

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

Birhanu Gizaw*

Microbial Biodiversity Directorate Ethiopian Biodiversity Institute. P.O. Box. 30726 Addis Ababa, Ethiopia.

***Corresponding Author:** Birhanu Gizaw, Microbial Biodiversity Directorate Ethiopian Biodiversity Institute. P.O. Box. 30726 Addis Ababa, Ethiopia. 0911862561. Email: gizachewbirhan@gmail.com

ABSTRACT

Microbs occupy majority of the biomass and biodiversity of life on the Earth. They play pivotal roles in all ecosystems in biogeochemical cycles and harbour novel genes and metabolites for several biotechnological applications in industry, medicine, agriculture, pharmaceutical and environmental sectors. Without microorganisms all life on earth would cease. The purpose of this review is to indicate ethiopian microbial niches and habitats potentials for exploration and strengthen exsitu conservation effort as well as future utilization in out manoeuvre microbial genetic resource in different sector. Understanding major microbial ecology helps to design microbial structural and functional diversity study associated with different habitats these are hyper extremophile environment, soil, rumen animals, aquatic ecosystem, rhizosphere, rhizoplane, phyllosphere and human microbiota helps to set priority and design microbial conservation strategy. In addition to this the use of metagenomic approaches led to the discovery of a large array of new genes and enabled the genome sequence of various uncultured microbes from this unique and versatile microbial ecology will grant sustainable conservation and utilization of untouched microbial genetic resource for biotechnological application for human and environmental use.

Keywords: Ecology, exsitu, extremophile, Microbs, rhizosphere, genes

INTRODUCTION

Microbial Diversity

Microorganism encompasses an extensive and diverse assemblage of organisms, such as bacteria, viruses, protists and fungi which exhibit widely different morphological, ecological and physiological characteristics. Inside our gut, in the mucky soil of a marsh, in Antarctic ice, in the hot springs and in habitats seemingly incompatible with life, microbes flourish. Microorganisms have been evolving for nearly 4 billion years and are capable of exploiting a vast range of energy sources and thriving in almost every habitat like surviving and thriving in extremes of heat, cold, radiation, pressure, salt, acidity and darkness. In these environments no other forms of life are found except microbes and the only nutrients come from inorganic matter. For 2 billion years microbes were the only form of life on Earth. During this long history, all of the basic biochemistries of life evolved, and all life forms have developed from these microbial ancestors. It is estimated that 50% of the living protoplasm on this planet is microbial [220]. Microorganisms

represent by far the richest repertoire of molecular and chemical diversity in nature. They live in highly organized and interactive communities that are versatile, complex and difficult to analyze from many perspectives. One of the challenges is that microbes are exceedingly small—only 1/8000th the volume of a human cell and spanning about 1/100th the diameter of a human hair. Investigating processes within this size range is challenging. Replicating quickly, exchanging genetic material with each other and with other organisms, not only are they everywhere, but these tiny organisms also manipulate the environments in which they live. Their presence has driven the development of new ecosystems, some of which allowed for the evolution of more complex organisms. They underlie basic ecosystem processes such as biogeochemical cycles and food chains, as well as maintain vital and often elegant relationships between themselves and higher organisms. Microbes provide the fundamental underpinning of all ecosystems. Diverse microorganisms are essential to sustainable biosphere. They are able to recycle nutrients, produce and consume gases

that affect global climate, destroy pollutants, treat our wastes and they can be used for biological control of plant and animal pests. Microbial genetic resources also play vital roles in improving local and national economies. Traditional food preparations, agro-industries, pharmaceuticals, soil mineralization, waste treatment, biofertilizer, biocontrol, biopesticide are among the major areas of applications of microbial genetic resources. In Ethiopia, microbes are vital in preparation of traditional foods and local drinks both in the rural and urban areas of the country. A large population of microbes can be rapidly scanned for their taxonomic grouping revealing new microbes, which have not been separated till date. These can be checked for their special characteristics like secondary metabolites for e.g., enzymes, antibiotics, hydrogen, methane, bioplastic, and bioremediation of oily sludge, bio wastes.

These and other properties can prove beneficial for improving the environment and consequently human health [122]. Without microorganisms, all life on earth would cease. Due to the innately small size of the microorganisms, environmental complexity plays a major role in determining diversity. Spatial heterogeneity is likely to lead to the formation of many niches within a habitat. Microbes communicate; some generate the signals for the formation of metabolically diverse communities. Some use sophisticated signaling to establish a complex relationship with higher organisms. Microbial ecology is thus used to describe the presence and contributions of microbes through their activities to the place where they are found.

Ethiopia is a country of great geographical diversity with high and rugged mountains, flat-topped plateaux, deep gorges, incised river, lakes, wetland, valleys and rolling plains. Altitude ranges from the highest peak at Ras Dejen, 4620 metres above sea level (masl), down to the Danakil depression 120meter below sea level. Physical conditions and variations in altitude have resulted in a great diversity of climatic conditions; soils and vegetation cover favors magnificent microbial diversity. Microbes are unseen natural resources that deserve greater attention. The fact that microbes are too small to be seen, does not mean they are too small to be studied and exploited or valued. These great potential of microbial ecology and diversity requiring exploration and molecular characterization beside of conventional study.

Reason of Studying Microbial Diversity and their Importance

It is clear that microbial communities drive the function of ecosystems and fundamentally underpin the biogeochemical cycles that our planet's life-support system. A better understanding and global awareness of the diversity found in microbes will be of value for the following reasons: · Microbes are important sources of knowledge about the strategies used by organisms to exist and limits of life · Microbes are of critical importance to the sustainability of life on our planet. The untapped diversity of microbes is a resource for new genes and organisms of value to biotechnology. Diversity patterns of microbes can be used for monitoring and predicting environmental change. Microbes play a role in conservation and restoration biology of higher organisms; Microbial communities are excellent models for understanding biological interactions and evolutionary history. Uniqueness of microbes and their often unpredictable nature and biosynthetic capabilities adapted to a specific set of environmental and cultural conditions, has made them likely candidates for solving particularly difficult problems facing the entire network of life on Earth. The various ways in which microbes have been used over the past five decades confirms that these organisms represent an untapped and extremely valuable resource to advance agricultural biotechnology, medical technology, human and animal health, food processing, food safety and quality, genetic engineering, environmental protection, and more effective treatment of agricultural and municipal wastes. Pharmaceutical products obtained from microbes is of recombinant proteins, insulin analogues, non-glycosylated humangrowth hormone [somatotropin, glucagon], vaccines [hepatitis B virus surface antigen [158]. Microbes have an active role to play in production of bio-fuels [224]. Many of these technological advances would not have been possible using straightforward chemical and physical engineering methods, or if they were, they would not have been practically or economically feasible. Microbes are restive engineers of our planet. Their versatile primary and secondary metabolite, enzymes, alkaloids, organic acids are great role in huge industries and in nature. Study on structural and functional diversity of microorganism in different pattern of ecology helps to exploit more in the era of molecular technology for Biotechnological application.

POTENTIAL INSITU MICROBIAL ECOLOGY IN ETHIOPIA

Hyper Extremophile and Extremophile Microbial Ecology

The extreme environment is characterized by low temperature (below 0°C); hydrothermal vents with temperatures up to 370 °C occur occasionally. The abyssal zone (3000-6000 m) and the hadal zone (>6000 m; the deepest part of the marine environment) are additionally characterized by high hydrostatic pressure (up to 110 MPa), absence of solar radiation, low nutrient availability and high content of dissolved oxygen (for example, about 4 ml dissolved oxygen per liter at 6000m depth [134,170]). Microbial life in terrestrial hot springs, such as present in Yellowstone National Park (USA), has been observed and studied since early the 1960s [37,33].

However, the discovery of microbial life in deep sea thermal vents and shallow marine seeps in volcanic regions of the world in the late 1970s and early 1980s led to the realization that the so called extreme thermophiles [119,78,106]. The extremophiles majorly include; Halophiles, Thermophiles, Barophiles, Psychrophiles and Acidophiles [194,15]. They have adapted to grow under extreme conditions such as high temperature (>100°C), high salinity (saturated NaCl), extremes of pH (<2.0, >10.0), High pressure (> 50 MPa), presence of organic solvents (e.g. > 1% toluene) or heavy metals and substrate stress. These kinds of extreme microbial growth conditions are found in exotic environments which were more widespread on primitive Earth.

Thermophilic and hyperthermophilic microorganisms are found as normal inhabitants of continental and submarine volcanic areas, geothermally heated sea-sediments, hydrothermal vents, solfataric fields; steam-heated soils, mud holes, surface waters; deep hot springs; geothermal power plants as well as submarine hot springs and fumaroles; hot sediments and vents, "black smokers" or "chimneys"; and active sea-mounts [67,50,200]. Thermophiles are further subcategorized on the basis of their temperature tolerance: for instance, facultative thermophiles, can grow at temperatures between 50°C-65°C, but also grow also at 37°C; obligative thermophiles have maximum growth temperatures of 65°C - 70°C, extremely thermophiles can grow between 40°C-70°C with an optimal growth temperature of about 65°C. Hyperthermophiles, mainly comprising of

archae, can grow over 90°C with a range of optimal temperatures between 80°C-115°C. Thermophiles are reported to have proteins which are thermostable and resist denaturation and proteolysis [149]. In addition, thermophilic bacteria, actinomycetes and archae adapt to high temperatures by increased electrostatic, disulphide and hydrophobic interactions in their proteins and produce biotechnologically valuable compounds, such as thermostable extremozymes through various adaptive mechanisms [175,135].

There are various extremozymes like cellulases, amylases, xylanases, proteases, pectinases, keratinases, lipases, esterases, catalases, peroxidases, phytases and DNA polymerases (e.g. Taq polymerase) which provide a clearer understanding of the origin of life. Currently, only 1-2 % of the microorganisms on the Earth have been commercially exploited and amongst these there are only a few examples of extremophiles [93]. Due to ever increasing industrial growth, the demand for thermostable enzymes has tremendously increased. An additional application for thermophilic enzymes is the development of new processes to reduce the release of environmentally harmful chemicals by replacement of existing chemical reactions with enzymatic reactions. A good example can be found in the paper-pulping industry. By adding thermostable xylanases to the unbleached pulp it is possible to remove parts of the lignin by hydrolysing the bonds that link the lignin, via xylan, to the cellulose fibers. The use of hemicellulases in bleaching is considered as one of the most important, new large scale industrial applications of enzymes [169]. There are many existing applications in which more thermally stable versions of enzymes now used will be advantageous.

This is especially true in the hydrolysis of corn starch to produce high fructose corn syrup. Amylolytic enzymes are now used at temperatures exceeding 100°C in some cases to hydrolyse liquified starch to oligosaccharides and eventually to glucose. Glucose is then partially isomerized to fructose using immobilized xylose (glucose) isomerase. Many of these same enzyme activities are available in extreme thermophiles. So far, about 70 species of hyperthermophilic bacteria and Archaea are known, which had been isolated from different terrestrial and marine thermal areas in the world. Hyperthermophiles are very divergent, both in terms of their phylogeny and physiological properties, and are grouped into 29 genera in 10

orders. Great variety of bacteria has been isolated from hot springs. These include, mats of cyanobacteria and other photosynthetic bacteria (purple and, green bacteria), *Thermus*, *Thermotogales*, *Aquificals* were commonly found in Hot springs environments. Certain Enterobacteria such as *Bacillus*, *Clostridium* and Thionic bacteria (*Thiobacillus*) were also inhibiting hot springs [201,55].

Hyperthermophiles are adapted to distinct environmental factors including composition of minerals and gasses, pH, redox potential, salinity and temperature. Most hyperthermophiles exhibit a chemo lithoautotrophic mode of nutrition: inorganic redox reactions serve as energy sources (chemolithotrophic), and CO₂ is the only carbon source required to build up organic cell material (autotrophic). Therefore, these organisms are fixing CO₂ by chemosynthesis and are designated chemolithoautotrophs.

The energy-yielding reactions in chemolithoautotrophic hyperthermophiles are an aerobic and aerobic types of respiration. A variety of hyperthermophiles are adapted to the high salinity of sea water of about 3% salt. They are represented by members of the archaeal genera *Pyrolobus*, *Pyrodictium*, *Hyperthermus*, *Stetteria*, *Thermodiscus*, *Igneococcus*, *Staphylothermus*, *Aeropyrum*, *Pyrobaculum*, *Methanopyrus*, *Pyrococcus*, *Thermococcus*, *Archaeoglobusa* and *Ferroglobus* and of the bacterial genera *Aquifex* and *Thermotoga*. The organism with the highest growth temperature is *Pyrolobus fumarii*, exhibiting an upper temperature border of growth above 113° C. In contrast to thermophilic microorganism recently a wide diversity of cold adapted microorganisms have been found in various low temperature environments and their enzymes attracted interests because of their biotechnological potential offering economical and ecological advantages such as energy saving, function in cold environment, minimizing undesirable chemical reactions that occur at high temperature, and inactivating easily by heating when required [92,185,153,39].

Psychrophilic microorganism living in cold environments, such as glacier silts, place of high altitude in Himalaya, Arctic soils and Antarctic environments, are potentially useful sources of cold-adapted enzymes. Cold active enzymes are attractive in food industry, e.g. processing of fruit juices and milk, as there is an increasing industrial trend to treat food stuffs under low temperature conditions in order to avoid changes in taste and nutritional value, and to

save energy [153,185]. Approximately 80% of our planet's biosphere is permanently cold that is, at temperatures below 5°C. This includes much of the world's oceans which cover 70% of the Earth's surface—the polar regions, which encompass Antarctica and parts of North America and Europe that are within the Arctic circle, montane regions (Alps, Himalayas and Rocky Mountains), the mesosphere and stratosphere, and to a lesser extent, man-made habitats such as fridges and freezers [40,152,184]. Psychrophilic prokaryotes are widespread among bacteria and archaea and can be found with in the genera *Aletromonas*, *Halobacterium*, *Shewanella*, *Psychrobacter*, *Pseudoalteromonas*, *Arthrobacter*, *Colwellia*, *Gelidibacter*, *Marinobacter*, *Psychroflexus*, *Pseudomonas*, *Methanobolus* and *Methanococcoides* [60].

Several species of eukaryotic microalgae have also adapted to growth at low temperature and thrive in melting snow and can color the snow pink, red, green, or yellow [105]. *Chlamydomonas nivalis* is the most common species of the snow algae. Other algae that grow on snow include species of the genera *Ankistrodesmis*, *Chloromonas* and *Raphidonema*. *Chlamydomonas nivalis* is a green alga that grows actively as the snow melts during the spring and summer and sunlight penetrates the snowpack. Although the vegetative cells of *Chlamydomonas nivalis* are green, it has bright red spores. Their presence in large numbers produces large expanses of red "watermelon snow". The lowest temperature for growth (-2°C) in marine polar ecosystems is recorded for the sulfate reducing bacteria, (*Desulfovibrio*, *Desulfosarcina*, *Desulfoto-maculum*, *Desulfobulbus*, *Desulfobacter*, and *Desulfobacterium*) were present in the lake [146]. Prokaryotic extremophile that grows at the lowest temperature (-10°C) and 10 % salinity currently known is the psychrotolerant mesophilic species *Psychrobacter cryohalolentis*, which was isolated from the permafrost of the Kolyma Lowlands of North Siberia [19]. *Psychrobacter submarinus* is the most halotolerant true psychrophile growing around 15 % salinity [144]. The true halophilic species within psychrophiles remain undiscovered. Methanotrophic psychrophilic species of the genus *Methylocella* tolerate acidic pH at 4.5, but the mesophilic species *Acidiphilum acidophilum* tolerates pH 1.5 at 15 °C (the minimum temperature for growth). True psychrophilic acidophiles are unknown or, most probably, do not exist at all. The alkaliphilic

psychrophiles, *Rhodonellum psychrophillum* and *Arsuki-bacterium ikkense*, are the “champions” growing at pH 10.5. In addition to adaptations cold environment microbes adapted for acidic environments, acidophiles are also typically adapted to environments with high temperatures, high salinity or heavy metal concentrations because these conditions often co-occur, for example, in areas of acid drainage [41,168,63].

