

CHARACTERIZATION OF DEHALOGENASE FOR THE DEGRADATION OF
3-CHLOROPROPIONIC ACID

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To all my Lovely family

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ABSTRACT

The use of herbicides that contain halogenated compounds, for example 3-chloropropionic acid (3-CP) poses significant environmental hazards as well as detrimental to human. The research detailed here investigated the isolation and identification of bacteria strains that could degrade 3-CP as its sole carbon source. Dehalogenase that can degrade 3-CP is rare in nature. In this study, two strains of dehalogenase producing bacteria capable of utilizing 3-CP were successfully isolated from abandoned agricultural land in Universiti Teknologi Malaysia. These bacteria were characterized by using 16S rRNA as well as biochemical analysis. Strain WH1 showed a 98 % sequence identity to *Burkholderia cepacia* with (accession number KU318403) whereas strain WH2 showed a 99% sequence identity to *Bacillus cereus* with (accession number KU721999). The results have shown that these bacteria were capable to grow in liquid minimal media supplied with 10 mM 3-CP as sole carbon source with doubling time of 43.62 h for WH1 and 14.75 h for WH2. Utilization of 3-CP was confirmed by detection of chloride ion released using halide ion assay technique for both strains which indicate their ability to degrade 3-CP. For further confirmation of 3-CP consumption, analysis by high performance liquid chromatography (HPLC) revealed that both *B. cepacia* WH1 and *B. cereus* WH2 effectively utilized ~100% of 10 mM 3-CP. This is the first report detailing both strains able to competently utilize 3-CP as their sole carbon source. Cell free extract of *B. cereus* strain WH2 was further characterized due to its faster growth on 3-CP compared to *B. cepacia* strain WH1. The intracellular dehalogenase from *B. cereus* WH2 was purified to homogeneity to afford a 2.5-fold (50 % yield) concentration with an estimated molecular mass of 37 kDa by SDS-PAGE analysis. Its highest enzyme activity was achieved at conditions of 30 °C and pH 7. While the activity of WH2 dehalogenase was substantially repressed by both Hg²⁺ and Ag²⁺, the enzyme was not inhibited by DTT and EDTA. Pertinently, kinetics evaluation revealed a higher affinity of the WH2 dehalogenase towards 3-CP than 3-chlorobutyric acid (3-CB), affording K_m values of 0.32 mM (k_{cat} 3.97 s⁻¹) and 0.52 mM (k_{cat} 4.35 s⁻¹), respectively. The WH2 dehalogenase was ~1.6-fold catalytically more efficient (k_{cat}/K_m) in dehalogenating the three-carbon, 3-CP (12.4 mM⁻¹ s⁻¹) over the four-carbon, 3-CB (8.27 mM⁻¹ s⁻¹). From the data, it was identified that 3-CP degradation was not stimulated by co-factors, such as NAD⁺, NADH, NADP⁺, NADPH, FAD and CoA that did not affect the enzyme activity by demonstrating activities of <0.1 unite (g protein)⁻¹. The amplified dehalogenase gene fragment was designated “*deh-wh2*” and subsequent analysis showed it belongs to Group II dehalogenase. Eight conserved residues that line the active site were identified: Asp10, Thr14, Ser117, Lys150, Tyr156, Ser174, Asn176 and Asp179. These residues are consistent with the residues found in the active site of DhlB, DehIVa and L-DEX. The product of 3-CP degradation was 3-hydroxypropionic acid based on HPLC. In conclusion, this study confirmed the presence of new dehalogenase isolated from various bacteria that have potential to utilize 3-CP, especially from contaminated environment.

