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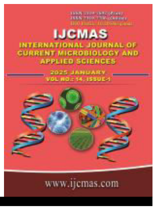

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Overview of Hot Water Springs and its Application

Patel Disha[1, 2]*, Dave Shailesh[2], Antony Suresh[1, 3], Braganza Vincent[2] and Modi Hasmukh[1]

[1]*Department of Lifesciences, Gujarat University, Ahmedabad, India*
[2]*Xavier Research Foundation, Loyola Centre for Research & Development, Ahmedabad, India*
[3]*St. Xavier`s College, Ahmedabad, India*

**Corresponding author*

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ABSTRACT

This review starts with a basic introduction of geothermal springs definations, classifications and its therapeutic values (Erfurt-Copper and Copper *et al.,* 2009; Eyton`s Earth *et al.,* 2010; Erfurt *et al.,* 2011). Also include Global scenario of hot springs location of India as well as worldwide and its significances. Furthermore, it focuses on microorganisms' growth insight extreme environment and they are capable to produce various potential industrial compounds as such enzymes, antibiotics, hormones etc. and its having attraction in present scenario (Sing *et al.,* 2006; Nayak *et al.,* 2013). This chapter describes combination methods like basic conventional methods, advance molecular based techniques and also next generation sequencing. Lastly, this chapter discusses thermophilic microbial diversity of hot water springs in Gujarat, India and also other countries and its role as a various application in different area.

Introduction

Hot Springs

A hot spring is a spring of geothermally heated ground water, rising up through the vents in the Earth`s Crust. Geothermal springs are a natural source of underground heated water under pressure near the vicinity of active volcanic environments (Simoneit *et al.,* 2000; Allaby and Allaby 2003).

The hot spring waters contain huge amount of minerals (Fe, Mn etc.) and also have traces of gases (CO_2, H_2, H_2S, CO) (Olive, 1990; Cown, 1992; Lengeler *et al.,* 1999; Resysenbach and Candy, 2001). The formation of hot water springs is shown in Figure 1.

Groundwater percolates through porous rock into fractures deep underground, where heat from a nearby magma chamber superheats the pressurized water to a temperature above the boiling point of water at surface pressure. In hot springs the rising superheated water is cooled below the boiling point by groundwater before reaching the surface. In geysers the superheated water collects in underground pockets. When the supply of steam and hot water is exhausted, the spouting stops and the cycles begin again. [Encyclopaedia Britannica Online.

http://global.britannica.com/EBchecked/media/91382/Cross-section-of-a-geyser-and-hot-spring-Groundwater-percolates. (Calderon, 2014)].

Geothermal springs have been defined and classified in various categories as shown in Table 1.

Traditionally, according to Indian mythology and Hindu beliefs hot springs have religious significance. Different types of minerals found in hot springs have different types of health benefits as shown in Table 2. Hot springs containing rich source of sulphur improve skin infections, skin inflammations and also respiratory problems (Eyton`s Earth, 2010; Erfurt, 2011). According to the World Health Organization (WHO), thermal spring waters are believed to positively impact different kinds of disease and conditions of fatigue such as joint, kidney, and respiratory problems, however, such health alleviations need to be confirmed by further scientific studies. Some other common benefits attributed to soaking in hot springs include strengthening the immune system, improving skin conditions, enhancing blood circulation, promoting detoxification, and relaxing mind and body. In pursuit of these health benefits, all types of people visit hot springs to not only deal with health problems, but also as a preventative measure in maintaining good health and vitality (Erfurt, 2011).

Hot springs are located in many countries in the world, as indicated in the map (Figure: 2). Each hot spring has its own biological and geophysical characteristics, thus endowing them with fascinating potential applications for research, from the point of view of biotechnological and ecological subject areas (Brock, 1997; Tirawongsaroj *et al.,* 2008; Lau *et al.,* 2009; Klatt *et al.,* 2011; Briggs *et al.,* 2014; Prieto-Barajas *et al.,* 2017). Microbial communities can be found from the hot water spring based on temperature of the channel of the hot springs (Lengeler *et al.,* 1999).

There are many hot water springs located in India as well as in other countries. Several significance studies have been reported on hot water springs all over the world. They have been described in Table: 3, 4 and 5.

Thermal environment and thermophilic bacteria

Earlier discovery made by Thomas D Brock in 1965 isolated *Thermus aquaticus* from hot water spring which are capable of producing thermostable Taq DNA polymerase (Brock and Freeze, 1969). The extremophiles discovered during the earlier studies aroused an interest and also gave a challenging platform for the researchers. The extremophiles mainly include: halophiles, thermophiles, barophiles, pscryophiles and acidophiles. Microorganisms growing under the extreme conditions, produce valuable industrial compounds like enzymes, antibiotics, hormones etc. which have gained attention in the present scenario (Herbert and Sharp, 1992; Austin, 1998; Sing, 2006; Nayak, 2013). The largest popular thermal biotopes are hydrothermal systems that include volcanic and geothermal i.e. volcanic area which gives sulphurous gases and steam, the natural geothermal springs and the submarine hydrothermal vents. The hot solfataric fields are made up of two layers, upper layer and the lower layer. Upper layer is having vital amount of oxygen; it imitates an ochre colour due to the presence of the ferric ions; whereas the layer below displays a blackish-blue colour because of ferrous ions. Similarly, the submarine thermal systems consist of the hot springs, hot vents and sediments with very high temperatures (Stetter, 1998). The submarine hydrothermal vent system has high NaCl concentration and pH range between 5 to 8, exhibiting an acidic to alkaline pH (Horikoshi, 1998; Kikani, 2013).

Thermophiles are a type of extremophile which love extreme environments. Thermophilic bacteria survive at a higher temperature range and these microbes mostly have habitats in hot spring's environment. Most of the studies have been reported on thermophiles, found from diverse environmental habitat sources such as hot water springs and geothermal location (Panda *et al.,* 2013). Sub-category of thermophiles is divided based on their thermotolerance temperature: Facultative thermophiles can grow at 37˚ C and 50˚ C - 65˚ C, Obligate thermophiles have 65˚ C - 70˚ C temperature showing maximum growth and they don't grow below 50˚ C, extreme thermophiles grow at 40˚ C - 70˚ C with an optimal growth at about 65 ˚C temperature and Hyperthermophiles can grow over 90˚ C with an optimal temperature ranging between 80˚ C -115˚ C (Nayak, 2013). Thermophilic microorganisms can not only survive at a higher temperature but their growth rate and metabolic activities are also responsive at higher temperature (Tsuei – Yun Fang *et al.,* 2005).

Thermophiles microorganisms are prokaryotes (include aechea and bacteria) and eukaryotes, their protein, nucleic acid, cytoplasmic membranes allow them to grow in temperatures beyond 45˚ C. At a lower temperature thermophile's cellular components do not perform their activity properly. On the other side, hyperthermophiles require over 80˚ C temperature for their optimal growth (Bauman, 2004). Thermophiles can survive in diverse habitats of high temperature, pH, salinity and extreme pressure (barophiles) (Kato, 2004). They were found to survive at 72˚ C (Kim *et al.,* 2001; Devi, 2015).

Thermophilic bacterial diversity provides their potential applications, which can be utilized for various purposes like, basic research knowledge and various biotechnological applications. Also study of thermophilic bacteria led to discovery of novel species (Huber *et al.,* 1991; Kozina *et al.,* 2010; Zhang *et al.,* 2010; Yohandini *et al.,* 2015). Due to their capability of the thermostability at a higher temperature thermophilic bacteria and their products have several potential applications in industries and also in biotechnological research processes, e.g. some enzymes (cellulases, amaylases, proteases, pectinases, xylanases, lipases, esterases, catalases, gelatinases, keratinases, ureases, peroxidases, phytases, glucosidase and alcohol dehydrogenases etc.), proteins and bioactive compounds (Rekadwad, 2015; Rekadwad and Pathak, 2016).

Culture-dependent and Culture-independent diversity

Bacterial classification within family, genus and species level depend on a broad range of phenotypic characterization (colony morphologies, Gram staining, endospore staining etc.). It gives details of the morphology of bacteria, conditions of the culture, appearance of the colony and their biochemical characterization (nutrient requirements - sugars, enzymatic activities, and /or metabolic activities) (Holt *et al.,* 1994).

Every new microbe requires biochemical analysis for its identification and metabolic activity. In India most of the laboratories depend on conventional methods for identification to find out the diversity of bacteria. During the 20th and 21st centuries, techniques for bacterial identification have undergone rapid growth. At the beginning, mostly conventional or phenotypic techniques were used (Petti *et al.,* 2005; Bailon-Salas *et al.,* 2017). Conventional method is used for bacterial classification and characterization based on their morphological, physiological and biochemical activities (Scow *et al.,* 2001). Based on the conventional methods, bacteria can be grouped into a number of natural assemblages depending on their characterization like shape, spore forming / non-spore forming, aerobic / anaerobic, Gram-positive / Gram-negative (Sigee, 2005). Classical methods like morphological and biochemical are used for identification and characterization of bacteria. It also includes isolation, laboratory culture and taxonomic characterization of individual (separate) bacterial species in environmental samples (Krishna, 2013).

Many microbial diversity studies have been done through culture-dependent and culture-independent approaches but researchers believe that traditional method approach, have many limitations in discovering a broad microbial diversity in the natural habitats. However, bacterial pure cultures are needed for their identification and characterization in understanding their physiology and at their genetical level (Ward *et al.,* 1998; Yohandini *et al.,* 2015).

In conventional methods, bacterial characterization is not steady, as it may be changed during stress conditions or evolution (Ocham *et al.,* 2005; Krishna, 2013). According to Verma *et al.,* in 2007, conventional techniques give information of only shape, size, colour, motility, staining properties, host-range, pathogenicity and assimilation of carbon sources and also these techniques do not provide a complete taxonomy of the microbes (Verma *et al.,* 2007). On the other hand, information on a successful concept of a microbial lineage (origin) is necessary to follow the complete approach. In the last few decades' appreciable development in the study of microbial taxonomy has taken place such as chemotaxonomy (Minnikin *et al.,* 1975), numerical taxonomy and DNA-DNA hybridization (Johnson, 1991), DNA amplification and sequencing (Konstantinidis and Tiedje, 2007) and whole genome sequencing (Janssen *et al.,* 2003; Das *et al.,* 2014). Thus, the use of a polyphasic approach, including a combined conventional and molecular based techniques is required to get a better knowledge of the bacterial diversity (Das *et al.,* 2014). Rastogi and Sani in 2011, mentioned that culture dependent traditional method can be allotted to only specific genera. Also, classical techniques take too much time for processing as well as depend upon the environmental conditions (Rastogi and Sani, 2011). Comparatively, the molecular based techniques are very fast, accurate with minor chances of error. The development of these advanced techniques has changed drastically, the definition of microorganisms as in many cases, sequence diversity within a species reveals multiple sequence clusters that are ecologically distinct (Cohan, 2002; Das *et al.,* 2014). 16S rRNA gene techniques give information of phylogenetic information to identify culturable isolates at a genus level.

On the earth most of the microbial species are unculturable, means they are not capable to grow under the laboratory conditions (Lewis *et al.,* 2010). There is major limitation of utilization approach of culturable media. Based on the microscopic observation, in environment more than 99% microorganisms are not cultivable in the laboratory condition (Hugenholtz, 2002). It was mentioned by Rondon in 1999 that only 1% of the obtained cells can be studied in the microbial cultures as the probability of unculturable cells to be grown in culture under various conditions is limited. Many researchers goal has been focused on different advanced molecular techniques for the better understanding of the unculturable microorganisms (Rondon *et al.,* 1999; Bailon-Salas *et al.,* 2017). The 16S rRNA gene sequencing molecular-based techniques have been very fruitful for the phylogenetic relationship between various types of microorganism from different ecosystems (Cai *et al.,* 2003; Clarridge, 2004; Mignard *et al.,* 2006; Nayak, 2013). Advance molecular-based techniques and bioinformatics implementations have provided significantly unexplored microbial diversity. However, conventional and molecular-based methods have their own values and limitations. So, the concept of the combination of traditional and advance molecular techniques is the best way to find out the whole microbial diversity from the nature (Kikani, 2013).

Metagenomics Study

Earlier reports on Yellowstone National Park hot spring were characterized by 5S rRNA sequencing from the mixed microbial flora and they found archaebacterial and eubacterial species related to *Thermus species* population (Stahl *et al.,* 1985).

“Metagenomics” term was first time used by Jo Handelsman in 1998. The metagenomics study involves collection of genetic material directly from the environmental samples (Handelsman *et al.,* 1998). Metagenomic approach helps to find out culturable and unculturable microbes from the mixed microbial communities of environmental samples. Metagenomic study has given great knowledge and better understanding about evolution, lifestyle and diversity of the microorganisms from the hidden world of the microbes (Qin *et al.,* 2010; Hess *et al.,* 2011; Pignatelli and Moya, 2011; Mishra and Khanolkar, 2017). Metagenomic study provides opportunity for yet to be cultivated 99% microbial diversity and their genetic material but still researcher’s final goal remains on microbial cultivation. The information given by metagenomics is used to flourish techniques of cultivation to isolate novel microorganisms and their products (Rondon *et al.,* 2000; Jiang *et al.,* 2011; Cai *et al.,* 2013; Gong *et al.,* 2013; Tan *et al.,* 2014; Grewal, 2014). The metagenomics process approach from the environmental samples has been shown in Figure 3.