Alkalophiles thrive in alkaline environments such as gypsum-based soils or soda lakes and are often halophiles. They encompass bacteria from different genera including among others *Bacillus*, *Halomonas* and *Pseudomonas* [186] as well as archaea belonging to the genera *Halalkalicoccus*, *Halobiforma*, *Halorubrum*, *Natrialba*, *Natronococcus* and *Natronorubrum* [35]. Deep-sea and deep subsurface environments host piezophiles (barophiles), a group of extremophiles that produce compatible solutes and polyunsaturated fatty acids and form multimeric and antioxidant proteins that enable them to survive under extremely high hydrostatic pressures [120,225]. Most piezophiles are psychrophilic gram-negative bacterial species that belong to the genera *Shewanella*, *Psychromonas*, *Photobacterium*, *Colwellia*, *Thiopfundum* and *Moritella*, but some are archaea derived and can be found among the genera *Thermococcus*, *Sulfolobus* and *Pyrococcus* [225]. Metallophiles are also acidophiles and include both bacteria from the genera *Acidithiobacillus*, *Leptospirillum*, *Alicyclobacillus*, *Acidiphilium*, *Acidimicrobium*, *Ferrimicrobium* and *Sulfobacillus* and archaea from the genera *Ferroplasma*, *Acidiplasma*, *Sulfolobus*, *Metallosphaera* and *Acidianus* [117,63]. Radiophiles are found among various microbial groups and species including bacteria from the genera *Deinococcus*, *Bacillus*, *Rubrobacter* and *Kineococcus*; the family *Geodermatophilaceae* and cyanobacteria including the genera *Nostoc* and *Chroococcidiopsis* [36, 94,21,84]. Ethiopia consists of different hyper extremophile and extremophile microbial ecology in different part of the country among these the Danakil Valley occurs in the Afar Triangle, within the Great Rift Valley, on north-east Ethiopian, south-east Eritrean and west Djiboutian territories are the most unexplored microbial ecosystem and also around 10 high pick above 3500m.a.s.l area. During global plate reorganisations, the East African rift system moved northward from the Mesozoic Anza rift system into the Afar depression and cut across

rift structures of the Red Sea and Gulf of Aden. The Red Sea, Gulf of Aden and Ethiopian rifts intersect in a complex zone within the central Afar depression, creating the typical rift-rift-rift triple junction zone [221,216]. It is an enormous unsettled area with barren soil. From the North to the South it is about 570 km long, and its width varies from 80 to 400 km (covering an area ~200000 km² [28]. Most of it lies below sea level. It also has the deepest depression of the African continent, the shoreline of lake Asal reaching 155 m b.s.l. [216]. Its geological, climatic, cultural and landscape features are unique on a global scale. Hot sulphur springs, multicolour salt and mineral crusts, rifts, faults, black lavas, vaporous geysers and active volcanoes create one of the most weird and beautiful landscapes on Earth. Nowhere else can so many unusual phenomena and geological processes be observed: plate divergence, tectonic rifts, faults, earthquakes, volcano eruptions, lava outflows, a lake of hot lava in a crater, hot springs, steam and gas exhalations, evaporation, deflation, corrosion, saline lakes, colourful salt crust and sand dunes. It is the hottest place on Earth, where during the dry season (in July and August) thermometers can read 50 °C [98]. Average temperature for the whole year is 34 °C [43]. Considering how inhospitable Danakil is for its inhabitants, the place seems to be even more interesting and worth visiting. The Danakil depression has lost its water because of desert evaporation and is dry down to Lake Dalol (acid water), 126 m below sea level. Lake Afrera is another salt lake which lies 118 m b.s.l. between these two lakes, there is the multiple shield of volcano of Erta Ale, occupying most of the depression floor. It is the largest and most active of all 34 volcanoes (5 active) situated in the Afar Triangle. The Erta Ale is a typical shield volcano with gentle slopes and elliptical shape due to its location over a major fissure zone along the axis of the Danakil depression both the central vents and the main parasitic vents. Its perimeter lies more than 100 m below sea level and the summit rises to 613 m above sea level. The Erta Ale is an unusual volcano because of the lake of hot, liquid lava in its crater.

At Danakil depression such as acidic or hot springs, saline and/or alkaline lakes, include high temperature, pH, pressure, salt concentration, high levels of radiation, harmful heavy metals and toxic compounds (organic solvents) are found, which are too harsh for normal life to exist. Microorganisms have evolved several

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

structural and chemical adaptations, which allow them to survive and grow in extreme environments. The enzymes of these microbes, which function in extreme environment is thermo stable (extremozymes) have several biotechnological applications. Antibiotics, compatible solutes and other compounds obtainable from these microbes are also finding a variety of uses (Table1).

Existence of these extreme environment support biotechnologically too important acidophil, alkalophil, halophilic microorganisms. This is the unique potential Ethiopian Hyper extremophile and extremophile microbial ecology still needs great exploration and scientific study for the contribution of biotechnologically important enzymes and understanding life process in primitive world and in astronomy study (Figure.1).

In addition to low land below sea level there is also high land above 3500m.a.s.l in Ethiopia for their psychrophilic microbial ecology and microbial community (Figure2).They also boasts of spectacular beauty. The Simien Mountains National Park, home to Mount Ras Dashen, Mount Ancua, and Mount Bwahi, is a

world heritage site. Despite the overall high elevation of Ethiopia, the Simen range is the only place in the country that is regularly snow-covered in winter. Bale Mountains National Park, which hosts Mount Tullu Dimtu, is waiting to be declared a world heritage site.

The Ethiopian Highlands share a similar flora and fauna of other mountainous regions of Africa; this distinctive flora and fauna is known as Afromontane but from the time of the last Ice Age has been populated with some Eurasian (palearctic) flora.

The habitats are somewhat different on either side of the Great Rift Valley that splits the highlands. Above 3000 meters elevation lie the high Ethiopian montane moorlands, the largest afroalpine region in Africa.

The montane moorlands lie above the tree line, and consist of grassland and moorland with abundant herbs and some shrubs that have adapted to the high mountain conditions. Around 10 Ethiopian highest mountains pick also great potential for psychrophilic microbial ecology still need exploration and metagenome study (Table.2).

Table1. Some of extremophil microbial enzymes

Species	T ⁰	Habitat	Enzyme	Reference
Sulfolobales				
<i>Sulfolobus acidocaldarius</i>	75	Terrestrial	DNA polymerase , Proteinase RNA polymerase ,Topoisomerase I,Topoisomerase II	[66,138,29,75]
<i>Sulfolobus solfataricus</i>	80	Terrestrial	DNA polymerase, s-Adenosyl- homocysteine-hydrolase	[177,179]
Thermoproteales				
<i>Thermoproteus tenax</i>	88	Terrestrial	RNA polymerase	[29]
<i>Pyrobaculum aerophilum</i>	100	Marin	Proteinase	[215]
<i>Methanopyrales</i>				
<i>Methanopyrus kandleri</i>	98	Marin	Topoisomerase type I	[197]
Pyrodictiales				
<i>Pyrodictium occultum</i>	105	Marin	DNA polymerase	[212]
Thermococcales				
<i>Pyrococcus furiosus</i>	100	Marin	Proteinase,DNA-polymerase	[212]
<i>Pyrococcus woesei</i>	100	Marin	Proteinase	[130]
<i>Thermococcus stetteri</i>	75	Marin	Proteinase	[130]
<i>Thermococcus ANI</i>	75-80	Terrestrial	Proteinase	[130]
<i>Thermococcus celer</i>	87	Marin	Proteinase	[130]
<i>Thermococcus litoralis</i>	88	Marin	Proteinase	[130]
Desulfurococcales				
<i>Desulfurococcus amylolyticus</i>	90	Terrestrial	Topoisomerase type I, Proteinase	[197]
<i>Desulfurococcus mucosus</i>	88	Terrestrial	RNA polymerase	[29]
<i>Staphylothermus marinus</i>	92	Marin	Proteinase	[130,54]
Thermoplasmatales				
<i>Thermoplasma acidophilum</i>	55-60	Terrestrial	DNA polymerase	[29]
			RNA polymerase	[29]
			Topoisomerase	[75]

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

Table 2. Highest Mountains in Ethiopia as a potential psychrophilic microbial ecology

	Mountain	Elevation
1	Ras Dashen	4,620 meters
2	Ancua	4,462 meters
3	Kidis Yared	4,453 meters
4	Bwahit	4,437 meters
5	Tullu Demtu	4,377 meters
6	Amba Farit	4,270 meters
7	Abune Yosef	4,260 meters
8	Ioll	4,220 meters
9	Bada	4,195 meters
10	Kaka	4,193 meters
11	Ch'ilalo Terara	4,036 meters
12	Gugē	4,200 meters
13	Āmba Ālagē	3,949 meters
14	Baylamt'u Terara	3,777 meters





Figure 1. (Thermophilic, acidophilic, Halophilic, Alkalophilic, Barophilic extremophil microbial ecology of Ethiopia) A. Small salt lake located about 5 km south of the Dallol Volcano, B. Gentle saline balloons in Dallol Volcano, C. Salt field, teepee structure, Asale Lake region, photo Z. Preisner, D. Salt mushrooms structures near the Dallol Volcano, (E-I). Acid lake with salt deposition inside the subsidence structure. Small salt pillars seen in the background Dallol below sea level -126m. (J,L,L) Afdera lake and Asle lake (Halophilic microbial Ecology), (M,N,O) Rift valley hot spring (Thermophilic microbial ecology), (P,Q,R) Ear tale (Fire lake Hyperthermophilic microbial ecology) (Photo Birhanu Gizaw 2011G.C).

SOIL MICROBIAL ECOLOGY

Soil microorganisms are considered hyper-diverse and ubiquitous however, shifts in community response have been documented under variable biotic or abiotic conditions [76]. The wide ranges of topographic and climatic factors, parent material and land use have in Ethiopia resulted in extreme variability of soils [71]. In different parts of the country, different soil forming factors have taken precedence. According to the Ministry of Agriculture about 19 soil types are identified throughout Ethiopia. (Table.4). Soil is a highly heterogeneous environment with its enormous microbial community and species diversity [56]. Microbial diversity in soil ecosystems exceeds, by far, that of eukaryotic organisms. One gram of soil may harbor up to 10 billion microorganisms of possibly, thousands of different species. Several hundreds of metres of fungal hyphae. Soil Studies based on molecular techniques have estimated about 4,000 microbial species per

gram of soil sample [160] (Table3). Microorganisms play an important role in the soil environment. They are the critical factors that determine soil organic matter decomposition, nutrient cycling, soil degradation and bioremediation of soil pollution [133,139]. Mineral composition, texture, SOC concentration, pedogenic processes, microbial activities, exchangeable ions, nutrient reserves, and moisture availability [123]. Due to different soil type and nutrient in side consisting divers and many microorganisms. Within the soil there exist many microbial interactions with, for example, soil invertebrates, the rhizosphere (the 3-4 mm layer of soil surrounding plant roots), mycorrhizal fungal associations and plant-pathogen relationships, and these associations contribute to the development and activity of microbial communities in soils, Thus 19 soil types with at different altitudinal ranges and vegetation as well as crop types favour a great diversity of microbial community in Ethiopia.



Figure2. Ethiopian high pick (A.Bale senate plato B.North mountain national park(Psychrophilic microbialecolgy above 4000m.a.s.l)

Table 3. Dominant bacterial phyla in soil (adapted from [115])

Phyla/Subphyla	Mean Contribution (%)	Range (%)	Examples
<i>α-Proteobacteria</i>	19	2–43	<i>Sphingomonas, Rhizobium, Mesorhizobium, Bradyrhizobium, Methylobacter, Methylophilus, Nitrospira, Nitrobacter, Rhodobacter</i>
<i>β-Proteobacteria</i>	10	2–31	<i>Burkholderia, Alcaligenes, Acidovorax, Collimonas, Nitrosospira, Thiobacillus, Rhodocyclus,</i>
<i>γ-Proteobacteria</i>	8	1–34	<i>Pseudomonas, Xanthamonas, Azotobacter, Thiocapsa, Chromatium</i>
<i>Verrucomicrobia</i>	7	0–21	<i>Chthoniobacter, Opitutus</i>
<i>Bacteroidetes</i>	5	0–16	<i>Chitinophaga</i>
<i>Firmicutes</i>	2	0–7	<i>Clostridium, Bacillus, Lactobacillus</i>
<i>Chlorofl exi</i>	3	0–16	
<i>Planctomycetes</i>	2	0–8	
<i>Gemmatimonadetes</i>	2	0–4	<i>Gemmatimonas</i>
<i>Other groups</i>	5	2–10	
<i>Unknown</i>	2	0–13	

Table 4. Soils Type and Distribution in Ethiopia.

Soil type	Area (km2)	Percent
Acrisol	55,726.5	5.0
Cambisol	124,038	11.1
Chernozems	814	0.07
Rendzinas	16,348	1.5
Gleysols	5,273.5	0.47
Phaeazems	32,551	2.9
Lithosol (Leptosols)	163,185	14.7
Fluvisols	88,261.5	7.9
Luvisols	64,063.5	5.8
Nitosols	150,089.5	13.5
Histosols	4,719.5	0.42
Arenosols	9,024	0.81
Regosols	133,596	12.0
Solonetz	495	0.04
Andosols	13,556	1.2
Vertisols	116,785	10.5
Xarosols	53,171	4.8
Yermosols	34,950	3.1
Solonchaks	47,217.5	4.2

PHYLOSHERIC, RHIZOSPHERIC, RHIZOPLAN AND ENDOPHYTIC PLANT AND CROPS MICROBIAL ECOLOGY

Ethiopia is one of the top 25 biodiversity-rich countries in the world [217] and hosts two of the world’s 34 biodiversity hotspots, namely the Eastern Afromontane and the Horn of Africa hotspots. It is also among the countries in the Horn of Africa regarded as major centre of diversity and endemism for several plant species. The phyllosphere is broadly defined as the surfaces and internal parts of the aerial structures of plants, including flowers, fruits, stems and leaves. Specialized microbial colonists, phytopathogens, spoilage organisms

and periodic immigrants have all been described as residents of this physically diverse habitat.

Bacteria are by far the most numerically abundant colonisers of the phyllosphere, and typical community densities in the order of 2×10^7 cells per cm^2 of leaf surface have been recorded [13] although these numbers can vary from as little as 10^5 to in excess of 1×10^{12} in arid and senescing leaves respectively. The abundance of life in the phyllosphere is matched by the habitat range that plants occupy in both terrestrial and aquatic environments. Plant leaves provide the greatest surface area on the planet, tolerating geographic and climatic extremes that can fluctuate on a daily cycle from sub-zero night time temperatures to leaf surface

temperatures that exceed 50°C in direct sunlight. Endophytes are organisms that inhabit internal plant tissues without apparent disease symptoms [176]. Endophytes are ubiquitous and probably all vascular and non-vascular terrestrial plants harbour them. They have also been isolated from fresh water and marine plants, and from lichens. Endophytes may be distributed in a hyper diverse pattern especially in tropical trees, of which single leaves may be colonised by numerous discrete individual mycelia, some occurring commonly, others being rare. [107]. Rhizosphere is microbial community around plant root; the rhizoplan is microbes adhering with plant root. Rhizosphere microbial colonies have dynamic association with biogeochemical cycling of nutrients (C, P, N, and S) and production of phytohormones or antibiotics [38]. PGPR are well known to colonize plant roots and stimulate plant growth [13]. *Azospirillum sp.*, *Bacillus subtilis sp.*, and *Pseudomonas sp.* have been well studied as plant rhizosphere-colonizing microorganisms [203].

