Systematic and Evolutionary Microbiology*, 54, 2067-2072. https://doi.org/10.1099/ijs.0.63124-0

Mariano, A. P., Kataoka, A. P. D. A. G., Angelis, D. D. F. D., and Bonotto, D. M. (2007). Laboratory study on the bioremediation of diesel oil contaminated soil from a petrol station. *Brazilian Journal of Microbiology*, 38, 346-353. http://dx.doi.org/10.1590/S1517-83822007000200030.

Martorell, M. M., Ruberto, L. A. M., de Castellanos, L. I. F., and Mac Cormack, W. P. (2019). Bioremediation abilities of Antarctic fungi. *Fungi in Extreme Environments: Ecological Role and Biotechnological Significance*, 517-534. https://doi.org/10.1007/978-3-030-19030-9_26

Maryam, A., Nur, M., Motharasan, M., Nur, A. Y., Siti, A. A., Siti, A. A., Smykl, J., Mohd, A. H., and Mohd, Y. (2019). Response surface-based optimization of the biodegradation of a simulated vegetable oily ballast wastewater under temperate conditions using the Antarctic bacterium *Rhodococcus erythropolis* ADL36. *Desalination and Water Treatment*, 144, 129-137. https://doi.org/10.5004/dwt.2019.23529

Mathews, I. I., Krishna, S. S., Schwarzenbacher, R., McMullan, D., Abdubek, P., Ambing, E., Canaves, J. M., Chiu, H. J., Deacon, A. M., DiDonato, M., and Elsliger, M. A. (2006). Crystal structure of phosphoribosylformylglycinamidine synthase II (smPurL) from *Thermotoga maritima* at 2.15 Å resolution. *Proteins: Structure, Function, and Bioinformatics*, 63, 1106-1111. https://doi.org/10.1002/prot.20650

Mazuki, T. A. T., Shukor, M. Y., and Ahmad, S. A. (2019). Bioremediation of phenol in Antarctic: a mini review. *Malaysian Journal of Biochemistry and Molecular Biology*, 22, 1-6.

McConnell, J. R., Maselli, O. J., Sigl, M., Vallelonga, P., Neumann, T., Anschütz, H., Bales, R. C., Curran, M. A., Das, S. B., Edwards, R., and Kipfstuhl, S. (2014). Antarctic-wide array of high-resolution ice core records reveals pervasive lead pollution began in 1889 and persists today. *Scientific Reports*, 4, 1-5. https://doi.org/10.1038/srep05848

McCormick, R. L., Ratcliff, M. A., Christensen, E., Fouts, L., Luecke, J., Chupka, G. M., Yanowitz, J., Tian, M., and Boot, M. (2015). Properties of oxygenates found in upgraded biomass pyrolysis oil as components of spark and compression ignition engine fuels. *Energy and Fuels*, 29, 2453-2461. https://doi.org/10.1021/ef502893q

McFarlin, K. M., Prince, R. C., Perkins, R., and Leigh, M. B. (2014). Biodegradation of dispersed oil in arctic seawater at-1 C. *PloS One*, 9, e84297. https://doi.org/10.1371/journal.pone.0084297

McWatters, R.S., Wilkins, D., Spedding, T., Hince, G., Raymond, B., Lagerewskij, G., Terry, D., Wise, L., and Snape, I. (2016). On site remediation of a fuel spill and soil reuse in Antarctica. *Science of the Total Environment*, 571, 963-973. https://doi.org/10.1016/j.scitotenv.2016.07.084

Megharaj, M., Ramakrishnan, B., Venkateswarlu, K., Sethunathan, N., and Naidu, R. (2011). Bioremediation approaches for organic pollutants: a critical perspective. *Environment International*, 37, 1362-1375. https://doi.org/10.1016/j.envint.2011.06.003

Miernyk, K. M., DeByle, C. K., and Rudolph, K. M. (2017). Evaluation of two matrices for long-term, ambient storage of bacterial DNA. *Biopreservation and Biobanking*, 15, 529-534. https://doi.org/10.1089/bio.2017.0040

Mignard, S. and Flandrois, J. P. (2006). 16S rRNA sequencing in routine bacterial identification: a 30-month experiment. *Journal of Microbiological Methods*, 67, 574-581. https://doi.org/10.1016/j.mimet.2006.05.009

Mohammadi, S., Kargari, A., Sanaeepur, H., Abbassian, K., Najafi, A., and Mofarrah, E. (2014). Phenol removal from industrial wastewaters: a short review. *Desalination and Water Treatment*, 53, 2215-2234. https://doi.org/10.1080/19443994.2014.883327

Mohanty, S. S. and Jena, H. M. (2017). Biodegradation of phenol by free and immobilized cells of a novel *Pseudomonas* sp. NBM11. *Brazilian Journal of Chemical Engineering*, 34, 75-84. https://doi.org/10.1590/0104-6632.20170341s20150388

Moon, J. S., Choi, H. S., Shin, S. Y., Noh, S. J., Jeon, C. O., and Han, N. S. (2015). Genome sequence analysis of potential probiotic strain *Leuconostoc lactis* EFEL005 isolated from kimchi. *Journal of Microbiology*, 53, 337-342. https://doi.org/10.1007/s12275-015-5090-8

Moradi, M., Fazlzadehdavil, M., Pirsaheb, M., Mansouri, Y., Khosravi, T., and Sharafi, K. (2016). Response surface methodology (RSM) and its application for optimization of ammonium ions removal from aqueous solutions by pumice as a natural and low cost adsorbent. *Archives of Environmental Protection*, 42, 33-43. https://doi.org/10.1515/aep-2016-0018

Morita, R. Y. (1975). Psychrophilic bacteria. *Bacteriological Reviews* 39, 144-167.

Mosaddegh, M. H., Jafarian, A., Ghasemi, A., and Mosaddegh, A. (2014). Phytoremediation of benzene, toluene, ethylbenzene and xylene contaminated air by D. deremensis and O. microdasys plants. *Journal of*

Environmental Health Science and Engineering, 12, 39. https://doi.org/10.1186/2052-336X-12-39

Mukherjee, D., Guha, D., Kumar, V., and Chakrabarty, S. (1991). Impairment of steroidogenesis and reproduction in sexually mature *Cyprinus carpio* by phenol sulfide under laboratory conditions. *Aquatic Toxicology*, 21, 29-39. https://doi.org/10.1016/0166-445X(91)90004-S

Mukred, A. M., Hamid, A. A., Hamzah, A., and Yusoff, W. W. (2008). Development of three bacteria consortium for the bioremediation of crude petroleum-oil in contaminated water. *Online Journal of Biological Sciences*, 8, 73-79. https://doi.org/10.3844/ojbsci.2008.73.79

Mustafa, S., Al-Douseri, A., Majki, K., and Al-Saleh, E. (2013). Potential of crude oil-degrading bacteria to co-resist heavy metals in soil. WIT *Transactions on Ecology and the Environment*, 173, 697-705. https://doi.org/10.2495/SDP130581

Mustapha, M. U., Halimoon, N., and Johari, W. L. W. (2020). Optimization of carbofuran insecticide degradation by *Enterobacter* sp. using response surface methodology (RSM). *Journal of King Saud University-Science*, 32, 2254-2262. https://doi.org/10.1016/j.jksus.2020.03.002

Mwangi, J. K., Lee, W.-J., Wang, L.-C., Sung, P.-J., Fang, L.-S., Lee, Y.-Y., and Chang-Chien, G.-P. (2016). Persistent organic pollutants in the Antarctic coastal environment and their bioaccumulation in penguins. *Environmental Pollution*, 216, 924-934. https://doi.org/10.1016/j.envpol.2016.07.001

Nair, C. I., Jayachandran, K., and Shashidhar, S. (2008). Biodegradation of phenol. *African Journal of Biotechnology*, 7, 4951-4958.

Nasr M. (2018) Modeling Applications in Bioremediation of Hydrocarbon Pollutants. In: Kumar V., Kumar M., Prasad R. (eds) *Microbial Action on Hydrocarbons*. Springer, Singapore. https://doi.org/10.1007/978-981-13-1840-5_8

Nawawi, N. M., Ahmad, S. A., Shukor, M. Y., Syed, M. A., Khalil, K. A., Ab Rahman, N. A., Dahalan, F. A., and Ibrahim, A. L. (2016). Statistical optimisation for improvement of phenol degradation by *Rhodococcus* sp. NAM 81. *Journal of Environmental Biology*, 37, 443-451.

Nawrocki, E. P. and Eddy, S. R. (2013). Computational identification of functional RNA homologs in metagenomic data. *RNA Biology*, 10, 1170-1179. https://doi.org/10.4161/rna.25038

Naz, S. and Afaque, F. (2017). Antibacterial Activity of Some Household Surface Cleaners against Common Pathogens. *RADS Journal of Biological Research and Applied Sciences*, 8, 23-25.

