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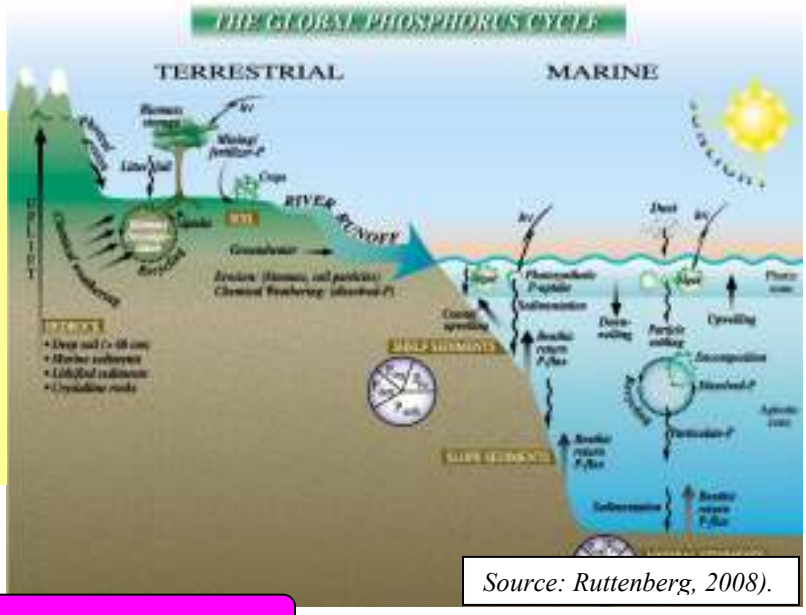
Content



Source: Ruttenberg, 2008).

FROM EDITOR'S DESK

The world over serious concerns are being expressed about the implications of climate change for water security, food security and biodiversity throughout the world. These issues have been hogging the limelight in print and electronic media in recent times. Understanding of biogeochemical cycles of various elements and in particular that of phosphorous is crucial not only from the viewpoint of quality of water but most importantly due to its role in agricultural production and therefore in ensuring food security. One of the articles in this issue covers the nature and distribution of phosphorus and its role in governing the productivity of an ecosystem has a role in changing climatic conditions over geological time-scale. Presented in this issue another article on an emerging research technique-Metagenomics and its application in characterization of microbial diversity which plays crucial role in maintaining the atmospheric and chemical condition required to sustain all larger life forms on earth.

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Prof. V.K. Jain

BIOAVAILABILITY OF PHOSPHORUS AND CLIMATE CHANGE

Amongst the pertinent environmental issues of climate change, natural resource conservation, and pollution etc., food security constitutes a major concern encompassing a range of environmental aspects. Food security, as defined by FAO, exists when all people, at all times, have access to sufficient, safe and nutritious food to meet dietary needs for an active and healthy life (FAO, 2005). In an attempt to meet the food and nutrition requirements of the growing population, the land resources are stressed to increase the yield. The stress comes in terms of applications of large amount of water, pesticides and fertilizers. In India, this stress is more visible as agriculture is the primary occupation and the natural fertility levels are unable to sustain the increasing demand of food grains. The requirement of primary nutrients like nitrogen and phosphorus is supplemented through fertilizers. Commonly used fertilizers include ammonium sulphate, single super phosphate, urea, calcium ammonium nitrate and NPK fertilizers. The factors like water, energy along with other myriad localized factors remain critical for meeting the future food grain demand. But the quantitative and qualitative enrichment can be achieved through application of fertilizers containing phosphorus.