The rhizosphere, influenced by root secretions, can contain up to 10¹¹ microbial cells per gram root [65] and more than 30,000 prokaryotic species [157]. Soil microorganisms (free-living, associative, and symbiotic rhizobacteria) belonging to the genera like *Acinetobacter*, *Burkholderia*, *Enterobacter*, *Alcaligenes*, *Arthrobacter*, *Azospirillum*, *Azotobacter*, *Bacillus*, *Erwinia*, *Flavobacterium*, *Rhizobium*, *Serratia*, *Xanthomonas*, *Proteus*, and *Pseudomonas* are the integral parts of rhizosphere biota [91] and exhibit successful rhizosphere colonization. Ethiopia constitute

about 6500-7000 species vegetation. Woody plants constitute about 1000 species [109]. Other source indicate that The Ethiopian flora is estimated to about 6000 species of higher plants of which 10% are considered to be endemic [99]. Woody plants constitute about 1000 species out of which 300 are trees. The natural vegetation is classified into 12 major vegetation types. Out of these, six are categorized as forest vegetation [109]. As the result of its diverse agroecology in Ethiopia is endowed with diverse crop genetic resources. Thus, the country is one of the Vavilovian centers of origin and diversity for various crops [214] Ethiopia is a centre of origin for many cultivated plants such as Tef (*Eragrostis tef*), noug (*Guizotia abyssinica*), Ethiopian mustard (*Brassica carinata*), enset (*Ensete ventricosum*), anchote (*Coccinia abyssinica*) and coffee (*Coffea arabica*). The country is also a centre of diversity for species such as wheat (*Triticum sp.*), barley (*Hordeum vulgare*), sorghum (*Sorghum bicolor*), pea (*Pisum sativum*), cowpea (*Vigna unguiculata*), chickpea (*Cicer arietinum*), lentil (*Lens culinaris*), chat (*Catha edulis*), shiny-leaf buckthorn (*Rhamnus prinoides*), cotton (*Gossypium herbaceum*), castor bean (*Ricinus communis*), oats (*Avena abyssinica*), and clovers (*Trifolium Sp.*). Wild relatives also exist for most of these species. All these diverse vegetation and crops in Ethiopia harbors magnificent number of Phyllospheric, Rhizospheric, Rhizoplan and endophytic microbial community are a source of phosphate solubilizer, nitrogen fixer, and Antibiotic, Hydrogen cyanides, siderophore, phytohormone, ACC diamase enzyme producer and these great microbial ecology needs to be explored for agricultural and environmental application. (Table 5)

Table 5. Plant growth promoting rhizobacteria and their use

PGPR	Activities	Microbs species/Genera	Reference
Nitrogen fixers	Enhancement in the nitrogen content of soil and hence improvement in plant growth and yield Enhancement in the nitrogen content of soil and improvement in plant growth and yield	<i>Enterobacter</i> , <i>Erwinia</i> , <i>Flavobacterium</i> , <i>Frankia</i> , <i>Klebsiella</i> , <i>Burkholderia</i> , <i>Pseudomonas</i> , <i>Rhizobium</i> , <i>Azospirillum</i> , <i>Alcaligenes</i> , <i>Azotobacter</i> , <i>Acetobacter</i> , <i>Bacillus</i> ,	[90,31,88,7]
Phytohormone production	Favorable influence on physiological plant processes leading to plant growth promotion	<i>Rhizobium</i> , <i>Pseudomonas</i> , <i>Azotobacter</i> , <i>Bacillus</i> , <i>Enterobacter</i> , <i>Alcaligenes</i> , <i>Bradyrhizobium</i> , <i>Xanthomonas</i>	[74,48,6]
Siderophore production	Enhancement in solubilization of ferric ions and hence improvement in iron availability for plants. Also contribute towards phytopathogen inhibition	<i>Pseudomonas</i> , <i>Bacillus</i> , <i>Serratia</i> , <i>Rhodococcus</i> , <i>Acinetobacter</i>	[49,132, 183,187]
Phosphate solubilization	Conversion of insoluble forms	<i>Bacillus</i> , <i>Pseudomonas</i> , <i>Rhizobium</i> ,	[110, 42,

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

	of phosphorus to plant accessible form, making it available to the plants	<i>Serratia, Kushneria, Rhodococcus, Arthrobacter</i>	[226]
Antibiotic production	Inhibition of soil borne phyto pathogens thus leading to suppression of the diseases	<i>Pseudomonas, Bacillus, Serratia, Streptomyces</i>	[209,10, 154,121, 147,116]
Lytic enzymes production (Chitinases, β -1,3 glucanases, proteases, cellulases and laminarinase)	Laminarinase Cell lysis of soil borne fungal pathogens of plants	<i>Pseudomonas, Bacillus, Serratia</i>	[79,83, 166]
ACC deaminase Hydrolysis of ACC	Reduction in ethylene production and plant growth promotion.	<i>Pseudomonas, Bacillus</i>	[23]
Salicylic acid production	Induced systemic resistance (ISR) in plants against pathogens	<i>Bacillus, Serratia</i>	[61,20]
organic acids Production	Solubilization of mineral nutrients for plant uptake	<i>Pseudomonas, Bacillus, rhizobiac</i>	[22,171]
Metal resistance	Effective metal sequestering	<i>Pseudomonas</i>	[143]

ETHIOPIA TRADITIONAL FOOD, CONDIMENTS AND BEVERAGE A POTENTIAL MICROBIAL ECOLOGY

Ethiopia is one of the countries where a wide variety of traditional fermented foods, beverages, suace and condiments are consumed during religious ceremonies, social gatherings, burial ceremonies, holidays, marriage ceremony, non religious ceremonies and iqub as well different festivals etc. The diverse above 80 ethnic groups in the country gave rise to the existence of cultural diversity and life style thus to use their own traditional foods such as Injera, Kocho, Bulla, Yoghurt, Curdle, Cheese and local drinks and condiment such as Tella, Tej, Borde, Cheka, Areke, Awaze, Shameta, Azo, Datta, siljo, keriboare a potential microbial ecology in Ethiopia, (Table 6 and Figure 3). Especially beverage lactic acid bacteria, acetic acid, yeast and filamentous fungi diversity are magnificent [77,9,89]. These microbes associated with fermented food and beverage has great health advantages. Fermented foods have high nutritional values (Vitamin K₂, trace minerals, B-vitamins), are easy to prepare and are

economical. Fermented foods contain healthy live bacteria known as probiotics, such as *Bifidobacteria* and various *Lactobacilli* improve immune status of the colon, and are involved in preventing and depleting pathogenic and infectious bacteria in the gastrointestinal tract. Further more, probiotic bacteria are effective against lactose intolerance and diarrhoea [141, 165]. These organisms are reported to have bacteriostatic, bactericidal, viricidal, anti-leukaemic and antitumor effects in the consumer [189,195]. Probiotic microorganisms have great physiological impact as their fermentation of complex, nondigestible carbohydrates in the colon produces short chain fatty acids that have numerous benefits. These short chain fatty acids are reported to play a role in prevention against colon cancer and other diseases [124,141]. This wide number of traditional food and beverages unique in raw material types, methods of preparation, types brewing equipment, fermentation nature and period, utilization culture harbor magnificent diversity of microorganisms in Ethiopia still need great exploration for health application and pharmaceutical industry. (Figure 4,5,6,7,8)

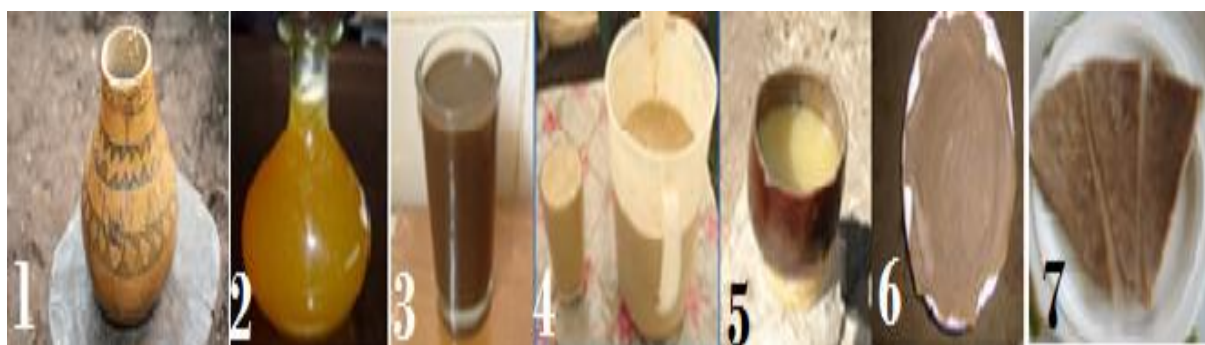


Figure 3. Some Ethiopian traditional food and Beverage 1. Cheka, 2. Tej, 3. Tella, 4. Borde, 5. korefe, 6. Injera, 7. Kocho bread

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort



Figure 4. Types of raw materials and equipment used for preparation and utilization of Cheka beverage in arbamich, konso, Jinka area of southern Ethiopia. (Photo, BirhanuG.)



Figure 5. Tella and Areki (Local Sprite) raw materials and equipment for brewing. (Photo, BirhanuG.)



Figure 6. Kocho fermentation process and utilization of Kocho bread with raw meat in southern Ethiopia



Figure 7. Milk processing equipment in Borena zone, Ethiopia. (Photo, BirhanuG.)



Figure 8. Some of traditional beverage drinking culture in different societies of Ethiopia (Photo Birhanu Gizaw 2012G.C)

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

Table 6. Ethiopian traditional food, condiments, beverage and their microbial association

		Microbial Species	Source
Fermented sausage	Wakalim	<i>Lactobacillus plantarum</i> , <i>Lactobacillus brevis</i> , <i>Lactobacillus delbrueckii</i> spp. <i>Lactis Lactobacillus pentosus</i>	[126]
Dairy product	Cottage cheese	<i>Lactobacillus plantarum</i> , <i>Lactobacillus fermenti</i> , <i>Kluyveromyces bulgaricus</i> , <i>Candida psudotropicalis</i> , <i>Kluyveromyces lactis</i>	[161]
	Curdle milk	<i>Lactobacillus</i> , <i>Lactococcus</i> , <i>Leuconostoc</i> , <i>Enterococcus</i> and <i>Streptococcus</i> (LAB). <i>Micrococcus</i> species	[8]
	Yoghurt	<i>St. thermophilus</i> , <i>L. delbrueckii</i> ssp. <i>bulgaricus</i>	
Fermented camel milk	Ititu	<i>Lactobacillus salivarius</i> , <i>Lactobacillus plantarum</i> , <i>Lactobacillus delbrueckii</i> subsp. <i>Bulgaricus</i> , <i>Lactococcus lactis</i> subspecies <i>cremoris</i> , <i>Lactococcus lactis</i> subspecies <i>lactis</i> , <i>Enterococcus faecalis</i>	[69]
Naturally fermented sour camel milk	Dhanaan	<i>Streptococcus</i> and <i>Lactococcus</i> (<i>Lactobacillus bulgaricus</i> and <i>Streptococcus thermophilus</i>)	[173,30]
Beverage	Tella	<i>L. pastotianumi</i> , <i>Saccharomyces carlsbergensis</i> , <i>Saccharomyces Cerevisiae</i> , <i>Acetobacter xylinum</i> <i>Lactobacillus pastorianum</i> , <i>Enterobacteriaceae</i> , <i>Lactobacillus</i> , <i>Lactococcus</i> ,	[188,24]
	Tej	<i>Sccharomyces cerevicieae</i> , <i>Kluyveromyces veronae</i> , <i>Kluyveromyces bulgaricus</i> , <i>Debaromyces phaffi</i> .	[25]
	Borde	<i>Weissella confusa</i> , <i>Lactobacillus brevis</i> , <i>Lactobacillus viridescens</i> , <i>Pediococcus pentosaceus</i> and <i>P. pentosaceus</i> subsp. <i>intermedius</i> <i>Lactobacillus curvatus</i> , <i>P. acidilactici</i> , <i>Lactobacillus collinoides</i> , <i>Lactobacillus sanfrancisco</i> , <i>Lactobacillus pontis</i> and <i>Lactobacillus delbrueckii</i> subsp. <i>delbrueckii</i>	[125]
	Cheka		
	Keneto		
	Keribo		
	korefe	<i>Lactic acid bacteria</i> ; (<i>Lactobacillus</i> , <i>Lactococcus</i> , <i>Pediococcus</i> , <i>Enterococcus</i> , <i>Weissella</i> Spp.)	[87]
	Bukire		
	Merissa		
	Booka		
	Sprite(Areke)		
	Bubugn	<i>Lactic acid bacteria</i> ; mold, yeast, mesophilic aerobic bacteria	[211]
	Imbushbush		
	Shamita	<i>Streptococci</i> , <i>micrococci</i> , <i>staphylococci</i> , <i>Bacillus</i> spp., <i>Saccaromyces</i> , <i>Rhodotrula</i> spp.	[127]
Food	Injera	<i>Pediococcus pentosaceus</i> <i>Lactobacillus fermentum</i> (28.04%), <i>Lactococcus piscium</i> , <i>Lactococcus plantarum</i> (<i>Pediococcus acidilactici</i> , <i>Leuconostoc mesenteriodes</i> subsp. <i>mesenteriodes</i> , <i>Lactococcus raffinolactis</i> , <i>L. mesenteriodes</i> subsp. <i>dextranicum</i> , <i>Enterococcus casseliflavus</i> , and <i>Saccharomyces cerevisiae</i> <i>Candida humilis</i> , <i>Candida tropicalis</i> <i>Saccharomyces exiguus</i> and <i>Pichia norvegensis</i> , <i>Lactobacillus plantarum</i> , <i>Lactobacillus brevis</i> , and <i>Lactobacillus fermentum</i>	[16]
	Kocho	<i>Lactobacillus</i> , <i>Leuconostoc</i> , <i>Pediococcus</i> and <i>Lactococcus</i> , <i>Cryptococcus albidus</i> var. <i>aerus</i> , <i>Guilliermondella selenospora</i> , <i>Rhodotrula acheniorum</i> <i>Trichosporon beigeli</i> , <i>Cryptococcus terreus</i> A, <i>Candida zeylandae</i> , <i>Kluyveromyces delphensis</i> , <i>luenstoc</i> , <i>Leuconostoc mesenteroides</i> , <i>Lactobacillus coryneformis</i> , <i>Lactobacillus plantarum</i> , <i>Clostridium butyricum</i> , <i>Clostridium beijerinckii</i> , <i>Clostridium sticklandii</i> , <i>Bacillus subtilis</i> , <i>Bacillus licheniformis</i> , <i>Bacillus cereus</i> , <i>Rhodotrula glutinis</i> , <i>Kluyveromyces maxianus</i> , <i>Pichia</i>	[167,32,164]

		<i>membranefaciens</i>	
	<i>Bulla</i>	<i>Lactobacillus</i> , <i>Leuconostoc</i> , <i>Pediococcus</i> and <i>Lactococcus</i> spp, [164] <i>Rhodotrula glutines</i> , <i>pichia membranefacanies</i> , <i>Bacillus</i> spp.	
<i>Condiments</i>	<i>siljo</i>	<i>Lactobacillus acidophilus</i> , <i>L. plantarum</i> and <i>L. delbruekii</i> , [208] <i>Saccharomyces cerevisiae</i> , <i>Rhodotorula glutinis</i> , <i>Yarrowia lipolyficu</i> and <i>S. rouxii</i> , <i>Micrococcus</i> , <i>Bacillus</i> , <i>Lactobacillus</i>	
	<i>Awaze</i>		
	<i>Azo</i>	<i>Lactobacillus plantarum</i> , <i>Lactobacillus delbrueckiisslactis</i> , [68] <i>Streptococcus criceti</i>	
	<i>Data</i>		

REMUN MICROBIAL ECOLOGY

The inhabitants of the rumen microbial ecosystem, a complex consortium of different microbial groups living in symbiotic relationship with the host, act synergistically for the bioconversion of lignocellulosic feeds into volatile fatty acids which serve as a source of energy for the animals. (Table7)The rumen is a suitable environment having unique characteristics such as temperature around 38 to 42°C, redox potential was found (-350 mV, with fluctuations between -250 and -450 mV), In the rumen, a, with result of a strong ambient environment due to the lack of oxygen. The rumen is usually well buffered, due to the presence of bicarbonates and phosphates founded in continuous flow of saliva, Saliva production can be high in a cow, reaching over 180 L/day. However, the pH can vary due the nature of the diet, but typically found between 5.5 and 7.0 when ruminants are fed with predominantly on forage diet [1, 178,181, 145,206].