Nešvera, J., Rucká, L., and Pátek, M. (2015). Catabolism of phenol and its derivatives in bacteria: genes, their regulation, and use in the

biodegradation of toxic pollutants. *Advances in Applied Microbiology*, 93, 107-160. https://doi.org/10.1016/bs.aambs.2015.06.002

Neto, E. de L., Guerra, M. B. B., Thomazini, A., Daher, M., Andrade, A. M. de, and Schaefer, C. E. G. R. (2017). Soil Contamination by Toxic Metals Near an Antarctic Refuge in Robert Island, Maritime Antarctica: A Monitoring Strategy. *Water, Air, and Soil Pollution*, 228, 66. https://doi.org/10.1007/s11270-017-3245-4

Niewerth, H., Schuldes, J., Parschat, K., Kiefer, P., Vorholt, J. A., Daniel, R., and Fetzner, S. (2012). Complete genome sequence and metabolic potential of the quinaldine-degrading bacterium *Arthrobacter* sp. Rue61a. *BMC Genomics*, 13, 1-19. https://doi.org/10.1186/1471-2164-13-534

Nogina, T., Fomina, M., Dumanskaya, T., Zelena, L., Khomenko, L., Mikhalovsky, S., Podgorskyi, V., and Gadd, G. M. (2020). A new *Rhodococcus aetherivorans* strain isolated from lubricant-contaminated soil as a prospective phenol-biodegrading agent. *Applied Microbiology and Biotechnology*, 104, 3611-3625. https://doi.org/10.1007/s00253-020-10385-6

Nor, N. M., Mohamed, M. S., Loh, T. C., Foo, H. L., Rahim, R. A., Tan, J. S., and Mohamad, R. (2017). Comparative analyses on medium optimization using one-factor-at-a-time, response surface methodology, and artificial neural network for lysine–methionine biosynthesis by *Pediococcus pentosaceus* RF-1. *Biotechnology and Biotechnological Equipment*, 31, 935-947. https://doi.org/10.1080/13102818.2017.1335177

Noubigh, A., Mgaidi, A., Abderrabba, M., Provost, E., and Fürst, W. (2007). Effect of salts on the solubility of phenolic compounds: experimental measurements and modelling. *Journal of the Science of Food and Agriculture*, 87, 783-788. https://doi.org/10.1002/jsfa.2762

Nunes, I., Jacquiod, S., Brejnrod, A., Holm, P. E., Johansen, A., Brandt, K. K., Priemé, A. and Sørensen, S. J. (2016). Coping with copper: legacy effect of copper on potential activity of soil bacteria following a century of exposure. *FEMS Microbiology Ecology*, 92, fiw175. https://doi.org/10.1093/femsec/fiw175

Nydahl, A. C., King, C. K., Wasley, J., Jolley, D. F., and Robinson, S. A. (2015). Toxicity of fuel-contaminated soil to Antarctic moss and terrestrial algae. *Environmental Toxicology and Chemistry*, 34, 2004-2012. https://doi.org/10.1002/etc.3021

Nzila, A. (2018). Current status of the degradation of aliphatic and aromatic petroleum hydrocarbons by thermophilic microbes and future perspectives. *International Journal of Environmental Research and Public Health*, 15, 2782. https://doi.org/10.3390/ijerph15122782

O'Neill, T. A., Aislabie, J., and Balks, M. R. (2015). Human Impacts on Soils. In: Bockheim, J. (eds) *The Soils of Antarctica. World Soils Book Series*. Springer, Cham. https://doi.org/10.1007/978-3-319-05497-1_15

Oaikhena, E. E., Makaije, D. B., Denwe, S. D., Namadi, M. M., and Haroun, A. A. (2016). Bioremediation potentials of heavy metal tolerant bacteria isolated from petroleum refinery effluent. *American Journal of Environmental Protection*, 5, 29-34. https://doi.org/10.11648/j.ajep.20160502.12

Ochyra, R., Bednarek-Ochyra, H., and Lewis Smith, R. I. (2008). New and rare moss species from the Antarctic. *Nova Hedwigia*, 87, 457-477. https://doi.org/10.1127/0029-5035/2008/0087-0457

Overbeek, R., Begley, T., Butler, R. M., Choudhuri, J. V., Chuang, H. Y., Cohoon, M., de Crécy-Lagard, V., Diaz, N., Disz, T., Edwards, R., and Fonstein, M. (2005). The subsystems approach to genome annotation and its use in the project to annotate 1000 genomes. *Nucleic Acids Research*, 33, 5691-5702. https://doi.org/10.1093/nar/gki866

Øvstedal, D. O. and Smith, R. L. (2001). Lichens of Antarctica and South Georgia: a guide to their identification and ecology. Cambridge University Press, United Kingdom

Oxford Analytica: Galapagos spill to fuel Ecuador government criticism. Emerald Expert Briefings (2019).

Paisio, C. E., Talano, M. A., González, P. S., Pajuelo-Domínguez, E., and Agostini, E. (2013). Characterization of a phenol-degrading bacterium isolated from an industrial effluent and its potential application for bioremediation. *Environmental Technology*, 34, 485-493.

Palanisamy, N., Ramya, J., Kumar, S., Vasanthi, N. S., Chandran, P., and Khan, S. (2014). Diesel biodegradation capacities of indigenous bacterial species isolated from diesel contaminated soil. *Journal of Environmental Health Science and Engineering*, 12, 1-8. https://doi.org/10.1186/s40201-014-0142-2

Pandey, V. C. and Bajpai, O. (2019). Phytoremediation: From theory toward practice. *In Phytomanagement of Polluted Sites* (pp. 1-49). Elsevier. https://doi.org/10.1016/B978-0-12-813912-7.00001-6

Park, J. S., Brown, M. T., and Han, T. (2012a). Phenol toxicity to the aquatic macrophyte *Lemna paucicostata*. *Aquatic Toxicology*, 106, 182-188. https://doi.org/10.1016/j.aquatox.2011.10.004

Park, S. H., Choi, S. R., and Choe, J. W. (2012b). *Bacillus subtilis* HmoB is a heme oxygenase with a novel structure. *BMB Reports*, 45, 239-241. https://doi.org/10.5483/BMBRep.2012.45.4.239

Patil, S. S. and Jena, H. M. (2015). Statistical optimization of phenol degradation by *Bacillus pumilus* OS1 using plackett–burman design and response surface methodology. *Arabian Journal for Science and Engineering*, 40, 2141-2151. https://doi.org/10.1007/s13369-015-1765-z

Penn, K., Jenkins, C., Nett, M., Udwary, D. W., Gontang, E. A., McGlinchey, R. P., Foster, B., Lapidus, A., Podell, S., Allen, E. E., and Moore, B. S. (2009). Genomic islands link secondary metabolism to functional adaptation in marine A*ctinobacteria*. *The ISME Journal*, 3, 1193-1203. https://doi.org/10.1038/ismej.2009.58

Perpetuo, E. A., Marques, R. C. P., Mendes, M. A., de Lima, W. C., Menck, C. F. M., and Do Nascimento, C. A. O. (2009). Characterization of the phenol monooxygenase gene from *Chromobacterium violaceum*: Potential use for phenol biodegradation. *Biotechnology and Bioprocess Engineering*, 14, 694-701. https://doi.org/10.1007/s12257-008-0266-2

Perruchon, C., Vasileiadis, S., Rousidou, C., Papadopoulou, E.S., Tanou, G., Samiotaki, M., Garagounis, C., Molassiotis, A., Papadopoulou, K. K., and Karpouzas, D. G. (2017). Metabolic pathway and cell adaptation mechanisms revealed through genomic, proteomic and transcription analysis of a *Sphingomonas haloaromaticamans* strain degrading ortho-phenylphenol. *Scientific Reports*, 7, 1-14. https://doi.org/10.1038/s41598-017-06727-6

Peter, H. U., Buesser, C., Mustafa, O., and Pfeiffer, S. (2008). Risk assessment for the Fildes Peninsula and Ardley Island, and development of management plans for their designation as Specially Protected or Specially Managed Areas. German Federal Environment Agency, Dessau.

Phadtare, S. (2004). Recent developments in bacterial cold-shock response. *Current Issues in Molecular Biology*, 6, 125-136.