Most of the microbial diversity are non-cultivable and it is very difficult to maintain bacterial pure culture in the laboratory condition, may be nutritional requirement and physical conditions like temperature, pH is responsible. During the process of culture-dependent method, sometimes it benefits to find microbial species, while on the other hand some microbes may be eliminated. Therefore, metagenomics (next generation sequencing) has in a way bypassed the bias of cultivation of the microbial strains by the enrichment techniques (Kikani, 2013). In Tanjung Sakti hot spring (South Sumatera), Indonesia, organisms have been cultivated and thermophilic bacteria have been identified through 16S rRNA sequencing and four distinct taxonomic groups: *Anoxybacillus*, *Geobacillus*, *Brevibacillus*, and *Bacillus* were found (Yohandini *et al.,* 2015).

Culture-independent metagenomics studies were done in Ganeshpuri (Nimbavali) hot spring, Mumbai region, Maharashtra, India. Proteobacteria, Firmicutes and Bacteriodetes were observed at a phylum level (Mishra and Khanolkar, 2017).

In the Tulsi Shyam hot spring, Gir Forest, Gujarat, India, thermophilic bacteria were isolated, identified, characterized and diversified using conventional method and Amplified Ribosomal DNA Restriction Analysis (ARDRA) approach. Based on conventional method, Gram-positive, rod shaped and catalase positive bacteria were obtained. Also molecular identification represented 3 Genera: *Anoxybacillus*, *Geobacillus/Aeribacillus* and *Bacillus* (Kikani *et al.,* 2015). Kikani in 2013 reported, culture-dependent seasonal diversity in Tulsi Shyam hot springs of Gujarat. A total of 64 bacterial strains were reported from water and soil samples. All the bacterial isolates exhibited Gram-positive features and were aerobic in nature. Catalase production was indicated positive in all of the isolates, whereas some of the isolates observed were oxidase positive. On the other hand, *Bacillus* and *Geobacillus* have been reported from

ARDRA profiles (Kikani, 2013). In Atri, Tarabalo and Taptapani hot springs of Odisha, Gram positive and rod shaped bacteria were observed with the help of traditional method and based on the molecular identification *Anoxybacillus*, *Geobacillus* and *Bacillus* species were observed (Nayak, 2013).

Actinomycetes/thermoactinomycetes were isolated and identified through biochemical tests and molecular method from Tulsi Shyam, Lasundra and TuvaTimba hot springs of Gujarat. All the isolates observed were Gram-positive and had large variation in Sugar profile (Shukla, 2015). Culture-independent study was done in Tulsi Shyam hot springs. In this metagenomic study (bacterial tag-encoded FLX amplicon pyrosequencing) most of the phyla indicated were Firmicutes, Proteobacteria and unclassified bacteria. Highest reported families were *Peptostreptococcaceae*, *Clostridiaceae* and *Enterobacteriaceae*. *Clostridium bifermentans*, *Clostridium lituseburense* and uncultured ubiquitous bacterial species were obtained (Ghelani *et al.,* 2015). Aerobic thermophilic *Bacillus* genus was isolated using culturable method and also antimicrobial study has been done from Ma'en hot springs in Jordan (Fandi *et al.,* 2014). Sahay *et al.,* in 2017 reported 14 different types of genera *Anoxybacillus*, *Bacillus,* *Brevibacillus*, *Brevundimonas*, *Burkholderia*, *Geobacillus*, *Paenibacillus*, *Planococcus*, *Pseudomonas*, *Rhodanobacter*, *Thermoactinomyces*, *Thermobacillus*, *Thermonema* and *Thiobacillus*, which were found using 16S rRNA sequencing molecular-based method from Manikaran and Yumthang hot springs of Indian Himalayas (Sahay *et al.,* 2017). *Thermodesulfobacterium* (Thermophilic sulphate reducing prokaryote) were identified with both manual biochemical method and 16S rRNA sequencing molecular-based method from Vajreshwari and Ganeshpuri hot springs, Thane, Maharashtra (Patil *et al.,* 2014a).

Identification of thermophilic bacterial study was carried out based on cultural method from Ulu Legong hot spring in Kedah, Malaysia (Akmar *et al.,* 2011). Khalil *et al.,* in 2018 reported *Brevibacillus brostelensis* thermophilic strain which grew between 45° C and 70 ° C temperature by extended genomic analysis as well as biochemical based method (phenotypic characterization) from "Al-Ain Alhara" hot spring, located in the southeast of Gazan city in Saudi Arabia (Khalil *et al.,* 2018). *Tepidimonas taiwanensis* novel bacterial strain was isolated on the basis of phylogenetic analysis of 16S rDNA sequences, DNA-DNA similarity data, whole cell protein analysis, fatty acid compositions as well as physiological and biochemical characterization from Sih-Chong-Si hot spring located in Pingtung county in southern Taiwan (Chen *et al.,* 2006). In Unkeshwar hot spring, Maharashtra, India, a total of 17 species were isolated based on morphological, biochemical and molecular analysis. These isolated strains belonged to Firmicute, Proteobacteria and Actinobacteria (Rekadwad and Pathak, 2016). Prieto-barajas *et al.,* in 2017 explored the culturable seasonal microbial diversity and physicochemical study on Tina and Bonita hot springs (Araro, Mexico). Total seventy-nine phylotypes were found using 16S rRNA sequences and they belong to Firmicutes, Proteobacteria and Actinobacteria phyla (Prieto-Barajas *et al.,* 2017).

In Manikaran hot spring, the bacterial diversity was investigated using culture-dependent method and it is predicted that it may be a maximum 0.1% of the total bacterial community (Ranjard *et al.,* 2000). In another study, foremost *Brevibacillus thermoruber*, *Paenibacillus sp*., *Bacillus licheniformis*, *Bacillus pumilus*, *Bacillus subtilis*, *Pseudomonas psychrophila*, *Exiguobacterium acetylicum*, *Rhodococcus baikunurensis*, *Pseudomonas fluorescens*, *Bacillus megaterium* and *Staphylococcus succinus* thermophilic and thermotolerant bacteria were isolated and identified from Manikaram hot spring (Verma *et al.,* 2014; Kumar *et al.,* 2014a; Devi, 2015).

Podar and Resysenbach in 2006, discovered Taq polymerase (thermotolerant DNA polymerase) from the *Thermus aquaticus*, thermophilic bacteria in Yellowstone hot springs in the United State of America that is patented and thus Polymerase Chain Reaction gained its application throughout the world. These lead researchers to study on biodiversity of hot springs (Podar and Reysenbach, 2006).

Several studies on bacterial biodiversity have been conducted using culture-dependent as well as culture-independent techniques from Indonesian hot springs and Indonesian acidic hot spring, Kawah Hujan B, at Kamojang geothermal field, West Java hot spring (Baker *et al.,* 2001; Aminin *et al.,* 2008; Adiawati *et al.,* 2009).

From their findings most of the clones are associated to Crenarcheota and Proteobacteria from culture-independent study. On the other hand, those findings which were from culture-dependent analysis observed the influence of Firmicutes and gamma Proteobacteria Phylum.

Table.1 Geothermal spring's definition and general classification

Classification Category	Definition
Geothermal Spring	It includes hot springs and extreme hot springs, naturally heated while passing through underground voids and pore spaces.
Natural Hot Spring	It is a generic term for geothermal springs generally identified as, at least at body temperature and pleasant bathing temperature, mainly used for medicinal purposes and bathing.
Thermal Spring	It includes warm and hot springs generally above 25˚ C temperature, used for medicinal purposes and bathing.
Mineral Spring	It can be a cold, warm, hot, extremely hot or artificially heated spring, used for medicinal purposes and bathing.
Thermo Mineral Spring	It is a geothermal mineral spring water and artesian water used for medicinal purposes and bathing.
Artesian Spring	It is naturally discharging from subsurface with warm to hot water at 25˚ C to 100˚ C, used for medicinal purposes.
Saline Spring	It varies in temperatures, has a very high amount of mineral salt content, possible sea water used for medicinal purposes and bathing.
Geyser	It is an extremely hot spring, water reaches boiling point and above, a visual tourist attraction in geo tourism.
Submarine Hot Spring	Submarine vents known as black smokers emitting extreme hot water enriched with mineral and metallic trace elements.

Source: (Erfurt-Cooper and Cooper, 2009; Erfurt, 2011).

Table.2 The therapeutic values of the mineral content of hot springs

Minerals in hot springs	Their therapeutic values
Arsenic	Limited amounts can assist the body with plasma and tissue growth. Foot bathing in mineral water with high content of arsenic, address fungal conditions of the feet.
Bicarbonate	Bicarbonate in hot springs can treat hypertension and mild atherosclerosis.
Boron	Boron is beneficial in building muscle mass, increasing brain activity and bones strengthening.
Chloride	It is beneficial for arthritis, rheumatic conditions, central nervous system conditions, posttraumatic and postoperative disorders, as well as orthopaedic and gynaecological disease.
Magnesium	Magnesium can convert blood sugar to energy and it also promotes healthy skin.
Potassium	It serves in the normalization of heart rhythms, assists in reducing high blood pressure, it also helps to eliminate body toxins and promotes healthy skin.
Sodium	Sodium and natural salts help in arthritic symptoms and it can stimulate the body`s lymphatic system when bathed in hot springs.
Sulphur and Sulphates	Sulphur is a rich in Hot Springs. It treats skin infections, respiratory problem and skin inflammations.

Source: (Eyton's Earth, 2010; Erfurt, 2011).

Table.3 List of Indian hot springs

Hot springs	States
TuvaTimba, Tulshishyam, Unai, Lasundara, Dholera	Gujarat
Vajreshwari, Ganeshpuri, Akloli, Aravali	Maharastra
Tatapani, Dhuni Pani, Chavalpani, Anhoni, Babeha	Madhya Pradesh
Ushnagudam, Rudrakund	Andhra Pradesh
Mannargudi	Tamil Nadu
Bendrutheertha, Bandaru, Irde	Karnataka
Tattapani, Tatwani, Manikaran, Khirganga, Vashisth, Jeori, Kasol, Kalath	Himachal Pradesh
Suryakund, Gaurikund, Taptkund, Rishikund	Uttarakhand
Yumthang, Borang, Phurchachu (Reshi), Ralang, Yumey Samdong, Taram – chu	Sikkim
Rameshkund, Lakshmikund, Tatal Pani, Janamkund, Shringshrishi, Rajgir, Sitakund, Bhaduri Bhur	Bihar
Atri, Taptapani, Tarabalo, Deulajhari	Orissa
Tantloi, Tantni, Bakreshwar of Birbhum, Kendughata, Bholeghata	West Bengal
Hot spring of Dirang area	Arunachal Pradesh
Tatta, Ram Kund, Brahma Kund, Jaron	Jharkhand
Chumathang, Panamik	Ladakh, Jammu and Kashmir
Jakrem	Meghalaya

Table.4 Location of hot springs in India and their significance

No.	Hot springs	Location	Significance
1	TuvaTimba	Gujarat	Isolated biosurfactant producing bacteria **(Joshi *et al.*, 2013)**. Thermophilic thermotolerant actinomycetes isolated for diversity phylogeny and biocatalytical potential **(Shukla, 2015)**. Reported metagenomics study using shotgun sequencing approach **(Mangrola *et al.*, 2015a)**. Seasonal thermophilic microbial diversity has been studied **(Patel *et al.*, 2019a)**.
2	Dholera	Gujarat	Isolation, screening and characterization of alkaline protease producing microorganisms **(Chudasama, 2012)**. Geothermal exploration case study was carried out **(Sircar *et al.*, 2015)**. Culturable thermophilic microbial diversity found out **(Patel *et al.*, 2019b)**.
3	Tulsi Shyam	Gujarat	*Bacillus amyloliquifaciens* strain was isolated and characterized and purified of a thermostable and calcium independent α amylase from this strain **(Kikani and Singh, 2011)**. Studies have been focused on molecular based diversity and bioctalytic perspectives of thermophilic and thermotolerent bacteria **(Kikani, 2013)**. Thermophilic thermotolerant actinomycetes isolated for diversity phylogeny and biocatalytical potential **(Shukla, 2015)**. Culture dependent diversity has been studied **(Kikani *et al.*, 2015)**. Amplicon pyrosequencing based metagenomics study was done **(Ghelani *et al.*, 2015)**. Studied alkaline protease producing thermotolerant alkaliphilic isolates **(Patel *et al.*, 2006)**.
4	Lasundra	Gujarat	Isolated biosurfactant producing bacteria **(Joshi *et al.*, 2013)**.