ABSTRAK

Penggunaan racun rumpai yang mengandungi sebatian, halogen seperti asid 3-kloropropionik (3-CP) boleh mendatangkan bahaya yang ketara kepada alam sekitar juga memudaratkan manusia sejagat. Penyelidikan yang dijalankan berkisar tentang pemencilan dan pengenalpastian strain bakteria yang boleh hidup menggunakan 3-CP sebagai sumber karbon tunggal. Dehalogenase yang boleh merendahkan 3-CP jarang ditemui secara semula jadi. Dalam kajian ini, dua strain bakteria yang menghasilkan dehalogenase seumpama ini yang mampu menggunakan 3-CP telah berjaya dipencilkan dari tanah pertanian yang terbiar di Universiti Teknologi Malaysia. Bakteria ini dicirikan dengan menggunakan 16S rRNA serta analisis biokimia. Strain WH1 menunjukkan 98% identiti dengan penjujukan kepada strain *Burkholderia cepacia* dengan (nombor akses KU318403) sedangkan Strain WH2 menunjukkan 99% identiti dengan penjujukan kepada strain *Bacillus cereus* dengan (nombor akses KU721999). Keputusan ujikaji telah menunjukkan bahawa bakteria ini boleh tumbuh dalam kultur media-minima cecair yang dibekalkan dengan 10 mM 3-CP sebagai sumber karbon tunggal dengan selang masa dua kali ganda lebih 43.62 jam untuk WH1 dan 14.75 jam untuk WH2. Penggunaan 3-CP sebagai sumber karbon, telah ditentukan melalui kaedah pengesanan pengeluaran ion klorida oleh kedua-dua strain yang menunjukkan keupayaannya untuk menguraikan 3-CP. Bagi mengesahkan penggunaan 3-CP, analisis menggunakan kromatografi cecair berprestasi tinggi (HPLC) mendedahkan bahawa *B. cepacia* WH1 dan *B. cereus* WH2 menggunakan secara berkesan ~100% 10 mM 3CP. Ini merupakan laporan yang pertama memperincikan kedua-dua strain yang mampu menggunakan 3-CP sebagai sumber karbon tunggal. Ekstrak dari sel *B. cereus* strain WH2 telah diuji selanjutnya kerana bakteria tersebut mempunyai kadar pertumbuhan yang jauh lebih tinggi daripada strain *B. cepacia* WH1. Dehalogenase yang diperolehi dari sel *B. cereus* WH2 telah ditulenkan, dan berupaya mencapai 2.5 kali ganda (50% hasil) kepekatan dengan anggaran jisim molekul 37 kDa melalui kaedah analisis SDS-PAGE. Aktiviti enzim yang tertinggi telah dicapai pada keadaan 30°C dan pH 7. Manakala aktiviti dehalogenase WH2 telah mengurang dengan kehadiran kedua-dua Hg^{2+} dan Ag^{2+} , tetapi sebaliknya dengan kehadiran DTT dan EDTA. Bersangkutan dengan penilaian kinetik menunjukkan 3-CP merupakan substrat yang lebih baik daripada asid 3-klorobutirik (3-CB) terhadap enzim dehalogenase WH2, dengan nilai K_m masing-masing 0.32 mM (k_{cat} 3.97 s⁻¹) dan 0.52 mM (k_{cat} 4.35 s⁻¹). Dehalogenase WH2 memangkinkan ~1.6 kali ganda lebih cekap (k_{cat}/K_m) terhadap bahan berhalogen yang mempunyai tiga karbon, 3-CP (12.4 mM⁻¹ s⁻¹) daripada empat-karbon, 3-CB (8.27 mM⁻¹ s⁻¹). Data telah membuktikan bahawa penguraian 3-CP tidak dirangsang oleh ko-faktor, seperti NAD⁺, NADH, NADP⁺, NADPH, FAD dan CoA yang tidak menjejaskan aktiviti enzim oleh aktiviti <0.1 unit (g protein)⁻¹. Serpihan gen dehalogenase diamplifikasikan yang telah diberi nama “*deh-wh2*” dan analisis berikutnya menunjukkan ia tergolong dalam kumpulan II dehalogenase. Lapan residu asid amino yang telah dikenal pasti melapisi tapak aktif terdiri daripada: Asp10, Thr14, Ser117, Lys150, Tyr156, Ser174, Asn176 dan Asp179. Penemuan residu asid amino ini selaras dengan residu yang ditemui pada tapak aktif DhIB, DehIVa dan L-DEX. Hasil penguraian 3-CP adalah asid 3-hidroksi propionik berdasarkan keputusan HPLC. Kesimpulannya, kajian ini mengesahkan kehadiran dehalogenase baharu yang telah dipencil dari pelbagai jenis bakteria yang berpotensi untuk menggunakan 3-CP, terutamanya dari persekitaran yang tercemar.