Pi, Y., Meng, L., Bao, M., Sun, P., and Lu, J. (2016). Degradation of crude oil and relationship with bacteria and enzymatic activities in laboratory testing. *International Biodeterioration and Biodegradation*, 106, 106-116. https://doi.org/10.1016/j.ibiod.2015.10.015

Plahuta, M., Tišler, T., Toman, M. J., and Pintar, A. (2017). Toxic and endocrine disrupting effects of wastewater treatment plant influents and effluents on a freshwater isopod *Asellus aquaticus* (Isopoda, Crustacea). *Chemosphere*, 174, 342-353. https://doi.org/10.1016/j.chemosphere.2017.01.137

Plewniak, F., Crognale, S., Rossetti, S., and Bertin, P. N. (2018). A genomic outlook on bioremediation: the case of arsenic removal. *Frontiers in Microbiology*, 9, 820. https://doi.org/10.3389/fmicb.2018.00820

Poi, G., Aburto-Medina, A., Mok, P. C., Ball, A. S., and Shahsavari, E. (2017). Bioremediation of phenol-contaminated industrial wastewater using a bacterial consortium—from laboratory to field. *Water, Air, and Soil Pollution*, 228, 89. https://doi.org/10.1007/s11270-017-3273-0

Poli, A., Finore, I., Romano, I., Gioiello, A., Lama, L., and Nicolaus, B. (2017). Microbial diversity in extreme marine habitats and their biomolecules. *Microorganisms*, 5, 25. https://doi.org/10.3390/microorganisms5020025

Poorsoleiman, M. S., Hosseini, S. A., Etminan, A., Abtahi, H., and Koolivand, A. (2020). Effect of two-step bioaugmentation of an indigenous bacterial strain isolated from oily waste sludge on petroleum hydrocarbons biodegradation: scaling-up from a liquid mineral medium to a two-stage composting process. *Environmental Technology and Innovation*, 17, Article ID 100558. https://doi.org/10.1016/j.eti.2019.100558

Powell, S. M., Bowman, J. P., Snape, I., and Stark, J. S. (2003). Microbial community variation in pristine and polluted nearshore Antarctic sediments. *FEMS Microbiology Ecology*, 45, 135-145. https://doi.org/10.1016/S0168-6496(03)00135-1

Powell, S., Forslund, K., Szklarczyk, D., Trachana, K., Roth, A., Huerta-Cepas, J., Gabaldon, T., Rattei, T., Creevey, C., Kuhn, M., and Jensen, L. J. (2014). eggNOG v4. 0: nested orthology inference across 3686 organisms. *Nucleic Acids Research*, 42, D231-D239. https://doi.org/10.1093/nar/gkt1253

Pradeep, N. V., Anupama, S., Navya, K., Shalini, H. N., Idris, M., and Hampannavar, U. S. (2015). Biological removal of phenol from wastewaters: a mini review. *Applied Water Science*, 5, 105-112. https://doi.org/10.1007/s13201-014-0176-8

Priyadharshini, S. D. and Bakthavatsalam, A. K. (2016). Optimization of phenol degradation by the microalga *Chlorella pyrenoidosa* using Plackett–Burman design and response surface methodology. *Bioresource Technology*, 207, 150-156. https://doi.org/10.1016/j.biortech.2016.01.138

Prosser, J. I. and Embley, T. M. (2002). Cultivation-based and molecular approaches to characterisation of terrestrial and aquatic nitrifiers. *Antonie van Leeuwenhoek*, 81, 165-179. https://doi.org/10.1023/A:1020598114104

Qin, X., Tang, J. C., Li, D. S., and Zhang, Q. M. (2012). Effect of salinity on the bioremediation of petroleum hydrocarbons in a saline-alkaline soil. *Letters in Applied Microbiology*, 55, 210-217. https://doi.org/10.1111/j.1472-765X.2012.03280.x

Quayle, W. C., Convey, P., Peck, L. S., Ellis-Evans, C. J., Butler, H. G., and Peat, H. J. (2003). Ecological responses of maritime Antarctic lakes to regional climate change. *Antarctic Research Series*, 79, 159-170. https://doi.org/10.1029/AR079p0159

Quayle, W. C., Peck, L. S., Peat, H., Ellis-Evans, J. C., and Harrigan, P. R. (2002). Extreme responses to climate change in Antarctic lakes. (Climate Change). *Science*, 295, 645-646.

Rahdar, S., Ahamadabadi, M., Khaksefidi, R., Saeidi, M., Narooie, M.R., Salimi, A., Biglari, H., and Baneshi, M. M. (2017). Evaluation of phenol removal from aqueous solution by banana leaf ash. *Journal of Global Pharma Technology*, 9, 20-28.

Ram Talib, N. S., Halmi, M. I. E., Abd Ghani, S. S., Zaidan, U. H., and Shukor, M. Y. A. (2019). Artificial neural networks (ANNs) and response surface methodology (RSM) approach for modelling the optimization of chromium (VI) reduction by newly isolated *Acinetobacter radioresistens* strain NS-MIE from agricultural soil. *BioMed Research International*, Article ID 5785387. https://doi.org/10.1155/2019/5785387

Ramasamy, S., Arumugam, A., and Chandran, P. (2017). Optimization of *Enterobacter cloacae* (KU923381) for diesel oil degradation using response surface methodology (RSM). *Journal of Microbiology*, 55, 104-111. https://doi.org/10.1007/s12275-017-6265-2

Rambeloarisoa, E., Rontani, J. F., Giusti, G., Duvnjak, Z., and Bertrand, J. C. (1984). Degradation of crude oil by a mixed population of bacteria isolated from sea-surface foams. *Marine Biology*, 83, 69-81. https://doi.org/10.1007/BF00393087

Ramírez, E. E. P., de la Luz Asunción, M., Rivalcoba, V. S., Hernández, A. L. M., and Santos, C. V. (2017). Removal of Phenolic Compounds from Water by Adsorption and Photocatalysis. In: *Phenolic Compounds-Natural Sources, Importance and Applications*, (pp. 343-372). InTech, Croatia.

Reed, S., Clark, M., Thompson, R., and Hughes, K. A. (2018). Microplastics in marine sediments near Rothera Research Station, Antarctica. *Marine Pollution Bulletin*, 133, 460-463. https://doi.org/10.1016/j.marpolbul.2018.05.068

Ren, L., Shi, Y., Jia, Y., and Yan, Y. (2015). Genome sequence of *Arthrobacter* sp. YC-RL1, an aromatic compound-degrading bacterium. *Genome Announcements*, 3, Article ID e00749-15. https://doi.org/10.1128/genomeA.00749-15

Reuter, J. A., Spacek, D. V., and Snyder, M. P. (2015). High-throughput sequencing technologies. *Molecular Cell*, 58, 586-597. https://doi.org/10.1016/j.molcel.2015.05.004

Rodríguez-Salazar, J., Almeida-Juarez, A. G., Ornelas-Ocampo, K., Millán-López, S., Raga-Carbajal, E., Rodríguez-Mejía, J. L., Muriel-Millán, L. F., Godoy-Lozano, E. E., Rivera-Gómez, N., Rudiño-Piñera, E., and Pardo-López, L. (2020). Characterization of a novel functional trimeric catechol 1, 2-dioxygenase from a *Pseudomonas stutzeri* isolated from the Gulf of Mexico. *Frontiers in Microbiology*, 11, 1100. https://doi.org/10.3389/fmicb.2020.01100

Romaniuk, K., Ciok, A., Decewicz, P., Uhrynowski, W., Budzik, K., Nieckarz, M., Pawlowska, J., Zdanowski, M. K., Bartosik, D., and Dziewit, L. (2018).

Insight into heavy metal resistome of soil psychrotolerant bacteria originating from King George Island (Antarctica). *Polar Biology*, 41, 1319-1333. https://doi.org/10.1007/s00300-018-2287-4

Romero-Rodríguez, A., Robledo-Casados, I., and Sánchez, S. (2015). An overview on transcriptional regulators in *Streptomyces*. *Biochimica et Biophysica Acta (BBA)-Gene Regulatory Mechanisms*, 1849, 1017-1039. https://doi.org/10.1016/j.bbagrm.2015.06.007

Rong, J. C., Liu, Y., Yu, S., Xi, L., Chi, N. Y., and Zhang, Q. F. (2020). Complete genome sequence of *Paenisporosarcina antarctica* CGMCC 1.6503 T, a marine psychrophilic bacterium isolated from Antarctica. *Marine Genomics*, 49, Article ID 100690. https://doi.org/10.1016/j.margen.2019.05.005

Roslee, A. F. A., Zakaria, N. N., Convey, P., Zulkharnain, A., Lee, G. L. Y., Gomez-Fuentes, C., and Ahmad, S. A. (2020). Statistical optimisation of growth conditions and diesel degradation by the Antarctic bacterium, *Rhodococcus* sp. strain AQ5–07. *Extremophiles*, 24, 277-291. https://doi.org/10.1007/s00792-019-01153-0

Rosselló-Móra, R. and Amann, R. (2015). Past and future species definitions for Bacteria and Archaea. *Systematic and Applied Microbiology*, 38, 209-216. https://doi.org/10.1016/j.syapm.2015.02.001