			Produced , purified and immobilized extracellular lipases Xrf11 strain and *Bacillus licheniformis* Xrf12 strain used for production of alkyl esters **(Gohel *et al.*, 2013)**. First study reported on metagenomics using Ion Torrent PGM platform **(Mangrola *et al.*, 2015b)**. Thermophilic thermotolerant actinomycetes isolated for diversity phylogeny and biocatalytical potential **(Shukla, 2015)**.
5	Unai	Gujarat	*Bacillus licheniformis*, thermophilic bacteria was isolated and characterized and its applications on thermostable and solevent-tolerant serine protease **(Dudhagara *et al.*, 2014)**. *Bacillus cohini*, thermophilic alkaline protease producing strain was isolated **(Dudhgara *et al.*, 2015)**. Ion Torrent based metagenomics approach was used to find out microbial diversity **(Mangrola *et al.*, 2018)**.
6	Ganeshpuri	Maharastra	Isolated and characterized *Thermodesulfobacterium* and its application in bioremediation process (Sulphate reduction) **(Patil *et al.*, 2014a)**. Isolated thermophilic bacillus species with extracellular enzymatic activities and that can be exploited for biotechnological purpose **(Lele and Deshmukh, 2016)**. Microbial diversity identified through metagenomics **(Mishra and Khanolkar, 2017)**. Isolated and purified bacteria from hot spring's soil samples **(Pednekar *et al.*, 2011).**
7	Unkeshwar	Maharastra	Physicochemical and microbial studies have been done **(Bhusare and Wakte, 2011)**. Studied water quality using Physical, chemical, ionic, biological parameter **(Yannawar *et al.*, 2013)**. Investigated microbial diversity based on metagenome sequencing **(Mehetre *et al.*, 2016)**.
8	Akoli	Maharastra	Thermophilic *Actinomycetes* isolated that are capable of producing industrial enzymes (**Chaudhary and Prabhu, 2016**).
9	Vajreshwari	Maharastra	Isolated biosurfactant producing bacteria **(Joshi *et al.*, 2013)**. Isolated and characterized *Thermodesulfobacterium* and its application in bioremediation process (Sulphate reduction) **(Patil *et al.*, 2014a)**. Thermophilic *Actinomycetes* isolated that are capable of producing industrial enzymes **(Chaudhary and Prabhu, 2016)**.
10	Tarabalo	Odisha	Isolated thermophilic bacteria and it was active for amaylase enzyme **(Khuntia *et al.*, 2010)**. Found true thermophiles and could be a source of thermostable protease enzymes, which can be used for pharmaceuticals and industrial applications **(Panda *et al.*, 2013)**. lated thermophilic microorganisms with the help of conventional and molecular based method. Determined heavy metal removal and amylase activity **(Nayak, 2013)**.
11	Taptapani	Odisha	Lipolytic thermophilic organisms were characterized **(Panda, 2011)**. Isolated thermophilic microorganisms with the help of conventional and molecular based methods. Determined heavy metal removal and amylase activity **(Nayak, 2013)**.
12	Atri	Odisha	Isolated thermophilic microorganisms with the help of conventional and molecular based methods. Determined heavy metal removal and amylase activity **(Nayak, 2013)**. They have studied a natural ecosystem for global warming research **(Mohanty, 2014).**
13	Vashist	Himachal Pradesh	Culturable microbial diversity of thermophilic bacteria was found to explore their potential industrial applications **(Sharma *et al.*, 2013)**.

			Evaluated thermotolerant bacteria using culturable method **(Kumar *et al.,* 2014b)**. Pigment producing bacteria were focused for their industrial applications **(Meenakshi, 2015)**. Isolated and characterized thermophilic bacteria **(Shirkot and Verma, 2015).**
14	Tattapani	Himachal Pradesh	Xylanase producing thermophilic bacteria isolated and characterized **(Chauhan, 2010).** Culturable microbial diversity of thermophilic bacteria found to explore their potential industrial applications **(Sharma *et al.,* 2013).** Pigment producing bacteria were focused for their industrial applications **(Meenakshi, 2015).** Microbial diversity using metagenomic approach **(Mahajan *et al.,* 2016).**
15	Manikaram	Himachal Pradesh	Xylanase producing thermophilic bacteria isolated and characterized **(Chauhan, 2010).** Culturable microbial diversity of thermophilic bacteria found to explore their potential industrial applications **(Sharma *et al.,* 2013).** Pigment producing bacteria were focused for their industrial applications **(Meenakshi, 2015).** Isolated and characterized thermophilic bacteria **(Shirkot and Verma, 2015).** Isolated, identified and characterized aerobic thermophiles to find out important thermostable enzymes from potential isolates **(Devi, 2015).**
16	Khiganga	Himachal Pradesh	Isolated and characterized thermophilic bacteria **(Shirkot and Verma, 2015)** .
17	Kasol		
18	Kalath		
19	Bakreshwar	West Bengal	Culture-independent approach has been used to investigate microbial diversity **(Ghosh et al. 2003)**. Cellulase activity by isolated thermophilic bacteria **(Acharya and Chaudhary, 2011)**. Isolated, characterized and molecular identified esterase producing thermophilic bacteria, has the ability of tributyrin degradation **(Ghati *et al.,* 2013)**. Evaluated thermotolerant bacteria using culturable method **(Kumar *et al.,* 2014a)**. Novel bacterium (BKH3) has been identified from hot spring water samples consortium **(Chaudhuri *et al.,* 2016)**.
20	Metaldanga	West Bengal	Novel bacterial strain was isolated and identified. This strain has application at industrial level and synthesis of nanoparticles **(Alam *et al.,* 2016)**.
21	Yumthang	Sikkim, Himalayas	Bacterial community found using Illumina platform (metagenomics) **(Panda *et al.,* 2016)**. Illumina sequencing platforms were used for bacterial metagenomics study **(Panda *et al.,* 2017)**. Diverse thermoactive enzymes were detected to be used for potential applications **(Sahay *et al.,* 2017)**.
22	Mani-karan	Himalyas	Diverse thermoactive enzymes were detected to be used for potential applications **(Sahay *et al.,* 2017)**.
23	Anhoni	Madhya Pradesh	Microbial community found through metagenomic analysis and the presence of chemoorganotrophic thermophilic community with the

			ability to utilize complex hydrocarbons as a source of energy **(Saxena *et al.*, 2017)**.
24	Surajkund	Jharkhand	Find out amylase, xylanase and cellulose producing bacteria though the culturedependent and culture-independent techniques **(Soy *et al.*, 2023).**
	Laxmankund		
	Brahmakund		
	Ramkund		
	Sitakund		
	Mixedkund		
24	Jakrem	Meghalaya	Bacterial community found using Illumina platform (metagenomics) **(Panda *et al.*, 2016)**.
25	Tattapani	Sarguja, Chhattisgarh	Microbial community found through metagenomic analysis and the presence of chemoorganotrophic thermophilic community with the ability to utilize complex hydrocarbons as a source of energy **(Saxena *et al.*, 2017)**.

Table.5 Global hot water springs other than India and their significance.

No.	**Hot springs**	**Location**	**Significance**
1	Yellowstone	USA	Case study was done on chemical analysis of thermal water **(Morey, 1973)**. Thermophilic bacteria were characterized **(Marsh and Don, 1953)**. Advanced Spaceborne Thermal Emission and Reflection Radiometer (ASTER) and the Airborne Visible/IR Image Spectrometer (AVIRIS) data were used to characterize hot spring deposits in the Lower, Midway, and Upper Geyser Basins of Yellowstone National Park from the visible/near infrared (VNIR) to thermal infrared (TIR) wavelengths **(Hellman and Michael, 2004)**. Presented bacterial diversity analysed by metagenomics from globally distributed terrestrial hot springs **(Menzel *et al.*, 2015)**.
2	Cahuelmo	North Patagonia, Chile (South America)	Microbial diversity, microheterogeneity and biogeography found out hot spring microbial mats (**Calderon, 2014)**.
3	Procelana		
4	Procelana geyser		
5	Elegedi	East Africa	Investigated pathogenic bacteria with the help of high-throughput sequencing technologies **(Ghilamicael *et al.*, 2018)**.
6	Akwar		
7	Maiwooi		
8	Garbanabra		
9	Gelti		
10	Ain Allah	Moroccan, North Africa	Thermophilic bacteria investigated and those strains are having important enzymes protease and amylase **(Tarik *et al.*, 2015)**.
12	Abaynou		
13	Moulay Yaacoub		
14	Ain Jerri		
15	Siloam	Limpopo, South Africa	First metagenomic bacterial diversity was done using 454 pyrosequencing **(Tekere *et al.*, 2011)**.
			Study has been done in metagenomics analysis of bacterial diversity **(Tekere *et al.*, 2015)**.

16	Die Eiland	Limpopo, South Africa	Bacterial metagenomics study has been done **(Tekere *et al.*, 2015)**.
17	Souting		
18	Tshipise		
19	Mphephu		
20	Sagole		
21	Sungai Tutung	Kerinci, Jambi (Indonsia)	Different thermophilic strains were identified and all these strains produced potential alkali proteases enzyme **(Arzita *et al.*, 2017)**.
22	Tanjung Sakti	South Sumatera (Indonesia)	Isolated thermophiles and also indicated hylogenetic analysis and clustered within distance of taxonomic groups of microbes **(Yohandini *et al.*, 2015a)**.
23	Cimanggu	Indonesia	Described bacterial classification using molecular based method directly amplified from the hot springs and also consortia **(Baker *et al.*, 2001)** .
24	Cibuni		
25	Domas		
26	Levunovo	Bulgaria, Europe	Microbial diversity investigated and 16S rRNA and GH-57 two genes explored **(Stefanova *et al.*, 2015)** .
27	Vetren Dol		
28	Pozzuoli	Italy	Presented bacterial diversity analysed by metagenomics from globally distributed terrestrial hot springs **(Menzel *et al.*, 2015)**.
29	Pisciarelli		
30	Bagnaccio	Viterbo, Italy	Isolated and identified a moderately thermophilic anaerobic bacteria from mixed sediments/water samples and also got novel species *Caloramator viterbensis* **(Seyfried et al. 2002)**.
31	Antun	Taiwan	A slightly thermophilic bacterial strain, *Tepidimonas fonticaldi* species isolated and characterized using a polyphasic taxonomic approach **(Chen *et al.*, 2013)**.
32	Rahsawarin	Thailand	Described bacterial count, physico-chemical analysis, metal analysis, ions and nutrients were measured **(Sudjaroen *et al.*, 2018)**.
33	Porn-Rang		
34	El Carrizal	Veracruz, Mexico	Isolated and identified thermophilic and alkalitolerant bacterial strains and the strains have capacity to produce hydrolytic enzymes under thermophilic conditions **(Pinzón-Martínez *et al.*, 2010)**.
35	Los Banos		
36	Lake Magadi	Kenya	Studied illumina sequencing and amplicon analysis of both total community rDNA and 16S rRNA, cDNA to determine the bacterial and community structure of bacteria and archaea **(Kambura *et al.*, 2016)**.
37	Little Magadi		
38	Grensdalur	Iceland	Presented bacterial diversity analysed by metagenomics from globally distributed terrestrial hot springs **(Menzel *et al.*, 2015)**.
39	Krisuvik		
40	Tibetan Plateu	Northwest China	Representeted work on biodiversity of thermophilic bacteria **(Wang *et al.*, 2013)**.
41	Tengchong	Yunnan Province, China	Temporal variation was observed in microbial diversity **(Huang, 2014)**.

42	Eryuan	China	Microbial diversity analysed based on metagenomics approach **(Menzel *et al.,* 2015)**. Tangchi and Bantang hot spring water samples collected in Hefei, China. Illumina MiSeq system was utilized to sequence and analyze the bacterial 16S rRNA gene **(Zhang *et al.,* 2023).**
43	Benguet	Philippines	First study was carried out to characterize thermophilic bacteria based on culture-dependent method and molecular method **(Socorro *et al.,* 2015)**.
44	Tatta Pani	Azad Kashmir, Pakistan	Facultative anaerobic bacteria were isolated and identified based on molecular method **(Zahoor *et al.,* 2012)**. Isolated and identified unexplored thermophilic bacteria with the help of morphological, biochemical, physiological and molecular attributes (**Ishaq *et al.,* 2023**).
45	Uzon Caldera	Kamchatka peninsula, Russia	Isolated and characterized nitrite-oxidizing moderately thermophilic bacteria **(Lebedeva *et al.,* 2011)**. Metagenomics studies have been done and also novel genes identified which are used for lipolytic and proteolytic enzyme activity **(Wemheuer *et al.,* 2013)**. Bacterial diversity identified using metagenomic method **(Menzel *et al.,* 2015)**. Investigated Aerobic, chemolithoautotrophic, hydrogen- and sulfur-oxidizing thermoacidophilic bacteria dominated the microbial population in the hydrothermal water and are principal producers of organic matter **(Maltseva *et al.,* 2023).**
46	Mutnovsky volcano	Kamchatka peninsula (Russia)	Novel gene identified based on metagenomics analysis and used for lipolytic and proteolytic enzyme activity **(Wemheuer *et al.,* 2013)**.
47	Gorjachinsk	Buryat Republic, Russia	Isolated and characterized nitrite-oxidizing moderately thermophilic bacteria **(Lebedeva *et al.,* 2011)**.
48	Neungam carbonate	Republic of Korea	In this study, Identification was done based on the full-length 16S rRNA gene sequence **(Lee *et al.,* 2022)**.
49	Mungang sulfur		
50	Deokgu		
51	Baegam		
52	Dongnae		
53	Sungai Klah	Malaysia	Identified thermophilic diversity using shotgun metagenomics platform **(Chan *et al.,* 2015)**.
54	Arzakan	Armenia, Eurasia	Microbial diversity studied using molecular and culture-based techniques **(Panosyan and Nils-Kare, 2014)**.
55	St. Lucia	Sou-friere, Eastern Caribbean, West Indies	Founded geochemistry and microbial diversity correlations **(Stout *et al.,* 2018)**.
56	Onikobeonsen-kyo	Miyagi, Japan	Isolated highly thermostable β-xylosidases enzymes from a soil microbial community of hot spring using a metagenomic approach **(Sato *et al.,* 2017)**.
57	Pamukcu	Balikesir, Turkey	Identified and characterized thermophilic bacteria with the help of phenotypic and genotypic methods including molecular based 16S rRNA sequencing, repPCR (Repetitive element sequence – based PCR) profile and fatty acid methyl ester **(Adiguzel *et al.,* 2009)**.
58	Llica	Erzurum, Turkey	
59	Akdag	Erzurum, Turkey	
60	Sorgun	Yozgat, Turkey	