The efficiency of ruminants to utilize such a wide variety of feeds is due to highly diversified rumen microbial ecosystem consisting of bacteria (10^{10} – 10^{11} cells/ml, representing more than 50 genera), 10^8 archaea per g digesta, ciliate protozoa (10^4 – 10^6 /ml, from 25 genera), anaerobic fungi (10^3 – 10^5 zoospores/ml, representing five genera) and bacteriophages (10^8 – 10^9 /ml)1.

These numbers might even be larger as majority of them are non-culturable. The diversity of bacterial and archaeal species in the rumen is estimated to be approximately 7,000 and 1,500 species, respectively. Which represented 19 existing phyla, with Firmicutes (~56%), Bacteroidetes (~31%), and Proteobacteria (~4%) being the predominant [113]. The synergism and antagonism among the different groups of microbes and even among different genera of the same group is so diverse and complicated that it is difficult to quantify the role played by

any particular group of microbes present in the rumen. Methanogens are present in the rumen in large numbers varying from 10^7 to 10^9 cells/ml of rumen liquor depending upon the type of diet given to the animals. Seven different species representing five genera of methanogens have been reported from the rumen of different animals, i.e. *Methanobacterium formicicum*, *Methanobacterium bryanti*, *Methanobrevibacter ruminantium*, *Methanobrevibacter smithii*, *Methanomicrobium mobile*, *Methanosarcina barkeri* and *Methanoculleus olentangyi* [118,114].

The methanogens play a vital role in the rumen of scavenging molecular hydrogen generated during rumen fermentation, thereby making rumen fermentation a continuous process, but this leads to a significant loss of gross energy consumed by the animals. There is also a close association between entodinio morphid protozoa and some of the bacteria, which attach to the pellicle of protozoa.

Eleven species of entodiniomorphid protozoa have been found to have adhered methanogens like *Entodinium longinucleatum*, *Eudiplodinium maggii*, *Entodinium bursa* and *Eremoplastron bovis*. The methanogens attach themselves with the ciliate protozoa to get a constant supply of hydrogen.

On pumping hydrogen in the rumen, the methanogens get detached from the protozoa [202]. In Ethiopia a total of 47.5 million cattle exists and 28 cattle breed [70] but other sources put the numbers higher 55.03 Million.

These are comprised 27.35 million sheep with 9 sheep breeds, 28.16 million with 8 goat breeds , 1.1 million with 7 camel breeds, 6.95 million with 6 donkey breeds , 1.96 million with 8 horse breeds, 0.36 million with 2 mule breeds and 51.35 million with 7 chicken breeds. This huge population of cattles with differs in breeds, geographical area, and grazing habits, feed and fodder type in Ethiopia which harbors

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

verydiver’s remun microbial community used for different biotechnological application and a

potential microbial ecology in Ethiopia still need great exploration.(Figure9).



Figure 9. Cattle at Borenazone (. (Photo, BirhanuGizaw.)

Table 7. Commonly known rumen microbial community.

Cellulytic bacteria	<i>Fibrobacter succinogenes</i>	[112,199, 219,159, 163,57, 104,47]	Acid utilizers	<i>Megasphaera elsdenii</i>	[46,150]	
	<i>Bacteroides succinogenes</i>			<i>Peptostreptococcus elsdenii</i>		
	<i>Ruminococcus flavefaciens</i>			<i>Wollinella succinogenes</i>		
	<i>Ruminococcus albus</i>			<i>(Vibrio succinogenes)</i>		
	<i>Clostridium cellobioparum</i>			<i>Veillonella gazogenes</i>		
	<i>Clostridium longisporum</i>			<i>(Veillonella alcalescens,</i>		
	<i>Clostridium lochheadii</i>			<i>Micrococcus lactolytica)</i>		
	<i>Eubacterium cellulosolvens</i>			<i>Oxalobacter formigenes</i>		
	<i>Butyrivibrio fibrisolvens</i>			<i>Desulphovibrio desulphuricans</i>		
	<i>Fibrobacter succinogenes</i>			<i>Desulphatamaculum ruminis</i>		
<i>Ruminococcus flavefaciens.</i>	<i>Succiniclasticum ruminis</i>					
Cellulytic fungi	<i>Neocallimastix frontalis</i>	[81]	Acetogenic bacteria	<i>Acetitomaculum ruminis</i>	[81]	
	<i>Piromyces communis</i>			<i>Eubacterium limosum</i>		
	<i>Orpinomyces joyonii</i>			<i>Streptococcus caprinus</i>		
Cellulytic Protozoa	<i>Enoploplastron triloricaatum</i>	[223,102, 162]	Tannin degraders	<i>Eubacterium oxidoreducens</i>	[223,102, 162]	
	<i>Eudiplodinium maggii</i>			Mimosine degraders		<i>Synergistes jonesii</i>
	<i>Ruminobacter amylophilus</i>		Methanogenic			<i>Methanobrevibacter ruminantium</i>
	<i>Bacteroides amylophilus</i>					<i>Archea Methanobacterium formicicum</i>
	<i>Prevotella ruminicola</i>			<i>Methanosarcina barkeri</i>		
<i>Bacteroides ruminicola</i>	<i>Methanomicrobium mobile</i>					
Dextrins Degradar	<i>Succinivibrio amyolytica</i>			<i>Mycoplasma Anaeroplasma bactoclasticum</i>		

	<i>Succinivibrio dextrinosolvens</i>			<i>Anaeroplasma abactoclasticum</i>	
	<i>Succinivibrio amylolytica</i>		Pectin	<i>Treponema saccharophilum</i>	[64]
	<i>Selenomonas ruminantium</i>			<i>Lachnospira multiparus</i>	
	<i>Lactobacillus acidophilus, L. casei</i>			<i>Pectin Treponema saccharophilum</i>	
	<i>L. fermentum, L. plantarum, L. brevis,</i>			<i>Succinivibrio dextrinosolvens</i>	
	<i>L. helveticus</i>			<i>Lachnospira multiparus</i>	
	<i>Bifidobacterium globosum, B. longum</i>				
	<i>B. thermophilum</i>		Protein degraders	<i>Prevotella ruminicola</i>	[111,73,51]
	<i>B. ruminale</i>			<i>Ruminobacter amylophilus</i>	
	<i>B. ruminantium</i>			<i>Entodinium caudatum</i>	
Other bacteria	<i>Actinobacillus succinogenes</i>	[103,198, 180,18,150]		<i>Eudiplodinium medium</i>	
	<i>Mannheimia succiniciproducen</i>			<i>Clostridium bifermentans</i>	
	<i>Desulfotomaculum ruminis</i>		<i>Bacteroides amylophilus</i>		
	<i>Treponema saccharophilum</i>		<i>Bacteroides rutminicola</i>		
	<i>Wolinella succinogenes</i>		<i>Butyrivibrio fibrisolvens</i>		
	<i>Lactobacillus ruminis</i>		Urea hydrolyzers	<i>Megasphaera elsdenii</i>	[172, 129]
	<i>Megasphaera elsdenii</i>			<i>Enterococcus faecium</i>	

HUMAN MICRO BIOTA

The human body is also an ecosystem. It is home to trillions of bacteria, viruses, fungi, and other tiny organisms estimated at between 75 trillion and 200 trillion. Together they form communities that make up the human microbiome. Like fingerprints, no two human microbiomes are the same. That makes each person just an ecosystem, but a unique ecosystem. (Table 8). According to a recent National Institutes of Health (NIH) estimate, 90% of cells in the human body are bacterial, fungal, or otherwise non-human cell, It may be no surprise that many of our body's most diverse populations of bacteria live on the skin, which is our point of contact with the world. There are at least 1,000 different species of skin bacteria, along with dozens of fungi and other microbes. Most aren't harmful, and many protect us. Currently, it is thought the human body contains 2-5 pounds of microbes, constituting ~1-3% of our body mass, As much of this is in our gastrointestinal tract, which represents ~10% of our mass, it is not surprising that it can exert profound effects on our physiology and well-being [151,182]. The microbial community inhabiting the gastrointestinal tract (GIT) is characterized by its high population density, wide diversity, and

complexity of interactions and are ten times more numerous than number of the body cells in total [44,59,101,96,174]. Nine of twenty five known Bacteria types were found within the human gastrointestinal tract microbiota. Predominating are Firmicutes (46-60%), Proteobacteria (10-30%), Bacteroidetes and Actinobacteria (8-28%) [204,140] The majority of GIT microbiota reside in colon their abundance reach 10^{12} cells/g of luminal content [96]. Population of upper parts of the human gastrointestinal tract (mouth, esophagus, stomach) is less differential and numerous. Human mouth is resided by members of 9 Bacteria types, 1 Archaea type and is considered to be the major population of upper GIT (10^8 cfu/g). 700 bacterial species were isolated from human mouth. Majority of them belong to *Streptococcus* sp. (type Firmicutes) which are characterized with the ability of adherence to various surfaces such as teeth, oral mucosa or tongue. Other bacterial species isolated from mouth belong to *Peptococcus*, *Staphylococcus*, *Bifidobacterium*, *Lactobacillus* and *Fusobacterium*. In addition to bacteria, the oral cavity is colonized by yeasts such as *Candida albicans* [227]. Intestinal microbiota includes microorganisms colonizing such parts of gastrointestinal tract as the small intestine

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

(jejunum and ileum), colon and rectum. Microbiota of these parts of the digestive system is much more diverse and larger than the population of upper parts of GIT. This complex ecosystem consists of 17 families, 45 genera and over 1,000 species of microorganisms [95]. Large intestine is inhabited by 800 species belonging to 9 Bacteria types and one type of Archaea. Among 9 Bacteria types, 2 types predominate Firmicutes (46-60%) and Bacteroidetes (with Actinobacteria 8-28%) [204,191]. More than 270 species out of 800 that can be found in colon belong to those 2 Bacteriatypes. Both Firmicutes and Bacteroidetes, characterize in high fermentation activity. [204]. In other literature the human colon only contains $> 10^{11}$ bacterial cells/g contents belonging to as many as 400 different species [45,136,190]. Gut microbiota can be divided into two groups' residents and travelers. Residents are autochthonous components, often symbiotic with human organism while travelers are allochthonous that are result of diet and other environmental factors. 70% of GIT microbiota is considered to be inconstant and its abundance depends on human organism. Composition of

microbiota in various parts of gastrointestinal tract differs due to variable environmental condition [140]. In addition to bacteria; the second fairly large groups are viruses. From the human fecal 1200 viral genotypes were isolated and their number reaches up to 10^9 virions per gram of dry weight [142]. The intestinal microbiota has three functions: metabolic, trophic and protective. The most important role is to build resistance to infection (protective function) by increasing the activity of the immune system and creating a natural barrier against colonization by exogenous pathogenic bacteria. This barrier is based on the competition (the living space and nutrients) by the production of bacteriocins and organic acids, which by lowering the pH inhibit the growth of pathogenic microorganisms. Which play a fundamental role in our well-being [95,128, 204,140,191,192]. Ethiopia is a multi-ethnic and diverse culture country which comprises with an estimated population of 104.34 million in 2017 [1]. The life style, settlement area, feeding habit and culture of this huge population are a source of magnificent potential for diverse microbial communities that still needs great exploration.

Table 8. Genera /species commonly human micro flora

Mouth	<i>Klebsiella sp.</i>	<i>Candida albicans</i>	<i>Staphylococcus aureus</i>	
<i>Staphylococci</i>	<i>Enterobacter sp.</i>	<i>Corynebacterium spp</i>	<i>Staphylococcus epidermidis</i>	[100,10,, 72,85, 155,19, 192]
<i>Enterococci</i>	<i>Proteus mirabilis</i>	<i>Corynebacterium parvum</i>	Eye	
<i>Streptococcus mutans</i>	<i>Lactobacillus spp.</i>	<i>Demodex folliculorum</i>	<i>Chlamydomphila pneumoniae</i>	
<i>Streptococcus sanguis</i>	<i>Peptostreptococcus Spp</i>	<i>Enterobacter cloacae</i>	<i>Haemophilus aegyptius</i>	
<i>Streptococcus mitis</i>	<i>Diphtheriods</i>	<i>Epidermophyton floccosum</i>	<i>Haemophilus influenzae</i>	
<i>Peptostreptococcus</i>	<i>Streptococci</i>	<i>Micrococcus spp</i>	<i>Moraxella spp</i>	
<i>Corynebacterium</i>	<i>Bacteriodes Spp.</i>	<i>Micrococcus luteus</i>	<i>Neisseria spp</i>	
<i>Lactobacillus</i>	<i>Candida Spp.</i>	<i>Mycobacterium spp</i>	<i>Staphylococcus aureus</i>	
<i>Nocardia</i>	<i>Gardnerella vaginalis</i>	<i>Neisseria spp</i>	<i>Staphylococcus epidermidis</i>	
<i>Odontomyces viscosus</i>	<i>Mycobacterium Spp</i>	<i>Peptostreptococcus spp</i>	<i>Streptococcus viridians</i>	
<i>Bacterionema matruchotii</i>	<i>Lactobacillus spp.</i>	<i>Malassezia ovale</i>	Stomach	
<i>Actinomyces bifidus</i>	Skin micro flora	<i>Propionibacterium spp</i>	<i>Helicobacter pylori</i>	
<i>Actinomyces israelii</i>	<i>Acinetobacter spp</i>	<i>Propionibacterium acnes</i>		
<i>Actinomyces naeslundii</i>	<i>Bacillus spp</i>	<i>Pseudomonas aeruginosa</i>		

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

<i>Actinomyces odontolyticus</i>	<i>Candida albicans</i>	<i>Sarcina spp</i>	
<i>Propionibacterium acnes</i>	<i>Corynebacterium spp</i>	<i>Staphylococcus aureus</i>	
Small intestine	<i>Corynebacterium parvum</i>	<i>Staphylococcus haemolyticus</i>	
<i>Lactobacillus spp.</i>	<i>Demodex folliculorum</i>	<i>Streptococcus viridans</i>	
<i>Bacteriodes Spp.</i>	<i>Enterobacter cloacae</i>	Vagina	
<i>Clostridium spp</i>	<i>Epidermophyton floccosum</i>	<i>L. iners</i>	
<i>MycobacteriumSpp</i>	<i>Micrococcus spp</i>	<i>L.crispatus</i>	
<i>Entrococci SPP</i>	<i>Micrococcus luteus</i>	<i>L. gasseri</i>	
<i>Entrobacterceae Spp.</i>	<i>Mycobacterium spp</i>	<i>L. jenesenii</i>	
Large Intestine	<i>Neisseria spp</i>	<i>L. acidophilus</i>	
<i>Bacteroides fragilis</i>	<i>Peptostreptococcus spp</i>	<i>L. fermentum</i>	
<i>Bacteroidesmelaninogenicus</i>	<i>Malassezia ovale</i>	<i>L. plantarum</i>	
<i>Bacteroides oralis</i>	<i>Propionibacterium spp</i>	<i>L. brevis</i>	
<i>Lactobacillus</i>	<i>Propionibacterium acnes</i>	<i>L. casei</i>	
<i>Clostridium perfringens</i>	<i>Pseudomonas aeruginosa</i>	<i>L. vaginalis</i>	
<i>Clostridium septicum</i>	<i>Sarcina spp</i>	<i>L. delbrueckii</i>	
<i>Clostridium tetani</i>	<i>Staphylococcus aureus</i>	<i>L. salivarius</i>	
<i>Bifidobacterium bifidum</i>	<i>Staphylococcus epidermidis</i>	<i>L. reuteri</i>	
<i>Staphylococcus aureus</i>	<i>Staphylococcus haemolyticus</i>	<i>L. rhamnosus</i>	
<i>Enterococcus faecalis</i>	<i>Streptococcus viridans</i>	Mucus membrain	
<i>Escherichia coli</i>	<i>Acinetobacter spp</i>	<i>Chlamydia trachomatis</i>	
<i>Salmonella enteritidis</i>	<i>Bacillus spp</i>	<i>Hemophilus influenzae</i>	
<i>Fusobacterium prausnitzii</i>			