Rouch, D. A., Lee, B. T., and Morby, A. P. (1995). Understanding cellular responses to toxic agents: a model for mechanism-choice in bacterial metal resistance. *Journal of Industrial Microbiology and Biotechnology*, 14, 132-141. https://doi.org/10.1007/BF01569895

Roy, S. M., Roy, D. R., and Sahoo, S. K. (2015). Toxicity prediction of PHDDs and phenols in the light of nucleic acid bases and DNA base pair interaction. *Journal of Molecular Graphics and Modelling*, 62, 128-137. https://doi.org/10.1016/j.jmgm.2015.09.004

Rückamp, M., Braun, M., Suckro, S., and Blindow, N. (2011). Observed glacial changes on the King George Island ice cap, Antarctica, in the last decade. *Global and Planetary Change*, 79, 99-109. https://doi.org/10.1016/j.gloplacha.2011.06.009

Ryter, S. W. and Tyrrell, R. M. (2000). The heme synthesis and degradation pathways: role in oxidant sensitivity: heme oxygenase has both pro-and antioxidant properties. *Free Radical Biology and Medicine*, 28, 289-309. https://doi.org/10.1016/S0891-5849(99)00223-3

Saarikoski, J., and Viluksela, M. (1981). Influence of pH on the toxicity of substituted phenols to fish. *Archives of Environmental Contamination and Toxicology*, 10, 747-753. https://doi.org/10.1007/BF01054858

Sachan, P., Madan, S., and Hussain, A. (2019). Isolation and screening of phenol-degrading bacteria from pulp and paper mill effluent. *Applied Water Science*, 9, 1-6. https://doi.org/10.1007/s13201-019-0994-9

Sachaniya, B. K., Gosai, H. B., Panseriya, H. Z., and Dave, B. P. (2020). Bioengineering for multiple PAHs degradation for contaminated sediments: Response surface methodology (RSM) and artificial neural network (ANN). *Chemometrics and Intelligent Laboratory Systems*, 202, 104033. https://doi.org/10.1016/j.chemolab.2020.104033

Saha, N. C., Bhunia, F., and Kaviraj, A. (1999). Toxicity of phenol to fish and aquatic ecosystems. *Bulletin of Environmental Contamination and Toxicology*, 63, 195-202.

Salaudeen, T., Okoh, O., and Okoh, A. (2019). Performance assessment of wastewater treatment plants with special reference to phenol removal. *International Journal of Environmental Science and Technology*, 16, 401-412. https://doi.org/10.1007/s13762-018-1684-0

Saługa, M., Ochyra, R., Żarnowiec, J., and Ronikier, M. (2018). Do Antarctic populations represent local or widespread phylogenetic and ecological lineages? Complicated fate of bipolar moss concepts with *Drepanocladus longifolius* as a case study. *Organisms Diversity and Evolution*, 18, 263-278. https://doi.org/10.1007/s13127-018-0372-8

Sandrin, T. R. and Maier, R. M. (2003). Impact of metals on the biodegradation of organic pollutants. *Environmental Health Perspectives*, 111, 1093-1101. https://doi.org/10.1289/ehp.5840

Sanger, F., Nicklen, S., and Coulson, A. R. (1977). DNA sequencing with chain-terminating inhibitors. *Proceedings of the National Academy of Sciences*, 74, 5463-5467. https://doi.org/10.1073/pnas.74.12.5463

Saravanan, P., Pakshirajan, K., and Saha, P. (2008). Growth kinetics of an indigenous mixed microbial consortium during phenol degradation in a batch reactor. *Bioresource Technology*, 99, 205-209. https://doi.org/10.1016/j.biortech.2006.11.045

Schadt, E. E., Turner, S., and Kasarskis, A. (2010). A window into third-generation sequencing. *Human Molecular Genetics*, 19, R227-R240. https://doi.org/10.1093/hmg/ddq416

Schattner, P., Brooks, A. N., and Lowe, T. M. (2005). The tRNAscan-SE, snoscan and snoGPS web servers for the detection of tRNAs and snoRNAs. *Nucleic Acids Research*, 33, W686-W689. https://doi.org/10.1093/nar/gki366

Schloss, J. A. (2008). How to get genomes at one ten-thousandth the cost. *Nature Biotechnology*, 26, 1113-1115. https://doi.org/10.1038/nbt1008-1113

Schink, S. J., Biselli, E., Ammar, C., and Gerland, U. (2019). Death rate of *E. coli* during starvation is set by maintenance cost and biomass recycling. *Cell Systems*, 9, 64-73. https://doi.org/10.1016/j.cels.2019.06.003

Schmid, M., Muri, J., Melidis, D., Varadarajan, A. R., Somerville, V., Wicki, A., Moser, A., Bourqui, M., Wenzel, C., Eugster-Meier, E., and Frey, J. E. (2018). Comparative genomics of completely sequenced *Lactobacillus helveticus* genomes provides insights into strain-specific genes and resolves metagenomics data down to the strain level. *Frontiers in Microbiology*, 9, 63. https://doi.org/10.3389/fmicb.2018.00063

Schröder, J. and Tauch, A. (2010). Transcriptional regulation of gene expression in *Corynebacterium glutamicum*: the role of global, master and local regulators in the modular and hierarchical gene regulatory network. *FEMS Microbiology Reviews*, 34, 685-737. https://doi.org/10.1111/j.1574-6976.2010.00228.x

Segata, N. and Huttenhower, C. (2011). Toward an efficient method of identifying core genes for evolutionary and functional microbial phylogenies. *PloS One*, 6, e24704. https://doi.org/10.1371/journal.pone.0024704

Semboung Lang, F., Tarayre, C., Destain, J., Delvigne, F., Druart, P., Ongena, M., and Thonart, P. (2016). The effect of nutrients on the degradation of hydrocarbons in mangrove ecosystems by microorganisms. *International Journal of Environmental Research*, 10, 583-592. https://doi.org/10.22059/IJER.2016.59903

Senthilvelan, T., Kanagaraj, J., Panda, R. C., and Mandal, A. B. (2014). Biodegradation of phenol by mixed microbial culture: an eco-friendly approach for the pollution reduction. *Clean Technologies and Environmental Policy*, 16, 113-126. Https://doi.org/10.1007/s10098-013-0598-2

Sepehr, S., Shahnavaz, B., Asoodeh, A., and Karrabi, M. (2019). Biodegradation of phenol by cold-tolerant bacteria isolated from alpine soils of Binaloud Mountains in Iran. *Journal of Environmental Science and Health*, Part A, 54, 367-379. https://doi.org/10.1080/10934529.2018.1553818

Setlhare, B., Kumar, A., Mokoena, M. P., and Olaniran, A. O. (2019). Catechol 1, 2-dioxygenase is an analogue of homogentisate 1, 2-dioxygenase in *Pseudomonas chlororaphis* strain UFB2. *International Journal of Molecular Sciences*, 20, 61. https://doi.org/10.3390/ijms20010061

Shah, M. P. (2018). Microbial degradation of phenol by an application of *Pseudomonas mendocina*. *Austin Journal Microbiology*, 4, 1-4.

Shahriari, M. M., Safaei, N., and Ebrahimipour, G. H. (2016). Optimization of phenol biodegradation by efficient bacteria isolated from petrochemical effluents. *Global Journal of Environmental Science and Management*, 2, 249-256.

Shen, X. H., Huang, Y., and Liu, S. J. (2005). Genomic analysis and identification of catabolic pathways for aromatic compounds in *Corynebacterium*

glutamicum. *Microbes and Environments*, 20, 160-167. https://doi.org/10.1264/jsme2.20.160

Shen, T., Pi, Y., Bao, M., Xu, N., Li, Y., and Lu, J. (2015). Biodegradation of different petroleum hydrocarbons by free and immobilized microbial consortia. *Environmental Science: Processes and Impacts*, 17, 2022-2033. https://doi.org/10.1039/C5EM00318K

Shin, H., Kim, Y., Han, D., and Hur, H. G. (2021). Emergence of high level carbapenem and extensively drug resistant *Escherichia coli* ST746 producing NDM-5 in influent of wastewater treatment plant, Seoul, South Korea. *Frontiers in Microbiology*, 12, Article ID 645411. https://doi.org/10.3389/fmicb.2021.645411

Shourian, M., Noghabi, K. A., Zahiri, H. S., Bagheri, T., Karbalaei, R., Mollaei, M., Rad, I., Ahadi, S., Raheb, J., and Abbasi, H. (2009). Efficient phenol degradation by a newly characterized *Pseudomonas* sp. SA01 isolated from pharmaceutical wastewaters. *Desalination*, 246, 577-594. https://doi.org/10.1016/j.desal.2008.07.015

Shukor, M. Y., Hassan, N. A. A., Jusoh, A. Z., Perumal, N., Shamaan, N. A., MacCormack, W. P., and Syed, M. A. (2009). Isolation and characterization of a *Pseudomonas* diesel-degrading strain from Antarctica. *Journal of Environmental Biology*, 30, 1-6.