61	Pasinler	Erzurum, Turkey	Studied thermophilic bacterial identification and characterization **(Adiguzel *et al.,* 2011)**.
62	Karakoc	Izmir, Turkey	Novel moderately thermophilic, *Brevibacillus aydinogluensis* species was isolated **(Inan *et al.,* 2012)**.
63	Sındırgı	Balikesir, Turkey	First reported study on microbial diversity using culture-dependent and culture-independent methods **(Cankili, 2016)**.
64	Havran		
65	Gure	Kuthaya, Turkey	
66	Eynal		
67	Kopru (Agri)	Eastern and Southeastern Anatolia Regions of Turkey	Isolated and identified bacteria with 16S rRNA sequencing **(Ulucay *et al.,* 2022).**
68	Hista (Siirt)		
69	Hasanabdal (Van)		
70	Davut (Agri)		
71	Guclukonak (Sirnak)		
72	Dargecit (Mardin)		
73	Pasinler (Erzurum)		
74	Afra	Jordan (Middle East)	Culture-dependent and Culture- independent bacterial diversity studies have been done **(Malkawi and Al-omari, 2010)**. Thermophiles study has been done **(Fandi *et al.,* 2014)**. Explored microbial diversity using metagenomic analysis **(Hussein *et al.,* 2017)**. Indicated new chemicals, microbiological data, antimicrobial activity and heavy-metals analysis **(Shakhatreh *et al.,* 2017).** Studied antimicrobial activity of *Streptomyces* strains **(Abussaud and Alanagreh, 2013)**. Isolated thermophilic bacteria and they showed ability to produce thermostable enzyme **(Mohammad *et al.,* 2017)**.
75	Ma'in		
64	Ashounah		
65	Waggas		
66	Zara		
67	Alshouneh		
68	Waggas		
69	Al-Mansheyah		
70	Deir Alla		
71	Hammamat		
72	Zara Dead Sea		
73	Hammamt Afra		
74	Al-Burbita		
75	Al-Hemma		
76	Bani Malik	Jazan (Saudi Arabia)	Studied thermophilic bacteria and highlighted their capability for the production of amylolytic and proteolytic enzymes **(El-Gayar *et al.,* 2017)**.
77	Rankihiriya	Shri lanka	Illumina MiSeq sequencing of the V3–V4 region of the 16S rRNA gene. heat-stable protease and amylase producers, nitrogen-fixing organisms, and potential bioremediation bacterial species, were detected in all the wells. **(Rupasinghe *et al.,* 2022)**.
78	Kanniya		
79	Nelum-wewa,		
80	Mahaoya		
81	Wahawa		
82	Madunagala		

Figure.1 Formation of hot water springs [(Source: (Calderon, 2014)].

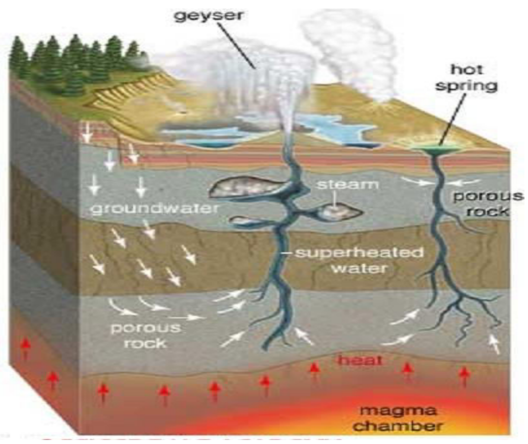
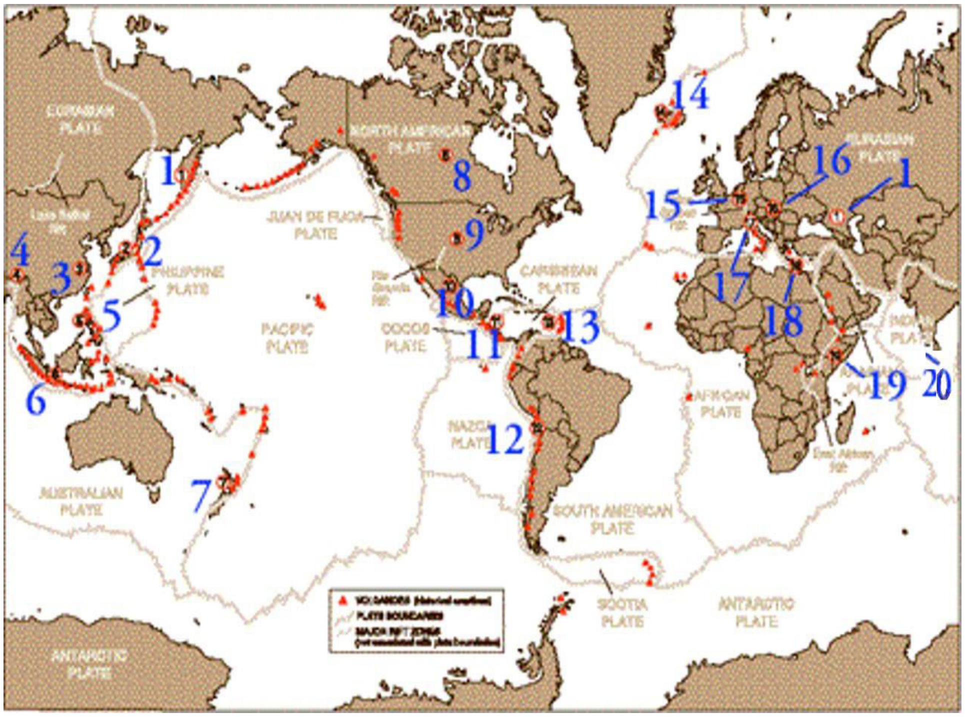
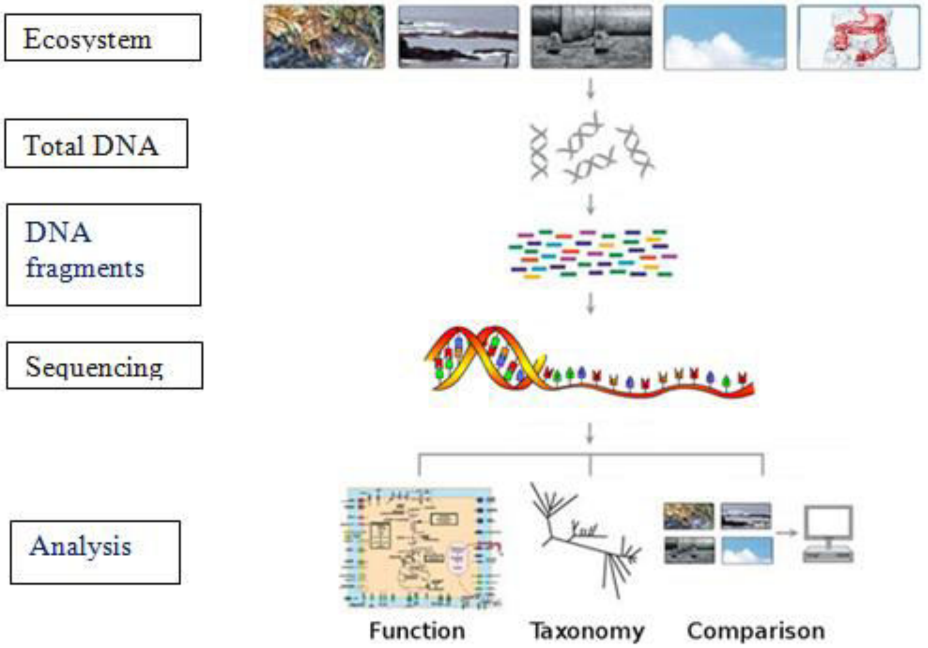


Figure.2 Worldwide location of hot springs (http://geothermal.marin.org/geomap_1.html)



1. Russia
2. Japan
3. Eastern China
4. Himalayan Geothermal Belt
5. The Philippines
6. Indonesia
7. New Zealand
8. Canada
9. United States
10. Mexico
11. Central American Volcanic Belt
12. Andean Volcanic Belt
13. The Caribbean Islands
14. Iceland and other Atlantic Islands
15. Northern Europe
16. Eastern Europe
17. Italy
18. Eastern and Southern Mediterranean
19. East Africa Rift System
20. India

Figure.3 Pipeline of Metagenomics Study (Ghazanfar *et al.,* 2010).



The presence and abundance of numerous kinds of extremophiles inside severe habitats can be revealed through amplicon sequencing of extreme locations. 16S rDNA amplicons from soil and water samples from Tuva Timba and water samples from Dholera in Gujarat, India, were utilized for identifying Firmicutes, Proteobacteria, and Actinobacteria as significant taxa. There was less diversity in the season-wise data (Patel *et al.,* 2020(a)).

In Bakreshwar hot springs microbial diversity was estimated by a culture-independent method (Malhotra *et al.,* 2000; Ghosh *et al.,* 2003). γ-Proteobacteria, cyanobacteria and green non-sulphur and low-GC Gram-positive bacteria were observed from 16S rDNA clones from sediment samples.

Geobacillus thermooleovorans thermophilic strains were isolated and identified from hot water spring (Sharma, 2000) and also effluent samples from paper pulp industry (Kashefi and Lovely, 2003). In the present study, physicochemical and microbiological diversity assessments of seven Indian hot springs |Ganeshpuri, Bendru Theertha, Tuwa, Vajreshwari, Akaloli, Sativali and Bhadrachalam. were undertaken. Culture-dependent and culture-independent microbial diversity analyses (Narsing Rao *et al.,* 2021).

Applications of Thermophilic bacteria

Thermophilic bacteria which mostly survive in high temperature are located in hot springs. Due to the thermophilic bacterial growth at high temperatures and their novel macromolecular properties, thermophilic bacteria have high metabolism, stable enzymes and higher yield of end products compared to the similar type of mesophilic species (Haki and Rakshit, 2003). Hot springs are a source of potential microorganisms that have the capacity to produce hydrogen (H_2) and ethanol. It was presumed by researchers that thermophilic bacteria are strongly capable of hydrogen production and cellulose degradation rather than mesophilic bacteria. Especially the amount of cellulolysis is assumably faster at a higher temperature (Wiegel and Ljungdahl, 1986; Blumer-Schuette *et al.,* 2008). It has been reported in 1998, in biological process, contamination risk factor by other organisms became less, where high temperature are necessary (Adams and Kelly, 1998).

Bioethanol product can also be obtained from thermophilic bacteria and it has numerous advantages like, distillation process is highly efficient at high temperature incubation period, do not require cooling process and some of the thermophiles have capability to direct fermentation of polysaccharides to ethanol. These type of properties of thermophilic bacteria indicate that they are better alternative source to yeast (Gough *et al.,* 1996).

Thermophiles also have potential and productive applications in various fields such as biomining, bioenergy, biosurfactant and thermozyme (Urbetia *et al.,* 2015). Many reported studies mentioned that anaerobic thermophilic bacteria have ability to produce biofuels (Canganella and Wiegel, 2014). Use of thermophilic bacteria in Consolidated Bioprocessing (CBP) offers a successful substitute for production of biohydrogen (Parisutham *et al.,* 2014). Reported studies have observed that moderate thermophiles microorganisms have best application for biomining and commercially applications of biomining process run below temperature at 40-50° C (Donati and Sand, 2007). Thermophilic bacteria can grow at high temperature and at high temperature rate of bioleaching process has been increased (Urbetia *et al.,* 2015). Thermophilic *Aeribacillus* and *Geobacillus* bacteria have been reported for bioremediation capability for many hydrocarbons and aromatic compounds (Mnif *et al.,* 2014). Reported studies have shown that *Anoxybacillus*, thermophilic strains have ability to degrade dye (Deive *et al.,* 2010). Thermophilic bacterial strains such as *Aneurinibacillus, Geobacillus, Alcaligenes, Bacillus* and *Brevibacillus* have been reported for higher production of biosurfactants (Bharali *et al.,* 2011; Joshi *et al.,* 2008; Mnif *et al.,* 2011; Sharafi *et al.,* 2014; Urbetia *et al.,* 2015).