AQUATIC ECOSYSTEM MICROBIAL ECOLOGY

Ethiopia, known as the 'water tower' of north-eastern Africa, on average, the surface water potential amounts to over 110 billion cubic metres per annum[5]. Ethiopia comprise the part of great rift valley and high land lakes, in general Water resources of Ethiopia:12 river basin, 11 fresh lakes,9 saline lakes, 4 crater lakes, >12 major swaps and wetlands. The Ethiopian rift valley also known as the Afro-Arabian rift is one of the greatest East African rift valleys that divides the Ethiopian highlands in to north and south halves. The volcano-tectonic basin so created as a result of faulting millions of years ago, later modulated in to beautiful lakes. There are several fresh water lakes found embedded in this basin, among them the most prominent are e.g., the Lake Abaya, Chamo, Koka, Beseka, Ziway, Abijata, Shala and Lake Hawasa. Due to its PH difference, alkalinity, salinity, shallowness, other physical and chemical nature of the lake comprise very rich algal diversity, cyanobacteria, archae, bacteria, phytoplankton and zooplankton. For example In Bishoftu crater lakes, dominance by green algae, diatoms

and cyanobacteria., mainly *Microcystis aeruginosa* and *Chroococcus sp.*, cyanobacterium, *Arthrospira fusiformis* (formerly called *Spirulina platensis*) are found [58]. *Spirulina (Arthrospira platensis)* is a micro-algae and one of the smallest, most ancient and robust organisms living on Earth and alone produces about 60% of the Earth's oxygen. Lake Arenguadi (Green Lake), Basaka, Shala, Chitu, Abijatta are source of *Spirulina (Arthrospira platensis)* [12] (Figure10). Different microlge genera identified from Arenguade and Killole lakes, Cyanophyta (*Microcystis*, *Dolichospermum*, *Anabaena*, *Aphanocapsa*, *Aphanizomenon*, *Cylindro-spermopsis*, *Nostoc*, *Merismopedia*, *Chroococcus*) Chlorophyta :- (*Spirogyra*, *Scendesmus*, *Pediastrum*, *Chlamydomonas*, *Closterium*, *Selenastrum*, *Cosmarium*, *Treubaria*, *Gonium*, *Chlorella*, *Volvox*, *Tetrastrum*, *Golenikia*, *Haematococcus*) Bacillarophyta: (*Melosira*, *Navicula*, *Nitzschia*) Dinoflagellated:- (*Ceratium*) [222], *A. hydrophila*, *A. caviae*, *A. sobria*, *A. salmonicida*, atypical, *E. aerogenes*, *E. coli*, *P. mirabilis*, *P. shigelloides*, *Y. enterocolitica* are bacteria are isolated from Tana lake[11]. There for the Ethiopia aquatic ecosystem are a potential source of microbial

community and microbial ecology for many biotechnological applications.

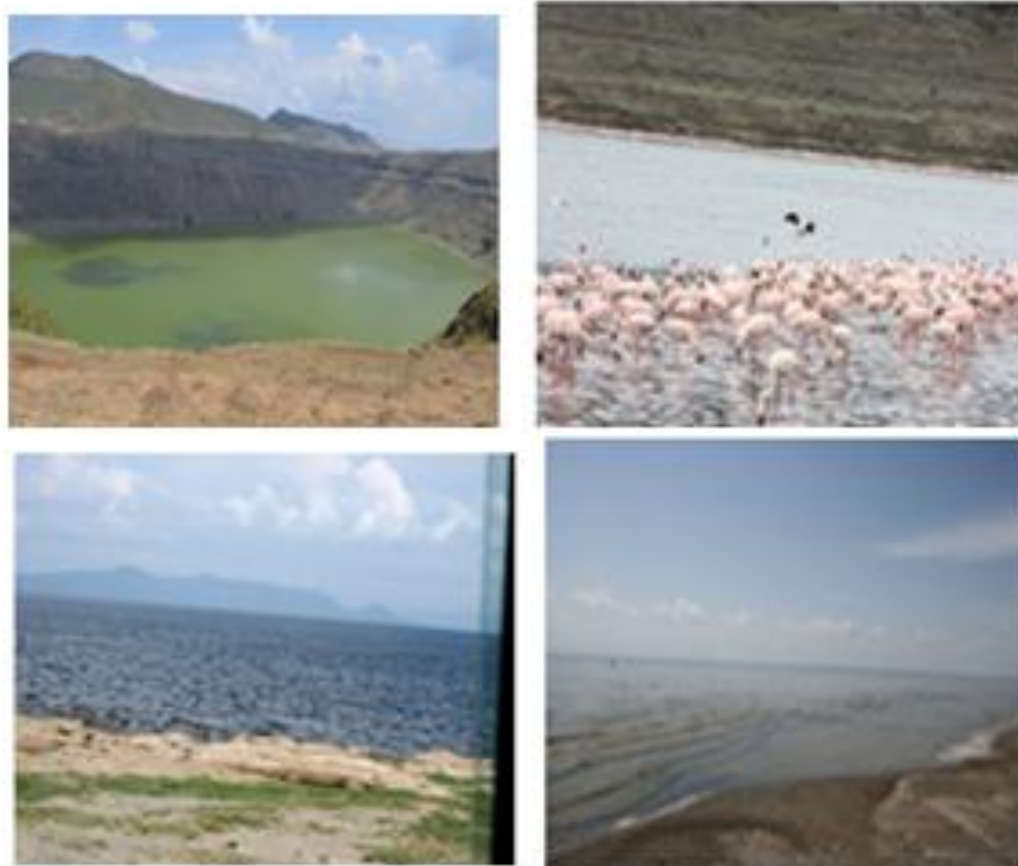


Figure 10. Lake Arenguade, Lake chitu, Lake shalla, Lake Abya Left to right (the source of spirulina)

TERMITE GUTS SYMBIONT MICROBIAL ECOLOGY

Termites are insects from the order Isoptera. They are usually called white ants. They are small to medium in size with a dull white to light and dark brown body and characterized by their colonial behavior [210,213]. Termites are among the most important lignocellulose-digesting insects and possess a variety of symbiotic microorganisms in their hindguts, including bacteria, Archaea and Eukarya [131].

Termites can be classified into six families and fifteen Subfamilies which the first five family belong to lower termites and the sixth family belongs to higher termites, 2600 described termite species world wide recorded [137]. The termite gut is bioreactor or, fermentation chambers' analogous to the rumen of sheep and cattle (i.e. anoxic environments for an anaerobic, oxygen-sensitive microbiota). [26,27].

Termite guts represent excellent models of highly structured microenvironments, high microbial diversity and community structure, physiological adaptations to various

environmental factors, metabolic interactions among microbial populations, and carbon and electron fluxes at the community level. There for Termites are recognized as "ecosystem engineers" Wood is the major substrate Posses a special gut for symbiosis with wood degrading protists and bacteria. The diversity of termite gut communities is extraordinarily high hemicelluloses - degrading bacteria [193], lignolytic bacteria [34], cellulolytic bacteria [218], aromatic-degrading bacteria [82] and nitrogen-fixing bacteria [80].

The genus *Macrotermes* is found throughout Ethiopia and so far 12 species have been described in the Ethiopian region and built tall mounds. (Figure, 11). In Africa they build large mounds which are a characteristic feature of many grasslands and savanna woodlands [196,4,2].

Macrotermes builds large epigeal mounds from which the termites forage outwards for distances of up to 50 m in galleries/runways either just below or on the soil surface [3].

The hindguts of *R. flavipes* and *Thoracotermes macrothorax* show a considerable genetic

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

diversity, and comprise strains belonging to the genera *Enterococcus* and *Lactococcus* [17], the methanogenic taxa *Methanobacteriaceae*, *Methanosarcinaceae*, and *Methanomicrobiaceae*, although in one study three clones grouped within the phylogenetic radiation of the non-methanogenic

Thermoplasmatales [205]. Termites are abundant in Ethiopia in central rift valley, Borena and in different part of Ethiopia where a great microbial communities symbiont is found that still requires detail study.



Figure 11. Termite mound at Borena, Ethiopia (Photo Birhanu Gizaw)

EXISITU MICROBIAL CONSERVATION EFFORT

Microorganism's Conservation Effort at Ethiopian Biodiversity Institute

The majority of the biomass and biodiversity of life on the Earth is accounted by microbes. "Microbes orchestrate life on earth" seems more a philosophy meaningful than a scientific assert. They live on this planet since more than three billion of years and their capability to adapt to several environments make them still the "highlanders. Because of the uncertainties associated with in-situ conservation of microorganisms, ex-situ preservation plays a major role in microbiology and include the gene banks, culture collections and microbial resource centers forming the repository for microbial isolates and do away with need for costly and time consuming re-isolation protocols. The CBD encourages adoption of measures for ex-situ conservation of biodiversity, preferably in the country of origin. Application of this approach is supported by the World Federation for Culture Collection (WFCC) and Directory of Collection of Cultures of Microorganisms. There are some 480 registered microbial culture collections worldwide, large service collections, who make their catalogues accessible include American Type Culture Collection (ATCC), the Belgian Coordinated collections of microorganisms in Louvain-la-Neuve, Brussels and Gent (BCCM), Centraalbureau voor Schimmel cultures in

Utrecht, Netherlands (CBS), the Czech Collection of microorganism, Brno (CCM), Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany (DSMZ), the Institute for Fermentation, Osaka, Japan (IFO), CABI bioscience.

Ethiopia has a well organized gene bank found in Ethiopian Biodiversity institute where dateback established in 1976 through the bilateral agreement between the Ethiopian Government and Government of the Federal Republic of Germany. Microbial Directorate one of the department in the at Ethiopian Biodiversity institute for few years acknowledged service in regards of institute establishment years and this directorate mandated for exploration, documentation, conserving and utilization of microbial genetic resource of the country. Microorganisms have great value of mankind because they benefits agriculture, industry, medicine & environment in various ways. The microbial diversity represents metabolic, structural, morphological and genetic diversity. Conventional methods for isolating and identifying microbes have been a limiting factor for exploring and exploiting microbial wealth. These methods have not been able to deliver new enzymes, molecules, products, antibiotics etc. due to very limited variability. Since, we are not able to culture majority of these organisms; there is a demand for novel techniques and effective strategies to tap the unexplored diversity [97]. A rich microbial diversity is anticipated

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

In Ethiopia due to altitude difference, climate, and edaphic versatility but a lack of adequate attention and awareness, demanding of high technology for exploration and budget, lack of number of experts in field of specialization for many years hampers the discovery and utilization of microbial genetic resource in organized manners for centuries.

However Microbial Directorate strengthens partially in expertise and materials beginning from 2012 G.C. For these reasons the conservation of microbial specific taxa should be a high priority and its ecosystems as well as microbial communities. It is usually impractical to protect individual species and strains in the natural environment but species and strains can be conserved by isolation and culturing at ex-situ in a

culture collection center [207,14]. However in Ethiopia a great potential for microbial ecology and microbial diversity requiring still great exploration and metagenomic study, currently there is great effort is delivered for ex-situ conservation under Microbial Gene Bank at Ethiopian Biodiversity Institute and in a great progress from year to year for the last 10 years (Figure 12). Microbial Directorate started building its capacity in materials and laboratory facility and 17 human power in mycology, bacteriology, micro algae and Molecular characterization and Microbial Gene Bank research team organized from 2010 G.C. till 2016 G.C. about 967 Bacteria species and strain, 226 Fungi Species, 10 Algae at genera level conserved genetic material and access for utilization in research and teaching reference.



Figure 12. Researcher team of Microbial Directorate from Ethiopian Biodiversity Institute at the core of Dallol for extremophilic microbial exploration (2012 G.C.) Photo Birhanu Gizaw

CONCLUSION AND RECOMMENDATION

Conclusion

Having knowledge on different microbial ecology helps for researcher to understand structural and functional microbial diversity represents metabolic, structural, morphological and genetic diversity for designing ex-situ conservation strategy and utilization of microbial genetic resource and access for benefit sharing. Magnificent habitat versatility

and variability in Ethiopia encompasses large array of microbial diversity, when later on supported by skilled man power and modern technology in molecular characterization approaches for exploring and exploiting microbial wealth to the biosphere and human welfare.

Recommendation

- Training for researcher with expertise in phylogeny, taxonomy and physiology of

environmental microorganisms to efficiently recognize and characterize the microbial diversity.

- Capacity building and supporting research on new methods and strategies for cultivation and isolation of microbes yet to be discovered.
- Fostering of multidisciplinary involvement in microbial biodiversity research by integrating molecular characterization and bioinformatics data analysis and physico-chemical disciplines of science
- Creating, maintaining and inter grade databases of microbial information including molecular, phenotypic, chemical, taxonomic, metabolic and ecological information and such databases would help in efficient comparison of the new biodiversity discoveries, their characterization and collection as well as curation of diverse isolates and maintenance and dissemination of data regarding them.
- Institutions, including environmental and conservation organizations, centres for diversity and university conservation biology departments should attempt to take a more active role in microbial conservation.
- Because of the overwhelming majority of non-cultured microbes in most microbial niches, metagenome searches and technology should be involved great attention is given for identification of unknown genes and proteins.

REFERENCE

- [1] <http://www.worldometers.info/world-population/ethiopia-population/>
- [2] Abdurahman Abdulahi, Abraham Tadesse, Mohammed Dawd (2010). Importance and Management of Termites in Ethiopia. *Pest Mgt. J. Eth.* 14: 1-18.
- [3] Abdurahman Abdulahi (1990). Foraging Activity and Control of Termites in Western Ethiopia, Ph.D. Thesis, University of London, pp. 277.
- [4] Adekayode FO, Ogunkoya MO (2009) Comparative study of clay and organic matter content of termite mounds and the surrounding soils. Conference Proceedings, African Crop Science, Uganda. Vol.9. pp. 379 – 384.
- [5] AdmasuGebeyehu (2014). Research and development in land and water resources) MoWR/EARO/IWMI/ILRI Workshop.
- [6] Ahmad F, Ahmad I, Khan MS (2008). Screening of free-living rhizospheric bacteria for their multiple plant growth promoting activities. *Microbiol Res* 168:173–181.
- [7] Akhtar MS, Siddiqui ZA (2009). Use of plant growth-promoting rhizobacteria for the biocontrol of root-rot disease complex of chickpea. *Australas Plant Pathol.* 38:44–50.
- [8] Almaz Gonfa, Alemu Fete, Kelbesa Urga and Birhanu Abegaz Gashe (1999). Microbiological Aspects of *fergo* (Ititu) Fermentation. *SINET: Ethiopia. Sci.* 22:283-289.
- [9] Alemu F, Amha-Selassie T, Kelbessa U, Elias S (1991). Methanol fuel oil and ethanol contents of some Ethiopian traditional alcoholic beverages. *SINET: Ethiop. J. Sci* 14:19-27.
- [10] Anukam KC, Osazuwa EO, Ahonkhai, and Reid G (2005) “16S rRNA gene sequence and phylogenetic tree of *Lactobacillus* species from the vagina of healthy Nigerian women,” *African Journal of Biotechnology*, vol. 4, no. 11, pp. 1222–1227.
- [11] Anwar Nuru, Bayleyegn, Molla Eshetu Yimer (2012). Occurrence and distribution of bacterial pathogens of fish in the southern gulf of Lake Tana, Bahir Dar, Ethiopia *Livestock Research for Rural Development*. 24 (8).
- [12] Antonio Piccolo, *Spirulina* production in the ESA-IO region -The way forward
- [13] Andrews JH and Harris RF (2000). The ecology and biogeography of microorganisms on plant surfaces. *Annual Review of Phytopathology* 38,145-180.
- [14] Arora D K, Saikia R, Dwivedi R and Smith D (2005) Current status, strategy and future prospects of microbial resource collections”, *Cur. Sc.* 89(3).
- [15] Austain B (1988). *Methods in Aquatic bacteriology*. A Wiley-Interscience Publication. 222-231.
- [16] Askal D, Kebede A (2013). Isolation, characterization and identification of lactic acid bacteria and yeast involved in fermentation of Teff (*Eragrostis Tef*) Batter. *Adv. Res. Biol. Sci.* 1(3):36-44.
- [17] Bauer S, Tholen A, Overmann J, Brune A (2000). Characterization of abundance and diversity of lactic acid bacteria in the hindgut of wood and soil feeding termites by molecular and culture dependent techniques. *Arch Microbiol* 173:126-137.
- [18] Baar C, Eppinger MG, Raddatz J, Simon C, Lanz O, Klimmek R, Nandakumar, Gross R, Rosinus A, H. Keller P, Jagtap B, Linke F, Meyer H, Lederer and Schuster SC (2003). Complete genome sequence and analysis of *Wolinella succinogenes*. *Proc. Natl. Acad. Sci. USA.* 100:11690–11695.
- [19] Bakermans C, Ayaladel Río HL, Ponder MA, Vishnivetskaya, Gilichinsky D, Thomashow M F and Tiedje JM (2006). *Psychrobacter*