Phosphorus is important because it is required by all living organisms in quantities, large or small. In plants it is crucial for the growth and development of roots and for strengthening tissues found in stems or stalks. Phosphorus is present in phosphoglycerate molecule trapping carbon in Calvin cycle in plants, it is part of structural components like phospholipids in cell membrane, hydroxyapatite in bones, and with fluoride in teeth (Ruttenberg, 2007). It is the medium of energy transfer as high energy bonds in Adenosine Triphospahte (ATP) (Corbridge, 1990), and is also present in genetic material in double helix DNA structure. The very presence and indispensable nature of P for life sustaining processes make it all the more essential. No wonder, approximately 1% of human body is P by weight corresponding to about 650 g of phosphorus or 1500 g of P_2O_5; 86% of which is in bones and teeth (Slansky, 1980). Apart from agriculture, which is by far the largest consumer of phosphate (http://www.nhm.ac.uk), it is an essential component of many foods and animal feed supplements. The use of phosphate in synthetic detergents in the middle of twentieth century revolutionized the laundry technology and still constitutes a part of total phosphate consumption. Other minor usage of phosphates is in metal surface treatment, corrosion inhibition, water treatment, ceramic production and as a flame retardant.

The prime source of phosphorus is rocks rich in phosphates, also known as phopshorites. About 90% of the world wide demand for rock phosphate is for food production (Smil, 2002; USGS, 2008) through fertilisers. Other minor sources include the Guano deposits, manure and biofertilsers. Mining of phosphate rock reserves since the beginning of the 20th century is used as an external source of phosphorus. Since the time of commercial exploitation of rock phosphates for the production of fertilizers, i.e. in the middle of 20th century, USA has been the world's largest producer of phosphate rock (Smil, 2000a). According to a survey by USGS in 2005, the present remaining reserves are with China (17%), USA (27%), and Morocco (17%) (Soon, 2008). The existing rate of population growth and the increasing food demand exerts immense pressure on the phosphate rock reserves. With the present rate of consumption, the current rock phosphate reserves are expected to last for another 50-100 years (Steen, 1998; Smil, 2000a; Gunther, 1997).

The consumption pattern of fertilizers in developing countries like India is different from that of developed nations where the agricultural soils have already crossed 'critical levels' of P and require only lighter applications (Cordell, 2009). Whereas in the developing and tropical countries like Africa and India the soils are subjected to over application of P fertilizers result in its accumulation in soils and water bodies leading to eutrophication (Steen, 1998; Gunther, 1997). India, being a developing nation is in the process of increasing crop yield along with adopting good agricultural practices. The critical level of nutrients in soils is yet to reach. Therefore the demand for phosphate and other fertilizers is expected to increase in the time to come. As the current level of phosphate resources and reserves with India are not sufficient to fulfil its demands, India relies on imports from other countries (Vuuren, 2010). With about 55% of the phosphorus being lost between 'farm to fork' (Smil, 2000b), five times more phosphorus is mined than what is actually consumed by the humans in food. This further enhances the threat to a sustainable use of phosphate rock reserves. Another important issue concerning the extraction of phosphate from open land mining is the exposure of harmful elements like Cd, As and radionuclides that are present in natural phosphate rocks of sedimentary origin (Mortvedt & Beaton, 1996). Furthermore, the processing of phosphate rocks require large amount of water, acids and in turn produces large amount of mineral

residues in the sands and clays (Straaten, 2008). Therefore, for the optimum utilization of resources and reserves, understanding natural existence and cycling of P is essential.

With atomic number 15 and atomic weight 31, phosphorus is the tenth most abundant element on earth with an average crustal abundance of 0.1%. (Nriagu and Moore, 1984; Slansky, 1986). The biogeochemical cycling of phosphorus in nature differs from other nutrients elements like C, N and S in many ways. The P containing rocks are its major reservoirs making the phosphorus cycle geological in nature with the minimal existence of gaseous phase (Figure 1). Also the time taken to complete one phosphorus cycle is of the order of 100-1000 Myrs (Trudinger and Swane, 1979) which is very long as compared to any other biogeochemical cycle. It is this long duration of cycling that makes the flow of phosphorus unidirectional from rock phosphates to the ocean for all practical purposes. Table 1 gives distribution of phosphorus concentration amongst the major reservoirs. During its movement from land to the ocean, P undergoes biogeochemical transformations and fractionation, binding/unbinding before finally settling down with sediments on the ocean floor.

