PRODUCTION AND CHARACTERIZATION OF PROTEASE FROM HALOPHILIC *VIRGIBACILLUS* SPECIES CD6

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Specially dedicated to my beloved family, future life partner, soulmates and friends

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ABSTRACT

In enzyme production industries, the major challenges that hinder the efficient and economic commercial scale application of proteases are their stability in broad range of pH, temperature, salinity, as well as their optimal activity in the presence of metal ions, organic solvents and detergents. Moreover, the enzyme purification steps also contribute to the cost of production. To overcome this problem, characterization and production of crude protease with attractive properties from wild bacterial isolate could be an alternative as it is a more cost-effective way compared to production of protease that involves purification steps and protein engineering approach. Therefore, crude protease of Virgibacillus sp. CD6 isolated from salted-fish was characterized in this study using azocasein assay and bioinformatics tools. Protease production was found to be highest when using soybean meal and yeast extract as nitrogen source compared to other organic nitrogen sources. The protease exhibited vast range of stability with optimum activity at 10.0 % (w/v) NaCl, 60°C, pH 7 and 10, indicating its polyextremophilicity. The enzyme activity was enhanced by Mg^{2+} , Mn^{2+} , Cd^{2+} and Al³⁺. Both PMSF and EDTA hindered protease activity, denoting the presence of serine protease and metalloprotease properties respectively. High protease stability (>80%) was demonstrated in presence of organic solvents and detergent constituents investigated, and surprisingly it is exceptionally compatible with commercial detergents. Phylogenetic analyses revealed that proteases of Virgibacillus sp. demonstrated far distance relationship with other species, which worth for further exploration. Attributes of this protease can actualize necessity of searching superlative enzymes from extremophiles for diverse applications, particularly in detergent industry.

ABSTRAK

Dalam industri penghasilan enzim, cabaran utama yang menghalang aplikasi komersial protease yang cekap dan ekonomi adalah ciri-ciri protease yang stabil dalam pelbagai pH, suhu, kadar garam serta aktiviti optimum dalam ion logam, pelarut organik, dan unsur detergen. Selain itu, proses penulenan enzim juga menyumbang kepada kos penghasilan. Bagi mengatasi masalah ini, pencirian dan penghasilan protease dari bakteria tanpa melibatkan proses penulenan boleh menjadi alternatif kerana ia adalah cara yang kos efektif berbanding dengan penghasilan protease yang melibatkan penulenan enzim dan kejuruteraan protein. Oleh itu, protease daripada Virgibacillus sp. CD6 yang dipencilkan daripada ikan masin telah dicirikan dalam kajian ini dengan penggunaan azocasein assay dan alat bioinformatik. Penghasilan protease didapati paling tinggi apabila menggunakan kacang soya dan ekstrak yis sebagai sumber nitrogen berbanding dengan sumber nitrogen organik yang lain. Protease tersebut mempamerkan luas kestabilan dengan aktiviti optimum pada 10.0% (w/v) NaCl, 60°C, pH 7 dan 10, menunjukkan ciri poli-ekstremofi. Aktiviti enzim telah dipertingkatkan oleh Mg^{2+} , Mn^{2+} , Cd^{2+} dan Al^{3+} . Kedua-dua PMSF dan EDTA didapati menghalang aktiviti protease, menandakan ciri protease serine dan metalloprotease masing-masing. Kestabilan protease yang tinggi (>80%) telah ditunjukkan dalam pelarut organik dan unsur detergen, serta amat serasi dengan bahan pencuci komersial. Analisis filogenetik menunjukkan bahawa protease daripada *Virgibacillus* sp. mempunyai hubungan yang jauh dengan spesies lain, bernilai untuk penerokaan selanjutnya. Sifat-sifat protease ini boleh merealisasi keperluan mencari enzim cemerlang dari esktremofi untuk pelbagai aplikasi, terutamanya dalam industri detergen.

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LIST OF SYMBOLS

A ₄₂₀	-	Absorbance at 420 nm
A ₇₅₀	-	Absorbance at 750 nm
α	-	Alpha
≈	-	Approximately
β	-	Beta
°C	-	Degree celcius
D	-	Diameter
=	-	Equal
γ	-	Gamma
g	-	Gram
g/L	-	Gram per liter
>	-	Greater than
h	-	Hour
kPa	-	Kilo Pascal
<	-	Less than
L	-	Liter
\log_{10}	-	Logarithm to base 10
mg/ml	-	Milligram per milliliter
μl	-	Microliter
mg	-	Milligram
mg/L	-	Milligram per liter
ml	-	Milliliter
mm	-	Millimeter
mM	-	Millimolar
Μ	-	Molar mass
nm	-	Nanometer

-	-	Negative
n	-	Number
OD_{600}	-	Optical density at 600 nm
/	-	Or
%	-	Percent
cm ⁻¹	-	Per centimeter
M^{-1}	-	Per molar
π	-	Pi
±	-	Plus-minus
+	-	Positive
R	-	Registered trademark
2	-	Square
×	-	Times
ТМ	-	Trademark
U/mg	-	Units per milligram
U/ml	-	Units per volume
v/v	-	Volume per volume
w/v	-	Weight per volume

LIST OF ABBREVIATIONS

А	-	Alanine
Al^{3+}	-	Aluminum ion
$Al_2(SO_4)_3$	-	Aluminum sulfate
APC	-	Activated protein C
ATP	-	Adenosine triphosphate
BLASTp	-	Protein-protein Basic Local Alignment Search Tool
BSA	-	Bovine serum albumin
С	-	Cysteine
C ₆ H ₅ Na ₃ O ₇	-	Trisodium citrate
C ₆ H ₅ Na ₃ O ₇ .2H ₂ O	-	Trisodium citrate dihydrate
Ca ²⁺	-	Calcium ion
CaCl ₂	-	Calcium chloride
Cd^{2+}	-	Cadmium ion
$Cd(NO_3)_2$	-	Cadmium nitrate
Cl	-	Chloride ion
Co ²⁺	-	Cobalt ion
CoCl ₂	-	Cobalt chloride
Cu^{2+}	-	Copper (II) ion
CuSO ₄	-	Copper (II) sulfate
CuSO ₄ .5H ₂ O	-	Copper (II) sulfate pentahydrate
D	-	Aspartic acid
DMSO	-	Dimethyl sulfoxide
DNA	-	Deoxyribonucleic Acid
DTT	-	Dithiothreitol
EC	-	Enzyme commission
EDTA	-	Ethylene Diamine Tetraacetic Acid

et al.	-	And friends
F	-	Phenylalanine
FDA	-	Food and Drug Administration
Fe ³⁺	-	Ferum (III) ion
FeCl ₃	-	Ferum (III) chloride
G	-	Glycine
Glu, E	-	Glutamic acid
H-bond	-	Hydrogen bond
H^+	-	Hydrogen ion
H_2O_2	-	Hydrogen peroxide
HCl	-	Hydrochloric acid
His, H	-	Histidine
Ι	-	Isoleucine
IAA	-	Iodoacetic acid
ID	-	Identifier
K	-	Lysine
\mathbf{K}^+	-	Potassium ion
K ₂ HPO ₄	-	Dipotassium hydrogen phosphate
KCl	-	Potassium chloride
KH ₂ PO ₄	-	Potassium dihydrogen phosphate
KNO ₃	-	Potassium nitrate
L	-	Leucine
Μ	-	Methionine
MEGA 7.0	-	Molecular Evolutionary Genetic Analysis version 7.0
Mg^{2+}	-	Magnesium ion
MgCl ₂	-	Magnesium chloride
MgSO ₄ .7H ₂ O	-	Magnesium sulfate heptahydrate
Mn^{2+}	-	Manganese ion
MnCl ₂	-	Manganese chloride
Ν	-	Asparagine
Na ⁺	-	Sodium ion
Na ₂ CO ₃	-	Sodium carbonate
NaCl	-	Sodium chloride