- cryohalolentis* sp. nov. and *Psychrobacter arcticus* sp.nov., isolated from Siberian permafrost. *Int J Syst Evol Microbiol* 56: 1285-1291.
- [20] Bargabus-Larson RL, Jacobsen BJ. (2007). Biocontrol elicited systemic resistance in sugar beet is salicylic acid independent and NPR1 dependent. *J Sugar Beet Res.* 44:17–33.
- [21] Bagwell CE, Bhat S, Hawkins GM, Smith BW, Biswas T, Hoover TR, Saunders E, Han CS, Tsodikov OV, ShimketsLJ (2008). Survival in nuclear waste, extreme resistance, and potential applications gleaned from the genome sequence of *Kineococcus radiotolerans*. *Applied and env microbiology*.74.1376-1384
- [22] Belimov AA, Kojemiakov AP, Chuvarliyeva CV (1995). Interaction between barley and mixed cultures of nitrogen fixing and phosphate-solubilizing bacteria. *Plant Soil.* 173:29–37.
- [23] Belimov AA, Safronova VI, Sergeyeva TA, Egorova TN, Matveyeva VA, Tsyganov VE, Borisov AY, Tikhonovich IA, Kluge C, Preisfeld A, Dietz K, Stepanok VV (2001). Characterization of plant growth promoting rhizobacteria isolated from polluted soils and containing 1-aminocyclopropane-1-carboxylate deaminase. *Can J Microbiol.* 47:642–652.
- [24] Belay Breza, Wolde A (2014) Fermenter Technology Modification Changes Microbiological and Physico-chemical Parameters, improves sensory characteristics in the fermentation of Tella: An Ethiopian Traditional Fermented Alcoholic Beverage. *J Food Process Technol* 5:4. 316.
- [25] Bekel Bahiru, Tetemke Mehari and Mogessie Ashenafi (2002). Yeast and lactic acid flora of Tej an indigenous Ethiopian honey wine: variations within and between production units: SINET. *J. Sci.* (Accepted).
- [26] Breznak JA, Brune A. (1994). Role of microorganisms in the digestion of lignocellulose by termites. *Annu Rev Entomol.* 39:453-487.
- [27] Brune A (1998). Termite guts: the world's smallest bioreactors. *Trends • Biotechnol.* 16:16-21.
- [28] Beyene A, Abdelsalam MG (2005). Tectonics of the Afar Depression: A review and synthesis. *Journal of African Earth Sciences*, 41: 41–59.
- [29] Bergquist PL, Morgan HW (1993). Extremely thermophilic Archaeobacteria. In: Herbert, R. A.; Sharp, R. S. (eds) *Molecular Biology and Biotechnology of Extremophiles*, Blackie, Glasgow. P.22-27.
- [30] Biratu K. and Seifu, E. (2016) Chemical composition and microbiological quality of Dhanaan: traditional fermented camel milk produced in eastern Ethiopia. *International Food Research Journal.* 23(5): 2223-2228.
- [31] Biswas JC, Ladha JK, Dazzo FB (2000) Rhizobia inoculation improves nutrient uptake and growth of lowland rice. *Soil Sci Soc Am J* 64:1644–1650.
- [32] Birhanu Gizaw, Zerihun Tsegay, Genene Tefera, Befikadu Teshome and Belay Tilahun. (2016). Fermenter Yeast Identified from *Ensete ventricosum* Product: Kocho and Bulla Collected from Angacha district. *Int. J. Curr. Trend. Pharmacobiol. Med. Sci* 1(4): 18-23.
- [33] Bott TL, Brock TD (1969). Bacterial growth rates above 90 degrees C in Yellowstone hot springs. *Science.* 164:1411-1412.
- [34] Borji M, Rahimi S, Ghorbani G, Vand Yoosefi J and Fazaeli H (2003). Isolation and identification of some bacteria from termites gut capable in degrading straw lignin and polysaccharides. *J. Fac. Vet. Med. Univ. Tehran.* 58: 249-256
- [35] Bowers KJ, Wiegel J (2011). Temperature and pH optima of extremely halophilic archaea: a mini review. *Extremophiles* 15(2):119-128.
- [36] Brim H, Venkateswaran A, Kostandarites HM, Fredrickson JK, Daly MJ (2003). Engineering *Deinococcus geothermalis* for bioremediation of high-temperature radioactive waste environments. *Appl Environ Microbiol.* 69:4575-4582.
- [37] Brock TD (1967). Life at high temperatures. Evolutionary ecological, and biochemical significance of organisms living in hot springs is discussed. *Science.* 158:1012-1019.
- [38] Cardoso EJBN, Freitas SS (1992). A rizosfera. In: Cardoso EJBN, Tsai SM, Neves PCP (eds) *Microbiologia do solo*. Sociedade Brasileira de Ciencia do Solo, Campinas, pp 41–57.
- [39] Cavicchioli R, Siddiqui KS, Andrews D, Sowers KR (2002). Low temperature extremophiles and their applications. *Curr. Opin. Biotechnol.* 13. 253-261.
- [40] Casanueva A, Tuffin M, Cary C, Cowan DA (2010). Molecular adaptations to psychrophily: the impact of 'omic' technologies. *Trends Microbiol.* 18:374 – 381.
- [41] Cárdenas JP, Valdés J, Quatrini R, Duarte F, Holmes DS (2010). Lessons from the genomes of extremely acidophilic bacteria and archaea with special emphasis on bioleaching microorganisms. *Appl Microbiol Biotechnol* 88:605-620.
- [42] Chen YP, Rekha PD, Arun AB, Shen FT, Lai WA, Young CC (2006). Phosphate solubilizing bacteria from subtropical soil and their tricalcium phosphate solubilizing abilities. *Appl Soil Ecol* 34:33–41.

- [43] Cieśluk K, Karasiewicz MT, Preisner Z (2014). Geotouristic attractions of the Danakil Depression. *Geotourism* 1(36): 33–42.
- [44] Clarke RTJ (1977). The gut and its microorganisms. In: Clarke RTJ, Bauchop T, eds. *Microbial ecology of the gut*. New York: Academic Press. 35–71.
- [45] Conway PL (1995). Microbial ecology of the human large intestine. In: Gibson GR, Macfarlane GT, eds. *Human colonic bacteria*. Boca Raton, FL: CRC Press. 1–24.
- [46] Counotte G, Prins R. (1981) Regulation of lactate metabolism in the rumen. *Vet Res Commun* 5, 101-115.
- [47] Coleman GS, Laurie JI, Bailey JE, Holdgate SA (1976). The Cultivation of Cellulolytic Protozoa Isolated from the Rumen. *J Gen Microbiol* 95, 144-150.
- [48] Costacurta A, Vanderleyden J (1995) Synthesis of phytohormones by plant-associated bacteria. *Critical Rev Microbiol* . 21:1–18.
- [49] Chaihan M, Chunhaleuchanon S, Lumyong S (2009). Screening siderophore producing bacteria as potential biological control agent for fungal rice pathogens in Thailand. *World J Microbiol Biotechnol*. 25.1919–1928.
- [50] Cowan DA (1995). Protein stability at high temperatures. *Essays Biochem*. 29: 193-207.
- [51] Cotta MA, RB Hespell (1986). Proteolytic activity of the ruminal bacterium *Butyrivibrio fibrisolvens*. *Appl Environ Microbiol* 52. 51-58.
- [52] Cotta MA (1988). Amylolytic activity of selected species of ruminal bacteria. *Appl Environ Microbiol* 54, 772-776.
- [53] Cotta MA (1992). Interaction of ruminal bacteria in the production and utilization of maltooligosaccharides from starch. *Appl Environ Microbiol*. 58. 48-54.
- [54] Cowan DA, Smolenski KA, Daniel RM, Morgan HW (1987). An extremely thermostable extracellular proteinase from a strain of the archaeobacterium *Desulfurococcus* growing at 88°C. *Biochem. J*. 247: 121-133.
- [55] Curtis TP, Sloan WT (2004). Prokaryotic diversity and its limits: microbial community structure in nature and implications for microbial ecology. *Curr Opin Microbiol*. 7, pp. 221 – 226.
- [56] Daniel R (2005). The metagenomics of soil. *Nature Reviews Microbiology* 3. 470–478.
- [57] Dashtban M, Schraft H, Qin W (2009). Fungal bioconversion of lignocellulosic residues; opportunities & perspectives. *Int J Biol Sci* 5. 578-595.
- [58] Degefu F, Herzig A, Jirsa F, Schagerl M (2014). First limnological records of highly threatened tropical high-mountain crater lakes in Ethiopia. *Trop. Conserv. Sci.* (In press).
- [59] Dehority BA (1997). Foregut fermentation. In: Mackie RI, White BA, eds. *Gastrointestinal microbiology*. Vol 1. New York: Chapman and Hall. 39–83.
- [60] DeMaayer P, Anderson D, and Cary C, Cowan DA (2014) .Some like it cold: understanding the survival strategies of psychrophiles. *EMBO Rep* 15:508-517.
- [61] De Meyer G, Hofte M (1997). Salicylic acid produced by the rhizobacterium *Pseudomonas aeruginosa* 7NSK2 induces resistance to leaf infection by *Botrytis cinerea* on bean. *Phytopathology* 87:588–593.
- [62] Dimkpa C. et al. (2009) Plant-rhizobacteria interactions alleviate abiotic stress conditions. *Plant, Cell and Environ*. 32. 1682–1694.
- [63] Dopson and Holmes (2014). Metal resistance in acidophilic microorganisms and its significance for biotechnologies. *Appl Microbiol Biotechnol*. 98(19):8133-44.
- [64] Duskova D, Marounek M (2001). Fermentation of pectin and glucose, and activity of pectin-degrading enzymes in the rumen bacterium *Lachnospira multiparus*. *Lett Appl Microbiol*. 33. 159-163.
- [65] Egamberdieva, D. et al. (2008). High incidence of plant growth stimulating bacteria associated with the rhizosphere of wheat grown on salinated soil in Uzbekistan. *Environ. Microbiol.* 10: 1–9.
- [66] Elie C, De Recondo A M, Forterre P (1989). Thermostable DNA polymerase from the archaeobacterium *Sulfolobus acidocaldarius*; purification, characterization and immunological properties. *Eur. J. Biochem*. 178: 619-626.
- [67] Erauso G, Reysenbach A, Godfroy A, Meunier J, Crump B, Partensky F, Baross J A, Marteinsson V, Barbier G, Pace N R, Prieur D (1993). *Pyrococcus abyssi* sp. nov., a new hyperthermophilic archaeon isolated from a deep-sea hydrothermal vent. *Arch. Microbiol*. 160: 338-349.
- [68] Endeshaw Abatenh, Birhanu Gizaw, Genete Tefera, Letay Gebrelibanos (2018), Lactic acid bacteria identified from fermented Azo condiment prepared from leaves of *Phytolaccadodecandra* and *Sorghum* in kafta Humera, Ethiopia, pesticides and bio fertilizers, 1:1-5.
- [69] Eyassu AA, Mohammed YK, Zelalem Y (2012). Isolation and characterization of lactic acid bacteria from Ititu: Ethiopian traditional fermented camel milk. *J. Sci.* 5:82-98.
- [70] Fadiga M, Amare S (2010). unpublished data assembled for structural modeling of Ethiopian livestock sector, Addis Ababa.
- [71] FAO (1984e). Farming system development, information Note. Rome.

- [72] Fredricks DN, Fiedler TL and MarrazzoJM (2005). "Molecular identification of bacteria associated with bacterial vaginosis," The New England Journal of Medicine, vol. 353, no. 18, pp. 1899–1911.
- [73] Forsberg CW, LK Lovelock, L Krumholz, JG Buchanan-Smith(1984).Protease activities of rumen protozoa. Appl Environ Microbiol 47, 101-110.
- [74] Frankenberger WTJ, Arshad M (1995) Phytohormones in soil: microbial production and function. Dekker, New York.
- [75] Forterre P, Ellie C, Sioud M, Hamal A(1989).Studies on DNA polymerases and topoisomerases in archaeobacteria.Can. J. Microbiol. 35: 228-233.
- [76] Finlay BJ, Esteban GF,OlmoJL and TylerPA. (1999). Global distribution of free-living microbial species. Ecography.22. 138-144.
- [77] Fite A, Tadesse A, Urga K, Seyoum E (1991) Methanol fusel oil and ethanol contents of some Ethiopian traditional alcoholic beverages. SINET: Ethiop J Sci 14: 19-27. 5.
- [78] Fiala G, Stetter KO (1986).*Pyrococcus furiosus* sp. nov. Represents a novel genus of marine heterotrophic archaeobacteria growing optimally at 100°C. Arch Microbiol, 145:56-61.
- [79] Fridlender M, Inbar J, Chet I (1993) Biological control of soilborne plant pathogens by a b-1, 3 glucanase-producing *Pseudomonas cepacia*. Soil Biol Biochem 25:1211–1221.
- [80] Frohlich J, Koustiane C, Kampf P, Roselle-MoraR, Valens M (2007). Occurrence of rhizobia in the gut of the higher termite *Nasutitermes nigriceps*. J. Syst. Appl. Microbiol., 30: 68-74.
- [81] Fuentes MC, Calsamiglia S, CardozoPW, Vlaeminck B (2009).Effect of pH and level of concentrate in the diet on the production of biohydrogenation intermediates in a dual-flow continuous culture. J Dairy Sci 92, 4456-4466.
- [82] Harazono KN, YamashitaN, ShinzatoH, WatanabeT, Fukatsuand Kurane R (2003). Isolation and characterization of aromatics degrading microorganisms from the gut of the lower *Coptotermes formosanus*. J. Biosci. Biotechnol. Biochem.67: 889-892.
- [83] Huang CJ, Wang TK, Chung SC, Chen CY (2005). Identification of an antifungal chitinase from a potential biocontrol agent, *Bacillus cereus* 28-9. J Biochem Mol Biol 38:82–88.
- [84] Gabani P, Singh OV (2013). Radiation-resistant extremophiles and their potential in biotechnology and therapeutics. Appl Microbiol Biotechnol. 97.993-1004.
- [85] GalaskRP (1988) "Vaginal colonization by bacteria and yeast," American Journal of Obstetrics & Gynecology. vol. 158. no. 4, pp. 993–995.
- [86] Gashe BA(1985).Involvement of lactic acid bacteria in the fermentation of tef (*Eragrostis tef*), an Ethiopian fermented food. J. Food Sci. 50. 800-801.
- [87] Getnet & Berhanu (2016). Microbial Dynamics, Roles and Physico-Chemical Properties of Korefe, A traditional fermented Ethiopian beverage biotechnology international 9(7): 156-175.
- [88] Gholami A, Shahsavani S, Nezarat S (2009). The effect of plant growth promoting rhizobacteria (PGPR) on germination, seedling growth and yield of maize. Int J Biol Life Sci1:35–40.
- [89] Ghebrekidan H(1992). The effect of different chemical and physical agents on the viability of *Cysticercus bovis*: a preliminary report. Ethiop Med J. 30: 23-31.
- [90] Gillis M, Kersters K, Hoste B, Janssens D, Kroppenstedt RM, Stephan MP, Teixeira KRS, Dobereiner J, de Ley J (1989). *Acetobacter diazotrophicus* sp. nov., a nitrogen fixing acetic acid bacterium associated with sugarcane. Int J SystBacteriol 39:361–364.
- [91] Glick BR (1995). The enhancement of plant growthby free-living bacteria. Can J Microbiol. 1995. 41. 109–117.
- [92] Groudieva T, Kambourova C, Yusef C, Royter C, Grote C, Trinks C,Antranikian C(2004). Diversity and cold-active hydrolytic enzymes of culturable bacteria associated with Arctic sea ice, Spitzbergen. Extremophiles.8(6). 475-488.
- [93] Gome J, Steiner W (2004). The biocatalytic potential of extremophiles and extremozymes. Food Technol. Biotechnol.42 (4): 223–235.
- [94] Gtari M, Essoussi I, Maaoui R, Sghaier H, Boujmil R, Gury J, Pujic P, Brusetti L, Chouaia B, Crotti E, Daffonchio D, Boudabous A, Normand P (2012). Contrasted resistance of stone dwelling *Geodermatophilaceae* species to stresses known to give rise to reactive oxygen species. FEMS Microbiol Ecol 80:566-577.
- [95] Guarner F, Malagelada JR(2003) Gut flora in health and disease. Lancet 361, 512-519.
- [96] Hattori M, Taylor TD (2009). The human intestinal microbiom: a new frontier of a human biology. DNA Res. 1. 1-12.
- [97] Handelsman JM R, Rondon SF, Brady J, Clardy and RM Goodman (1998). Molecular biological access to the chemistry of unknown soilmicrobes: a new frontier for natural products. Chem. Biol. 5:245–249.
- [98] Harris S (2008). Salt Investment S.A.Z.F (SI SAZF), Lake Assal Salt Project, Djibouti. Geographic Environmental Solutions. Briggs P., 2010. Etiopia, Global PWN, Warszawa
- [99] Hedberg I, Friis I, Person E(2009).General Part and Index to Vol. 1-7.Flora of Ethiopia and