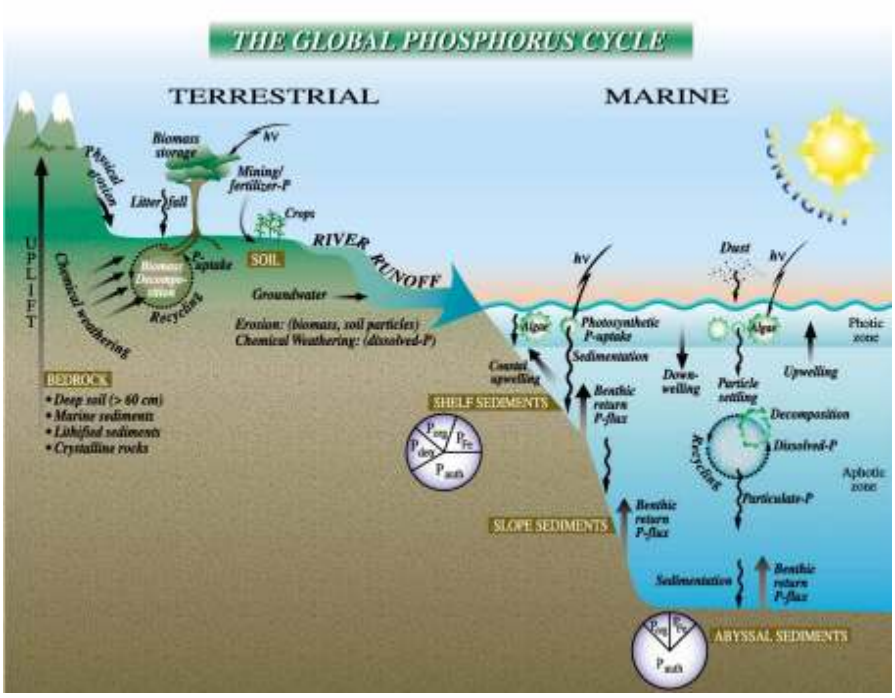

Figure 1 Diagrammatic representation of Phosphorus cycle (Source: Ruttenberg, 2008).

Table1.1: Major reservoirs active in the global phosphorus cycle (Ruttenberg, 2008).

Reservoir description	Reservoir size Moles P X 10^{12}
Sediments (Crustal rocks and soil>60 cm deep and marine sediments	0.27x 10^{8} -1.3 x10^{8}
Land (total soil< 60cm deep: organic+ inorganic)	3,100-6,450
Land biota	83.9-96.8
Surface Ocean (total dissolved phosphorus)	87.4
Deep sea (total dissolved phosphorus)	2,810
Oceanic biota	1.61-4.45
Minable phosphorus	323-645
Atmospheric phosphorus	0.0009

Phosphorus is a productivity limiting nutrient. Based on its chemical speciation and fractionation it determines productivity in terrestrial, and aquatic (lakes, rivers and oceans) ecosystems. In the terrestrial ecosystems, weathering is the only process by which the P bound in minerals is made available to living system through soil. Due to reactivity of the orthophosphate ion (available P) it does not remain available for a long time and gets occluded with Fe, Al and Ca species, becoming non-available to plants. In lakes, when present in more than required available concentration, it can cause eutrophication and deterioration of the water body. In the riverine ecosystems chemical fractionation of P determines the fertility of floodplains and the deltas. Apart from that rivers act as the most important carrier of phosphorus from continent to the ocean. The three main routes through which phosphate migrates from terrestrial zone to hydrosphere include leaching of soils, soil erosion and crop harvesting (through waste water). This transfer of P from continent to oceans can occur in soluble as well as particulate form. According to Jahnke (2000), around 95% of P occurs in particulate form while the remaining 5% is in the soluble form reaching the estuaries and oceans, its largest reservoir.