Silva, C. C., Hayden, H., Sawbridge, T., Mele, P., De Paula, S. O., Silva, L. C., Vidigal, P. M., Vicentini, R., Sousa, M. P., Torres, A. P., and Santiago, V. M. (2013). Identification of genes and pathways related to phenol degradation in metagenomic libraries from petroleum refinery wastewater. *PloS one*, 8, Article ID e61811. https://doi.org/10.1371/journal.pone.0061811

Singh, A., Kumar, V., and Srivastava, J. N. (2013). Assessment of bioremediation of oil and phenol contents in refinery waste water via bacterial consortium. *Journal of Petroleum and Environmental Biotechnology*, 4, 1-4. https://doi.org/10.4172/2157-7463.1000145

Singh, O. V. and Jain, R. K. (2003). Phytoremediation of toxic aromatic pollutants from soil. *Applied Microbiology and Biotechnology*, 63, 128-135. https://doi.org/10.1007/s00253-003-1425-1

Singh, R., Gautam, N., Mishra, A., and Gupta, R. (2011). Heavy metals and living systems: An overview. *Indian Journal of Pharmacology*, 43, 246. https://doi.org/10.4103/0253-7613.81505

Singh, S., Eapen, S., Thorat, V., Kaushik, C. P., Raj, K., and D'souza, S. F. (2008). Phytoremediation of ^{137}cesium and ^{90}strontium from solutions and low-level nuclear waste by *Vetiveria zizanoides*. *Ecotoxicology and Environmental Safety*, 69, 306-311. https://doi.org/10.1016/j.ecoenv.2006.12.004

Singh, V., Khan, M., Khan, S., and Tripathi, C. K. M. (2009). Optimization of actinomycin V production by *Streptomyces triostinicus* using artificial neural network and genetic algorithm. *Applied Microbiology and Biotechnology*, 82, 379-385. https://doi.org/10.1007/s00253-008-1828-0

Sivakumar, D., Kandaswamy, A. N., Gomathi, V., Rajeshwaran, R., and Murugan, N. (2014). Bioremediation studies on reduction of heavy metals toxicity. *Pollution Research*, 33, 553-558.

Sivaraman, B., Jeyasekaran, G., Shakila, R. J., Wilwet, L., Alamelu, V., Aanand, S., and Sukumar, D. (2019). Molecular identification of Lutjanus species by PCR-RFLP analysis of mitochondrial 12S rRNA region. *Journal of Food Composition and Analysis*, 84, Article ID 103329. https://doi.org/10.1016/j.jfca.2019.103329

Sivasubramanian, S. and Namasivayam, S. K. R. (2015). Phenol degradation studies using microbial consortium isolated from environmental sources. *Journal of Environmental Chemical Engineering*, 3, 243-252. https://doi.org/10.1016/j.jece.2014.12.014

Šmarda, P., Bureš, P., Horová, L., Leitch, I. J., Mucina, L., Pacini, E., Tichý, L., Grulich, V., and Rotreklová, O. (2014). Ecological and evolutionary significance of genomic GC content diversity in monocots. *Proceedings of the National Academy of Sciences*, 111, E4096-E4102. https://doi.org/10.1073/pnas.1321152111

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, 413-421. https://doi.org/10.1007/s00248-006-9022-3

Song, Z. and Huang, G. (2007). Toxic effects of pentachlorophenol on *Lemna polyrhiza*. *Ecotoxicology and Environmental Safety*, 66, 343-347. https://doi.org/10.1016/j.ecoenv.2005.10.001

Souza, E. C., Vessoni-Penna, T. C., and de Souza Oliveira, R. P. (2014). Biosurfactant-enhanced hydrocarbon bioremediation: An overview. *International Biodeterioration and Biodegradation*, 89, 88-94. https://doi.org/10.1016/j.ibiod.2014.01.007

Springael, D. and Top, E. M. (2004). Horizontal gene transfer and microbial adaptation to xenobiotics: new types of mobile genetic elements and lessons from ecological studies. *Trends in Microbiology*, 12, 53-58. https://doi.org/10.1016/j.tim.2003.12.010

Sridevi, V., Lakshmi, M. V. V. C., Manasa, M., and Sravani, M. (2012). Metabolic pathways for the biodegradation of phenol. *International Journal of Engineering Science and Advanced Technology*, 2, 695-705.

Stackebrandt, E. and Schumann, P. E. T. E. R. (2006). Introduction to the taxonomy of actinobacteria. *Prokaryotes*, 3, 297-321. https://doi.org/10.1007/0-387-30743-5_16

Stackebrandt, E., Fowler, V. J., Fiedler, F., and Seiler, H. (1983). Taxonomic studies on *Arthrobacter nicotianae* and related taxa: description of *Arthrobacter uratoxydans* sp. nov. and *Arthrobacter sulfureus* sp. nov. and reclassification of *Brevibacterium protophormiae* as *Arthrobacter protophormiae* comb. nov. *Systematic and Applied Microbiology*, 4, 470-486. https://doi.org/10.1016/S0723-2020(83)80005-8

Stark, J. S., Kim, S. L., and Oliver, J. S. (2014). Anthropogenic disturbance and biodiversity of marine benthic communities in Antarctica: a regional comparison. *PloS One*, 9, Article ID e98802. https://doi.org/10.1371/journal.pone.0098802

Stark, J. S., Mohammad, M., McMinn, A., and Ingels, J. (2017). The effects of hydrocarbons on meiofauna in marine sediments in Antarctica. *Journal of Experimental Marine Biology and Ecology*, 496, 56-73. https://doi.org/10.1016/j.jembe.2017.07.009

Steliga, T., Wojtowicz, K., Kapusta, P., and Brzeszcz, J. (2020). Assessment of biodegradation efficiency of polychlorinated biphenyls (PCBs) and petroleum hydrocarbons (TPH) in soil using three individual bacterial strains and their mixed culture. *Molecules*, 25, 709. https://doi.org/10.3390/molecules25030709

Sterner, R., Merz, A., Thoma, R., and Kirschner, K. (2001). Phosphoribosylanthranilate isomerase and indoleglycerol-phosphate synthase: Tryptophan biosynthetic enzymes from *Thermotoga maritima*. *Methods in Enzymology*, 331, 270-280. https://doi.org/10.1016/S0076-6879(01)31064-9

Su, X., Wang, Y., Xue, B., Hashmi, M. Z., Lin, H., Chen, J., Wang, Z., Mei, R., and Sun, F. (2019). Impact of resuscitation promoting factor (Rpf) in membrane bioreactor treating high-saline phenolic wastewater: performance robustness and Rpf-responsive bacterial populations. *Chemical Engineering Journal*, 357, 715-723. https://doi.org/10.1016/j.cej.2018.09.197

Suárez-García, L. I., Cuervo-López, F. M., and Texier, A. C. (2019). Biological removal of mixtures of ammonium, phenol, cresol isomers, and sulfide in a sequencing batch reactor. *Revista Mexicana de Ingeniería Química*, 18, 1189-1202. https://doi.org/10.24275/uam/izt/dcbi/revmexingquim/2019v18n3/Suarez

Suenaga, H., Koyama, Y., Miyakoshi, M., Miyazaki, R., Yano, H., Sota, M., Ohtsubo, Y., Tsuda, M., and Miyazaki, K. (2009). Novel organization of aromatic degradation pathway genes in a microbial community as revealed by metagenomic analysis. *The ISME Journal*, 3, 1335-1348. https://doi.org/10.1038/ismej.2009.76

Suhaila, Y. N., Ramanan, R. N., Rosfarizan, M., Latif, I. A., and Ariff, A. B. (2013a). Optimization of parameters for improvement of phenol degradation

by *Rhodococcus* UKMP-5M using response surface methodology. *Annals of Microbiology*, 63, 513-521. https://doi.org/10.1007/s13213-012-0496-6

Suhaila, Y. N., Rosfarizan, M., Ahmad, S. A., Latif, I. A., and Ariff, A. B. (2013b). Nutrients and culture conditions requirements for the degradation of phenol by *Rhodococcus* UKMP-5M. *Journal of Environmental Biology*, 34, 635-643.