NaHCO ₃	-	Sodium bicarbonate
NaNO ₂	-	Sodium nitrite
NaOH	-	Sodium hydroxide
NH ₄ Cl	-	Ammonium chloride
Ni ²⁺	-	Nickel ion
NiSO ₄	-	Nickel sulfate
OH	-	Hydroxide ion
Р	-	Proline
PHB	-	Polyhydroxybutyrate
PMSF	-	Phenylmethylsulfonyl fluoride
pI	-	Isoelectric point
PSI-BLAST	-	Position-Specific Iterated Basic Local Alignment
		Search Tool
Q	-	Glutamine
R	-	Arginine
rcf	-	Relative centrifugal force
rpm	-	Rotary per minute
rRNA	-	Ribosomal ribonucleic acid
SAPS	-	Statistical Analysis of Protein Sequences
SD	-	Standard deviation
SDS	-	Sodium dodecyl sulfate
SDS-PAGE	-	Sodium dodecyl sulfate polyacrylamide gel
		electrophoresis
Ser, S	-	Serine
sp.	-	Species (singular)
spp.	-	Species (plural)
Т	-	Threonine
t-PA	-	Tissue plasminogen activator
TCA	-	Trichloroacetic acid
Tris	-	2-Amino-2-(hydroxymethyl)propane-1,3-diol
u-PA	-	Urokinase type plasminogen activator
USA	-	United States of America
USD	-	United States dollar

UV	-	Ultraviolet
V	-	Valine
W	-	Tryptophan
X, Xaa	-	Unknown amino acid
Y	-	Tyrosine
Zn^{2+}	-	Zinc ion
ZnSO ₄	-	Zinc sulfate

LIST OF APPENDICES

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CHAPTER 1

INTRODUCTION

1.1 Background of study

Halophilic bacteria has been recognized as one of the extremophiles that has valuable applications in industry and environment (Oren, 2010; Edbeib *et al.*, 2016; Yin *et al.*, 2015). They are found in natural saline and hypersaline habitats such as seawater, salt marshes and lagoon. Occurrence of halophiles can be from seawater to brines (Brock, 1979), some habitats include Dead Sea between Israel and Jordan and also Great Salt Lake in Utah (Oren, 2006). Besides that, salty environments inhabited by halophilic and halotolerant bacteria include food products such as salted fish and fermented food (Enache *et al.*, 2012), and these type of foods are commonly found in Malaysia.

Well-adapted strategies in saline environments utilized by halophilic bacteria made them useful in industrial applications. These halophilic bacteria has been used for production of valuable metabolites and solutes such as stress protectants (DasSarma and DasSarma, 2006), saline wastewater treatments (Shivanand and Mugeraya, 2011) and biodegradation of organic pollutants in environmental biotechnology (Le Borgne *et al.*, 2008). Halophilic bacteria can be classified under different phyla. Under different phylum, halophilic bacteria have different physiological requirements such as compatible solute used and salt concentration required. This diversity makes the halophilic bacteria as one of the source of opportunity and abundance, including industrial enzymes. One of the enzymes produced by halophilic bacteria is protease, which is a type of hydrolase. Protease can be produced from animal, plant and microbial source. Protease from microbial source has been extensively used in various application especially in detergent industry since 1960 (Rao *et al.*, 1998) due their effectiveness in removing protein stains (Karn and Kumar, 2015). Until today, proteases contributed approximately 60% of the global industrial enzymes market (Anithajothi *et al.*, 2014). While from this amount, microbial proteases constitute 40% of total enzyme production (Raval *et al.*, 2014) which applied in various industries. The largest market undeniable is detergent industry, as this industry contributed to production of 13.5 billion tons per year (Adrio and Demain, 2014).

Apart from that, use of eco-friendly protease recovered from industrial sludge for bio-conversion of proteinaceous waste material into value-added products has become an increasingly concern due to it is a cost effective process (Karn and Kumar, 2015). And also, protease has been engineered using rational design and directed evolution approach to improve its properties and functions to be applied as therapeutic agents and in food processing (Li *et al.*, 2013). Based on huge demand of protease market and its application, new candidate of protease remained a worth for further discovery.

1.2 Problem statement / significance of study

Halophilic bacteria produce polyextremophilic enzymes that may have useful application in various biotechnological field. For instance, protease can act as fibrinolytic agent and also removing protein based stains such as blood and sweat effectively (Karn and Kumar, 2015). Most of the commercial bacterial proteases used in detergent industry are produced from Bacillus sp. (Gupta et al., 2002b), lesser investigation on protease from Virgibacillus sp., and until today, no commercial protease is originated from genus Virgibacillus as well. Furthermore, expenditure cost in detergent industry such as purification, production (Niyonzima and More, 2015b) and protein engineering to increase protease efficiency (Li et al., 2013) are expensive. To sort out these problems, a single step of production with the use of crude enzyme is required (Niyonzima and More, 2015a), a more cost effective way compared to purification. Moreover, exploration on novel enzymes with extraordinary properties from extremophiles is always in demand and continuously in research field. Therefore, this study was conducted to characterize extracellular protease produced from a halophilic bacterium, Virgibacillus sp. strain CD6 that is potentially to be applied in various industries, especially in detergent formulation.

1.3 Objectives of study

The objectives of this research are:

- i. To select the best nitrogen source for protease production.
- ii. To assess the effect of physico-chemical factors on the activity and stability of protease from *Virgibacillus* sp. CD6.
- iii. To analyze extracellular protease sequences encoded for Virgibacillus sp.

1.4 Scope of study

The previously isolated halophilic bacteria, *Virgibacillus* sp. strain CD6 was initially screened for extracellular protease activity by using qualitative approaches, (skim milk agar and gelatin liquefaction). After that, medium for protease production was formulated and effect of nitrogen sources on protease production was investigated. The optimum conditions of protease activity and its stability in terms of pH, temperature and salt concentration were determined. Then, protease stability in presence of metal ions, inhibitors, detergent constituents and organic solvent was assessed. Compatibility of protease with commercial detergents and substrate specificity of protease were also investigated. Lastly, annotated protein sequences of extracellular proteases of *Virgibacillus* sp. were analyzed using bioinformatics approach and phylogenetic protein tree was constructed.

REFERENCES

- Abraham, J., Gea, T., and Sánchez, A. (2014). Substitution of chemical dehairing by proteases from solid-state fermentation of hair wastes. *Journal of Cleaner Production*. 74, 191-198.
- Adamiak, J., Otlewska, A., and Gutarowska, B. (2015). Halophilic microbial communities in deteriorated buildings. World Journal of Microbiology and Biotechnology. 31, 1489-1499.
- Adrio, J. L., and Demain, A. L. (2014). Microbial enzymes: tools for biotechnological processes. *Biomolecules*. 4, 117-139.
- Altschul, S. F., Madden, T. L., Schäffer, A. A., Zhang, J., Zhang, Z., Miller, W., and Lipman, D. J. (1997). Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research*. 25, 3389-3402.
- An, S.-Y., Asahara, M., Goto, K., Kasai, H., and Yokota, A. (2007). Virgibacillus halophilus sp. nov., spore-forming bacteria isolated from soil in Japan. International Journal of Systematic and Evolutionary Microbiology. 57, 1607-1611.
- Andersen, L. P. (1998). US 5834299 A. Retrieved on 15 December, 2016, from https://www.google.ch/patents/US5834299
- Anithajothi, R., Nagarani, N., Umagowsalya, G., Duraikannu, K., and Ramakritinan, C. M. (2014). Screening, isolation and characterization of protease producing moderately halophilic microorganism *Halomonas meridiana* associated with coral mucus. *Toxicological & Environmental Chemistry*. 96, 296-306.
- Annamalai, N., Rajeswari, M. V., and Balasubramanian, T. (2014). Extraction, purification and application of thermostable and halostable alkaline protease from *Bacillus alveayuensis* CAS 5 using marine wastes. *Food and Bioproducts Processing*. 92, 335-342.