The average global concentration of Soluble Reactive Phosphorus in the oceans is 2.3 micromoles/ litre and this pool is by far the largest reservoir of dissolved P (Nelson, 2000). The distribution of phosphorus in ocean is stratified i.e., the variation is found in both, horizontal and vertical profiles of the ocean (Fig. 1). The consumption of phosphorus in its simplest composition as orthophosphate by the phytoplanktons creates a differentiation in vertical profile. For defining the optimum productivity, Alfred Redfield et al., (1963) identified the molar ratio of C: N: P in organic matter as 106C: 16N: 1P to understand the ideal system and nutrient limitation. The ratio would depend on the

nutrient availability and the nutritive state of the phytoplankton. When compared with the inorganic C: N: P ratio of the sea water which is 1000: 15: 1 (HCO_3^-, NO^-_3, HPO_4^-) reflects that the nitrogen and phosphorus are limiting the productivity. In the absence of orthophosphate the planktons break down other complex forms, hence removing P from the upper layers while there is a build up of P in the deeper layers. The respiration of the biogenic particles, microbial activity during diagenesis causes this build-up in sediment pore waters. Horizontally, the variation in P distribution is dependent on the distance from the continents. Continental shelf and slope sediments vary from the deep sea. The productivity is higher in the continent shelf and slope as it receives higher P, Si, N and Fe and other continent derived nutrients via rivers, accompanied by the retention of sedimentary P. Therefore, the shelf and abyssal sediments have completely different P distribution. But the common thing is that both are dominated by Ca-P (mostly authigenic apatite). This comprises the larger fraction of total P in pelagic sediments. In the hemipelagic sediments, the remaining P is partitioned between iron bound P (mostly Fe oxyhydroxides), detrital apatite and organic apatite, while the organic and detrital fractions are insignificant in the pelagic sediments (Ruttenberg, 2007). Marine phosphate deposition or phosphorus removal mechanisms are discussed by Follmi (1996), Delaney (1998) and Rao (1998). The only major P removal mechanism is through burial in sediments that includes organic matter burial (Mach et al, 1987), P sorption and precipitation with clays and iron oxyhydroxides (Delaney 1998), phosphorite burial (Tribble et al. 1995) and hydrothermal processes (Froelich 1982). P removal rate from the oceans is controlled by the burial of sediments with organic matter as their primary content. Upon subduction of the oceanic plate, the P is recycled into the mantle with carbon and nitrogen. Sedimentary organic phosphorus, on subduction is likely to be incorporated into the crystalline apatite during subduction zone metamorphism. The result is that subducted organic P does not return to the earth's surface at the same rate as carbon and nitrogen and thus the Phosphorus cycle is decoupled from that of carbon and nitrogen during subduction and metamorphism. This crystallized mass upon exposure gets weathered to produce bioavailable phosphorus (Ruttenberg, 2007; Guidry et al, 2000).

P is considered limiting in marine ecosystems on a geological time scale. Some authors (Ruttenberg, 2007; Compton et al., 2000; Filippelli & Delaney, 1996) consider

the weathering controlled input of phosphorus to be responsible for its limiting nature on geological time scales, while others owe it to the long residence time for its limiting nature. The estimates of residence time of Phosphorus in oceans are variable and are based on difference in calculation of P flux from rivers and atmospheric sources. It may vary from 10,000-80,000 years. Considering the increase in rate of burial of phosphorus, the residence time may further decrease (Nelson, 2000). It is this long residence time of phosphorus in deep water sediments as compared to other potentially bio-limiting nutrients such as Fe and Si accompanied by the vast atmospheric reserve for nitrogen that makes P the ultimate nutrient limiting factor for the biological productivity (Redfield, 1958; Howarth, 1995; Tyrell, 1999).