Sukumaran, D. (2013). Phytoremediation of heavy metals from industrial effluent using constructed wetland technology. *Applied Ecology and Environmental Sciences*, 1, 92-97. https://doi.org/10.12691/aees-1-5-4

Sun, J. Q., Xu, L., Tang, Y. Q., Chen, F. M., Zhao, J. J., and Wu, X. L. (2014). Bacterial pyridine hydroxylation is ubiquitous in environment. *Applied Microbiology and Biotechnology*, 98, 455-464. https://doi.org/10.1007/s00253-013-4818-9

Sun, Z., Tan, H. Y., Bianco, P. R., and Lyubchenko, Y. L. (2015). Remodeling of RecG helicase at the DNA replication fork by SSB protein. *Scientific Reports*, 5, 1-7. https://doi.org/10.1038/srep09625

Syahri, Y. F. and Yani, A. (2019). Biochemical tests and identification of potential indigenous bacteria from nickel post-mining land in Pomalaa. *In IOP Conference Series: Earth and Environmental Science* (p. 012020). IOP Publishing, Kolaka, Indonesia.

Szőköl, J., Rucká, L., Šimčíková, M., Halada, P., Nešvera, J., and Pátek, M. (2014). Induction and carbon catabolite repression of phenol degradation genes in *Rhodococcus erythropolis* and *Rhodococcus jostii*. *Applied Microbiology and Biotechnology*, 98, 8267-8279. https://doi.org/10.1007/s00253-014-5881-6

Tao, K., Liu, X., Chen, X., Hu, X., Cao, L., and Yuan, X. (2017). Biodegradation of crude oil by a defined co-culture of indigenous bacterial consortium and exogenous *Bacillus subtilis*. *Bioresource Technology*, 224, 327-332. https://doi.org/10.1016/j.biortech.2016.10.073

Tatusov, R. L., Fedorova, N. D., Jackson, J. D., Jacobs, A. R., Kiryutin, B., Koonin, E. V., Krylov, D. M., Mazumder, R., Mekhedov, S. L., Nikolskaya, A. N., and Rao, B. S. (2003). The COG database: an updated version includes eukaryotes. *BMC Bioinformatics*, 4, 1-14. https://doi.org/10.1186/1471-2105-4-41

Tavakoli, A. and Hamzah, A. (2017). Characterization and evaluation of catechol oxygenases by twelve bacteria, isolated from oil contaminated soils in Malaysia. *Biological Journal of Microorganism*, 5, 71-80.

Tchounwou P. B., Yedjou C. G., Patlolla A. K., Sutton D. J. (2012). Heavy Metal Toxicity and the Environment. In: Luch A. (eds) *Molecular, Clinical and Environmental Toxicology* (pp. 133-164). Springer, Basel.

Tengku-Mazuki, T. A., Subramaniam, K., Zakaria, N. N., Convey, P., Khalil, K. A., Lee, G. L. Y., Zulkharnain, A., Shaharuddin, N. A., and Ahmad, S. A. (2020). Optimization of phenol degradation by Antarctic bacterium *Rhodococcus* sp. *Antarctic Science*, 32, 486-495. https://doi.org/10.1017/S0954102020000358

Teixeira, L. C., Peixoto, R. S., Cury, J. C., Sul, W. J., Pellizari, V. H., Tiedje, J., and Rosado, A. S. (2010). Bacterial diversity in rhizosphere soil from Antarctic vascular plants of Admiralty Bay, maritime Antarctica. *The ISME Journal*, 4, 989-1001. https://doi.org/10.1007/s11274-008-9743-1

Terauds, A., Chown, S. L., Morgan, F., J. Peat, H., Watts, D. J., Keys, H., Convey, P., and Bergstrom, D. M. (2012). Conservation biogeography of the Antarctic. *Diversity and Distributions*, 18, 726-741. https://doi.org/10.1111/j.1472-4642.2012.00925.x

Tian, M., Du, D., Zhou, W., Zeng, X., and Cheng, G. (2017). Phenol degradation and genotypic analysis of dioxygenase genes in bacteria isolated from sediments. *Brazilian Journal of Microbiology*, 48, 305-313. https://doi.org/10.1016/j.bjm.2016.12.002

Tin, T., Fleming, Z. L., Hughes, K. A., Ainley, D. G., Convey, P., Moreno, C. A., Pfeiffer, S., Scott, J., and Snape, I. (2009). Impacts of local human activities on the Antarctic environment. *Antarctic Science*, 21, 3-33. https://doi.org/10.1017/S0954102009001722

Titah, H. S., Halmi, M. I. E. B., Abdullah, S. R. S., Hasan, H. A., Idris, M., and Anuar, N. (2018). Statistical optimization of the phytoremediation of arsenic by *Ludwigia octovalvis*-in a pilot reed bed using response surface methodology (RSM) versus an artificial neural network (ANN). *International Journal of Phytoremediation*, 20, 721-729. https://doi.org/10.1080/15226514.2017.1413337

Top, E. M. and Springael, D. (2003). The role of mobile genetic elements in bacterial adaptation to xenobiotic organic compounds. *Current Opinion in Biotechnology*, 14, 262-269. https://doi.org/10.1016/S0958-1669(03)00066-1

Treaty, A. (1991). Annex III to the protocol on environmental protection to the Antarctic Treaty (Madrid protocol).

Trevizani, T. H., Figueira, R. C. L., Ribeiro, A. P., Theophilo, C. Y. S., Majer, A. P., Petti, M. A. V., Corbisier, T. N., and Montone, R. C. (2016). Bioaccumulation of heavy metals in marine organisms and sediments from Admiralty Bay, King George Island, Antarctica. *Marine Pollution Bulletin*, 106, 366-371. https://doi.org/10.1016/j.marpolbul.2016.02.056

Trevizani, T. H., Petti, M. A. V., Ribeiro, A. P., Corbisier, T. N., and Figueira, R. C. L. (2018). Heavy metal concentrations in the benthic trophic web of Martel Inlet, Admiralty Bay (King George Island, Antarctica). *Marine*

Pollution Bulletin, 130, 198-205. https://doi.org/10.1016/j.marpolbul.2018.03.031

Troisi, G., Barton, S., and Bexton, S. (2016). Impacts of oil spills on seabirds: Unsustainable impacts of non-renewable energy. *International Journal of Hydrogen Energy*, 41, 16549-16555. https://doi.org/10.1016/j.ijhydene.2016.04.011

Tschech, A. and Fuchs, G. (1987). Anaerobic degradation of phenol by pure cultures of newly isolated denitrifying pseudomonads. *Archives of Microbiology*, 148, 213-217. https://doi.org/10.1007/BF00414814

Tulloch, V. J., Plagányi, É. E., Matear, R., Brown, C. J., and Richardson, A. J. (2018). Ecosystem modelling to quantify the impact of historical whaling on Southern Hemisphere baleen whales. *Fish and Fisheries*, 19, 117-137. https://doi.org/10.1111/faf.12241

Turner, J., Lu, H., King, J., Marshall, G. J., Phillips, T., Bannister, D., and Colwell, S. (2021). Extreme temperatures in the Antarctic. *Journal of Climate*, 34, 2653-2668. https://doi.org/10.1175/JCLI-D-20-0538.1

Tyagi, M., da Fonseca, M. M. R., and de Carvalho, C. C. (2011). Bioaugmentation and biostimulation strategies to improve the effectiveness of bioremediation processes. *Biodegradation*, 22, 231-241. https://doi.org/10.1007/s10532-010-9394-4

Unell, M., Nordin, K., Jernberg, C., Stenström, J., and Jansson, J. K. (2008). Degradation of mixtures of phenolic compounds by *Arthrobacter chlorophenolicus* A6. *Biodegradation*, 19, 495-505. https://doi.org/10.1007/s10532-007-9154-2

UniProt Consortium. (2015). UniProt: a hub for protein information. *Nucleic Acids Research*, 43, D204-D212. https://doi.org/10.1093/nar/gku989

Utturkar, S. M., Klingeman, D. M., Hurt Jr, R. A., and Brown, S. D. (2017). A case study into microbial genome assembly gap sequences and finishing strategies. *Frontiers in Microbiology*, 8, 1272. https://doi.org/10.3389/fmicb.2017.01272

Vaiano, V., Matarangolo, M., Murcia, J. J., Rojas, H., Navío, J. A., and Hidalgo, M. C. (2018). Enhanced photocatalytic removal of phenol from aqueous solutions using ZnO modified with Ag. *Applied Catalysis B: Environmental*, 225, 197-206. https://doi.org/10.1016/j.apcatb.2017.11.075

Vajić, U. J., Grujić-Milanović, J., Živković, J., Šavikin, K., Gođevac, D., Miloradović, Z., Bugarski, B., and Mihailović-Stanojević, N. (2015). Optimization of extraction of stinging nettle leaf phenolic compounds using response surface methodology. *Industrial Crops and Products*, 74, 912-917. https://doi.org/10.1016/j.indcrop.2015.06.032

van Dijk, E. L., Jaszczyszyn, Y., Naquin, D., and Thermes, C. (2018). The third revolution in sequencing technology. *Trends in Genetics*, 34, 666-681. https://doi.org/10.1016/j.tig.2018.05.008

van Schie, P. M. and Young, L. Y. (2000). Biodegradation of phenol: mechanisms and applications. *Bioremediation Journal*, 4, 1-18. https://doi.org/10.1080/10588330008951128

van Wyk, R., van Wyk, M., Mashele, S. S., Nelson, D. R., and Syed, K. (2019). Comprehensive comparative analysis of cholesterol catabolic genes/proteins in mycobacterial species. *International Journal of Molecular Sciences*, 20, 1032. https://doi.org/10.3390/ijms20051032