Clostridium thermocellum, *Clostridium stercorarium*, *Clostridium straminisolvens*, *Caldicellulosiruptor saccharolyticus*, and *Caldicellu-losiruptor obsidiansis* anaerobic thermophilic bacteria have capacity to utilize cellulose (Madden, 1983; Wiegel and Dykstra, 1984; Freier *et al.,* 1988; Rainey *et al.,* 1994; Kato *et al.,* 2004; Hamilton-Brehm *et al.,* 2010). Verma and Shirkot in 2014 purified laccase enzyme from *Geobacillus thermocatenulatus*, thermophilic species and it can be effectively used in removal of the industrial dyes which can cause environmental pollution (Verma and Shirkot, 2014). Thermophilic *Bacillus* species have a potential application in environment pollution degradation. Indigenous thermophilic hydrocarbon degraders are of special significance for the bioremediation of oil-polluted desert soil (Margesin and Schinner, 2001). Nowadays due to the industrial activity metal contamination problem is increasing day by day, and microorganisms when in contact with heavy metals can decrease metal solubility and mobility. The metal and sulphate-reducing bacteria have suitable physiology for metal precipitation and immobilization. The activities of these microbes provide metabolic products such as iron and hydrogen sulphide, which lead to mineral formation. These minerals can react with heavy metals, resulting in precipitation and hence detoxification (Chalaal and Islam, 2001; Mehta *et al.,* 2016).

This study uses thermophilic bacteria obtained from Gujarat's Tuva Timba and Dholera hot springs to demonstrate the degradation of low density polyethylene (LDPE) (Patel *et al.,* 2020(b)).

Gram-positive strains of Bacillus subtillis, Bacillus licheniformis, Bacillus sonorensis, and Gram-negative strains of Tepidimonas taiwanesis were chosen for biofilm production in this investigation. By employing the 96-well microtiter plate technology, the quantification of biofilm development and enhanced capacity were examined. Additionally, examine the impact on biofilm formation by adding a carbon source, a nitrogen source, and a combination of inhibitors, such as sodium salicylate and thioglycolate (Patel *et al.,* 2021).

Bakreshwar hot spring in West Bengal, India could be a source of cellulase activities and bacteria are found as a novel source of endoglucanases and exoglucanase fuction at higher temperature (Acharya and Chaudhary, 2011).

Previous study from Jordan thermal springs, mentioned thermophilic bacteria have a great antimicrobial activity and also indicated that *Bacillus* strains may be a good producer of antibiotics and also have antimicrobial effects against Gram-positive bacteria at higher temperature (Fandi *et al.,* 2014).

The three highly populated nations of China, India, and Pakistan are surrounded by the Himalayan Geothermal Belt (HGB), which is home to a large number of hot springs. Proteobacteria, Firmicutes, Bacteroidetes, and Actinobacteria are the most common bacterial phyla found in the hot springs found throughout these countries, according to studies on the subject. There is a noteworthy positive link between the diversity of bacteria and physicochemical parameters such as pH, temperature, Na+, HCO3-, and so on. The water in these hot springs is primarily of the Na-Cl, Na-HCO3, SO4-Cl, and mixed types, according to physicochemical investigations. The temperature ranges between 100 and 250◦C, as indicated by different geothermometers (Nabi Najar *et al.,* 2022). The present study examined the variety of thermophilic microorganisms found in bacteria in thermal hot springs located in the Indian Himalayan Region (IHR). It is also noted that the development of thermophilic bacteria isolated from IHR's thermal hot springs occurs at temperatures between 40 and 100 °C and pH values between 3.5-8, producing a variety of enzymes and metabolites that have been documented in literature through metagenomics research (Verma *et al.,* 2022).

Author Contributions

Patel Disha: Investigation, formal analysis, writing—original draft. Dave Shailesh: Validation, methodology, writing—reviewing. Antony Suresh:—Formal analysis, writing—review and editing. Braganza Vincent: Investigation, writing—reviewing. Modi Hasmukh: Resources, investigation writing—reviewing.

Data Availability

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Ethical Approval Not applicable.

Consent to Participate Not applicable.

Consent to Publish Not applicable.

Conflict of Interest The authors declare no competing interests.

References

Abussaud MJ and Alanagreh L. Isolation, Characterization and Antimicrobial Activity of Streptomyces Strains from Hot Spring Areas in the Northern Part of Jordan. African Journal of Biotechnology 12(51): 7124–32. (2013).

Acharya S and Chaudhary A. Effect of Nutritional and Environmental Factors on Cellulases Activity by Thermophilic Bacteria Isolated from Hot Spring. Journal of Scientific & Industrial Research. 70: 142–148. (2011).

Adams MW and Kelly RM. Finding and using hyperthermophilic enzymes. Trends in biotechnology. 16(8):329-332. (1998).

Adiawati P, Yohandini H, Madayanti F and Akhmaloka. Microbial diversity of acidic hot spring (Kawah Hujan B) in geothermal area West Java-Indonesia. Open Microbiology Journal. 3(1):58-66. (2009).

Adiguzel A, Inan K, Sahin F, Arasoglu T, Gulluce M, Belduz A and Baris O. Molecular Diversity of Thermophilic Bacteria Isolated from Pasinler Hot Spring (Erzurum, Turkey). Turkish Journal of Biology. 35: 267-274. (2011).

Adiguzel A, Ozkan H, Baris O, Inan K, Gulluce M and Sahin F. Identification and Characterization of Thermophilic Bacteria Isolated from Hot Springs in Turkey. Journal of Microbiological Methods. 79(3): 321-328. (2009).

Akmar HN, Asma I, Venugopal B, Latha YL and Sasidharan S. Identification of Appropriate Sample and Culture Method for Isolation of New Thermophilic Bacteria from Hot Spring. African Journal of Microbiology Research. 5(3): 217-221. (2011).

Alam N, Sarkar M, Chowdhury T, Ghosh D and Chattopadhyay B. Characterization of a Novel MDH1 Bacterium from a Virgin Hot Spring Applicable for Gold Nanoparticle (GNPs) Synthesis. Advances in Microbiology. 06(09): 724-732. (2016).

Allaby A and Allaby M. Oxford Dictionary of Earth Science, Oxford University Press, UK. (2003).

Aminin ALN, Warganegara FM, Aditiawati P and Akhmaloka. Simple enrichment and independent cultures to expand bacterial community analysis from Gedongsongo Hot Spring. Journal of Bioscience and Bioengineering. 106(2):211-214. (2008).

Arzita S, Anthoni A and Yetria R. The Diversity of the Alkaline Protease Producers, Thermophilic Obligate Bacillus Spp., from Sungai Tutung Hot Spring, Kerinci, Jambi, Indonesia. Journal of Pure and Applied Microbiology 11(4): 1789-1797. (2017).

Austain B. Methods in Aquatic Bacteriology. In: A Wiley-Interscience Publication, 222-231. (1988).

Bailon-Salas AM, Medrano-Roldan H, Valle-Cervantes S, Ordaz-Diaz LA, Urtiz-Estrada N and Rojas-Contreras JA. Review of Molecular Techniques for the Identification of Bacterial Communities in Biological Effluent Treatment Facilities at Pulp and Paper Mills. BioResources. 12(2): 4384–4409. (2017).

Baker CG, Shabarni Gr, Don CA and Adrian SR. Bacterial Community Analysis of Indonesian Hot Springs. FEMS Microbiology Letters 200(1): 103-109. (2001).

Bauman RW, Machunt-Masuoka E and Tizard I. Microbiology. Pearson Education Publishssing, Inc. San Francisco, USA. (2004).

Bharali P, Das S, Konwar B and Thakur A. Crude biosurfactant from thermophilic Alcaligenes faecalis: feasibility in petro-spill bioremediation. International Biodeterioration Biodegradation. 65:682-690. (2011).

Bhusare DU and Wakte PS. Microbiological and Physiochemical Attributes of Hot Water Sulphur Spring of Unkeshwar. Journal of experimental sciences. 2(4): 4–6. (2011).

Blumer-Schuette SE, Kataeva I, Westpheling J, Adams MWWand Kelly RM. Extremely thermophilic microorganisms for biomass conversion: status and prospects. Current Opinion in Biotechnology. 19:210–217. (2008).

Briggs BR, Brodie EL, Tom LM, Dong H, Jiang H, Huang Q, Wang S, Hou W, Wu G, Haung L, Hedlund BP, Zhang C, Dijkstra P and Hungate BA. Seasonal patterns in microbial communities inhabiting the hot springs of Tengchong, Yunnan Province China. Environmental Microbiology. 16, 1579–1591. (2014).

Brock TD. The value of basic research: discovery of Thermus aquaticus and other extreme thermophiles. Genetics. 146, 1207–1210. (1997).

Brock Thomas and Freeze Hudson. Thermus aquaticus gen. n. and sp. n., a Nonsporulating Extreme Thermophile. Journal of Bacteriology. 98:289-297. (1969).

Cai H, Archambault M and Prescott JF. 16S ribosomal RNA sequence- based identification of veterinary clinical bacteria. Journal of Veterinary Diagnostic Investigation. 15(5): 465-469. (2003).

Cai W, Wannemuehler Y, Dell'anna G, Nicholson B, Barbieri NL, Kariyawasam S, Feng Y, Logue CM, Nolan LK and Li G. A novel two-component signaling system facilitates uropathogenic Escherichia coli's ability to exploit abundant host metabolites. PLoS Pathog. 9(6):e1003428. (2013).

Calderon RM. Ecology of Hot Spring Microbial Mats : Diversity, Microheterogeneity, and Biogeography". PhD Thesis. University of Autonoma de Barcelona. (2014).

Canganella F and Wiegel J. Anaerobic thermophiles. Life. 4(1):77–104. (2014).

Cankili Y. Prokaryotic diversity of hot springs in Balikesir and Kutahya, Turkey. Applied Ecology and Environmental Research. 14(4): 429–440. (2016).

Chalaal O and Islam MR. Integrated management of radioactive strontium contamination in aqueous stream systems. Journal of Environmental Management. 61:51–59. (2001).

Chan CS, Chan KG, Tay YL, Chua YH and Goh KM. Diversity of Thermophiles in a Malaysian Hot Spring Determined Using 16S RRNA and Shotgun Metagenome Sequencing. Frontiers in Microbiology. 6: 1–15. (2015).

Chaudhary N and Prabhu S. Thermophilic Actinomycetes from Hot Water Spring Capable of Producing Enzymes of Industrial Importance. International Journal of Research Studies in Biosciences. 4(6): 29–35. (2016).

Chaudhuri B, Nurul A, Manas S and Chowdhury T. Phylogenetic Characterization of BKH3 Bacterium Isolated from a Hot Spring Consortium of Bakreshwar (India) and Its Application. Advances in Microbiology 6: 453–461. (2016).

Chauhan S. Isolation, Characterization and Genetic Improvement of Xylanase Producing Thermophilic Microorganisms from Hot Springs of Himachal Pradesh. PhD Thesis. Shoolini University of Biotechnology and Management Sciences. Solan, H.P., India. (2010).

Chen TL, Chou YJ, Chen WM, Bhagwath A and Young CC. Tepidimonas Taiwanensis Sp. Nov., a Novel Alkaline-Protease-Producing Bacterium Isolated from a Hot Spring. Extremophiles. 10(1): 35–40. (2006).

Chen, WM, Huang HW, Chang JS, Han YL, Guo TR and Sheuet SY. Tepidimonas Fonticaldi Sp. Nov., a Slightly Thermophilic Betaproteobacterium Isolated from a Hot Spring. International Journal of Systematic and Evolutionary Microbiology. 63: 1810–16. (2013).

Chudasama CJ. Isolation, Screening and Characterization of Alkaline Protease Producing Microorganisms. PhD thesis. Sardar Patel University. (2012).

Clarridge JE. Impact of 16S rRNA gene sequence analysis for identification of bacteria on clinical microbiology and infectious diseases. Clinical microbiology reviews. 17: 840-862. (2004).

Cohan FM. What are bacterial species? Annual Review of Microbiology. 56:457–487. (2002).

Cowan DA. Enzymes from thermophilic Archaebacteria: Current and future applications in biotechnology. Biochemical Society Symposium. 58:149-169. (1992).

Das S, Dash HR, Mangwani N, Chakraborty J and Kumari S. Understanding Molecular Identification and Polyphasic Taxonomic Approaches for Genetic Relatedness and Phylogenetic Relationships of Microorganisms. Journal of Microbiological Methods. 103:80–100. (2014).

Deive F, Dominguez A, Barrio T, Moscoso F, Moran P, LongoM and Sanroman M. Decolorization of dye Reactive Black 5 by newly isolated thermophilic microorganisms from geothermal sites in Galicia (Spain). Journal of Hazardous Materials.182:735–742. (2010).

Devi S. Microbial diversity of aerobic culturable thermophiles in the hot spring of Manikaran. PhD Thesis. Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur (H.P.) India. (2015).

Donati, E. R., & Sand, W. (Eds.). Microbial processing of metal sulfides (Vol. 130). Dordrecht: Springer. (2007).

Dudhagara P, Bhavasar S, Ghelani A and Bhatt S. Isolation, Characterization and Investing the Industrial Applications of Thermostable and Solvent Tolerant Serine Protease from Hot Spring Isolated Thermophilic Bacillus licheniformis U1. International Journal of Applied Sciences and Biotechnology. 2(1): 75–82. (2014).

Dudhgara PR, Bhavsar S and Ghelani A. Hide Dehairing and Laundry Detergent Compatibility Testing of Thermostable and Solvents Tolerant Alkaline Protease from Hot Spring Isolate Bacillus Cohnii U3. Journal of Biological Sciences Original. 15(3): 152–161. (2015).