- Anwar, T., and Chauhan, R. S. (2012). Computational analysis of halotolerance genes from halophilic prokaryotes to infer their signature sequences *International Journal of Advance Biotechnology and Bioinformatics*. 1, 69-78.
- Armstrong, E., Yan, L., Boyd, K. G., Wright, P. C., and Burgess, J. G. (2001). The symbiotic role of marine microbes on living surfaces. *Hydrobiologia*. 461, 37-40.
- Atsushi, I. K. A. I. (1980). Thermostability and aliphatic index of globular proteins. *Journal of Biochemistry*. 88, 1895-1898.
- Averhoff, B., and Müller, V. (2010). Exploring research frontiers in microbiology: recent advances in halophilic and thermophilic extremophiles. *Research in Microbiology*. 161, 506-514.
- Bajpai, D., and Tyagi, V. (2007). Laundry detergents: an overview. *Journal of Oleo Science*. 56, 327-340.
- Banbula, A., Potempa, J., Travis, J., Fernandez-Catalén, C., Mann, K., Huber, R., Bode,
 W., and Medrano, F. (1998). Amino-acid sequence and three-dimensional structure of the *Staphylococcus aureus* metalloproteinase at 1.72 Å resolution. *Structure*. 6, 1185-1193.
- Barrett, A. J. (1994). *Proteolytic enzymes: serine and cysteine peptidases*. United States: Elsevier.
- Barrett, A. J., Woessner, J. F., and Rawlings, N. D. (2012). *Handbook of proteolytic enzymes*. United States: Elsevier.
- Benavente, D., Sanchez-Moral, S., Fernandez-Cortes, A., Cañaveras, J. C., Elez, J., and Sáiz-Jiménez, C. (2011). Salt damage and microclimate in the Postumius Tomb, Roman Necropolis of Carmona, Spain. *Environmental Earth Sciences*. 63, 1529-1543.
- Bhunia, B., Basak, B., and Dey, A. (2012). A review on production of serine alkaline protease by *Bacillus* spp. *Journal of Biochemical Technology*. 3, 448-457.
- Blinkovsky, A. M., Byun, T., Brown, K. M., Golightly, E. J., and Klotz, A. V. (2000).
 A non-specific aminopeptidase from *Aspergillus*. *Biochimica et Biophysica* Acta (BBA)-Protein Structure and Molecular Enzymology. 1480, 171-181.
- Boeuf, G. (2011). Marine biodiversity characteristics. *Comptes Rendus Biologies*. 334, 435-440.

- Bork, P., Holm, L., and Sander, C. (1994). The immunoglobulin fold: structural classification, sequence patterns and common core. *Journal of Molecular Biology*. 242, 309-320.
- Bowman, J. P., McCammon, S. A., Rea, S. M., and McMeekin, T. A. (2000). The microbial composition of three limnologically disparate hypersaline Antarctic lakes. *FEMS Microbiology Letters*. 183, 81-88.
- Brendel, V., Bucher, P., Nourbakhsh, I. R., Blaisdell, B. E., and Karlin, S. (1992).
 Methods and algorithms for statistical analysis of protein sequences. *Proceedings of the National Academy of Sciences*. 89, 2002-2006.
- Britton, K. L., Stillman, T. J., Yip, K. S., Forterre, P., Engel, P. C., and Rice, D. W. (1998). Insights into the molecular basis of salt tolerance from the study of glutamate dehydrogenase from *Halobacterium salinarum*. *Journal of Biological Chemistry*. 273, 9023-9030.
- Brock, T. (1979). Ecology of saline lakes. Strategies of Microbial Life in Extreme environments. 29-47.
- Brown, A. (1976). Microbial water stress. Bacteriological Reviews. 40, 803.
- Cao, Z.-J., Zhang, Q., Wei, D.-K., Chen, L., Wang, J., Zhang, X.-Q., and Zhou, M.-H. (2009). Characterization of a novel *Stenotrophomonas* isolate with high keratinase activity and purification of the enzyme. *Journal of Industrial Microbiology and Biotechnology*. 36, 181-188.
- Carrasco, I. J., Márquez, M. C., and Ventosa, A. (2009). Virgibacillus salinus sp. nov., a moderately halophilic bacterium from sediment of a saline lake. International Journal of Systematic and Evolutionary Microbiology. 59, 3068-3073.
- Carter, P., Nilsson, B., Burnier, J. P., Burdick, D., and Wells, J. A. (1989). Engineering subtilisin BPN' for site-specific proteolysis. *Proteins: Structure, Function, and Bioinformatics*. 6, 240-248.
- Chaiyanan, S., Chaiyanan, S., Maugel, T., Huq, A., Robb, F. T., and Colwell, R. R. (1999). Polyphasic taxonomy of a novel *Halobacillus*, *Halobacillus thailandensis* sp. nov. isolated from fish sauce. Systematic and Applied Microbiology. 22, 360-365.
- Chamroensaksri, N., Akaracharanya, A., Visessanguan, W., and Tanasupawat, S. (2008). Characterization of halophilic bacterium NB2-1 from pla-ra and its protease production. *Journal of Food Biochemistry*. 32, 536-555.

- Charney, J., and Tomarelli, R. M. (1947). A colonmetric method for the determination of the proteolytic activity of duodenal juice. *Journal of Biological Chemistry*. 171, 501-505.
- Chen, Y.-G., Cui, X.-L., Fritze, D., Chai, L.-H., Schumann, P., Wen, M.-L., Wang, Y.-X., Xu, L.-H., and Jiang, C.-L. (2008). Virgibacillus kekensis sp. nov., a moderately halophilic bacterium isolated from a salt lake in China. International Journal of Systematic and Evolutionary Microbiology. 58, 647-653.
- Chung, C. H., and Goldberg, A. L. (1981). The product of the lon (capR) gene in Escherichia coli is the ATP-dependent protease, protease La. Proceedings of the National Academy of Sciences. 78, 4931-4935.
- Cleland, W. (1964). Dithiothreitol, a new protective reagent for SH groups*. *Biochemistry*. 3, 480-482.
- Collins, K. D. (1997). Charge density-dependent strength of hydration and biological structure. *Biophysical Journal*. 72, 65.
- Cotta, M. A., and Hespell, R. B. (1986). Proteolytic activity of the ruminal bacterium *Butyrivibrio fibrisolvens. Applied and environmental microbiology.* 52, 51-58.
- Craik, C. S., Page, M. J., and Madison, E. L. (2011). Proteases as therapeutics. *Biochemical Journal*. 435, 1-16.
- Csonka, L. N. (1989). Physiological and genetic responses of bacteria to osmotic stress. *Microbiological Reviews*. 53, 121-147.
- Dash, H. R., Mangwani, N., Chakraborty, J., Kumari, S., and Das, S. (2013). Marine bacteria: potential candidates for enhanced bioremediation. *Applied Microbiology and Biotechnology*. 97, 561-571.
- DasSarma, S., and DasSarma, P. (2006). Halophiles. In Gregg P. (Eds.) *Encyclopedia of Life Sciences*. Chichester: John Wiley & Sons Ltd.
- Davies, J., Anderson, G., Beveridge, T., and Clark, H. (1983). Chemical mechanism of the Gram stain and synthesis of a new electron-opaque marker for electron microscopy which replaces the iodine mordant of the stain. *Journal of Bacteriology*. 156, 837-845.
- De Castro, E., Sigrist, C. J., Gattiker, A., Bulliard, V., Langendijk-Genevaux, P. S., Gasteiger, E., Bairoch, A., and Hulo, N. (2006). ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. *Nucleic Acids Research*. 34, W362-W365.