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LIST OF ABBREVIATIONS

(v/v)	-	Volume percentage per 100 mL volume
(w/v)	-	Mass percentage per 100 mL volume
°C	-	Centigrade
β-HA	-	β-halo carboxylic acid
μL	-	Microliter
μm	-	Micrometre
μmol	-	Micromole
16S rRNA	-	ribosomal RNA gene
2,2,3-TB	-	2,2,3-trichlorobutyric acid
2,2,3-TCP	-	2,2,3-trichloropropionic acid
2,2-DCB	-	2,2-dichlorobutyric acid
2,2-DCP	-	2, 2-dichloropropionic acid
2-CB	-	2-chlorobutanoic acid
2-CP	-	2-chloropropionic acid
3,3-DCP	-	3,3-dichloropropanoic acid
3-CB	-	3-chlorobutanoic
3-CP	-	3-chloropropionic acid
3-HP	-	3-hydroxypropionic acid
Ag ²⁺	-	Silver ion
A _{nm}	-	Absorption spectroscopy at nm light source
APS	-	Ammonium persulfate

bar	-	Barometer
BLAST	-	Basic local alignment search tool
BLASTn	-	Basic local alignment search tool – nucleotide
bp	-	Base pairs
BS	-	Basal salts
BSA	-	Bovine serum albumin
Ca ²⁺	-	Calcium ions
CFE	-	Cell free extract
Co ²⁺	-	Cobalt ion
CoA	-	Coenzyme A
Cu ²⁺	-	Copper ion
DDT	-	Dichlorodiphenyltrichloroethane
<i>deh</i>	-	Dehalogenase
dH ₂ O	-	Distilled water
DNA	-	Deoxyribonucleic acid
EtBr	-	Ethidium bromide
FAD	-	Flavin adenine dinucleotide
g	-	Gram
h	-	Hour
Hg ²⁺	-	Mercury ion
HPLC	-	High performance liquid chromatography
HTUs	-	Hypothetical taxonomic units
kbp	-	Kilo base pair
KDa	-	kilodalton
LB	-	Luria Broth
LC-MS	-	Liquid chromatography–mass spectrometry

M	-	Molarity (molar)
MEGA	-	Molecular Evolutionary Genetics Analysis
mg	-	Milligram
Mg ²⁺	-	Magnesium ion
Min	-	Minute
mL	-	Milliliter
mM	-	Millimolar
mm	-	millimetre
MSA	-	multiple progression alignment
NaCl	-	Sodium chloride
NAD ⁺	-	Nicotinamide adenine dinucleotide
NADP ⁺	-	Nicotinamide adenine dinucleotide phosphate
NCBI	-	National center for biotechnology information
OD	-	Optical density
OTUs	-	Operational taxonomic units
PCBs	-	polychlorinated biphenyls
PCR	-	Polymerase chain reaction
Pfu		Plaque-forming unit
pKa	-	Acid dissociation constant
RNAse	-	Ribonuclease
rpm	-	Revolution Pper minute
rRNA	-	Ribosomal ribonucleic acid
RSM	-	response surface methodology
Rt	-	Retention time
s	-	Second

SDS- PAGE	-	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
TAE	-	Buffer solution containing a mixture of tris base, acetic acid and ethidium bromide
TEMED	-	Tetramethylethylenediamine
TS	-	Trace metal
W	-	Watt
WHO	-	World Health Organization
Zn ²⁺	-	Zinc ion

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CHAPTER 1

INTRODUCTION

1.1 Background of Study

In recent time, rapid escalation of industrial and agricultural activities witnessed an excessive production of xenobiotic compounds and caused grave environmental concern. These man-made compounds are often described as non-naturally occurring chemicals (Rieger *et al.*, 2002). Such chemicals at high concentrations are responsible for environmental pollution unless inhibited. The contamination of water and soil that is caused due to the presence of xenobiotic substances requires remediation. Lately, degradation of hazardous wastes including xenobiotic compounds using microbes became a prominent route (Yan *et al.*, 2009).