El-Gayar KE, Al Abboud MA, and Essa AMM. Characterization of Thermophilic Bacteria Isolated from Two Hot Springs in Jazan, Saudi Arabia. Journal of Pure and Applied Microbiology. 11(2): 743–752.

(2017).

Erfurt PJ. An assessment of the role of natural hot and mineral springs in health, wellness and recreational tourism. PhD thesis, James Cook University. (2011).

Erfurt-Cooper P and Cooper M. Health and Wellness Tourism: Spas and Hot Springs. Bristol, UK: Channel View Publications. (2009)

Eytons' Earth. Balneotherapy and Balneology - The Science and Art of Mineral Water Therapy. Document: www.eytonsearth.org/balneology-balneotherapy.php#hot_spring. (2010).

Fandi K, Nayef Al-muaikel and Fouad Al-momani. Antimicrobial Activities of Some Thermophiles Isolated from Jordan Hot Springs. International Journal of Chemical, Environmental & Biological Sciences. 2(1): 2320–4087. (2014).

Feng‑Qin Zhang, Jun Liu, Xiao‑Ju Chen. Comparative analysis of bacterial diversity in two hot springs in Hefei, China. Scientific Reports. 13:5832. (2023).

Freier D, Mothershed CP and Wiegel J. Characterization of Clostridium thermocellum JW20. Applied and Environmental Microbiology. 54:204–211. (1988).

Ghati A, Kaushik S and Paul G. Isolation, Characterization and Molecular Identification of Esterolytic Thermophilic Bacteria from an Indian Hot Spring. Current Research in Microbiology and Biotechnology. 1(4): 196–202. (2013).

Ghazanfar S, Azim A, Ghazanfar MA, Anjuman MI and Begum I. Metagenomics and its application in soil microbial community studies: biotechnological prospects. Journal of Animal and Plant Sciences. 6(2). 611-622. (2010).

Ghelani A, Patel R, Mangrola A and Dudhagara P. Cultivation-Independent Comprehensive Survey of Bacterial Diversity in Tulsi Shyam Hot Springs, India. Genomics Data. 54–56. (2015).

Ghilamicael AM, Boga HI, Anami SE, Mehari T and Budambula NLM. Potential Human Pathogenic Bacteria in Five Hot Springs in Eritrea Revealed by next Generation Sequencing. PLoS ONE. 13(3): 1–12. (2018).

Ghosh D, Bal B, Kashyap VK and Pal S. Molecular Phylogenetic Exploration of Bacterial Diversity in a Bakreshwar (India) Hot Spring and Culture of Shewanella-Related Thermophiles. Applied and Environmental Microbiology. 69(7): 4332–36. (2003)

Gohel HR, Ghosh SK and Braganza VJ. Production, Purification and Immobilization of Extracellular Lipases Xrf11 and Bacillus Licheniformis Xrf12 for Production of Alkyl Esters. International Journal of Life Sciences Biotechnology and Pharma Research 2(3): 278–86. (2013).

Gong JS, Lu ZM, Li H, Zhou ZM, Shi JS and Xu ZH. Metagenomic technology and genome mining: emerging areas for exploring novel nitrilases. Applied Microbiology and Biotechnology. 97: 6603- 6611. (2013).

Gough S, Flynn O, Hack CJ and Marchant R. Fermentation of molasses using a thermotolerant yeast, Kluyveromyces marxianus IMB3: simplex optimisation of media supplements. Applied microbiology and biotechnology. 46(2), 187-190. (1996).

Grewal S. Assessment of Microbial Diversity in Metagenome of Totemic Soil of Chambyal, Samba, J & K State. PhD Thesis. University of Jammu, School of Biotechnology. (2014).

Haki GD and Rakshit SK. Developments in industrially important thermostable enzymes. Bioresource Technology. 89:17–34. (2003).

Hamilton-Brehm SD, Mosher JJ, Vishnivetskaya T, Podar M, Carroll S, Allman S, Phelps TJ and Keller M. Caldicellulosiruptor obsidiansis sp nov, an anaerobic, extremely thermophilic, cellulolytic bacterium isolated from Obsidian Pool, Yellowstone National Park. Applied and Environmental Microbiology. 76:1014–1020. (2010).

Handelsman J, Rondon MR, Brady SF, Clardy J and Goodman RM. Inception of Metagenomic. Chemistry and Biology. 5(10): 245-249. (1998).

Hellman MJ and Michael RS. Analysis of Hot Springs and Associated Deposits in Yellowstone National Park Using ASTER and AVIRIS Remote Sensing. Journal of Volcanology and Geothermal Research. 135: 195–219. (2004).

Herbert and Sharp RJ. Molecular biology and biotechnology of extremophiles. Chapman and Hall, New York. p 44-75. (1992).

Hess M, Sczyrba A, Egan R, Kim TW, Chokhawala H, Schroth G, Luo S, Clark DS, Chen F, Zhang T, Mackie RI, Pennacchio LA, Tringe SG, Visel A, Woyke T, Wang Z and Rubin EM. Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. Science. 331: 463-467. (2011).

Holt JG, Kneg NR, Sneath PHA, Staley JT and Williams ST. Bergey's Manual of Determinative Bactenology, (9th Ed) Hensyl, W R, Willians and Wilkins Company, Baltimore, USA. (1994).

Horikoshi K. Alkalophiles. In: Horikoshi, K., Grant, W. (Ed.) Extremophiles: Microbial Life in Extreme Environments. Wiley-Liss, Inc. New York, pp. 35-56. (1998).

Huang L. Greater Temporal Changes of Sediment Microbial Community than Its Waterborne Counterpart in Tengchong Hot Springs, Yunnan Province, China. Scientific Reports. 1–11. (2014)

Huber G, Huber R, Jones BE, Lauerer G, Neuner A, Segerer A, Stetter KO and Degens ET. Hyperthermophilic archaea and bacteria occurring within Indonesian hydrothermal areas. Systematic and Applied Microbiology. 14:397-404. (1991).

Hugenholtz P. Exploring prokaryotic diversity in the genomic era. Genome Biology. 3(2):1-8. (2002).

Hussein EI, Jacob JH, Shakhatreh MAK, Abd Al-razaq MA, Juhmani AF and Cornelison CT. Exploring the Microbial Diversity in Jordanian Hot Springs by Comparative Metagenomic Analysis. Wiley Microbiology Open. 1–8. (2017).

Inan K, Sabriye C, Ali OB and Fikrettin S. Brevibacillus Aydinogluensis Sp. Nov., a Moderately Thermophilic Bacterium Isolated from Karakoc Hot Spring. International Journal of Systematic and Evolutionary Microbiology. 62: 849–55. (2012).

Ishaq K, Shah AH, Fariq A, Rasheed S, Jannat S. Diversity of culturable thermophilic bacteria from Tata Pani hotspring of Kotli Azad Jammu and Kashmir. Biodiversity Data Journal 11: e99224. (2023).

Jagdish Verma, Anuradha Sourirajan, Kamal Dev. Bacterial diversity in 110 thermal hot springs of Indian Himalayan Region (IHR). 3 Biotech. 12: 238. (2022).

Janssen P, Audit B, Cases I, Darzentas N, Goldovsky L, Kunin V, Lopez-Bigas N, Peregrin-Alvarez JM, Pereira-Leal JB, Tsoka S and Ouzounis CA. Beyond 100 genomes. Genome Biology. 4:402. (2003).

Jiang C, Li SX, Luo FF, Jin K, Wang Q, Hao ZY, Wu LL, Zhao GC, Ma GF, Shen PH, Tang XL and Wu B. Biochemical characterization of two novel β glucosidase genes by metagenome expression cloning. Bioresource Technology. 102: 3272-3278. (2011).

Johnson JL. DNA reassociation experiments. In Nucleic Acid Techniques in Bacteri- al Systematics. In: Stackebrandt, E., Goodfellow, M. (Eds.), Wiley, Chichester. 21-44. (1991).

Joshi S, Bharucha C, Jha S, Yadav S, Nerurkar A and Desai AJ. Biosurfactant production usingmo- lasses and whey under thermophilic conditions. Bioresource Technology. 99:195-199. (2008).

Joshi SJ, Suthar H, Yadav A, Hingurao K and Nerukar A. Occurrence of Biosurfactant Producing Bacillus Spp. in Diverse Habitats. International Scholarly Research Notices Biotechnology. Article ID - 52340, 6 pages, (2013). http://dx.doi.org/10.5402/2013/652340.

Kambura AK, Mwirichia RK, Kasili RW, Karanja EN, Makonde HM, Boga HI. Bacteria and Archaea diversity within the hot springs of Lake Magadi and Little Magadi in Kenya. BMC Microbiol. 7;16(1):136. (2016). doi: 10.1186/s12866-016-0748-x. PMID: 27388368; PMCID: PMC4936230.

Kambura, Anne & Mwirichia, Romano & Kasili, Remmy & Karanja, Edward & Makonde, Huxley & Boga, Hamadi. Bacteria and Archaea diversity within the hot springs of Lake Magadi and Little Magadi in Kenya. BMC Microbiology. 16:136. (2016). DOI 10.1186/s12866-016-0748-x

Kashefi K and Lovely DR. Extending the upper temperature limit for life. Science. 301: 934-941. (2003).

Kato S, Haruta S, Cui ZJ, Ishii M, Yokota A and Igarashi Y. Clostridium straminisolvens sp nov, a moderately thermophilic, aerotolerant and cellulolytic bacterium isolated from a cellulose- degrading bacterial community. International Journal of Systematic and Evolutionary Microbiology. 54:2043-2047. (2004).

Khalil AB, Sivakumar N, Arslan M, Saleem H and Qarawi S. Insights into Brevibacillus Borstelensis AK1 through Whole Genome Sequencing: A Thermophilic Bacterium Isolated from a Hot Spring in Saudi Arabia. BioMed Research International. Article ID 5862437. (2018).

Khuntia HK, Samal S, Sahoo RK, Kar SK, Pal BB and Bihari KM. Isolation and Characterization of Thermophilic Bacteria from Hot Spring in Orissa, India. Biosciences, Biotechnology Research Asia. 7(1): 449-451. (2010).

Kikani B. Molecular Diversity and Biocatalytic Potential of Thermophilic and Thermotolerant Bacteria from a Hot Spring Reservoir in Tulsi Shyam, Junagadh (Gujarat)". PhD Thesis. Saurashtra University. (2013).

Kikani BA and Singh SP. Single Step Purification and Characterization of a Thermostable and Calcium Independent α-Amylase from Bacillus Amyloliquifaciens TSWK1-1 Isolated from Tulsi Shyam Hot Spring Reservoir, Gujarat (India). International Journal of Biological Macromolecules. 48(4): 676-681. (2011).

Kikani BA, Sharma AK and Singh SP. Culture Dependent Diversity and Phylogeny of Thermophilic Bacilli from a Natural Hot Spring Reservoir in the Gir Forest, Gujarat (India). Microbiology. 84(5): 687–700. (2015a)

Kikani BA, Sharma AK and Singh SP. Culture Dependent Diversity and Phylogeny of Thermophilic Bacilli from a Natural Hot Spring Reservoir in the Gir Forest, Gujarat (India). Microbiology Pleiades Publishing, Ltd. 84(5): 687-688. (2015b).

Kim B, Grote R, Lee D, Antranikian G and Pyum Y. Thermoanaerobacter yonseiensis sp. nov., a novel extremely thermophilic, xylose utilizing bacterium that grows up to 85°C. International Journal of Systematic and Evolutionary Microbiology. 51: 1539-1548. (2001).

Klatt C, Wood J, Rusch D, Bateson M, Hamamura N, Heidelberg, J, Grossman A, Bhaya D, Cohan F, Kuhl M, Bryant D and Ward D. Community ecology of hot spring cyanobacterial mats: predominant populations and their functional potential. International Society for Microbial Ecology Journal. 5:1262–1278. (2011).

Konstantinidis KT and Tiedje JM. Prokaryotic taxonomy and phylogeny in the geno- mic era: advancements and challenges ahead. Current Opinion in Microbiology. 10:504–509. (2007).

Kozina IV, Kublanov IV, Kolganova TV, Chernyh NA and Bonch-Osmolovskaya EA. Caldanaerobacter uzonensis sp. nov., ananaerobic, thermophilic, heterotrophic bacterium isolated from a hot spring. International Journal of Systematic and Evolutionary Microbiology. 60:1372-1375. (2010).

Krishna. Molecular DIiversity of Bacterial Population of Kaveri River Belt of Kodagu District, India. PhD Thesis. Manglore University. (2013)

Kumar M, Yadav AN, Tiwari R, Prasanna R and Saxena AK. Deciphering the diversity of culturable thermotolerant bacteria from Manikaran hot springs. Annals of Microbiology. 64:741-751. (2014a)

Kumar MK, Yadav AN, Tiwari R, Prasanna R and Saxena AK. Bioprospecting Evaluating the Diversity of Culturable Thermotolerant Bacteria from Four Hot Springs of India. Journal of Biodiversity, Bioprospecting and Development. 1(3):1-9. (2014).

Lau MCY, Aitchison JC and Pointing SB. Bacterial community composition in thermophilic microbial mats from five hot springs in central Tibet. Extremophiles. 13:139-149. (2009).