- Debette, J. (1991). Isolation and characterization of an extracellular proteinase produced by a soil strain of *Xanthomonas maltophilia*. *Current Microbiology*. 22, 85-90.
- DeMaere, M. Z., Williams, T. J., Allen, M. A., Brown, M. V., Gibson, J. A., Rich, J., Lauro, F. M., Dyall-Smith, M., Davenport, K. W., and Woyke, T. (2013). High level of intergenera gene exchange shapes the evolution of haloarchaea in an isolated Antarctic lake. *Proceedings of the National Academy of Sciences*. 110, 16939-16944.
- Deng, A., Wu, J., Zhang, Y., Zhang, G., and Wen, T. (2010). Purification and characterization of a surfactant-stable high-alkaline protease from *Bacillus* sp. B001. *Bioresource Technology*. 101, 7100-7106.
- Díez, B., Pedrós-Alió, C., Marsh, T. L., and Massana, R. (2001). Application of denaturing gradient gel electrophoresis (DGGE) to study the diversity of marine picoeukaryotic assemblages and comparison of DGGE with other molecular techniques. *Applied and Environmental Microbiology*. 67, 2942-2951.
- Dobson, S., and Franzmann, P. (1996). Unification of the genera *Deleya* (Baumann et al. 1983), *Halomonas* (Vreeland et al. 1980), and *Halovibrio* (Fendrich 1988) and the species *Paracoccus halodenitrificans* (Robinson and Gibbons 1952) into a single genus, *Halomonas*, and placement of the genus *Zymobacter* in the family *Halomonadaceae*. *International Journal of Systematic and Evolutionary Microbiology*. 46, 550-558.
- Dodson, G., and Wlodawer, A. (1998). Catalytic triads and their relatives. *Trends in Biochemical Sciences*. 23, 347-352.
- Dohrmann, A.-B., and Müller, V. (1999). Chloride dependence of endospore germination in *Halobacillus halophilus*. Archives of Microbiology. 172, 264-267.
- Doroshchuk, N., Gelfand, M., and Rodionov, D. (2006). Regulation of nitrogen metabolism in gram-positive bacteria. *Molecular Biology*. 40, 829-836.
- Dubnovitsky, A. P., Kapetaniou, E. G., and Papageorgiou, A. C. (2005). Enzyme adaptation to alkaline pH: atomic resolution (1.08 Å) structure of phosphoserine aminotransferase from *Bacillus alcalophilus*. *Protein Science*. 14, 97-110.

- Edbeib, M. F., Wahab, R. A., and Huyop, F. (2016). Halophiles: biology, adaptation, and their role in decontamination of hypersaline environments. *World Journal of Microbiology and Biotechnology*. 32, 1-23.
- Embaby, A. M., Saeed, H., and Hussein, A. (2016). SHG10 keratinolytic alkaline protease from *Bacillus licheniformis* SHG10 DSM 28096: Robust stability and unusual non-cumbersome purification. *Journal of Basic Microbiology*. 56(12), 1317-1330.
- Enache, M., Popescu, G., Itoh, T., and Kamekura, M. (2012). Halophilic microorganisms from man-made and natural hypersaline environments: Physiology, ecology, and biotechnological potential. In Stan-Lotter H., Fendrihan, S. (Eds.) *Adaption of Microbial Life to Environmental Extremes*. United States: Springer.
- Esmon, C. T., Fukudome, K., Mather, T., Bode, W., Regan, L. M., Stearns-Kurosawa, D. J., and Kurosawa, S. (1999). Inflammation, sepsis, and coagulation. *Haematologica*. 84, 254-259.
- Estell, D. A., Graycar, T. P., and Wells, J. A. (1985). Engineering an enzyme by sitedirected mutagenesis to be resistant to chemical oxidation. *Journal of Biological Chemistry*. 260, 6518-6521.
- Ettenauer, J. D., Jurado, V., Piñar, G., Miller, A. Z., Santner, M., Saiz-Jimenez, C., and Sterflinger, K. (2014). Halophilic microorganisms are responsible for the rosy discolouration of saline environments in three historical buildings with mural paintings. *PloS One*. 9, e103844.
- Felsenstein, J. (1985). Confidence limits on phylogenies: an approach using the bootstrap. *Evolution*. 783-791.
- Fendrich, C. (1988). Halovibrio variabilis gen. nov. sp. nov., Pseudomonas halophila sp. nov. and a new halophilic aerobic coccoid Eubacterium from Great Salt Lake, Utah, USA. Systematic and Applied Microbiology. 11, 36-43.
- Fujiwara, N., and Yamamoto, K. (1987). Production of alkaline protease in a low-cost medium by alkalophilic *Bacillus* sp. and properties of the enzyme. *Journal of Fermentation Technology*. 65, 345-348.
- Gasteiger, E., Hoogland, C., Gattiker, A., Wilkins, M. R., Appel, R. D., and Bairoch,A. (2005). *Protein identification and analysis tools on the ExPASy server*.United States: Springer.

- Gensberg, K., Jan, S., and Matthews, G. M. (1998). Subtilisin-related serine proteases in the mammalian constitutive secretory pathway. *Seminars in cell & developmental biology*. 9(1), 11-17.
- Ghorbel, B., Sellami-Kamoun, A., and Nasri, M. (2003). Stability studies of protease from *Bacillus cereus* BG1. *Enzyme and Microbial Technology*. 32, 513-518.
- Gill, S. C., and Von Hippel, P. H. (1989). Calculation of protein extinction coefficients from amino acid sequence data. *Analytical Biochemistry*. 182, 319-326.
- Goh, K. M., Hong, G. P., Chyi, N. H., Ng, P., Piaw, C. K., and Rahman, R. N. Z. R.
 A. (2012). Trends and tips in protein engineering, A Review. *Jurnal Teknologi*. 59.
- Graziano, G., and Merlino, A. (2014). Molecular bases of protein halotolerance. Biochimica et Biophysica Acta (BBA)-Proteins and Proteomics. 1844, 850-858.
- Guasch, A., Coll, M., Avilés, F. X., and Huber, R. (1992). Three-dimensional structure of porcine pancreatic procarboxypeptidase A: A comparison of the A and B zymogens and their determinants for inhibition and activation. *Journal of Molecular Biology*. 224, 141-157.
- Gupta, A., Joseph, B., Mani, A., and Thomas, G. (2008). Biosynthesis and properties of an extracellular thermostable serine alkaline protease from *Virgibacillus pantothenticus*. World Journal of Microbiology and Biotechnology. 24, 237-243.
- Gupta, R., Beg, Q., Khan, S., and Chauhan, B. (2002a). An overview on fermentation, downstream processing and properties of microbial alkaline proteases. *Applied Microbiology and Biotechnology*. 60, 381-395.
- Gupta, R., Beg, Q., and Lorenz, P. (2002b). Bacterial alkaline proteases: molecular approaches and industrial applications. *Applied Microbiology and Biotechnology*. 59, 15-32.
- Guruprasad, K., Reddy, B. B., and Pandit, M. W. (1990). Correlation between stability of a protein and its dipeptide composition: a novel approach for predicting in vivo stability of a protein from its primary sequence. *Protein Engineering*. 4, 155-161.
- Haddar, A., Agrebi, R., Bougatef, A., Hmidet, N., Sellami-Kamoun, A., and Nasri, M. (2009). Two detergent stable alkaline serine-proteases from *Bacillus mojavensis* A21: Purification, characterization and potential application as a laundry detergent additive. *Bioresource Technology*. 100, 3366-3373.