The nature and distribution of phosphorus and its role in governing the productivity of an ecosystem has a role in changing climatic conditions over geological time-scale. Raymo & Rudiman (1992) tried to link the rise of Himalayan-Tibetan Plateau leading to dramatic increase in chemical weathering bringing the CO_2 level down, resulting in global cooling. Following this, Filippelli (1997) and Filippelli and Souch (1999), tried to establish a relationship between the oceanic productivity and the glacial time scales. In context to oceans, P being the limiting nutrient will determine the surface ocean productivity and in turn the carbon dioxide sequestration that is regulated by biomass production (Boyle, 1990; Bakun, 1990; Ruttenberg, 1993; Follmi, 1996). Geologically, Cambrian explosion supposedly resulted in excess of phosphorus in environment and as an adaptation of life forms with hard body parts appeared to convert excess P into apatite (Narbonne et al, 1994; Morris, 2000). In a recent study, Planavsky et al., (2010) have used the P/Fe ratios and dissolved silica concentrations to determine the dissolved phosphate concentrations in ancient sea water. A peak in phosphorus to iron ratios in Neoproterozoic iron formations dating from ~750 to ~635 Myr found in aftermath of widespread low latitude ‘snowball earth’ glaciations. This resulted from higher weathering rates in the glaciated settings leading to availability of large quantities of dissolved P, increasing the ocean’s primary productivity, leading to higher organic matter production and increased carbon burial. This large scale nutrient supply can result in change of climatic regimes over geological time scales.

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Metagenomics: A tool to exploit the uncultured microbial diversity

Abstract

More than three billion years ago life started on earth with too small organism to be seen by eye, which later on evolved into the complex form of life. Although the complex form of life draw the most attention, these tiny form of life are abundant and diverse and they play crucial role in maintaining the atmospheric and chemical condition required to sustain all larger life forms on earth. Vast majority of these microbial organisms are still completely unknown due to their inability to grow under culture condition. These microorganisms can be the source of some enzymes or catalysts which are of great importance to mankind. Metagenomics is a promising tool for the study of such organisms, which bypass the need to cultivate organism for their study. This is a discipline by which complete microbial community representing a particular environment can be studied and can be accessed for the gene or protein of interest.

Ninety-nine per cent of all micro-organisms in almost every environment on earth remain, as yet, uncultured (1). The discipline of metagenomics, defined as the culture-independent genomic analysis of all the micro-organisms in a particular environmental niche (2), evolved as an effort to discover more about the microbial diversity of natural environments such as soil, marine water and the gastrointestinal tracts of vertebrates and invertebrates (3). Metagenomics is a fast developing field of research, with a vast application in the identification and charectecterization of novel molecules from the microbial community found in a particular environment. In 1985 Pace et al (4) were the first to propose direct cloning of environmental DNA; they cloned the planktonic DNA in a phage vector to study the 16S rRNA sequence. The construction of metagenomic libraries require the isolation of high quality DNA from environmental sample, this poses a challenge as many microbes in the diverse environment are either reluctant to lysis method developed mainly for the mesophilic cells or produce stable nucleases upon lysis. Nevertheless, significant progress has been made, and various methods allowing the isolation of high quality DNA from a variety of environments, i.e., soil (5, 6, 7, 8), marine picoplankton (9), contaminated subsurface sediments (10), groundwater (11), hot springs and mud holes in solfataric fields (12), surface water from rivers (13), glacier ice (14), Antarctic desert soil (15), and buffalo rumens (16), have been developed. Sampling microbes or DNA from a given environment constitutes the first step of all metagenomic approaches. Different considerations influence the selection of a habitat to be sampled. In general, it may be reasonable to select either environments with a high microbial diversity such as soils or sediments (17, 18) or extreme environments that typically harbour few but highly specialized organisms perfectly adapted to the hostile conditions of the respective habitat (19). Therefore the selection of particular habitat predetermines the diversity and general properties of the putative biocatalyst to be discovered. For