Lebedeva EV, Off S, Zumbragel S, Kruse M, Shagzhina A, Lucker S, Maixner F, Lipski A, Daims H and Spieck E. Isolation and Characterization of a Moderately Thermophilic Nitrite-Oxidizing Bacterium from a Geothermal Spring. FEMS Microbiology Ecology. 75:195–204. (2011).

Lee, Y.-J.; Ganbat, D.; Oh, D.; Kim, H.; Jeong, G.E.; Cha, I.-T.; Kim, S.-B.; Nam, G.; Jung, Y.-J.; Lee, S.-J. Isolation and Characterization of Thermophilic Bacteria from Hot Springs in Republic of Korea. Microorganisms, 10, 2375. (2022). https://doi.org/10.3390/microorganisms10122375

Lele OH and Deshmukh PV. Isolation and characterization of thermophilic Bacillus sp. with extracellular enzymatic activities from hot spring of Ganeshpuri, Maharashtra, India. International Journal of Applied Research. 2(5): 427–430. (2016).

Lengeler JW, Drews G and Schelgel HG. Biology of Prokaryote. Blackwell Science Inc., New York, USA. 652-915. (1999).

Lewis K, Epstein S, D'Onofrio A and Ling LL. Uncultured microorganisms as a source of secondary metabolites. Journal of Antibiotics. 63(8):468-476. (2010).

Madden RH. Isolation and characterization of Clostridium stercorarium sp nov, cellulolytic thermophile. International Journal of Systematic Bacteriology. 33:837-840. (1983).

Mahajan MM, Singh DP, Kanika K, Goyal E and Singh AK. Deciphering the microbial diversity of Tattapani hot water spring using. International Journal of Agricultural Science and Research (IJASR). 6(2):371-382. (2016).

Malhotra R, Noorwez SM and Satyanarayana T. Production and partial characterization of thermostable and calcium-independent α-amylase of an extreme thermophile Bacillus thermoleovorans NP54. Letters in Applied Microbiology. 31: 378- 384. (2000).

Malkawi HI and Al-omari MN. Approaches to Study the Bacterial and Archaeal Diversity from Jordanian Hot Springs. African Journal of Microbiology Research. 4(10): 923–932. (2010).

Maltseva, A.I.; Klyukina, A.A.; Elcheninov, A.G.; Pimenov, N.V.; Rusanov, I.I.; Kublanov, I.V.; Kochetkova, T.V.; Frolov, E.N. Water and Sediments of an Acidic Hot Spring—Distinct Differentiation with Regard to the Microbial Community Composition and Functions. Water, 15, 3415. (2023).https://doi.org/10.3390/w15193415.

Mangrola AV, Dudhagara PR, Koringa PG, Joshi CG and Patel RK. Metagenomic Microbial Community Profiling of Unnai Hot Spring by Ion-Torrent Based Shotgun Sequencing. Microbiology. 87(1): 143–146. (2018).

Mangrola AV, Dudhagara PR, Koringa PG, Joshi CG and Patel RK. Shotgun Metagenomic Sequencing Based Microbial Diversity Assessment of Lasundra Hot Spring, India. Genomics Data. 4: 73–75. (2015).

Mangrola AV, Dudhagara PR, Koringa PG, Joshi CG, Parmar M and Patel RK. (2015). Deciphering the Microbiota of Tuwa Hot Spring, India Using Shotgun Metagenomic Sequencing Approach. Genomic Data. 4: 153–155.

Margesin R and Schinner F. Biodegradation and bioremediation of hydrocarbons in extreme environments. Applied Microbiology and Biotechnology. 56:650–663. (2001).

Marsh CL and Don LH. Characterization of some thermophilic bacteria from the hot springs of Yellowstone National. Journal of Bacteriology. 65(2): 193–197. (1953).

Meenakshi. (2015). Biocolor production from bacteria inhabiting hot water springs of Himachal Pradesh. PhD Thesis. University of Horticulture and Forestry, Nauni, Solan. (2015).

Mehetre GT, Paranjpe A, Syed DG and Dharne MS. Investigation of Microbial Diversity in Geothermal Hot Springs In. American Society For Microbiology. 4(1): 4–5. (2016).

Mehta R, Singhal P, Singh H and Damle D. Insight into Thermophiles and Their Wide-Spectrum Applications. 3 Biotech. 6(81): 1–9. (2016).

Menzel P, Gudbergsdottir SR, Rike AG, Lin L, Zhang Q, Contursi P, Moracci M, Kristjansson JK, Bolduc B, Gavrilov S, Ravin N, Mardanov A, Bonch-Osmolovskaya E, Young M, Krogh A and Peng X. Comparative metagenomics of eight geographically remote terrestrial hot springs. Microbial Ecology. 70:411–424. (2015).

Menzel P, Gudbergsdóttir SR, Rike AG, Lin L, Zhang Q, Contursi P, Moracci M, Kristjansson JK, Bolduc B, Gavrilov S, Ravin N, Mardanov A, Bonch-Osmolovskaya E, Young M, Krogh A, Peng X. Comparative Metagenomics of Eight Geographically Remote Terrestrial Hot Springs. Microb Ecol. Aug;70(2):411-24. doi: 10.1007/s00248-015-0576-9. Epub 2015 Feb 25. PMID: 25712554. (2015).

Mignard S and Flandrois JP. 16S rRNA sequencing in routine bacterial identification: a 30-month experiment. Journal of microbiological methods. 67:574- 581. (2006).

Minnikin DE, Alshamaony L and Goodfellow M. Differentiation of Mycobacterium, Nocardia and related taxa by thin-layer chromatographic analysis ofwhole-organism methanolysates. Journal of General

Microbiology. 88:200–204. (1975).

Mishra D and Khanolkar N. Metagenomic Analysis : Microbial Diversity of Hot Spring Water Near Mumbai Region (India). International Journal of Interdisciplinary and Multidisciplinary Studies (IJIMS.) 4(3):575–593. (2017).

Mnif S, Chamkha M, Labat M and Sayadi S. Simultaneous hydrocarbon biodegradation and biosurfactant production by oilfield-selected bacteria. Journal of Applied Microbiology. 111: 525–536. (2011).

Mnif S, Sayadi S and Chamkha M. Biodegradative potential and characterization of a novel aromatic-degrading bacterium isolated from a geothermal oil field under saline and thermophilic conditions. International Biodeteriaration and Biodegradation. 86:258–264. (2014).

Mohammad BT, Al DH, Jaouani A, Abdel-Latif S and Kennes C. Isolation and Characterization of Thermophilic Bacteria from Jordanian Hot Springs: Bacillus Licheniformis and Thermomonas Hydrothermalis Isolates as Potential Producers of Thermostable Enzymes. International Journal of Microbiology. Article ID 6943952: 1-13. (2017).

Mohanty S. The Atri hot spring in Odisha - A Natural Ecosystem for Global Warming Research. International Journal of Geology, Earth and Environmental Sciences 4(1):85–90. (2014).

Morey GW. Chemical Analysis of Thermal Waters in Yellowstone National Park, Wyoming. Geological Survey Bulletin. 1960-1965. (1973).

Nabi NI, Sharma P, Das S, Thandu SM, Kumar S, Thakur N. Bacterial diversity, physicochemical and geothermometry of South Asian hot springs. Current Research in Microbial Sciences 3 - 100125. (2022).

Narsing Rao MP, Dong Z-Y, Luo Z-H, Li M-M, Liu B-B, Guo S-X, Hozzein WN, Xiao M and Li W-J. Physicochemical and Microbial Diversity Analyses of Indian Hot Springs. Front. Microbiol. 12:627200. doi: 10.3389/fmicb.2021.627200. (2021).

Nayak SP. Identification and Characterization of thermophilic bacteria from hot springs of Odisha and their potential applications. PhD Thesis. Orissa University of Agriculture and Technology, Bhubaneswar, Odisha, India. (2013).

Ocham H, Lerat E and Daubm V. Examining Bacterial Species under the Specter of Gene Transfer and Exchange. Proceedings of the National Academy of Sciences, USA. 102:6595-6599. (2005).

Olive E. Thermophilic blue-green algae and the thermal environment. Bacteriological Reviews. 33:476-504. (1990).

Orhan Ulucay. Arzu Gormez. Cem Ozic. Identification, characterization and hydrolase producing performance of thermophilic bacteria: geothermal hot springs in the Eastern and Southeastern Anatolia Regions of Turkey. Antonie van Leeuwenhoek. 115:253–270. (2022).

Panda AK, Bisht SS, Kaushal BR, Mandal SD, Nachimuthu SK and Basistha BC. Bacterial Diversity Analysis of Yumthang Hot Spring, North Sikkim, India by Illumina Sequencing. Big Data Analysis. 7(2): 1–7. (2017).

Panda AK, Bisht SS, Mandal SS and Nachimuthu SK. Bacterial and Archeal Community Composition in Hot Springs from Indo - Burma Region, North - East India. AMB Express. 6(111):1–12. (2016).

Panda MK, Sahu MK and Kumananda T. Isolation and Characterization of a Thermophilic Bacillus Sp. with Protease Activity Isolated from Hot Spring of Tarabalo, Odisha, India. Iranian Journal of Microbiology. 5(2):159–165. (2013).

Panosyan H and Nils-kare B. Microbial Diversity in an Armenian Geothermal Spring Assessed by Molecular and Culture-Based Methods. Journal of Basic Microbiology. 54: 1240–1250. (2014).

Parisutham V, Kim TH and Lee SK. Feasibilities of consolidated bioprocessing microbes: from pretreatment to biofuel production. Bioresource Technology. 161:431–440. (2014).

Patel DN, Dave SR, Braganza VJ and Modi HA. Assessment of culturable microbial diversity of Dholera thermal springs of Gujarat, India. Journal of Experimental Biology and Agricultural Sciences. 7(1):57–64. (2019b).

Patel DN, Dave SR, Braganza VJ and Modi HA. Seasonal variation in bacterial diversity of TuvaTimba thermal springs of Gujarat, India. International Research Journal of Biological Sciences. 8(2):6-14. (2019a).

Patel DN, Dave SR, Braganza VJ, Modi HA. Biodegradation potential of polyethylene by thermophilic bacterial isolates from TuvaTimba and Dholera hot water springs from Gujarat, India. National Seminar on Present Day Biology: Impact of Research on Cellular and Molecular Biology. Conference Proceedings. ISBN: 978-93-90996-18-6. (2020b).

Patel DN, Dave SR, Braganza VJ, Modi HA. Preparation and quantification of biofilm formation using thermophilic bacterial isolates from TuvaTimba and Dholera hot water springs, Gujarat, India. Journal of Biological Sciences and Medicine. 7(1): 1-9. (2021).

Patel DN, Thakkar JR, Braganza VJ, Modi HA. Metagenomics Assessment by Amplicon Sequencing of TuvaTimba and Dholera Hot Water Springs, India. Current Science. 119(10):1663-1670. (2020a).

Patel RK, Oza SM, Kamani SS, Sangani SR and Rawal CM. Production and Characterization of Alkaline Protease from Thermotolerant Alkaliphilic Isolates from Natural Hot Spring of Tulshi Shyam, Gujarat, India. International Journal of Bioscience Reporter. 4(1):147–151. (2006).

Patil SZ, Unnithan AR and Unnikrishnan G. Biosulphidogenesis : Isolation and Characterization of Thermodesulfobacterium Commune Sp. Nov. Isolated from Hot Water Springs of Thane, Maharashtra. Journal of Pharmacy and Biological Science. 9(3):09-13. (2014).

Pednekar P, Jain R, Mahajan G. Anti-infective potential of hot-spring bacteria. J Global Infect Dis; 3:241-5. (2011).

Petti CA, Polage CR and Schreckenberger P. The role of 16S rRNA gene sequencing in identification of microorganisms misidentified by conventional methods. Journal of Clinical Microbiology. 43(12):6123-6125. (2005).

Pignatelli M and Moya A. Evaluating the fidelity of de novo short read metagenomic assembly using simulated data. PLoS One. 6:e19984. (2011).

Pinzon-Martinez DL, Rodriguez-Gomeza C, Minana-Galbisb D, Carrillo-Chavezc JA, Valerio-Alfaroa G and Oliart-Ros R. Thermophilic Bacteria from Mexican Thermal Environments: Isolation and Potential Applications. Environmental Technology. 31(8–9):957–966. (2010).

Podar M and Reysenbach AL. New opportunities revealed by biotechnological explorations of extremophiles. Current Opinion in Biotechnology. 17:250-255. (2006).

Prieto-barajas, Cristina M, Ruth A, Eduardo V and Gustavo S. Revista Mexicana de Biodiversidad Effect of Seasonality and Physicochemical Parameters on Bacterial Communities in Two Hot Spring Microbial Mats from Araro, Mexico. Revista Mexicana de Biodiversidad 88(3):616–624. (2017).

Qin J, Lil R, Rase J, Arumugam M, Burgdorf KS, Manichanh C, Nielsen T, Pons N, Levenez F, Yamada T, Mende DR, Li JL, Xu J, Li S, Li D, Caol J, Wang B, Liang H, Zheng H, Xiel Y, Tap J, Lepage P, Bertalan M, Batto JM, Hansen T, Paslier DL, Linneberg A, Nielsen BH, Pelletier E, Renault P, Thomas SP, Turner K, Zhu H, Yu C, Li S, Jian M, Zhou Y, Lil Y, Zhang X, Li S, Qin N, Yang H, Wang J, Brunak S, Dore J, Guarner F, Kristiansen K, Pedersen O, Parkhil J, Weissenbach J, Ehrlich DS and Wang J. A human gut microbial gene catalogue established by metagenomic sequencing. Nature. 464: 59-65. (2010).