- Haki, G., and Rakshit, S. (2003). Developments in industrially important thermostable enzymes: a review. *Bioresource Technology*. 89, 17-34.
- Hänelt, I., and Müller, V. (2013). Molecular mechanisms of adaptation of the moderately halophilic bacterium *Halobacillis halophilus* to its environment. *Life*. 3, 234-243.
- Heerd, D., Yegin, S., Tari, C., and Fernandez-Lahore, M. (2012). Pectinase enzymecomplex production by *Aspergillus* spp. in solid-state fermentation: A comparative study. *Food and Bioproducts Processing*. 90, 102-110.
- Heyndrickx, M., Lebbe, L., Kersters, K., De Vos, P., Forsyth, G., and Logan, N. A. (1998). Virgibacillus: a new genus to accommodate Bacillus pantothenticus (Proom and Knight 1950). Emended description of Virgibacillus pantothenticus. International Journal of Systematic and Evolutionary Microbiology. 48, 99-106.
- Heyrman, J., Logan, N. A., Busse, H.-J., Balcaen, A., Lebbe, L., Rodriguez-Diaz, M., Swings, J., and De Vos, P. (2003). *Virgibacillus carmonensis* sp. nov., *Virgibacillus necropolis* sp. nov. and *Virgibacillus picturae* sp. nov., three novel species isolated from deteriorated mural paintings, transfer of the species of the genus *Salibacillus* to *Virgibacillus*, as *Virgibacillus marismortui* comb. nov. and *Virgibacillus salexigens* comb. nov., and emended description of the genus *Virgibacillus*. *International Journal of Systematic and Evolutionary Microbiology*. 53, 501-511.
- Ibrahim, A. S., Al-Salamah, A. A., Elbadawi, Y. B., El-Tayeb, M. A., and Ibrahim, S. S. S. (2015). Production of extracellular alkaline protease by new halotolerant alkaliphilic *Bacillus* sp. NPST-AK15 isolated from hyper saline soda lakes. *Electronic Journal of Biotechnology*. 18, 236-243.
- Jackson, D. P., and Cotter, D. A. (1984). Expression of proteolytic enzymes during Dictyostelium discoideum spore germination. Archives of Microbiology. 137, 205-208.
- James, H. (2005). Bio Chemistry. India: Lotus Press.
- Jones, P., Binns, D., Chang, H.-Y., Fraser, M., Li, W., McAnulla, C., McWilliam, H., Maslen, J., Mitchell, A., and Nuka, G. (2014). InterProScan 5: genome-scale protein function classification. *Bioinformatics*. 30, 1236-1240.

- Joo, H.-S., and Chang, C.-S. (2005). Production of protease from a new alkalophilic Bacillus sp. I-312 grown on soybean meal: optimization and some properties. Process Biochemistry. 40, 1263-1270.
- Joo, H. S., Kumar, C., Park, G. C., Paik, S., and Chang, C. S. (2003). Oxidant and SDS-stable alkaline protease from *Bacillus clausii* I-52: Production and some properties. *Journal of Applied Microbiology*. 95, 267-272.
- Kalisz, H. M. (1988). Microbial proteinases. Enzyme Studies (pp. 1-65). Springer.
- Kämpfer, P., Arun, A., Busse, H.-J., Langer, S., Young, C.-C., Chen, W.-M., Syed, A., and Rekha, P. (2011). Virgibacillus soli sp. nov., isolated from mountain soil. International Journal of Systematic and Evolutionary Microbiology. 61, 275-280.
- Kanekar, P., Kanekar, S., Kelkar, A., and Dhakephalkar, P. (2012). Halophiles– Taxonomy, diversity, physiology and applications. *Microorganisms in Environmental Management* (pp. 1-34). Springer.
- Karbalaei-Heidari, H. R., Amoozegar, M. A., Hajighasemi, M., Ziaee, A.-A., and Ventosa, A. (2009). Production, optimization and purification of a novel extracellular protease from the moderately halophilic bacterium *Halobacillus karajensis*. *Journal of Industrial Microbiology and Biotechnology*. 36, 21-27.
- Karlström, A., and Levine, R. L. (1991). Copper inhibits the protease from human immunodeficiency virus 1 by both cysteine-dependent and cysteineindependent mechanisms. *Proceedings of the National Academy of Sciences*. 88, 5552-5556.
- Karn, S. K., and Kumar, A. (2015). Hydrolytic enzyme protease in sludge: Recovery and its application. *Biotechnology and Bioprocess Engineering*. 20, 652-661.
- Kim, J., Jung, M.-J., Roh, S. W., Nam, Y.-D., Shin, K.-S., and Bae, J.-W. (2011). Virgibacillus alimentarius sp. nov., isolated from a traditional Korean food. International Journal of Systematic and Evolutionary Microbiology. 61, 2851-2855.
- Koka, R., and Weimer, B. C. (2000). Investigation of the ability of a purified protease from *Pseudomonas fluorescens* RO98 to hydrolyze bitter peptides from cheese. *International Dairy Journal*. 10, 75-79.
- Kornberg, A., Spudich, J. A., Nelson, D. L., and Deutscher, M. P. (1968). Origin of proteins in sporulation. *Annual Review of Biochemistry*. 37, 51-78.

- Kulpreecha, S., Boonruangthavorn, A., Meksiriporn, B., and Thongchul, N. (2009). Inexpensive fed-batch cultivation for high poly(3-hydroxybutyrate) production by a new isolate of *Bacillus megaterium*. *Journal of Bioscience and Bioengineering*. 107, 240-245.
- Kumar, C. G., and Takagi, H. (1999). Microbial alkaline proteases: From a bioindustrial viewpoint. *Biotechnology Advances*. 17, 561-594.
- Kumar, S., Stecher, G., and Tamura, K. (2016). MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Molecular Biology and Evolution*.
- Kumar, S., Tsai, C.-J., and Nussinov, R. (2000). Factors enhancing protein thermostability. *Protein Engineering*. 13, 179-191.
- Kushner, D. (1978). Microbial life in extreme environments. London: Academic Press.
- Lapsongphon, N., Rodtong, S., and Yongsawatdigul, J. (2013). Spent brewery yeast sludge as a single nitrogen source for fibrinolytic enzyme production of *Virgibacillus* sp. SK37. *Food Science and Biotechnology*. 22, 71-78.
- Lauro, F. M., McDougald, D., Thomas, T., Williams, T. J., Egan, S., Rice, S., DeMaere, M. Z., Ting, L., Ertan, H., and Johnson, J. (2009). The genomic basis of trophic strategy in marine bacteria. *Proceedings of the National Academy of Sciences*. 106, 15527-15533.
- Laxman, R. S., Sonawane, A. P., More, S. V., Rao, B. S., Rele, M. V., Jogdand, V. V., Deshpande, V. V., and Rao, M. B. (2005). Optimization and scale up of production of alkaline protease from *Conidiobolus coronatus*. *Process Biochemistry*. 40, 3152-3158.
- Le Borgne, S., Paniagua, D., and Vazquez-Duhalt, R. (2008). Biodegradation of organic pollutants by halophilic bacteria and archaea. *Journal of Molecular Microbiology and Biotechnology*. 15, 74-92.
- Lee, J.-S., Lim, J.-M., Lee, K. C., Lee, J.-C., Park, Y.-H., and Kim, C.-J. (2006). Virgibacillus koreensis sp. nov., a novel bacterium from a salt field, and transfer of Virgibacillus picturae to the genus Oceanobacillus as Oceanobacillus picturae comb. nov. with emended descriptions. International Journal of Systematic and Evolutionary Microbiology. 56, 251-257.
- Lee, S.-Y., Kang, C.-H., Oh, T.-K., and Yoon, J.-H. (2012). Virgibacillus campisalis sp. nov., from a marine solar saltern. International Journal of Systematic and Evolutionary Microbiology. 62, 347-351.