instance, to identify novel enzymes with specific properties (e.g., stability against high temperature, pH, pressure, or salt tolerance) extreme environments may be mined. However, in this context, one has to consider that intracellular enzymes of extremophiles are not necessarily adapted to these conditions, too (19, 20). In addition, it is also possible to select an environment that is naturally enriched for target biocatalysts (21) or to enrich samples in the laboratory e.g., by iterative incubation cycles in the presence of defined, which are expected to select for the enzymatic activity of choice (20, 22–24). Both strategies increase the chance to find genes of interest. Nevertheless, a major drawback of employing any enrichment steps is the loss of microbial diversity by favouring fast growing and culturable parts of microbial consortia (25–27). Basically there are two fundamentally different approaches for metagenomic studies, namely sequence based and functional based (Fig. 1). Both approaches has their own limitation and advantages, while sequences based approach rely on sequence homology to the known gene, therefore cannot identify the fundamentally new gene, the function based approach is based on the expression of target gene and therefore can identify fundamentally new gene, however the drawback of this approach is that it cannot identify those genes which could not express due to some reason and there the sequence based approach has the advantage.

MINING OF METAGENOMES FROM EXTREME ENVIRONMENTS

To date, the majority of biomolecules are derived from metagenomic libraries which have been constructed from temperate soil samples (28, 29). However, extreme environments, such as solfataric hot springs (12), Urania hypersaline basins (30), glacier soil (31), glacial ice (14), and Antarctic/Arctic soil (15, 32, 33), represent an almost untapped reservoir of novel biomolecules with biotechnologically valuable properties. Although the diversity of microbial communities present in most extreme habitats is likely to be low, these environments are nevertheless an interesting source for novel biocatalysts that are active under extreme conditions (34). Recently, a number of metagenomic libraries

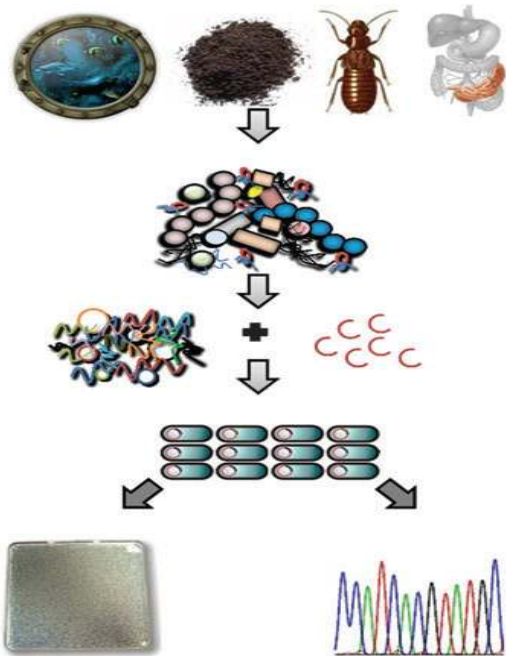

Figure 1 Schematic overview of the metagenomics, divided into functional and sequence-based approaches. While functional screening is focused on the identification of novel processes and proteins produced by heterologous gene expression against a

surrogate host,sequence-based analysis provides insights into the metabolic potential and ecological diversity of an environmental community by comparing DNA databases.(Metagenomics under the microscope, 2008)

derived from the above-mentioned extreme habitats have been constructed. The majority of these libraries have been mined for novel lipases/esterases. Rhee et al. (12) constructed large-insert fosmid libraries from environmental samples originating from solfataric hot springs in Indonesia. Function-driven screening resulted in the identification of a novel esterase, which was classified as a new member of the hormone-sensitive lipase family. This enzyme exhibited a high temperature optimum and high thermal stability. Additionally, Ferrer et al. (35) constructed a metagenomic library derived from the brine seawater interface of Urania hypersaline basins. Five novel esterases which showed no significant amino acid sequence similarity to known esterases were identified. All of these enzymes displayed habitat-specific properties, such as a preference for high hydrostatic pressure and salinity. Samples of an extreme environment were also used to isolate the first metagenome-derived DNA-modifying enzymes by a function-based approach. Small-insert and large-insert metagenomic libraries derived from glacier ice were constructed (14). An *E. coli* mutant that carries a cold-sensitive lethal mutation in the 5'-3'exonuclease domain of the DNA polymerase I was employed as a host for the metagenomic libraries. Only recombinant *E. coli* strains complemented by a gene conferring DNA polymerase activity were able to grow. Nine novel DNA polymerases or domains typical of these enzymes were identified and exhibited only weak similarities to known genes.