Varadaraju, C., Tamilselvan, G., Enoch, I. M. V. M., and Selvakumar, M. (2018). Phenol sensing studies by 4-aminoantipyrine method-a review. *International Journal of Organic and Medicinal Chemistry*, 5, 1-7. https://doi.org/10.19080/OMCIJ.2018.05.555657

Varjani, S. J. and Upasani, V. N. (2017). A new look on factors affecting microbial degradation of petroleum hydrocarbon pollutants. *International Biodeterioration and Biodegradation*, 120, 71-83. https://doi.org/10.1016/j.ibiod.2017.02.006

Varjani, S., Thaker, M., and Upasani, V. (2014). Optimization of growth conditions of native hydrocarbon utilizing bacterial consortium "HUBC" obtained from petroleum pollutant contaminated sites. *Indian Journal of Applied Research*, 4, 474-476.

Vázquez, S., Monien, P., Minetti, R. P., Jürgens, J., Curtosi, A., Primitz, J. V., Frickenhaus, S., Abele, D., Mac Cormack, W., and Helmke, E. (2017). Bacterial communities and chemical parameters in soils and coastal sediments in response to diesel spills at Carlini Station, Antarctica. *Science of The Total Environment*, 605, 26-37. https://doi.org/10.1016/j.scitotenv.2017.06.129

Vázquez, S., Monien, P., Minetti, R. P., Jürgens, J., Curtosi, A., Primitz, J. V., Frickenhaus, S., Abele, D., Mac Cormack, W., and Helmke, E. (2017). Bacterial communities and chemical parameters in soils and coastal sediments in response to diesel spills at Carlini Station, Antarctica. *Science of the Total Environment*, 605, 26-37. https://doi.org/10.1016/j.scitotenv.2017.06.129

Veenagayathri, K., and Vasudevan, N. (2010). Effect of pH, nitrogen sources and salts on the degradation of phenol by the bacterial consortium under saline conditions. *International Journal of Biotechnology and Biochemistry*, 6, 783-792.

Víctor-Ortega, M. D., Ochando-Pulido, J. M., and Martínez-Férez, A. (2016). Phenols removal from industrial effluents through novel polymeric resins: kinetics and equilibrium studies. *Separation and Purification Technology,* 160, 136-144. https://doi.org/10.1016/j.seppur.2016.01.023

Vilímková, L., Páca, J., Kremláčková, V., and Stiborová, M. (2008). Isolation of cytoplasmic NADPH-dependent phenol hydroxylase and catechol-1, 2-dioxygenase from *Candida tropicalis* yeast. *Interdisciplinary Toxicology*, 1, 225-230. https://doi.org/10.2478/v10102-010-0046-7

Villegas, L. G. C., Mashhadi, N., Chen, M., Mukherjee, D., Taylor, K. E., and Biswas, N. (2016). A short review of techniques for phenol removal from wastewater. *Current Pollution Reports*, 2, 157-167. https://doi.org/10.1007/s40726-016-0035-3

Waller, C. L., Griffiths, H. J., Waluda, C. M., Thorpe, S. E., Loaiza, I., Moreno, B., Pacherres, C. O., and Hughes, K. A. (2017). Microplastics in the Antarctic marine system: an emerging area of research. *Science of the Total Environment*, 598, 220-227. https://doi.org/10.1016/j.scitotenv.2017.03.283

Wang, F., Li, C., Wang, H., Chen, W., and Huang, Q. (2016). Characterization of a phenanthrene-degrading microbial consortium enriched from petrochemical contaminated environment. *International Biodeterioration and Biodegradation*, 115, 286-292. https://doi.org/10.1016/j.ibiod.2016.08.028

Wang, L., Li, Y., Yu, P., Xie, Z., Luo, Y., and Lin, Y. (2010). Biodegradation of phenol at high concentration by a novel fungal strain *Paecilomyces variotii* JH6. *Journal of Hazardous Materials*, 183, 366-371. https://doi.org/10.1016/j.jhazmat.2010.07.033

Wang, N. F., Zhang, T., Zhang, F., Wang, E. T., He, J. F., Ding, H., Zhang, B.T., Liu, J., Ran, X.B., and Zang, J. Y. (2015). Diversity and structure of soil bacterial communities in the Fildes Region (maritime Antarctica) as revealed by 454 pyrosequencing. *Frontiers in Microbiology*, 6, https://doi.org/10.3389/fmicb.2015.01188

Wang, P., Hu, X., He, Q., Waigi, M., Wang, J., and Ling, W. (2018). Using calcination remediation to stabilize heavy metals and simultaneously remove polycyclic aromatic hydrocarbons in soil. *International Journal of Environmental Research and Public Health*, 15, 1731-1739. https://doi.org/10.3390/ijerph15081731

Wang, P., Qu, Y., and Zhou, J. (2009). Biodegradation of mixed phenolic compounds under high salt conditions and salinity fluctuations by *Arthrobacter* sp. W1. *Applied Biochemistry and Biotechnology*, 159, 623-633. https://doi.org/10.1007/s12010-008-8494-7

Wang, Q. and Xie, S. (2012). Isolation and characterization of a high-efficiency soil atrazine-degrading *Arthrobacter* sp. strain. *International Biodeterioration and Biodegradation*, 71, 61-66. https://doi.org/10.1016/j.ibiod.2012.04.005

Wang, Y. and Tam, N. F. (2019). Microbial Remediation of Organic Pollutants. *In World Seas: An Environmental Evaluation* (pp. 283-303). Academic Press. https://doi.org/10.1016/B978-0-12-805052-1.00016-4

Wang, Z., Xie, Z., Mi, W., Möller, A., Wolschke, H., and Ebinghaus, R. (2015). Neutral Poly/Per-Fluoroalkyl Substances in Air from the Atlantic to the Southern Ocean and in Antarctic Snow. *Environmental Science and Technology*, 49, 7770-7775. https://doi.org/10.1021/acs.est.5b00920

Wang, Z., Zhang, J., Zhang, Y., Hesham, A. L., and Yang, M. (2006). Molecular characterization of a bacterial consortium enriched from an oilfield that degrades phenanthrene. *Biotechnology Letters*, 28, 617-621. https://doi.org/10.1007/s10529-006-0023-6

Wasi, S., Tabrez, S., and Ahmad, M. (2013). Toxicological effects of major environmental pollutants: an overview. *Environmental monitoring and assessment*, 185, 2585-2593. https://doi.org/10.1007/s10661-012-2732-8

Wilkness, P. (1990). Fuel spill clean up in the Antarctic. *Antarctic Journal of the United States*, 25, 3-8.

Winnacker, M. (2019). Polyhydroxyalkanoates: recent advances in their synthesis and applications. *European Journal of Lipid Science and Technology*, 121, 1900101. https://doi.org/10.1002/ejlt.201900101

Woehler E.J., Ainley D., Jabour J. (2014) Human Impacts to Antarctic Wildlife: Predictions and Speculations for 2060. In: Tin T., Liggett D., Maher P., Lamers M. (eds.) *Antarctic Futures*. Springer, Dordrecht. https://doi.org/10.1007/978-94-007-6582-5_2

Wong, J. W. C., Lai, K. M., Wan, C. K., Ma, K. K., and Fang, M. (2002). Isolation and optimization of PAH-degradative bacteria from contaminated soil for PAHs bioremediation. Water, Air, and Soil Pollution, 139, 1-13. https://doi.org/10.1023/A:1015883924901

Wu, L., Ali, D. C., Liu, P., Peng, C., Zhai, J., Wang, Y., and Ye, B. (2018). Degradation of phenol via ortho-pathway by *Kocuria* sp. strain TIBETAN4 isolated from the soils around Qinghai Lake in China. *PloS One*, 13, e0199572. https://doi.org/10.1371/journal.pone.0199572

Xie, X. and Müller, N. (2018). Enzymes involved in the anaerobic degradation of phenol by the sulfate-reducing bacterium *Desulfatiglans anilini*. *BMC Microbiology*, 18, 93. https://doi.org/10.1186/s12866-018-1238-0

Yaacob, N. S., Mohamad, R., Ahmad, S. A., Abdullah, H., Ibrahim, A. L., and Ariff, A.B. (2016). The influence of different modes of bioreactor operation on the efficiency of phenol degradation by *Rhodococcus* UKMP-5M. *Rendiconti Lincei*, 27, 749-760. https://doi.org/10.1007/s12210-016-0567-x