Rainey FA, Donnison AM, Jansen PH, Saul D and Rodrigo A. Description of Caldicellulosiruptor saccharolyticus gen nov, sp nov: an obligately anaerobic, extremely thermophilic, cellu- lolytic bacterium. FEMS Microbiology Letters. 120:263–266. (1994).

Ranjard L, Poly F and Nazaret S. Monitoring complex bacterial communities using culture-independent molecular techniques: application to soil environment. Research in Microbiology. 151:167–177. (2000).

Rastogi G and Sani RS. Molecular techniques to asses microbial community structure, function and dynamics in the environment. In Microbes and microbial technology: agricultural and environmental applications. Ahmad I, Ahmad F, Pichtel J, eds, pp 29–57. Springer, New York. (2011).

Rekadwad B and Pathak A. First Report on Revelatory Prokaryotic Diversity of Unkeshwar Hot Spring (India) Having Biotechnological Potential. Indian Journal of Biotechnology.15:195–200. (2016).

Rekadwad BN. Access to prokaryotic diversity of Unkeshwar hot springs, India. (LAP-LAMBERT Academic Publishers, Germany). 148. (2015).

Reysenbach AL and Cady S. Microbiology of ancient and modern hydrothermal systems. Trends in Microbiology. 9:79-86. (2001).

Rondon MR, August PR, Bettermann AD, Brady SF, Grossman TH, Liles MR, Loiacono KA, Lynch BA, MacNeil IA, Minor C, Tiong CL, Gilman M, Osburne MS, Clardy J, Handelsman J and Goodman RM. Cloning the soil metagenome: a strategy for accessing the genetic and functional diversity of uncultured microorganisms. Appllied and Environmental Microbiology. 66:2541-2547. (2000).

Rondon MR, Goodman RM, and Handelsman J. The Earth's bounty: Assessing and accessing soil microbial diversity. Trends in Biotechnology 17(10), 403-409. (1999).

Ruwini R, Sathya A, Sudeera W, Biggs PJ, Rohana Chandrajith, Saumya Wickramasinghe. Microbial diversity and ecology of geothermal springs in the high-grade metamorphic terrain of Sri Lanka. Environmental Advances 7 - 100166. (2022).

SaAK. Isolation and Identification of new lipolytic thermophilic bacteria from an Indian hot spring. International Journal of Pharma and Bio Sciences. 2(2):229–235. (2011).

Sahay H, Yadav NA, Singh AK, Singh S, Kaushik R and Saxena AK. Hot Springs of Indian Himalayas : Potential Sources of Microbial Diversity and Thermostable Hydrolytic Enzymes. 3 Biotech. 7(2): 1–11. (2017).

Sato M, Suda M, Okuma J, Katol T, Hirose Y, Nishimura A, Kondo Y and Shibata D. Isolation of Highly Thermostable b -Xylosidases from a Hot Spring Soil Microbial Community Using a Metagenomic Approach. Dna Research. 24(6):649–656. (2017).

Saxena R, Dhakan DB, Mittal P and Waiker P. Metagenomic Analysis of Hot Springs in Central India Reveals Hydrocarbon Degrading Thermophiles and Pathways Essential for Survival in Extreme Environments. Frontiers in Microbiology 7:2123. (2017).

Scow KM, Schwartz E, Johnson MJ and Macalady JL. Microbial biodiversity, measurement of Levin, SA, Editor. 177-190. (2001).

Seyfried M, Delina L, Fred RA and Juergen W. Caloramator Viterbensis Sp. Nov., a Novel Thermophilic, Glycerol-Fermenting Bacterium Isolated from a Hot Spring in Italy. International Journal of Systematic and Evolutionary Microbiology 52:1177–1184. (2002).

Shakhatreha MA, Jacobb JH, Husseinc EI, Masadehd MM, Obeidate SM, Juhmanic AF and Abd Al-razaq MA. Microbiological Analysis, Antimicrobial Activity, and Heavy-Metals Content of Jordanian Ma'in Hot-Springs Water. Journal of Infection and Public Health. 10(6):789–793. (2017).

Sharafi H, Abdoli M, Hajfarajollah H, Samie N, Alidoust L, Abbasi H, Fooladi J, Zahiri H and Noghabi K. First report of a lipopeptide biosurfactant from thermophilic bacterium Aneurinibacillus thermoaerophilus MK01 newly isolated from municipal landfill site. Applied Biochemistry and Biotechnology. 173:1236–1249. (2014).

Sharma A. Thermo-alkali stable celluase-free Xylanase of an Extreme Thermophile Bacillus (Geobacillus) thermoleovorans. Ph.D Thesis. University of Delhi, New Delhi. (2000).

Sharma N, Vyas G and Pathania S. Culturable Diversity of Thermophilic Microorganisms Found in Hot Springs of Northern Himalayas and to Explore Their Potential for Production of Industrially Important Enzymes. Scholars Academic Journal of Biosciences (SAJB) 1(5):165–78. (2013).

Shikotar P and Verma A. Assessment of Thermophilic Bacterial Diversity of Thermal Springs of Himachal Pradesh. ENVIS Bulletin Himalayan Ecology. 23:1–8. (2015).

Shukla R. Diversity Phylogeny and Biocatalytical Prospective of Thermophilic Thermotolerant Actinomycetes Thermoactinomycetes from Hot Spring Reservoirs in Gujarat. PhD Thesis. Saurashtra University. (2015).

Sigee DC. Bacteria The main Heterotrophic Microorganisms in Freshwater System. In Freshwater Microbiology (1st Ed.) John Wily and Sons, Ltd, England, 287-317. (2005).

Simoneit TRB, Aboul-Kassim TAT and Tiercelin JJ. Hydrothermal petroleum from lacrustrine sedimentary organic matter in the East African Rift. Applied Geochemistry. 15:355-368. (2000).

Singh SP. Extreme Environments and Extremophiles. In: National Science Digital Library, CSIR, India. E-Book. Environmental Microbiology. 1-35. (2006).

Sircar A, Shah M, Sahajpal S, Vaidya D, Dhale S and Chaudhary A. Geothermal Exploration in Gujarat : Case Study from Dholera. Geothermal Energy. 3(22):1–26. (2015).

Socorro M, Megay DV and Windell RL. Isolation and Characterization of Extremely Thermophilic Bacteria from Hot Springs. International Journal of Phillippine Science and Technology 08(2):1–5. (2015).

Soy S, Lakra U, Prakash P, Suravajhala P, Nigam V.K, Sharma S.R. & Baya N. Exploring microbial diversity in hot springs of Surajkund, India through 16S rRNA analysis and thermozyme characterization from endogenous isolates. Scientific Reports, 13:14221. (2023).

Stahl DA, Lane DJ, Olsen GJ and Pace NR. Characterization of a Yellowstone Hot Spring Microbial Community by 5S rRNA Sequences. Applied and Environmental Microbiology 49(6):1379–1384. (1985).

Stefanova K, Tomova I, Tomova A, Radchenkova N, Atanassov I and Kambourova M. Archaeal and Bacterial Diversity in Two Hot Springs from Geothermal Regions in Bulgaria as Demostrated by 16S rRNA and GH-57 Genes. International Microbiology 18(4):217–223. (2015).

Stetter K. Hyperthermophiles: Isolation, Classification and Properties. In: Horikoshi, K., Grant, W. (Eds.). Extremophiles: Microbial Life in Extreme Environments. Wiley-Liss, Inc. New York, 1-24. (1998).

Stout LM, Blake RE, Greenwood JP, Martini AM and Rose EC. Microbial Diversity of Boron-Rich Volcanic Hot Springs of St. Lucia, Lesser Antilles. FEMS Microbiology Ecology. 70:402–412. (2018).

Sudjaroen Y, Kanittada T and Kowit S. Characteristics of Mineral Water from Nature Hot Springs in Ranong Province, Thailand. Annals of Tropical Medicine and Public Health 10(2): 2017–2019. (2018).

Tan H, Barret M, Harrington C and Gara FO. Environmental Microbiology and Engineering: Identification of Novel Phytase Genes from an Agricultural Soil-Derived Metagenome. Journal of Microbiology and Biotechnology. 24:113- 118. (2014).

Tarik A, Mouna O, Marouane M, Jean S, Elmostafa E, Jamal I, Mohamed I and Mohamed A. Thermophilic Bacteria in Moroccan Hot Springs, Salt Marshes and Desert Soils. Brazilian Journal of Microbiology 46(2):443-453. (2015).

Tekere M, Lotter A, Olivier J, and Venter S. Bacterial Diversity in Some South African Thermal Springs : A Metagenomic Analysis. Proceedings World Geotheral Congress. 19–25. (2015).

Tekere M, Lotter A, Olivier J, Jonker N and Venter S. Metagenomic Analysis of Bacterial Diversity of Siloam Hot Water Spring, Limpopo, South Africa. African Journal of Biotechnology 10(78): 18005–18012. (2011).

Tirawongsaroj P, Sriprang R, Harnpicharnchai P, Thongaram T, Champreda V, Tanapongpipat S, Pootanakit K and Eurwilaichitr L. Novel thermophilic and thermostable lipolytic enzymes from Thailand hot spring metagenomic library. Journal of Biotechnology. 133:42–49. (2008).

Tsuei-Yun F, Wen-Chi T, Ching-Ju Y and Tong-Yuan S. Characterization of the thermophilic isoamylase from the thermophilic archaeon Sulfolobus solfataricus ATCC 35092. Journal of Molecular Catalysis B: Enzymatic. 33:99–107. (2005).

Urbieta MS, Donati ER, Chan KG, Shahar S, Sin LL and Goh KM. Thermophiles in the genomic era: biodiversity, science, and applications. Biotechnology Advances. 33(6):633-647. (2015).

Verma A and Shirkot P. Purification and characterization of thermostable laccase from thermophilic Geobacillus thermo- catenulatus MS5 and its applications in removal of textile dyes. Scholars Academic Journal of Biosciences. 2(8):479–485. (2014).

Verma A, Dhiman K, Gupta M and Shirkot P. Bioprospecting of Thermotolerant Bacteria from Hot Water Springs of

Himachal Pradesh for the Production of Taq DNA Polymerase. Proceedings of the National Academy of Sciences, India Section B: Biological Sciences. 85(3):739-749. (2014).

Verma PO., Verma M, Sharma P, Kumar M, Kumari K, Singh A, Kumari H, Jit S, Gupta SK, Khanna M and Lal R. Polyphasic approach of bacterial classification - an overview of recent advances. Indian Journal of Microbiology. 47:98–108. (2007).

Wang S, Hou W, Dong H, Jiang H, Huang L, Wu G, Zhang C, Song Z, Zhang Y, Ren H, Zhang J and Zhang L. Control of Temperature on Microbial Community Structure in Hot Springs of the Tibetan Plateau. PLoS ONE. 8(5):e62901. (2013).

Ward DM, Ferris MJ, Nold SC and Bateson MM. A natural view of microbial biodiversity within hot spring cyanobacterial mat communities. Microbiology and Molecular Biology Reviews. 62:1353-1370. (1998).

Wemheuer B, Taube R, Akyol P, Wemheuer F and Daniel R. Microbial Diversity and Biochemical Potential Encoded by Thermal Spring Metagenomes Derived from the Kamchatka Peninsula. Hindawi Publishing Corporation. 13: 136714. (2013).

Wiegel J and Dykstra M. Clostridium thermocellum: adhesion and sporulation while adhered to cellulose and hemicellulose. Applied Microbiology and Biotechnology. 20:59–65. (1984).

Wiegel J and Ljungdahl LG. The importance of thermophilic bacteria in biotechnology. Critical Review in Biotechnology. 3:39–108. (1986).

Yannawar VB, Bhosle AB, Shaikh PR and Gaikwad SR. Water Quality of Hot Water Unkeshwar Spring of Maharashtra, India. International Journal of Innovation and Applied Studies. 3(2):541–551. (2013).

Yohandini, Heni, Julinar, and Muharni. Isolation and Phylogenetic Analysis of Thermophile Community Within Tanjung Sakti Hot Spring, South Sumatera, Indonesia. Journal of Biosciences. 22(3):143–148. (2015).

Zahoor S, Muhammad MJ and Muhammad NA. Isolation and Molecular Identification of a Facultatively Anaerobic Bacterium From The Hot Spring of Azad Kashmir. Pakistan Journal of Biotechnology. 44:329–333. (2012).

Zhang FQ, Liu J, Chen XJ. Comparative analysis of bacterial diversity in two hot springs in Hefei, China. Sci Rep. Apr 10;13(1):5832. doi: 10.1038/s41598-023-32853-5. PMID: 37037855; PMCID: PMC10086057. (2023).

Zhang J, Tang S, Zhang Y, Yu L, Klenk H and Li W. *Laceyella tengchongensis* sp. nov., a thermophile isolated from soil of a volcano. International Journal of Systematic Evolutionary and Microbiology. 60:2226-2230. (2010).

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