- Eritrea Volume 8. The National Herbarium, Addis Ababa, Ethiopia and Uppsala, Sweden.
- [100] Heinemann C and Reid G (2005) "Vaginal microbial diversity among postmenopausal women with and without hormone replacement therapy," *Canadian Journal of Microbiology*, vol. 51, no. 9, pp. 777–781.
- [101] Hespell RB, Akin DE, Dehority BA (1997). Bacteria, fungi and protozoa of the rumen. In: Mackie RI, White BA, Isaacson RE, eds. *Gastrointestinal microbiology*. Vol 2. New York: Chapman and Hall, 59–141.
- [102] Hook SE, AD Wright, BW McBride (2010) Methanogens: methane producers of the rumen and mitigation strategies. *Archaea* Volume. 2010, 1-11.
- [103] Hong SH, Kim JS, Lee YH, In Choi SS, Rih JK, Kim CH, Jeong H, Molecular approaches for understanding the rumen microbial ecosystem C. G. Hur, and J. J. Kim (2004). The genome sequence of the capnophilic rumen bacterium *Mannheimia succiniciproducens*. *Nat. Biotechnol.* 22:1275–1281.
- [104] Hodrova BJ, Kopecny O, Petr (1995). Interaction of the rumen fungus *Orpinomyces joyonii* with *Megasphaera elsdenii* and *Eubacterium limosum*. *Lett Appl Microbiol* 21, 34-37.
- [105] Hoham RW (1975). Optimum temperatures and range for the growth of snow alga. *Arct. and Antarct Alp Res* 7: 13-24.
- [106] Huber R, Langworthy TA, Konig H, Thomm M, Woese CR, Sleytr UB, Stetter KO (1986). *Thermotoga maritima* sp. nov. represents a new genus of unique extremely thermophilic eubacteria growing up to 90°C. *Arch Microbiol.* 144:324-333.
- [107] Hyde KD, Frohlich J and Taylor J (1997) Diversity of ascomycetes on palms in the tropics. In: Hyde, K.D. (ed.) *Biodiversity of Tropical Microfungi*. Hong Kong University Press, Hong Kong, pp. 141-156.
- [108] Hwang BK, Ahn SJ, Moon SS (1994) Production, purification and antifungal activity of the antibiotic nucleoside, tubercidin, produced by *Streptomyces violaceoniger*. *Can. J. Bot* 72:480–485.
- [109] IBC (2012a). The State of Forest Genetic Resource of Ethiopia. Country Report Submitted to FAO, Addis Ababa, Ethiopia.
- [110] Igual JM, Valverde A, Cervantes E, Velazquez E (2001) Phosphate-solubilizing bacteria as inoculants for agriculture: use of updated molecular techniques in their study. *Agronomie* 21:561–568
- [111] Ivan ML, Neill T, Entz (2000). Rumen fermentation and duodenal flow following progressive inoculations of fauna-free wethers with major individual species of ciliate protozoa or total fauna. *J Anim Sci* 78, 750-759.
- [112] Ivan M, HV Petit, J Chiquette, AD Wright (2012). Rumen fermentation and microbial population in lactating dairy cows receiving diets containing oilseeds rich in C-18 fatty acids. *Br J Nutr* 31, 1-8.
- [113] Jami E, Mizrahi I. (2012a). Composition and similarity of bovine rumen microbiota across individual animals. *PLoS ONE* 7(3). 33306
- [114] Jarvis GN, Strompl C, Burgess DM, Skillman LC, Moore ERB, Joblin KN. (2000). Isolation and identification of ruminal methanogens from grazing cattle. *Curr. Microbiol.* 40, 327–332.
- [115] Janssen PH (2006). Identifying the dominant soil bacterial taxa in libraries of 16S rRNA and 16S rRNA genes. *Applied and Environmental Microbiology* 72. 1719–1728.
- [116] Jayaprakashvel M, Mutheszilan R, Srinivasan R, Hussain J A, Gobalakrishnan S, Bhagat J, Kaarthikeyan C, Muthulakshmi, R (2010). Hydrogen cyanide mediated biocontrol potential of *Pseudomonas* sp. AMET1055 isolated from the rhizosphere of coastal sand dune vegetation. *Adv Biotech* 9:39–42.
- [117] Johnson DB (2014). Biomining biotechnologies for extracting and recovering metals from ores and waste materials. *Curr Opin Biotechnol* 30:24-31.
- [118] Joblin KN, Naylor GE and Williams AG (1990). Effect of *Methanobrevibacter smithii* on xylanolytic activity of anaerobic ruminal fungi. *Appl. Environ. Microbiol.* 56, 2287–2295.
- [119] Jones WJ, Leigh JA, Mayer F, Woese CR, Wolfe RS (1983). *Methanococcus jannaschii* sp. nov., an extremely thermophilic methanogen from a submarine hydrothermal vent. *Arch Microbiol.* 136:254-261.
- [120] Kawamoto J, Sato T, Nakasone K, Kato C, Mihara H, Esaki N, Kurihara T (2011) Favourable effects of eicosapentaenoic acid on the late step of the cell division in a piezophilic bacterium, *Shewanella violacea* DSS12, at high-hydrostatic pressures. *Environ Microbiol* 7 13:2293-2298.
- [121] Kamensky M, Ovadis M, Chet I, Chernin L (2003) Soil-borne strain IC14 of *Serratia plymuthica* with multiple mechanisms of antifungal activity provides biocontrol of *Botrytis cinerea* and *Sclerotinia sclerotiorum* diseases. *Soil Biol Biochem* 35:323–331.
- [122] Kalia VC, Purohit HJ (2008). Microbial diversity and genomics in aid of bioenergy. *J Ind Microbiol Biotechnol.* 35(5):403-419.
- [123] Kay BD (1998). Soil structure and organic carbon: a review. In: Lal, R., Kimble, J.M., Follett, R.F., Stewart, B.A. (Eds.), *Soil*

- Processes and the Carbon Cycle. CRC Press, Boca Raton, FL, pp. 169–197.
- [124] Kalui CM, Mathara JM, Kutima PM (2010). Probiotic potential of spontaneously fermented cereal based foods. *Afr. J. Biotechnol.* 9(17): 2490-2498.
- [125] Kebede Abegaz (2014). Isolation, characterization and identification of lactic acid bacteria involved in traditional fermentation of *borde*, an Ethiopian cereal beverage. *International Journal of Food and Nutrition Sciences* Vol. 1(1). pp. 007-015.
- [126] Ketema Bacha, Tetemke Mehari and Mogessie Ashenafi (2007). Microbiological study of Wakalim, a traditional Ethiopian fermented sausage. *Ethiop. J. Biol. Sci.*, 6(2): 129-145.
- [127] Ketema Bacha, Tetemke Mehari and Mogessie Ashenafi (1999). Microbiology of the fermentation of shamita, a traditional Ethiopian Fermented Beverage. *SINET: Ethiop. J. Sci.*, 22(1): 113-126.
- [128] Klaassens ES, de Vos WM, Vaughan EE (2007). Metaproteomics approach to study the functionality of the microbiota in the human infant gastrointestinal tract. *Appl. Environ. Microbiol.* 73, 1388-1392.
- [129] Khattab MSA, Ebeid HM (2014). Isolation of *Enterococcus Faecium* and *Enterococcus Cecorum* from Bovine Rumen Using Modern Techniques. *J. Anim. Prod. Adv.* 4(10):514-519.
- [130] Klingeberg M, Galunsky B, Sjöholm C, Kasche V, Antranikian G. (1995). Purification and Properties of a Highly Thermostable, Sodium Dodecyl Sulphate-Resistant and Stereospecific Proteinase from the Extremely Thermophilic Archaeon *Thermococcus stetteri*. *Appl. Environ. Microbiol.* 61(8): 3098-3104.
- [131] König H (2006). *Bacillus* species in the intestine of termites and other soil invertebrates. *J. Applied Microbiol.*, 101: 620-627.
- [132] Koo SY, Cho KS (2009). Isolation and characterization of a plant growth-promoting rhizobacterium, *Serratia* sp. SY5. *J Microbiol Biotechnol* 19:1431–1438.
- [133] Larkin RP (2003). Characterization of soil microbial communities under different potato cropping systems by microbial population dynamics, substrate utilization and fatty acid profiles. *Soil Biol. Biochem.*, 35: 1451-1466.
- [134] Lauro FM, Bartlett DH (2008). Prokaryotic lifestyles in deep sea habitats. *Extremophiles* 12, 15-25.
- [135] Ladenstein R, Ren B (2006). Protein disulfides and protein disulfide oxidoreductases in hyperthermophiles. *FEBS Journal* 273:4170–4185.
- [136] Lee A (1984). Neglected niches: the microbial ecology of the gastrointestinal tract. In: Marshall K, ed. *Advances in microbial ecology*. New York: Plenum Press. 115–62.
- [137] Lee KE and Wood TG (1971). *Termites and Soil*. Acad. Press, New York, London, pp: 1-100.
- [138] Lin X, Tang J (1990). Purification, characterization and gene cloning of thermolysin, a thermostable acid protease from *Sulfolobus acidocaldarius*. *J. Biol. Chem.* 265: 1490-1495.
- [139] Li XR (2012). *Eco-hydrology of biological soil crusts in desert regions of China*, China Higher Education Press.
- [140] Libudzisz Z, Nowak A (2008). Mikroorganizmy jelitowe człowieka. *Standardy Medyczne* 2, 372-379.
- [141] Lorraine (2003). In the relevance of biotechnology in the development of functional foods for improved nutritional and health quality in developing countries. *Afr. j. biotechnol.* 2: 631-635.
- [142] Rajilic-Stojanovi M, Smidt H, de Vos WM (2007). Diversity of the human gastrointestinal tract microbiota. *Revised. Environ. Microbiol.* 9, 2125-2136.
- [143] Rajkumar M, Freitas H (2008). Influence of metal resistant-plant growth-promoting bacteria on the growth of *Ricinus communis* in soil contaminated with heavy metals. *Chemosphere* 71:834–842.
- [144] Romanenko VG, Rothblat GH and Levitan I (2002). B. Modulation of endothelial inward rectifier K⁺ current by optical isomers of cholesterol. *Biophys. J.* 83:3211–3222.
- [145] Røjen BA, Kristensen NB (2012). Effect of time duration of ruminal urea infusions on ruminal ammonia concentrations and portal-drained visceral extraction of arterial urea-N in lactating Holstein cows. *J. Dairy Sci.* 95:1395-1409.
- [146] Karr EA, Sattley W M, Rice MR, Jung DO, Madigan MT, Achenbach L (2005). Diversity and distribution of sulphate-reducing bacteria in permanently frozen Lake Fryxell, McMurdo Dry Valleys, Antarctica. *Appl Environ Microbiol* 71: 6353-6359.
- [147] Kim PI, Bai H, Bai D, Chae H, Chung S, Kim Y, Park R, Chi YT (2004). Purification and characterization of a lipopeptide produced by *Bacillus thuringiensis* CMB. *J Appl Microbiol* 97:942–949.
- [148] Klingeberg M, Hashwa F, Antranikian G (1991). Properties of extremely thermostable proteases from anaerobic hyperthermophilic bacteria. *Appl. Microbiol. Biotechnol.* 34:715-719.