It is needless to mention that some of these xenobiotic compounds are resistant to degradation. Studies revealed that specific microorganisms are not only capable of degrading such complexes but also remains resistant to such xenobiotics (Van Pée and Unversucht, 2003; Niknam *et al.*, 2014). In this regard, halogenated organic compounds are considered as largest groups of xenobiotic compounds. They are known as prevalent pollutants. They are found in soil, air, water, and sediment. Halogenated organic compounds being extensively produced as industrial products are mostly used as herbicides, insecticides, fungicides, and solvents. Besides, they are considered as an important class of environmental pollutants. These halogenated compounds cause several human health problems due to its persistence, toxicity and hazardous metabolites (Fetzner, 1998; Fetzner and Lingens, 1994).

Since the beginning of the 20th century, physiologists and biochemists started realizing that halogenated compounds can affect our metabolic systems due to their toxicity (Slater *et al.*, 1995). Penfold (1913) first reported the microorganisms assisted degradation of halogenated compounds. Interestingly, these microorganisms owing to their short life cycle are capable of evolving new enzymes, pathways and regulatory mechanisms for the degradation of almost all xenobiotic compounds. Thus, the evolution of dehalogenase producing microorganisms exploiting some of these halogenated compounds is not only scientifically interesting but also have practical significance in terms of environmental pollution remediation via green chemical route (Penfold, 1913; Timmis and Pieper, 1999).

The compound, 3-chloropropionic acid (3-CP) belongs to the class of chlorinated monocarboxylic acid or β -chloro substituted haloalkanoic acids. It originates from the possible chemical inclusion in pesticides. This compound is a carcinogenic and genotoxic to the animals and humans (Alexander, 1981). Generally, they degrade into harmless substances *via* both non-biological and biological pathways in which the later are considered to be more economical, safer and environmentally amiable (Janssen *et al.*, 2005). Primarily, biodegradation using microorganisms is a natural process that allows the removal of xenobiotic chemicals such as chloro-aliphatic compounds from the environment (Sinha *et al.*, 2009; Abel *et al.*, 2012; Edbeib *et al.*, 2016).

Several studies are performed to isolate the bacterial species by enrichment and laboratory culture which used halogen-substituted organic acids as their carbon and energy resources (Janssen *et al.*, 2005). However, only a few organisms are found capable to degrade the β -halo carboxylic acid (β -HA) (Jing and Huyop, 2007; Mesri *et al.*, 2009; Yusn and Huyop, 2009; Hamid *et al.*, 2011; Muslem *et al.*, 2015). The proposed reaction for dehalogenation of 3-CP by hydrolytic dehalogenation is similar to Group II dehalogenase enzyme. During nucleophilic substitution, the hydroxide ion of water attacks the partially positively charged carbon atom bonded to the electronegative chlorine atom. This causes the transfer of the electron pair from the electron-rich hydroxide to the partially positively charged carbon atom. Since the carbon atom can only accommodate four electron pairs (four covalent

bonds) in its valence state, this reaction subsequently results in the breaking of the carbon-chlorine bond to form the carbon-oxygen bond (van Pée and Unversucht, 2003). The chlorine atom is now liberated as a chloride ion carrying with it a pair of electrons.