- Li, Q., Yi, L., Marek, P., and Iverson, B. L. (2013). Commercial proteases: Present and future. *FEBS Letters*. 587, 1155-1163.
- Li, W. F., Zhou, X. X., and Lu, P. (2005). Structural features of thermozymes. *Biotechnology Advances*. 23, 271-281.
- Li, Y., Shoemaker, C. F., Ma, J., Luo, C., and Zhong, F. (2009). Effects of alcalase/protease N treatments on rice starch isolation and their effects on its properties. *Food Chemistry*. 114, 821-828.
- Lippert, K., and Galinski, E. A. (1992). Enzyme stabilization be ectoine-type compatible solutes: protection against heating, freezing and drying. *Applied Microbiology and Biotechnology*. 37, 61-65.
- Lowry, O. H., Rosebrough, N. J., Farr, A. L., and Randall, R. J. (1951). Protein measurement with the Folin phenol reagent. *Journal of Biological Chemistry*. 193, 265-275.
- Lozano, P., de Diego, T., and Iborra, J. L. (1996). Influence of water-miscible aprotic solvents on α-chymotrypsin stability. *Biotechnology progress*. 12, 488-493.
- Lukesh III, J. C., Palte, M. J., and Raines, R. T. (2012). A potent, versatile disulfidereducing agent from aspartic acid. *Journal of the American Chemical Society*. 134, 4057-4059.
- Luo, X., and Hofmann, K. (2001). The protease-associated domain: a homology domain associated with multiple classes of proteases. *Trends in Biochemical Sciences*. 26, 147-148.
- Madern, D., Camacho, M., Rodríguez-Arnedo, A., Bonete, M.-J., and Zaccai, G. (2004). Salt-dependent studies of NADP-dependent isocitrate dehydrogenase from the halophilic archaeon *Haloferax volcanii*. *Extremophiles*. 8, 377-384.
- Madern, D., and Zaccai, G. (2004). Molecular adaptation: the malate dehydrogenase from the extreme halophilic bacterium *Salinibacter ruber* behaves like a non-halophilic protein. *Biochimie*. 86, 295-303.
- Madigan, M. T., and Orent, A. (1999). Thermophilic and halophilic extremophiles. *Current Opinion in Microbiology*. 2, 265-269.
- Matzke, J., Schwermann, B., and Bakker, E. P. (1997). Acidostable and acidophilic proteins: the example of the α-amylase from *Alicyclobacillus acidocaldarius*. *Comparative Biochemistry and Physiology Part A: Physiology*. 118, 475-479.
- Mehta, V. J., Thumar, J. T., and Singh, S. P. (2006). Production of alkaline protease from an alkaliphilic actinomycete. *Bioresource Technology*. 97, 1650-1654.

- Meissner, D. (2010). Proteolytic processing of fungal and insect proteins involved in chitin synthesis. PhD dissertation, University of Osnabrück, Osnabrück, Germany.
- Mitchinson, C., and Wells, J. A. (1989). Protein engineering of disulfide bonds in subtilisin BPN'. *Biochemistry*. 28, 4807-4815.
- Miyoshi, S.-i., and Shinoda, S. (2000). Microbial metalloproteases and pathogenesis. *Microbes and Infection*. 2, 91-98.
- Montriwong, A., Rodtong, S., and Yongsawatdigul, J. (2015). Detergent-Stable Salt-Activated Proteinases from Virgibacillus halodenitrificans SK1-3-7 Isolated from Fish Sauce Fermentation. Applied Biochemistry and Biotechnology. 176, 505-517.
- Murray, A. E., and Fritsen, C. H. (2007). Microbiota within the perennial ice cover of Lake Vida, Antarctica. *FEMS Microbiology Ecology*. 59, 274-288.
- Namwong, S., Tanasupawat, S., Smitinont, T., Visessanguan, W., Kudo, T., and Itoh, T. (2005). Isolation of *Lentibacillus salicampi* strains and *Lentibacillus juripiscarius* sp. nov. from fish sauce in Thailand. *International Journal of Systematic and Evolutionary Microbiology*. 55, 315-320.
- Neelakantan, S., Mohanty, A., and Kaushik, J. K. (1999). Production and use of microbial enzymes for dairy processing. *Current Science*. 77, 143-148.
- Newport, G., and Agabian, N. (1997). KEX2 influences *Candida albicans* proteinase secretion and hyphal formation. *Journal of Biological Chemistry*. 272, 28954-28961.
- Niederberger, T. D., Steven, B., Charvet, S., Barbier, B., and Whyte, L. G. (2009). *Virgibacillus arcticus* sp. nov., a moderately halophilic, endospore-forming bacterium from permafrost in the Canadian high Arctic. *International Journal* of Systematic and Evolutionary Microbiology. 59, 2219-2225.
- Niyonzima, F. N., and More, S. (2015a). Detergent-compatible proteases: microbial production, properties, and stain removal analysis. *Preparative Biochemistry and Biotechnology*. 45, 233-258.
- Niyonzima, F. N., and More, S. S. (2015b). Coproduction of detergent compatible bacterial enzymes and stain removal evaluation. *Journal of Basic Microbiology*. 55, 1149-1158.
- North, M. J. (1982). Comparative biochemistry of the proteinases of eucaryotic microorganisms. *Microbiological Reviews*. 46, 308.

- Oren, A. (1990). The use of protein synthesis inhibitors in the estimation of the contribution of halophilic archaebacteria to bacterial activity in hypersaline environments. *FEMS Microbiology Ecology*. 6, 187-192.
- Oren, A. (2002). Molecular ecology of extremely halophilic Archaea and Bacteria. *FEMS Microbiology Ecology*. 39, 1-7.
- Oren, A. (2006). The Prokaryotes. United States: Springer.
- Oren, A. (2008). Microbial life at high salt concentrations: phylogenetic and metabolic diversity. *Saline Systems*. 4, 1.
- Oren, A. (2010). Industrial and environmental applications of halophilic microorganisms. *Environmental Technology*. 31, 825-834.
- Oren, A. (2015). Halophilic microbial communities and their environments. *Current Opinion in Biotechnology*. 33, 119-124.
- Oren, A., Heldal, M., and Norland, S. (1997). X-ray microanalysis of intracellular ions in the anaerobic halophilic eubacterium *Haloanaerobium praevalens*. *Canadian Journal of Microbiology*. 43, 588-592.
- Ortiz, G. E., Noseda, D. G., Ponce Mora, M. C., Recupero, M. N., Blasco, M., and Albertó, E. (2016). A comparative study of new *Aspergillus* strains for proteolytic enzymes production by solid state fermentation. *Enzyme research*. 2016.
- Otlewska, A., Adamiak, J., and Gutarowska, B. (2015). Clone-based comparative sequence analysis of 16S rRNA genes retrieved from biodeteriorating brick buildings of the former Auschwitz II–Birkenau concentration and extermination camp. *Systematic and Applied Microbiology*. 38, 48-55.
- Pantoliano, M. W., Whitlow, M., Wood, J. F., Rollence, M. L., Finzel, B. C., Gilliland, G. L., Poulos, T. L., and Bryan, P. N. (1988). The engineering of binding affinity at metal ion binding sites for the stabilization of proteins: subtilisin as a test case. *Biochemistry*. 27, 8311-8317.
- Paul, S., Bag, S. K., Das, S., Harvill, E. T., and Dutta, C. (2008). Molecular signature of hypersaline adaptation: insights from genome and proteome composition of halophilic prokaryotes. *Genome Biology*. 9, 1.
- Petersen, T. N., Brunak, S., von Heijne, G., and Nielsen, H. (2011). SignalP 4.0: discriminating signal peptides from transmembrane regions. *Nature Methods*. 8, 785-786.