Yan, N., Marschner, P., Cao, W., Zuo, C., and Qin, W. (2015). Influence of salinity and water content on soil microorganisms. *International Soil and Water Conservation Research*, 3, 316-323. https://doi.org/10.1016/j.iswcr.2015.11.003

Yao, Y., Meng, X.-Z., Wu, C.-C., Bao, L.-J., Wang, F., Wu, F.-C., and Zeng, E. Y. (2016). Tracking human footprints in Antarctica through passive sampling of polycyclic aromatic hydrocarbons in inland lakes. *Environmental Pollution*, 213, 412-419. https://doi.org/10.1016/j.envpol.2016.02.035

Yin, K., Lv, M., Wang, Q., Wu, Y., Liao, C., Zhang, W., and Chen, L. (2016). Simultaneous bioremediation and biodetection of mercury ion through surface display of carboxylesterase E2 from *Pseudomonas aeruginosa* PA1. *Water Research*, 103, 383-390. https://doi.org/10.1016/j.watres.2016.07.053

Yin, K., Wang, Q., Lv, M., and Chen, L. (2019). Microorganism remediation strategies towards heavy metals. *Chemical Engineering Journal*, 360, 1553-1563. https://doi.org/10.1016/j.cej.2018.10.226

Ying, G. G., Williams, B., and Kookana, R. (2002). Environmental fate of alkylphenols and alkylphenol ethoxylates—a review. *Environment International*, 28, 215-226. https://doi.org/10.1016/S0160-4120(02)00017-X

Ying, W., Ye, T., Bin, H., Zhao, H. B., Bi, J. N., and Cai, B. L. (2007). Biodegradation of phenol by free and immobilized *Acinetobacter* sp. strain PD12. *Journal of Environmental Sciences*, 19, 222-225. https://doi.org/10.1016/S1001-0742(07)60036-9

Yoo, J. Y., Choi, J., Lee, T., and Park, J. W. (2004). Organobentonite for sorption and degradation of phenol in the presence of heavy metals. *Water, Air, and Soil Pollution*, 154, 225-237. https://doi.org/10.1023/B:WATE.0000022970.21712.64

Youssef, M., El-Shatoury, E. H., Ali, S. S., and El-Taweel, G. E. (2019). Enhancement of phenol degradation by free and immobilized mixed culture of *Providencia stuartii* PL4 and *Pseudomonas aeruginosa* PDM isolated from activated sludge. *Bioremediation Journal*, 23, 53-71. https://doi.org/10.1080/10889868.2019.1602106

Yu, Z., Hu, Z., Xu, Q., Zhang, M., Yuan, N., Liu, J., Meng, Q., and Yin, J. (2020). The LuxI/LuxR-type quorum sensing system regulates degradation of polycyclic aromatic hydrocarbons via two mechanisms. *International Journal of Molecular Sciences*, 21, 5548. https://doi.org/10.3390/ijms21155548

Yusuf, I., Ahmad, S. A., Phang, L. Y., Syed, M. A., Shamaan, N. A., Khalil, K. A., Dahalan, F. A., and Shukor, M. Y. (2016). Keratinase production and biodegradation of polluted secondary chicken feather wastes by a newly isolated multi heavy metal tolerant bacterium-*Alcaligenes* sp. AQ05-001.

Journal of Environmental Management, 183, 182-195. https://doi.org/10.1016/j.jenvman.2016.08.059

Zahri, K. N. M., Gomez-Fuentes, C., Sabri, S., Zulkharnain, A., Khalil, K. A., Lim, S., and Ahmad, S. A. (2021). Evaluation of heavy metal tolerance level of the Antarctic bacterial community in biodegradation of waste canola oil. *Sustainability*, 13, 10749. https://doi.org/10.3390/su131910749

Zakaria, N. N., Ahmad, S. A., Lee, G. L. Y., Yasid, N. A., Manogaran, M., Subramaniam, K., Tengku Mazuki, T. A., Nawawi, N. M., and Shukor, M. Y. (2018). Biodegradation of phenol by Antarctic bacterium *Rhodococcus baikonurensis* strain AQ5-001 in the presence of heavy metals. *Malaysian Journal of Biochemistry and Molecular Biology*, 21, 29-36.

Zakaria, N. N., Roslee, A. F. A., Gomez-Fuentes, C., Zulkharnain, A., Abdulrasheed, M., Sabri, S., Ramirez-Moreno, N., Calisto-Ulloa, N., and Ahmad, S. A. (2020). Kinetic studies of marine psychrotolerant microorganisms capable of degrading diesel in the presence of heavy metals. *Revista Mexicana de Ingeniería Química*, 19, 1375-1388. https://doi.org/10.24275/rmiq/Bio1072

Zangrando, R., Barbaro, E., Vecchiato, M., Kehrwald, N. M., Barbante, C., and Gambaro, A. (2016). Levoglucosan and phenols in Antarctic marine, coastal and plateau aerosols. *Science of The Total Environment*, 544, 606-616. https://doi.org/10.1016/j.scitotenv.2015.11.166

Zeng, H.-Y., Cao, X.-L., Xiong, L.-B., Cai, X.-L., Huang, L.-Q., Zhang, C.-Y., and Li, Y.-Q. (2014). Microbiological degradation of phenol using two co-aggregating bacterial strains. *Environmental Earth Sciences*, 71, 1339-1348. https://doi.org/10.1007/s12665-013-2540-7

Zeng, Y. H., Cai, Z. H., Zhu, J. M., Du, X. P., and Zhou, J. (2020). Two hierarchical LuxR-LuxI type quorum sensing systems in *Novosphingobium* activate microcystin degradation through transcriptional regulation of the mlr pathway. *Water Research*, 183, Article ID 116092. https://doi.org/10.1016/j.watres.2020.116092

Zhang, D., Hu, P., Liu, T., Wang, J., Jiang, S., Xu, Q., and Chen, L. (2018a). GC bias lead to increased small amino acids and random coils of proteins in cold-water fishes. *BMC Genomics*, 19, 1-10. https://doi.org/10.1186/s12864-018-4684-z

Zhang, K., Liu, Y., Chen, Q., Luo, H., Zhu, Z., Chen, W., Chen, J., and Mo, Y. (2018b). Biochemical pathways and enhanced degradation of di-n-octyl phthalate (DOP) in sequencing batch reactor (SBR) by *Arthrobacter* sp. SLG-4 and *Rhodococcus* sp. SLG-6 isolated from activated sludge. *Biodegradation*, 29, 171-185. https://doi.org/10.1007/s10532-018-9822-4

Zhang, Q., Chen, Z., Li, Y., Wang, P., Zhu, C., Gao, G., Xiao, K., Sun, H., Zheng, S., Liang, Y., and Jiang, G. (2015). Occurrence of organochlorine pesticides in the environmental matrices from King George Island, west Antarctica.

Environmental Pollution, 206, 142-149. https://doi.org/10.1016/j.envpol.2015.06.025

Zhao, T., Gao, Y., Yu, T., Zhang, Y., Zhang, Z., Zhang, L., and Zhang, L. (2021). Biodegradation of phenol by a highly tolerant strain *Rhodococcus ruber* C1: Biochemical characterization and comparative genome analysis. *Ecotoxicology and Environmental Safety*, 208, Article ID 111709. https://doi.org/10.1016/j.ecoenv.2020.111709

Zhou, J., Yu, X., Ding, C., Wang, Z., Zhou, Q., Pao, H., and Cai, W. (2011). Optimization of phenol degradation by *Candida tropicalis* Z-04 using Plackett-Burman design and response surface methodology. *Journal of Environmental Sciences*, 23, 22-30. https://doi.org/10.1016/S1001-0742(10)60369-5

Zhou, M., Dong, B., and Shao, Z. (2020). Complete genome sequence of *Marinobacter* sp. LQ44, a haloalkaliphilic phenol-degrading bacterium isolated from a deep-sea hydrothermal vent. *Marine Genomics*, 50, Article ID 100697. https://doi.org/10.1016/j.margen.2019.100697

Zhou, W., Guo, W., Zhou, H., and Chen, X. (2016). Phenol degradation by *Sulfobacillus acidophilus* TPY via the meta-pathway. *Microbiological Research*, 190, 37-45. https://doi.org/10.1016/j.micres.2016.05.005

Zvěřina, O., Coufalík, P., Barták, M., Petrov, M., and Komárek, J. (2018). The contents and distributions of cadmium, mercury, and lead in *Usnea antarctica* lichens from Solorina Valley, James Ross Island (Antarctica). *Environmental Monitoring and Assessment*, 190, 13. https://doi.org/10.1007/s10661-017-6397-1