It is known that long term exposure of microorganism to halogenated compounds found in soil and water triggers certain microorganisms to produce specialized enzymes that enable the utilization of such compounds as their energy and carbon source. Generally, the aforementioned bacterial species possess certain common characteristics in utilizing halogenated organic compounds as sole carbon and energy source. However, some fundamental characteristics must be satisfied for the bacteria to be able to utilize halogenated organic compounds for their growth. The bacteria must either possess or synthesize dehalogenase in response to the halogenated compound which, in turn confer the bacteria special abilities to remove the halogenated substituent(s) from the compound. Furthermore, the product of the dehalogenation must be non-toxic and easily convertible to an intermediate in the central metabolic pathway of the bacteria. Next, the halogenated compound must enter the cell either *via* passive or active transport mechanism to reach the active site of dehalogenase. Finally and most importantly, the halogenated compound must be non-toxic to the bacteria at normal intracellular concentrations. These halogenated organic compounds (herbicides) are widespread in agriculture sectors including 2-chloropropionic acid (2-CP); 2, 2-dichloropropionic acid (2,2-DCP) and 3-chloropropionic acid (3-CP). Despite some studies, following intensive literature search, the available information on 3-CP degradation is still lacking. Chan *et al.* (2010) had acknowledged that many microbial genomes carrying enzyme families contain dehalogenases that are useful for xenobiotic compounds remediation.

It is pertinent to highlight here the degradation of 3-CP, a representative of the β -substituted chloroalkanoic acids has been quite problematic as compared to that of the α -chloro-substituted haloalkanoic acids such as 2, 2-DCP. This is because the α -chloroalkanoic acid-degrading microorganisms cannot utilize/degrade the β -substituted chloroalkanoic acids as the former secrete α -specific dehalogenases that only cleave α -chloro-substituted haloalkanoic acids. Furthermore, only a few isolated

microorganisms have been described to be able to degrade the β -halocarboxylic acids (β -HA) (Mesri *et al.*, 2009; Yusn and Huyop, 2009). The present work proposes the isolation of bacteria from soil taken from an abandoned agricultural land and characterizes them to determine their potency in degrading 3-CP. Evaluation of the dehalogenating capacity of such bacteria towards 3-CP was the main aim of this study. The knowledge gathered from the abovementioned evaluation can be beneficial for the application of *in situ* bioremediation of contaminated soil and waterways, especially those containing pollutants comprising of chlorinated xenobiotics. Degradation of 3-CP was the prime focus of this study because the compound represents a group of commonplace bioactive ingredient (β -substituted chloroalkanoic acids) prevalent in formulations of herbicides used extensively in the agricultural sector to manage weed growth in plantations (Jing and Huyop, 2007). Furthermore, 3-CP is a more complex structure than the α -chloro-substituted haloalkanoic acids i.e. 2, 2-DCP, as 3-CP is resistant to enzymatic attack as well as being a representative of a well-known group of pollutants in the environment. Hence, 3-CP has been chosen as a model pollutant associated with pesticides in this study.

1.2 Problem Statement

The expansion of agricultural area, crop production, and subsequent use of pesticides and herbicides result in the liberation of high concentrations of the xenobiotic compounds that pollutes the environment. The major environmental pollutants namely the xenobiotic halogenated compounds i.e. β -substituted chloroalkanoic acids are weakly degradable chemicals. Presently, the tendency of such environmentally hazardous compounds towards bioaccumulation is harmful to human health and hygiene (Birnbaum and Fenton, 2003; Hayes *et al.*, 2006; Qing Li *et al.*, 2006) as well as their intractability remains a global concern. Consequently, dedicated efforts are needed to develop safe, economic and effective strategies to eliminate such toxic substances from the environment.

It is known that certain microbes are effective in degrading β -substituted chloroalkanoic acids; hence the exploitation of such beneficial microbes for the safer removal of such compounds from the environment is of great interest. Herein, the study suggests a greener biotechnological approach which involves the isolation, identification, characterization and evaluation of bio-degradation efficacy of β -producing bacteria. The study believes the natural ability of the bacteria to utilize such toxic compounds for growth while rendering these compounds safer to the environment and makes them perfect bioremediation agents for neutralizing the toxicity of β -substituted chloroalkanoic acids.