- Phadatare, S., Srinivasan, M., and Deshpande, M. (1989). Evidence for the involvement of serine protease in the conidial discharge of *Conidiobolus coronatus*. Archives of Microbiology. 153, 47-49.
- Phrommao, E., Yongsawatdigul, J., Rodtong, S., and Yamabhai, M. (2011). A novel subtilase with NaCl-activated and oxidant-stable activity from *Virgibacillus* sp. SK37. *BMC Biotechnology*. 11, 1.
- Piñar, G., Kraková, L., Pangallo, D., Piombino-Mascali, D., Maixner, F., Zink, A., and Sterflinger, K. (2014). Halophilic bacteria are colonizing the exhibition areas of the Capuchin Catacombs in Palermo, Italy. *Extremophiles*. 18, 677-691.
- Pinar, G., Piombino-Mascali, D., Maixner, F., Zink, A., and Sterflinger, K. (2013). Microbial survey of the mummies from the Capuchin Catacombs of Palermo, Italy: biodeterioration risk and contamination of the indoor air. *FEMS Microbiology Ecology*. 86, 341-356.
- Priest, F. G. (1977). Extracellular enzyme synthesis in the genus *Bacillus*. *Bacteriological Reviews*. 41, 711.
- Quesada, E., Ventosa, A., Rodriguez-Valera, F., Megias, L., and Ramos-Cormenzana,
 A. (1983). Numerical taxonomy of moderately halophilic Gram-negative bacteria from hypersaline soils. *Microbiology*. 129, 2649-2657.
- Rajamani, S., and Hilda, A. (1987). Plate assay to screen fungi for proteolytic activity. *Current Science Bangalore*. 56, 1179-1181.
- Rajeswari, V. D., Jayaraman, G., and Sridharan, T. (2012). Purification and characterization of extracellular protease from halotolerant bacterium *Virgibacillus dokdonensis* VITP14. *Asian Journal of Biochemistry*. 7, 123-132.
- Raju, N. B. (2002). Meiosis and ascospore development in nonlinear asci of Neurospora pannonica. *Mycologia*. 94, 99-104.
- Rao, M. B., Tanksale, A. M., Ghatge, M. S., and Deshpande, V. V. (1998). Molecular and biotechnological aspects of microbial proteases. *Microbiology and Molecular Biology Reviews*. 62, 597-635.
- Raval, V. H., Pillai, S., Rawal, C. M., and Singh, S. P. (2014). Biochemical and structural characterization of a detergent-stable serine alkaline protease from seawater haloalkaliphilic bacteria. *Process Biochemistry*. 49, 955-962.
- Rawlings, N. D. (1995). Evolutionary families of metallopeptidases. *Methods Enzymology*. 248, 183-228.

- Rees, D., Lewis, M., and Lipscomb, W. (1983). Refined crystal structure of carboxypeptidase A at 1.54 Å resolution. *Journal of Molecular Biology*. 168, 367-387.
- Roeßler, M., and Müller, V. (1998). Quantitative and physiological analyses of chloride dependence of growth of *Halobacillus halophilus*. Applied and Environmental Microbiology. 64, 3813-3817.
- Rohban, R., Amoozegar, M. A., and Ventosa, A. (2009). Screening and isolation of halophilic bacteria producing extracellular hydrolyses from Howz Soltan Lake, Iran. *Journal of Industrial Microbiology and Biotechnology*. 36, 333-340.
- Rothschild, L. J., and Mancinelli, R. L. (2001). Life in extreme environments. *Nature*. 409, 1092-1101.
- Rudner, D. Z., Fawcett, P., and Losick, R. (1999). A family of membrane-embedded metalloproteases involved in regulated proteolysis of membrane-associated transcription factors. *Proceedings of the National Academy of Sciences*. 96, 14765-14770.
- Saitou, N., and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution*. 4, 406-425.
- Sáiz-Jiménez, C., and Laiz, L. (2000). Occurrence of halotolerant/halophilic bacterial communities in deteriorated monuments. *International Biodeterioration & Biodegradation*. 46, 319-326.
- Sarkar, P., Hasenack, B., and Nout, M. (2002). Diversity and functionality of *Bacillus* and related genera isolated from spontaneously fermented soybeans (Indian Kinema) and locust beans (African Soumbala). *International Journal of Food Microbiology*. 77, 175-186.
- Sathishkumar, R., Ananthan, G., and Raghunathan, C. (2015). Production and characterization of haloalkaline protease from ascidian-associated *Virgibacillus halodenitrificans* RSK CAS1 using marine wastes. *Annals of Microbiology*. 65, 1481-1493.
- Saum, S. H., and Müller, V. (2008). Regulation of osmoadaptation in the moderate halophile *Halobacillus halophilus*: chloride, glutamate and switching osmolyte strategies. *Saline Systems*. 4, 1.

- Saum, S. H., Pfeiffer, F., Palm, P., Rampp, M., Schuster, S. C., Müller, V., and Oesterhelt, D. (2013). Chloride and organic osmolytes: a hybrid strategy to cope with elevated salinities by the moderately halophilic, chloride-dependent bacterium *Halobacillus halophilus*. *Environmental Microbiology*. 15, 1619-1633.
- Schechter, I., and Berger, A. (1967). On the size of the active site in proteases. I. Papain. Biochemical and Biophysical Research Communications. 27, 157-162.
- Scott, A. B. (1980). Botulinum toxin injection into extraocular muscles as an alternative to strabismus surgery. *Journal of Pediatric Ophthalmology and Strabismus*. 17, 21-25.
- Secades, P., and Guijarro, J. (1999). Purification and characterization of an extracellular protease from the fish pathogen *Yersinia ruckeri* and effect of culture conditions on production. *Applied and Environmental Microbiology*. 65, 3969-3975.
- Secor, E. R., Carson, W. F., Cloutier, M. M., Guernsey, L. A., Schramm, C. M., Wu, C. A., and Thrall, R. S. (2005). Bromelain exerts anti-inflammatory effects in an ovalbumin-induced murine model of allergic airway disease. *Cellular Immunology*. 237, 68-75.
- Setyorini, E., Takenaka, S., Murakami, S., and Aoki, K. (2006). Purification and characterization of two novel halotolerant extracellular proteases from *Bacillus subtilis* strain FP-133. *Bioscience, Biotechnology, and Biochemistry*. 70, 433-440.
- Shivanand, P., and Mugeraya, G. (2011). Halophilic bacteria and their compatible solutes-osmoregulation and potential applications. *Current Science(Bangalore)*. 100, 1516-1521.
- Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., and Söding, J. (2011). Fast, scalable generation of high-quality protein multiple sequence alignments using Clustal Omega. *Molecular Systems Biology*. 7, 539.
- Siezen, R. J., de Vos, W. M., Leunissen, J. A., and Dijkstra, B. W. (1991). Homology modelling and protein engineering strategy of subtilases, the family of subtilisin-like serine proteinases. *Protein Engineering*. 4, 719-737.

- Siglioccolo, A., Paiardini, A., Piscitelli, M., and Pascarella, S. (2011). Structural adaptation of extreme halophilic proteins through decrease of conserved hydrophobic contact surface. *BMC Structural Biology*. 11, 1.
- Sinha, R., and Khare, S. (2012). Isolation of a halophilic Virgibacillus sp. EMB 13: Characterization of its protease for detergent application. Indian Journal of Biotechnology. 11, 416-426.
- Sinsuwan, S., Rodtong, S., and Yongsawatdigul, J. (2007). NaCl-Activated Extracellular Proteinase from *Virgibacillus* sp. SK37 Isolated from Fish Sauce Fermentation. *Journal of Food Science*. 72, C264-C269.
- Sinsuwan, S., Rodtong, S., and Yongsawatdigul, J. (2008). Production and characterization of NaCl-activated proteinases from *Virgibacillus* sp. SK33 isolated from fish sauce fermentation. *Process Biochemistry*. 43, 185-192.
- Sinsuwan, S., Rodtong, S., and Yongsawatdigul, J. (2009). Purification and characterization of a salt-activated and organic solvent-stable heterotrimer proteinase from *Virgibacillus* sp. SK33 isolated from Thai fish sauce. *Journal* of Agricultural and Food Chemistry. 58, 248-256.
- Sivaprakasam, S., Dhandapani, B., and Mahadevan, S. (2011). Optimization studies on production of a salt-tolerant protease from *Pseudomonas aeruginosa* strain BC1 and its application on tannery saline wastewater treatment. *Brazilian Journal of Microbiology*. 42, 1506-1515.
- Sogin, M. L., Morrison, H. G., Huber, J. A., Welch, D. M., Huse, S. M., Neal, P. R., Arrieta, J. M., and Herndl, G. J. (2006). Microbial diversity in the deep sea and the underexplored "rare biosphere". *Proceedings of the National Academy of Sciences*. 103, 12115-12120.
- Sousa, M., Ardö, Y., and McSweeney, P. (2001). Advances in the study of proteolysis during cheese ripening. *International Dairy Journal*. 11, 327-345.
- Spížek, J., Novotná, J., Řezanka, T., and Demain, A. L. (2010). Do we need new antibiotics? The search for new targets and new compounds. *Journal of Industrial Microbiology and Biotechnology*. 37, 1241-1248.
- Spring, S., Ludwig, W., Marquez, M., Ventosa, A., and Schleifer, K.-H. (1996). Halobacillus gen. nov., with Descriptions of Halobacillus litoralis sp. nov. and Halobacillus trueperi sp. nov., and Transfer of Sporosarcina halophila to Halobacillus halophilus comb. nov. International Journal of Systematic and Evolutionary Microbiology. 46, 492-496.