Recent discoveries on the physiology of non-cultured microbes and their significance for biogeochemical cycles

Sequence analysis of large insert libraries with environmental DNA combined with genetic and functional analysis has the potential to provide significant insight into the genomic potential and ecological roles of cultured and uncultured microbes (Figure 1). The importance of this potential for understanding complex environments can be estimated by the following six very recent examples. First, bacteriorhodopsins capable of generating a chemiosmotic membrane potential in response to light have been demonstrated only for halophilic archaea [36]. However, recent analysis of genome fragments recovered directly from marine bacterioplankton suggested the presence of a new bacterial rhodopsin, proteorhodopsin (37, 38). Biochemical and biophysical analyses of this gproteobacterial rhodopsin protein expressed heterologously in *E. coli* and analyses of the native protein present in ocean surface waters demonstrated its ability to function as a light-driven proton pump. They discovered widespread distribution of proteorhodopsin genes among divergent marine bacterial taxa (38), the high abundance and spectra adaptation of proteorhodopsin proteins to different habitats combined with the genetic and biophysical data indicate that proteorhodopsin-based bacterialphototrophy is a globally significant oceanic microbial process (37, 39 ,40–43). Second, culture-independent partial or nearly complete recovery of microbial genomes from an environmental sample by an extended random shotgun-sequencing approach offers a highly intriguing approach to study natural microbial communities. A recent example gave significant insights into the community structure and the metabolism of a natural acidophilic biofilm growing on the surface of a flowing acid mine drainage [44]. This was mainly possible through reconstruction of the microbial genomes present in this niche. For this purpose the near-complete genomes of Leptospirillum group II and Ferroplasma type II were reconstructed. A detailed analysis of these genomes allowed

pathway reconstruction of carbon fixation and energy generation and provided insights into survival strategies in the extreme acidic environment; for example, genes for biosynthesis of isoprenoid- based lipids and for a variety of proton efflux systems were identified. However, this information has to be confirmed by biochemical and biophysical approaches. Third, another field for which significant insights in structure, metabolism and gene expression of mixed microbial communities are of high medical interest are biofilms of indwelling medical devices. Recently, Wenderoth and colleagues (45) investigated the community composition of biliary stent biofilms by a cultivation independent approach, i.e. PCR amplification of 16S rRNA/rDNA, SSCP (single-stranded confirmation polymorphism) fingerprinting of the amplificons and sequencing the major SSCP species. Using this approach, novel uncultured bacteria were identified as the major members of biliary stent biofilms and a sequential colonization process of the stent surface was observed, with *Pseudomonas aeruginosa* being the pioneer colonizer followed by *Klebsiella pneumoniae* and an uncultured microbe (45).Fourth, another example is the analysis of the complex metagenome of model biofilms growing on rubber-coated valves within drinking water networks using the cultivation - independent approach. This analysis revealed significant insights into phylogenetic, catabolic and metabolic abilities of the analyzed microbial community [46]. Concerning the potential health risk of the studied biofilm, no DNA or protein sequences directly linked to pathogenic traits were identified. Fifth, the major sequencing approach of the Sargasso Sea has identified a by far greater number of DNA sequences than described in any of the above cited references (47, 48). This study is most likely to open up the possibility of new investigations of the microbial world and of its evolution. However, it will require new bioinformatics tools and it also highlights how generalist databases such as Genbank or EMBL are not adapted to the overflow of new sequences. In brief, the functions of these many novel sequences and their significance for the ecosystems need to be elucidated over the next decade. Sixth, most recently mixed microbial communities of interest have been investigated by monitoring gene expression using DNA microarrays [49,50]. This approach however, identifies only those genes transcribed in the analyzed community and is therefore very valuable for the identification of functional genes with relevance to the ecosystem. Though several challenges still remain to be overcome to most effectively apply microarray technology to monitoring gene expression in complex microbial ecosystems (e.g. increasing the sensitivity), the potential and capability of this promising in situ technology appears to be highly attractive. Finally, a completely different but highly intriguing approach was recently reported by Kruger et al. [51__].- independent biochemical studies of microbial mats of a north western Black Sea shelf, which oxidize methane under anaerobic conditions, resulted in the identification of a prominent nickel-containing protein. Biochemical analyses of this nickel protein isolated from the natural system and its abundance in the methaneoxidizing mat (7% of extracted proteins) indicated that it is likely to catalyze the crucial step in anaerobic methane oxidation (methane activation). This approach is not only remarkable because of the biochemical and ecological findings but also because it first uncovered the function of the novel protein and subsequently applied metagenome technologies to determine the corresponding gene (Metagenomic past and future trend).