The study hypothesized the bioprospecting for dehalogenase-producing bacteria from environments previously exposed to continuous spraying of herbicides (i.e. agricultural land in Universiti Teknologi Malaysia (UTM) would yield bacterial isolates competent for *in-situ* bioremediation of 3-CP (i.e. β -substituted chloroalkanoic acid) as its sole source of carbon and energy for growth. It was expected the environmental stress from growing in an environment high in concentrations of β -substituted chloroalkanoic acid would trigger certain bacteria to develop exceptional catalytic machinery that allows them to utilize the abovementioned toxic compound.

It is pertinent to indicate here, isolation studies focusing on the biodegradation effectiveness of certain bacterial isolates to degrade β -chlorosubstituted haloalkanoic acids such as a 3-CP (Mesri *et al.*, 2009; Muslem *et al.*, 2015) remain lacking. Similarly, the precise mechanism for the β -chlorosubstituted degradation by such unique bacterial isolates is poorly understood. Even the product of the degradation of 3-CP has never been accumulated as proof of their degradation pathway. Moreover, there is yet any detailed report on the physicochemical characteristics and the full gene sequence of these β -specific dehalogenases.

1.3 Objectives of the Study

Based on the abovementioned problem statement the following objectives are set:

1. To isolate and identify the dehalogenase-producing bacteria effective in degrading 3-CP as the sole source of carbon and energy.
2. To characterize the biochemical properties and evaluate 3-CP dehalogenation efficiency of the bacterial isolates.
3. To purify and study the physicochemical characteristics of the β -haloalkanoic acid dehalogenase.
4. To amplify and analyse the full gene sequence of the β -haloalkanoic acid dehalogenase.

1.4 Scope of the Study

The soil sample expected to harbor β -specific haloalkanoic acid degrading bacteria was collected from soil samples in an abandoned agricultural land in UTM. The study used enrichment techniques that utilized only 3-CP as the sole carbon source. Hence, only bacteria effective in utilizing the 3-CP-enriched broth as the sole source of carbon would be isolated from the soil samples and used in the subsequent evaluation of the study. The bacterial isolates were initially subjected to halo ion assay for confirming their ability to utilize 3-CP for their growth by using HPLC. Subsequently, the morphological and molecular identification on the isolates using 16S rRNA was used to determine the gene sequence of 16S rRNA gene of bacterial DNA. Results are further used to make a comparison with genomic database for determining microorganism's identity. Phylogeny tree was constructed to identify the evolutionary relationship distance of the microorganism to the nearest known microorganisms.

The identified bacterial isolates were assessed for their biochemical properties using BiologTM Gen III. Next, their efficacy for degrading 3-CP using a time course growth profile versus the production of the degraded product i.e. 3-hydroxypropionic

acid (3-HP) using HPLC. The degradation efficiency of the 3-CP for the selected bacterial isolates was assessed over an unstipulated period until the degradation of 3-CP was almost completed. After this, only the bacterium showing the fastest degradation of 3-CP was selected for the subsequent study.

The next scope was to obtain the pure form of the β -specific haloalkanoic acid dehalogenase for the physicochemical assessments on the enzyme. The purification was carried using ammonium sulphate precipitation and subsequently dialyzed to obtain the pure form of the dehalogenase. The purified dehalogenase was characterized for parameters: enzyme substrate assays, pH, temperature, co-factors, substrate specificity and kinetic parameter.

The study then determines the full gene sequence of the β -haloalkanoic acid dehalogenase using primers from the Group II dehalogenase. Lastly, the study carried out qualitative and quantitative assay to monitor the liberation of 3-CP degraded product i.e. 3-HP monitored by HPLC catalyzed by the purified β -specific haloalkanoic acid dehalogenase.

1.5 Significance of the Study

This study hopes to provide new knowledge on the safe remediation of environmentally hazardous xenobiotic halogenated compounds such as β -haloalkanoic acids through the use of an exceptional dehalogenase producing bacteria. Furthermore, the properties of the β -haloalkanoic acid dehalogenase isolated in this study will be better understood while the product of the 3-CP degradation can be confirmed. For that particular reason, it will be interesting to study this β -specific novel dehalogenase enzyme which can degrade 3-CP, in order to recognize their catalytic properties and the biodegradation adopted by their catalytic machinery.