- Sumantha, A., Larroche, C., and Pandey, A. (2006). Microbiology and industrial biotechnology of food-grade proteases: a perspective. *Food Technology and Biotechnology*. 44, 211.
- Takács, B. J. (2000). Protein purification: Theoretical and methodological considerations. United States: Wiley Online Library.
- Tangrea, M. A., Bryan, P. N., Sari, N., and Orban, J. (2002). Solution structure of the pro-hormone convertase 1 pro-domain from Mus musculus. *Journal of Molecular Biology*. 320, 801-812.
- Tavano, O. L. (2013). Protein hydrolysis using proteases: an important tool for food biotechnology. *Journal of Molecular Catalysis B: Enzymatic*. 90, 1-11.
- Teplyakov, A. V., Kuranova, I. P., Harutyunyan, E. H., Vainshtein, B. K., Fro, C., Ho, W. E., and Wilson, K. S. (1990). Crystal structure of thermitase at 1.4 A resolution. *Journal of Molecular Biology*. 214, 261-279.
- Vandeputte-Rutten, L., and Gros, P. (2002). Novel proteases: common themes and surprising features. *Current Opinion in Structural Biology*. 12, 704-708.
- Veloorvalappil, N. J., Robinson, B. S., Selvanesan, P., Sasidharan, S., Kizhakkepawothail, N. U., Sreedharan, S., Prakasan, P., Moolakkariyil, S. J., and Sailas, B. (2013). Versatility of microbial proteases. *Advances in Enzyme Research*. 2013.
- Veltman, O. R., Vriend, G., Berendsen, H. J., Van den Burg, B., Venema, G., and Eijsink, V. G. (1998). A single calcium binding site is crucial for the calciumdependent thermal stability of thermolysin-like proteases. *Biochemistry*. 37, 5312-5319.
- Ventosa, A., de la Haba, R. R., Sánchez-Porro, C., and Papke, R. T. (2015). Microbial diversity of hypersaline environments: a metagenomic approach. *Current Opinion in Microbiology*. 25, 80-87.
- Ventosa, A., Nieto, J. J., and Oren, A. (1998). Biology of moderately halophilic aerobic bacteria. *Microbiology and Molecular Biology Reviews*. 62, 504-544.
- Venugopal, M., and Saramma, A. V. (2006). Characterization of alkaline protease from *Vibrio fluvialis* strain VM10 isolated from a mangrove sediment sample and its application as a laundry detergent additive. *Process Biochemistry*. 41, 1239-1243.

- Venugopal, M., and Saramma, A. V. (2008). An alkaline protease from *Bacillus circulans* BM15, newly isolated from a mangrove station: characterization and application in laundry detergent formulations. *Indian Journal of Microbiology*. 47, 298.
- Vermelho, A. B., Meirelles, M. N. L., Lopes, A., Petinate, S. D. G., Chaia, A. A., and Branquinha, M. H. (1996). Detection of extracellular proteases from microorganisms on agar plates. *Memórias do Instituto Oswaldo Cruz*. 91, 755-760.
- Vieille, C., and Gregory Zeikus, J. (1996). Thermozymes: Identifying molecular determinants of protein structural and functional stability. *Trends in Biotechnology*. 14, 183-190.
- Vieille, C., and Zeikus, G. J. (2001). Hyperthermophilic enzymes: sources, uses, and molecular mechanisms for thermostability. *Microbiology and Molecular Biology Reviews*. 65, 1-43.
- Vijayaraghavan, P., and Vincent, S. G. P. (2012). Cow dung as a novel, inexpensive substrate for the production of a halo-tolerant alkaline protease by *Halomonas* sp. PV1 for eco-friendly applications. *Biochemical Engineering Journal*. 69, 57-60.
- Wang, L., and Wang, Y.-J. (2004). Rice starch isolation by neutral protease and highintensity ultrasound. *Journal of Cereal Science*. 39, 291-296.
- Ward, O., Rao, M., and Kulkarni, A. (2009). Proteases production. Applied Microbiology Industrial. 495-511.
- Watson, R. R. (1976). Chapter I substrate specificities of aminopeptidases: a specific method for microbial differentiation. *Methods in Microbiology*. 9, 1-14.
- Williams, T. J., Allen, M. A., DeMaere, M. Z., Kyrpides, N. C., Tringe, S. G., Woyke, T., and Cavicchioli, R. (2014). Microbial ecology of an Antarctic hypersaline lake: genomic assessment of ecophysiology among dominant haloarchaea. *The ISME Journal*. 8, 1645-1658.
- Xiang, W., Guo, J., Feng, W., Huang, M., Chen, H., Zhao, J., Zhang, J., Yang, Z., and Sun, Q. (2008). Community of extremely halophilic bacteria in historic Dagong Brine Well in southwestern China. *World Journal of Microbiology and Biotechnology*. 24, 2297-2305.

- Yancey, P. H. (2005). Organic osmolytes as compatible, metabolic and counteracting cytoprotectants in high osmolarity and other stresses. *Journal of Experimental Biology*. 208, 2819-2830.
- Yau, S., Lauro, F. M., DeMaere, M. Z., Brown, M. V., Thomas, T., Raftery, M. J., Andrews-Pfannkoch, C., Lewis, M., Hoffman, J. M., and Gibson, J. A. (2011). Virophage control of antarctic algal host-virus dynamics. *Proceedings of the National Academy of Sciences*. 108, 6163-6168.
- Yau, S., Lauro, F. M., Williams, T. J., DeMaere, M. Z., Brown, M. V., Rich, J., Gibson, J. A., and Cavicchioli, R. (2013). Metagenomic insights into strategies of carbon conservation and unusual sulfur biogeochemistry in a hypersaline Antarctic lake. *The ISME Journal*. 7, 1944-1961.
- Yin, J., Chen, J.-C., Wu, Q., and Chen, G.-Q. (2015). Halophiles, coming stars for industrial biotechnology. *Biotechnology Advances*. 33, 1433-1442.
- Yoon, J.-H., Oh, T.-K., and Park, Y.-H. (2004). Transfer of Bacillus halodenitrificans Denariaz et al. 1989 to the genus Virgibacillus as Virgibacillus halodenitrificans comb. nov. International Journal of Systematic and Evolutionary Microbiology. 54, 2163-2167.
- Zahran, H. (1997). Diversity, adaptation and activity of the bacterial flora in saline environments. *Biology and Fertility of Soils*. 25, 211-223.
- Zuckerkandl, E., and Pauling, L. (1965). Evolutionary divergence and convergence in proteins. *Evolving Genes and Proteins*. 97, 97-166.