- [149]KumarS, NussinovR(2001). How do thermophilic proteins deal with heat?.CMLS, Cell. Mol. Life Sci. 58: 1216–1233
- [150]Marx H, Graf AB, Tatto NE, Thallinger GG, Mattanovich D, Sauer M (2011). Genome sequence of the ruminal bacterium *Megasphaera elsdenii*. J. Bacteriol. 193(19):5578-5579.
- [151]MacDougall R NIH (2012). Human Microbiome Project defines normal bacterial makeup of the body. NIH.
- [152]Margesin R, Miteva V (2011). Diversity and ecology of psychrophilic microorganisms. Res Microbiol 162: 346 – 361.
- [153]Margesin R, Schinner F (1994). Properties of cold-adapted microorganisms and their potential role in biotechnology. J. Biotechnol., 33: 1-14.
- [154]Maurhofer M, Keel C, Haas D, Defago G (1994) Pyoluteorin production by *Pseudomonas fluorescens* strain CHAO is involved in the suppression of *Pythium damping-off* of cress but not of cucumber. Eur J Plant Pathol 100:221–232.
- [155]Majumdar S, Singh BA (2014). Normal Microbial Flora of Oral Cavity. J Adv Med Dent Sci Res; 2(4):62-66.
- [156]McAllister TA, LM Rode, DJ Major, KJ Cheng, JG Buchanan-Smith(1990). Effect of ruminal microbial colonization on cereal grain digestion. Can J Anim Sci 70, 571-579.
- [157]Mendes R. et al. (2011) Deciphering the rhizosphere microbiome for disease-suppressive bacteria. Science 332, 1097–1100.
- [158]MirallesNF, Espin JD, Corchero JL, Vilaverde A (2009). Microbial factories for recombinant pharmaceuticals. Microbial cell factories Cell Factories. 17:1-8.
- [159]Michalet-Doreau B, I Fernandez, G Fonty(2002). A comparison of enzymatic and molecular approaches to characterize the cellulolytic microbial ecosystems of the rumen and the cecum. J Anim Sci 80. 790-796.
- [160]Montesinos E (2003) Plant-associated microorganisms: a view from the scope of microbiology. Int Microbiol 6:221–223.
- [161]Mogessie Ashenafi(1989a). Proteolytic, lipolytic and fermentative properties of yeasts isolated from Ayib a traditional Ethiopian cottage cheese SINET:Ethiop.J.Sci.12:131-139.
- [162]Mosoni P, Martin C, Forano E, Morgavi DP (2011). Long-term defaunation increases the abundance of cellulolytic Ruminococci and Methanogens but does not affect the bacterial and methanogen diversity in the rumen of sheep. J Anim Sci 89, 783-791.
- [163]Moniello G, AJ Richardson, SH Duncan, CS Stewart (1996). Effects of coumarin and sparteine on attachment to cellulose and cellulolysis by *Neocallimastix frontalis* RE1. Appl Environ Microbiol 62, 4666-4668.
- [164]Mogessie Ashenafi (1996a). Effect of container smoking and incubation temperature on the microbiological and some biochemical qualities of fermenting Ergo a traditional Ethiopian sour milk. Int. Dairy. J. 6:95-104.
- [165]Mugula JK, Nnko sam, Narvuhus JA and Sorhaug T(2003). Use of starter cultures of lactic acid bacteria and yeasts in the preparation of togwa, a Tanzanian fermented food. Int. J. food microbiol. 83(3): 307-318.
- [166]Nandakumar R, Babu S, Raguchander T, Samiyappan R (2007). Chitinolytic activity of native *Pseudomonas fluorescens* strains. J Agri Sci Technol 9:61–68.
- [167]Negasi A, Fassil A, Asnake D (2017). In vitro evaluation of lactic acid bacteria isolated from traditional fermented Shamita and Kocho for their desirable characteristics as probiotics Afr. J. Biotechnol. 16(12):594-606.
- [168]Navarro CA, von Bernath D, Jerez CA (2013) Heavy metal resistance strategies of acidophilic bacteria and their acquisition: importance for biomining and bioremediation. Biol Res 46:363-371.
- [169]Nissen, Anker ANL, Munk N, Lange NK (1992). Xylanases for the Pulp and Paper Industry. In: Visser J, Beldman G, Kusters -van Someren MA, Voragen AGJ (eds) Xylan and Xylanases, Elsevier Science Publishers, Amsterdam, p.325-337.
- [170]Nogi Y (2008) Bacteria in the deep sea: psychrophiles. In: Margesin, R., Schinner, F., Marx, J.C., Gerday, C. (Eds.), Psychrophiles: From Biodiversity to Biotechnology. Springer Verlag, Berlin Heidelberg, pp. 73-82.
- [171]Noel TC, Sheng C, Yost CK, Pharis RP, Hynes MF(1996). *Rhizobium leguminosarum* as a plant growth promoting Rev Environ Sci Biotechnol 123 Author's personal copy rhizobacterium: direct growth promotion of canola and lettuce. Can J Microbiol 42:279–293.
- [172]Orpin CG, Joblin KN. The rumen anaerobic fungi. In: Hobson PH, ed. The rumen microbial ecosystem. New York: Elsevier Applied Science, 1988:129–50.
- [173]Osman MA, Abdel Rahman IE and Dirar HA(2010). Biochemical changes occurring during fermentation of camel milk by selected bacterial starter cultures. African Journal of Biotechnology 9(43): 7331-7336.
- [174]Palmer C, Bik EM, DiGiulio DB, Relman DA, Brown PO(2007). Development of the human infant intestinal microbiota. PLoS Biol. 5,177.
- [175]Pebone E, Limauro D, Bartolucci S. (2008). The machinery for oxidative protein folding in

- Thermophiles. *Antioxid Redox Signal.* 10(1): 157-169.
- [176]Petrini O, Petrini LE and Rodrigues K (1995) *Xylariaceae* endophytes: an exercise in biodiversity. *Fitopatologica Brasiliensis* 20, 531-539.
- [177]Pisani F, Rossi M (1994).Evidence that an archaeal alpha-like DNA polymerase has a modular organisation of its associated catalytic activities. *J. Biol. Chem.* 269: 7887-7892.
- [178]Pourazad P, Khiaosaard R, Kumar M (2015). Transient feeding of a concentrate-rich diet increases the severity of subacute ruminalacidosis in dairy cattle. *J. Anim. Sci.* (in Press).
- [179]Porcelli, M et al., (1993) "S Adenosylhomocysteine hydrolase from the thermophilic archaeon *Sulfolobus solfataricus*: purification, physico-chemical and immunological properties," *Biochimica et Biophysica acta*, 1164. pp. 179-188.
- [180]Pukall RA, Lapidus M, Nolan A, Copeland T, Glavina Del Rio, S. Lucas, F. Chen, H. Tice, J. F. Cheng, O. Chertkov, D. Bruce, L. Goodwin, C. Kuske, T. Brettin, J. C. Detter, C. Han, S. Pitluck, A. Pati, K. Mavrommatis, N. Ivanova, G. Ovchinnikova, A. Chen, K. Palaniappan, S. Schneider, M. Rohde, P. Chain, P. D'haeseleer, M. Göker, J. Bristow, J. A. Eisen, V. Markowitz, N. C. Kyrpides, H. P. Klenk, and P. Hugenholtz. (2009). Complete genome sequence of *Slackia heliotrinireducens* strain (RHS 1). *Stand. Genomic Sci.* 1:234-241.
- [181]Puggaard L, Kristensen NB, Sehested J (2011). Effect of decreasing dietary (2010).phosphorus supply on net recycling of inorganic phosphate in lactating dairy cows. *J. Dairy Sci.* 94:1420-1429.
- [182]Reid A, Greene S (2013) FAQ human microbiome.
- [183]Rokhbakhsh-Zamin F, Sachdev D, Kazemi-Pour N, Engineer A, Pardesi KR, Zinjarde S, Dhakephalkar PK, Chopade BA (2011) Characterization of plant-growth-promoting traits of *Acinetobacter* species isolated from rhizosphere of *Pennisetum glaucum*. *J Microbiol Biotechnol* 21:556-566.
- [184]Rodrigues DF, Tiedje JM (2008). Coping with our cold planet. *Appl Environ Microbiol* 74: 1677 – 1686.
- [185]Russell NJ (1998). Molecular adaptations in psychrophilic bacteria: potential for biotechnological applications. *Adv. Biochem. Engin. Biotechnol.*, 61: 1-21.
- [186]Sarethy IP, Saxena Y, Kapoor A, Sharma M, Sharma SK, Gupta V, Gupta S (2011) Alkaliphilic bacteria: applications in industrial biotechnology. *J Ind Microbiol Biotechnol* 38:769-790.
- [187]Sahu GK, Sindhu SS (2011) Disease control and plant growth promotion of green gram by siderophore producing *Pseudomonas sp.* *Res J Microbiol* 6:735-749.
- [188]Sahle S, Gashe BA (1991).The microbiology of tella fermentation. *SINET: Ethiop J.Sci.* 14:81-92.
- [189]Sanni AI (1993). The need for process optimisation of African fermented foods and beverages. *Int. J. Food Microbiol.* 18: 85-95
- [190]Savage DS (1977). Microbial ecology of the gastrointestinal tract. *Annu Rev Microbiol*; 31:107-33.
- [191]Salizewska K, Klewicka E, Motyl I (2008) Mikroflora człowieka. In: *Mikrobiologia Techniczna. Mikroorganizmy i środowiska ich występowania*. Red. Libudzisz Z., Kowal K., akowska Z. PWN, Warszawa, 240-248.
- [192]Sai Manasa Jandhyala, Rupjyoti Talukdar, Chivkula Subramanyam, Harish Vuyuru, Mitnala Sasikala, and D Nageshwar Reddy. (2015). Role of the normal gut microbiota *World J Gastroenterol.* 721(29): 8787-8803.
- [193]Schafer A, Konrad R, Kuhnigk T, Kampfer P., Hertel H, König H (1996). Hemicellulose-degradating bacteria and yeasts from the termite gut. *J. Applied Microbiol.*, 80: 471-478.
- [194]Singh SP (2006). Extreme Environments and Extremophiles, in *National Science Digital Library (CSIR): E Book, Environmental Microbiology*. CSIR. India. 1-35.
- [195]Simango C and Grukure (1992) survival of bacterial enteric pathogens in traditional fermented food. *j. appl. bacteriol.* 73: 37-40.
- [196]Sileshi G, Nyeko P, Nkunica P, Sekemate B, Akinnifesi F, Ajayi O (2009). Integrating ethno-ecological and scientific knowledge of termites for sustainable termite management and human welfare in Africa. *Ecology and Society.* 14(1): 48.
- [197]Slesarev AI, Lake JA, Stetter KO, Gellert M, Kozyavkin SA (1994). Purification and characterization of DNA topoisomerase V. *J. Biol. Chem.* 269: 3295-3303.
- [198]Spring SM, Visser M, Lu A, Copeland A, Lapidus S, Lucas, J. F. Cheng, C. Han, R. Tapia, L. A. Goodwin, S. Pitluck, N. Ivanova, M. Land, L. Hauser, F. Larimer, M. Rohde, M. Göker, J. C. Detter, N. C. Kyrpides, T. Woyke, P. J. Schaap, C. M. Plugge, G. Muzer, J. Kuever, I. A. Pereira, S. N. Parshina, R. Bernier-Latmani, A. J. Stams, and H. P. Klenk. (2012). Complete genome sequence of

- the sulfate-reducing firmicute *Desulfotomaculum ruminis* type strain (DL(T)). *Stand. Genomic Sci.* 7:304–319.
- [199] Suen G, Stevenson DM, Bruce DC, Chertkov O, Copeland A, Cheng JF, Detter C, Detter JC, Goodwin LA, Han CS, Hauser LJ (2011). Complete genome of the cellulolytic ruminal bacterium *Ruminococcus albus*. *J. Bacteriol.* 193(19):5574–5575.
- [200] Stetter KO (1996). Hyperthermophilic prokaryotes. *FEMS Microbiol. Rev.* 18:149–158.
- [201] Stetter (2006) Hyperthermophilic life in the history of life. *Philos Trans R Soc Lond B.* 361:1837–1842.
- [202] Stumm C K, Gijzen HJ and Vogels GD (1982). Association of methanogenic bacteria with ovine rumen ciliates. *Br. J. Nutr.* 47, 95–99.
- [203] Steenhoudt O, Vanderleyden J (2000) *Azospirillum*, a free-living nitrogen-fixing bacterium closely associated with grasses: genetic, biochemical and ecological aspects. *FEMS Microbiol Rev* 24:487–506.
- [204] Stolarczyk A, Libudzisz Z, Socha P, Socha J (2008) Rola probiotyków i prebiotyków w profilaktyce i leczeniu zespołu metabolicznego u dzieci i młodzieży. *Standardy Medyczne* 2, 175–171.
- [205] Shinzato N, Matsumoto T, Yamaoka I, Oshima T, Yamagishi A (1999) Phylogenetic diversity of symbiotic methanogens living in the hindgut of the lower termite *Reticulitermes speratus* analyzed by PCR and in situ hybridization. *Appl Environ Microbiol.* 65:837–840.
- [206] Storm AC, Kristensen NB, Røjen BA, Larsen M (2014). Technical note: A method for quantification of saliva secretion and salivary flux of metabolites in dairy cows. *J. Anim. Sci.* 91:5769–5774.
- [207] Supardiyono EK and Smith D (1997). Microbial diversity: ex situ conservation of Indonesian microorganisms. *World Journal of Microbiology and Biotechnology* Volume 13, Issue 3, pp 359–361.
- [208] Tetemke Mehari, Mogessese Ashenafi (1995). Microbiology of siljo, a traditional Ethiopian fermented legume product. *World Journal of Microbiology and Biotechnology* Volume 11, Issue 3, pp 338–342.
- [209] Thomashow LS, Weller DM (1988). Role of a phenazine antibiotic from *Pseudomonas fluorescens* in biological control of *Gaeumannomyces graminis* var. *tritici*. *J Bacteriol* 170:3499–3508.
- [210] Thorne BL, Carpenter JM (1992). Phylogeny of the dictyoptera. *J. Syst. Entomol.* 17: 253–268.
- [211] Tigist, M, Getnet B (2018). The microbiological and physicochemical characteristics of bubugn, a traditional fermented Ethiopian low alcoholic beverage. *Biotechnology International* 11(1): 1–11
- [212] Uemori T, Ishino Y, Toh H, Asada K, Kato I. (1993) Organisation and nucleotide sequence of the DNA polymerase gene from *Pyrococcus furiosus* nuclacid res. 21: 259–265.
- [213] Varma A, Krishna B, Kolli J, Paul S, Saxena and König H (1994). Lignocellulose degradation by microorganisms from termite hills and termite guts: A survey on the present state of art. *FEMS Microbiol. Rev.*, 15: 9–28.
- [214] Vavilov NI (1951) The Origin, Variation, Immunity and Breeding of Cultivated Plants (Translated by S. K. Chestitee). *Chronica Botanica*, 13, 1–366.
- [215] Völkl PR, Huber E, Drobner R, Rachel S, Burggraf A, Trincone and Stetter KO (1993). *Pyrobaculum aerophilum* sp. nov., a novel nitrate-reducing hyperthermophilic archaeum. *Appl. Environ. Microbiol.* 59:2918–2926.
- [216] Waltham T (2010) Afar Triangle: Rift Valleys and Volcanoes over Plate Divergence. In: Migoń P. (ed.), *Geomorphological landscapes of the world*. Springer Science + Business Media, Dordrecht: 183–190.
- [217] WCMC (1994). Biodiversity Data Sourcebook. World Conservation Monitoring Centre, World Conservation Press, Cambridge, UK.
- [218] Wenzel MI, Schonig M, Berchtold P, Kampfer and König H (2002). Aerobic and facultatively anaerobic cellulolytic bacteria from the gut of the termite *Zootermopsis angusticollis*. *J. Applied Microbiol.*, 92: 32–40
- [219] Weimer PJ (1996). Why Don't Ruminant Bacteria Digest Cellulose Faster? *J Dairy Sci* 79, 1496–1502
- [220] Whitman WB, Coleman DC, Wiebe WJ (1998). Prokaryotes: the unseen majority. *Proc. Natl. Acad. Sci. USA*, 95:6578–6583.
- [221] Wolfenden E, Ebinger C, Yirgu G, Deino A, Ayalew D (2004) Evolution of the northern Main Ethiopian rift: birth of a triple junction. *Earth and Planetary Science Letters*, 224: 213–228.
- [222] Woynshet Lule Roman Nega Damtew Etisa (2015). Microalgal Diversity of Middle Rift Valley Lakes (Arenguade and Killole) Oromia Region, Ethiopia. Volume 5, Issue 4 .282–287.
- [223] Yanagita K, Kamagata Y, Kawaharasaki M, Suzuki T, Nakamura Y, Minato H (2000). Phylogenetic analysis of methanogens in sheep rumen ecosystem and detection of *Methanomicrobium mobile* by fluorescence in situ hybridization. *Biosci Biotechnol Biochem* 64, 1737–1742.
- [224] Zhang GC, Lui JJ, Ding WT (2012). Decreased xylitol formation during xylolse fermentation in

Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort

- Saccharomyces cerevisiae due to over expression of Water Forming NADH oxidase. *Apple Environ Microbiol.* 78:1081-1086.
- [225] Zhang Y, Li X, Bartlett DH, Xiao X (2015) Current developments in marine microbiology: high pressure biotechnology and the genetic engineering of piezophiles. *Curr Opin Biotechnol.* 29 33:157-164.
- [226] Zhu F, Qu L, Hong X, Sun X (2011) Isolation and characterization of a phosphate-solubilizing halophilic bacterium *Kushneria* sp. YCWA18 from Daqiao Saltern on the coast of yellow sea of China. *J Evid Based Complement Altern* 2011:1–6.
- [227] Zilberstein B, Quintanilha AG, Santos MAA, Pajecki D, Moura EG, Alves PRA, Filho FM, de Souza JAU, Gama-Rodrigues J (2007). Digestive tract microbiota in healthy volunteers. *Clinics* 62, 47-54.

Citation: Birhanu Gizaw. "Potential Microbial Ecology in Ethiopia and Ex-situ Conservation Effort". (2018) *Annals of Microbiology and Infectious Diseases*, 1(4), pp. 08-39

Copyright: © 2018 Birhanu Gizaw. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.