1.6 Operational Framework of the Research

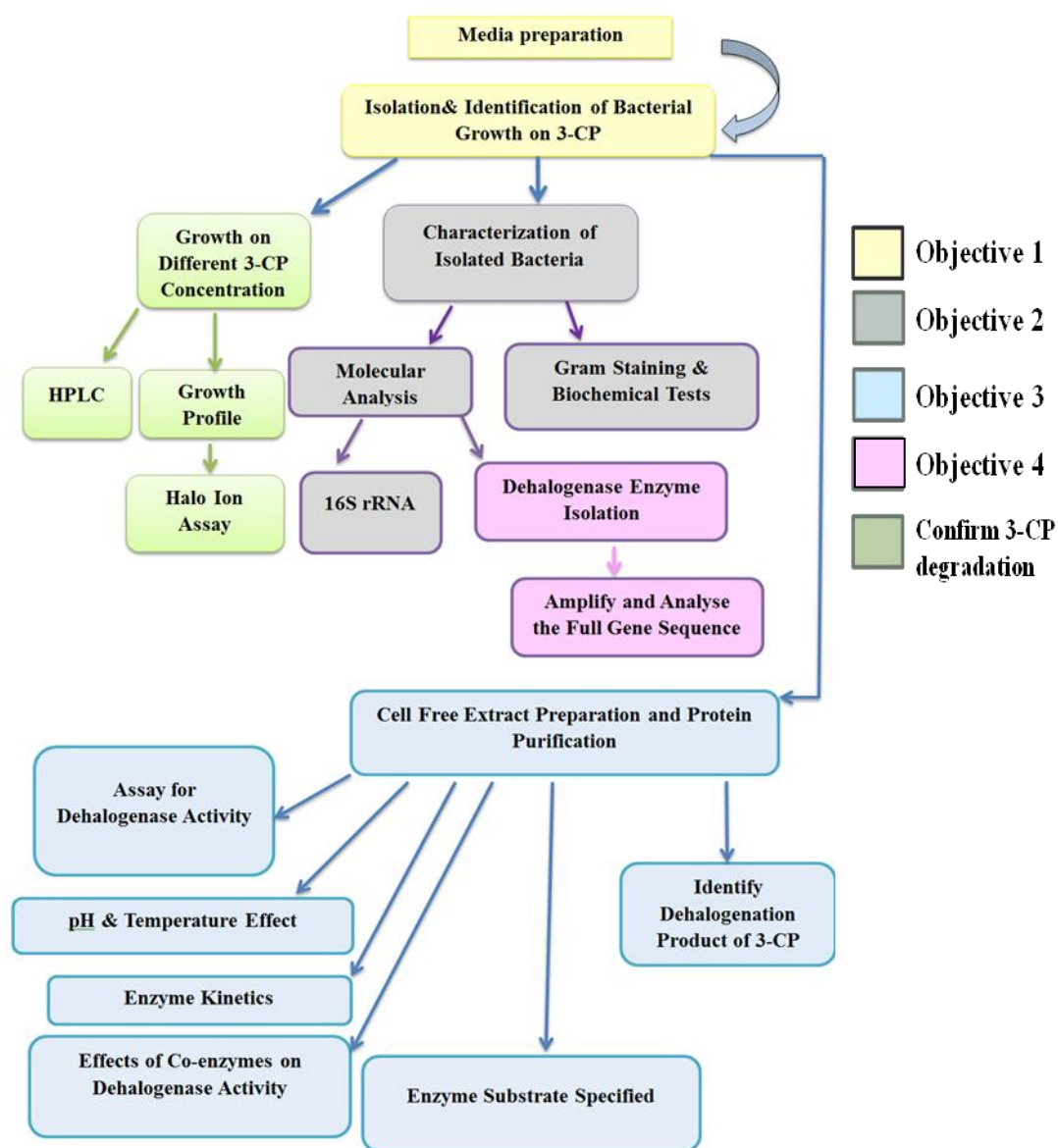


Figure 1.1: Operational framework of the research methodology.

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