Degradation of xenobiotics

Xenobiotics are defined as compounds that are foreign to a living organism. These molecules are not easily recognized by existing degradative enzymes and tend to

accumulate in soils and water. Among the xenobiotics, polyaromatic, chlorinated and nitroaromatic compounds were shown to be toxic, mutagenic and carcinogenic for living organisms. Nevertheless, thanks to their diversity, versatility and plasticity for adaptation, micro-organisms are the best candidates among all living organisms tofunnel xenobiotic compounds into natural biogeochemical cycles. Indeed, more and more micro-organisms are being described as able to degrade these anthropogenic molecules. However, some xenobiotics have been shown to be unusually recalcitrant, i.e., micro-organisms either do not metabolize these xenobiotics or transform them into metabolites that accumulate. For example, in the case of nitroaromatic compounds and 2,4,6-trinitrotoluene (TNT) in particular, several species (mainly Pseudomonas and Clostridia) are able to transform TNT through characterized metabolic pathways into products, which are however as toxic as the parent molecule (52). Therefore, the discovery of new catabolic pathways leading to complete mineralization of the pollutant would be more valuable. In addition, the degradation pathways of many other xenobiotics remain to a large extent poorly characterized, if not totally unknown. A better knowledge of the diversity of catabolic pathways for the degradation of xenobiotics would certainly bring valuable information for bioremediation processes.

Conclusion and future prospective

Metagenomics is a wide area of research interest, with application in several industrial processes. In last few decades there has been acute depletion of fossil fuels which are widely used as a tranportation fuel, this necessitates the discovery of an alternative non renewable source of fuel, Plant biomass, the most abundant biopolymer on earth, has long been recognized as a potential sustainable source of mixed sugars for biofuel production. Efficient degradation of lignocellulosic plant biomass can be a promising alternative source but the recalcitrant nature of these materials is a challenge and limits their efficiency, therefore the intensive metagenomic study of the rumen or gut microbiota of plant biomass feeding organism can unravel the genes involved in the complete deconstruction of these material.

Pollution is a major problem of today's world, resulting in the accumulation of xenobitics in diferrent strata of atmosphere, among the xenobiotics, polyaromatic, chlorinated and nitroaromatic compounds were shown to be toxic, mutagenic and carcinogenic for living organisms. Nevertheless, thanks to their diversity, versatility and plasticity for adaptation, micro-organisms are the best candidates among all living organisms to funnel xenobiotic compounds into natural biogeochemical cycles.

Aditionally metagenomic study of microbes inhabiting extreme habitat can potentiate the discovery of several novel enzymes and biocatalyst with biotechnologically valuable properties.

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