Those Who Can See Invisible Can Do Impossible!

Gaya Prasad

© Association of Microbiologists of India 2011

Early history of microbiology is a story of some common people, like amateur lens grinders, janitors, hobbyists, chemists, physicians, botanists and housewives with a quest for discovery. These early explorers were sometimes driven by chance or curiosity, and sometimes by a problem for which no one had an answer at that point of time [1]. Now we know that microbes are pervasive. They are everywhere, in land, water and air. Microbes play a major role in the life history of humans, animals, and plants, in the quality and safety of our food supplies, in the health and sustainability of our air, land, and water; in bio-warfare and national security. Microbiology in twentieth century has evolved into an extremely interactive discipline among the sciences.

Today, we realize that we are outnumbered by the microbial community; that each of us has a microbiota

which exceeds in numbers our own body cells. It is estimated that nine out of ten cells in our body are microbes. Our own body microbes, collectively called as 'Human Microbiome', carry 100 times as many genes as our own DNA, and also exceed in sheer diversity of those genes [2]. Understanding how the magic balance between the gastrointestinal microbiota and human body influences human health and disease is of prime importance. Some microbes make us sick which is known to us since a very long time, but we realized only recently how the microbial genes affect how much energy we absorb from our foods [3] and how microbes and viruses modulate our immune system in a positive manner [4]. The understanding of variability between individuals and its implication will be one of the most challenging tasks, which will go far beyond understanding mechanisms of microbial pathogenesis in infectious diseases [5]. I have no doubt that the next few years will reveal remarkable findings related to our body microbiota, which will benefit public health tremendously. The use of probiotics, prebiotics, and nutraceuticals throughout the world, including India, has become widespread without any in-depth understanding of their use. However, the future will reveal to us the true relationship.

The high complexity of the microbial communities in various ecological niches will continue to challenge us for decades, since most of them are unculturable. According to an estimate more than 99% of microbes in the environment cannot be cultured in artificial media in the laboratory, a characteristic that limits our understanding of microbial physiology, genetics, molecular biology and community ecology [6]. One way to address this problem is metagenomics, the culture-independent cloning and analysis of microbial DNA extracted directly from an environmental sample. However, metagenomics has its limitation as is evident from several studies including the most ambitious

G. Prasad (✉)
Association of Microbiologists of India, ADG (AH), ICAR,
Krishi Bhavan, New Delhi, India
e-mail: gprasad1986@gmail.com

one conducted by Craig Venter and coworkers [7] using water of the Sargasso Sea. For example, in the Sargasso Sea sequences, 69% of the ORFs could not be associated with known function. This analysis points to a major limitation in annotating sequences from uncultured microorganisms. Hence, a fundamental challenge in understanding microbial communities is to chronicle genetic conservation across time and location and to delineate the smallest complement of genes conserved in genomes across different communities.

Another challenge is to develop culture media which could allow laboratory culture of thousands of microorganisms, which are currently not culturable. The recent development of a growth medium by Robert Heinzen and colleagues for *Coxiella* is a very good example of the combination of post-genomic analyses, basic bacterial metabolism and physiology to formulate the composition of the medium to allow growth of an obligate intracellular bacterium [8]. This is a significant achievement that will definitely enhance the development of genetic tools to dissect various aspects of microbe–host interaction.

Synthetic microbiology is another fascinating new area opened by the recent achievements of a functional synthetic microbial genome and creation of *Mycoplasma laboratorium* by Craig Venter and his co-workers. This is expected to become a powerful tool that will speed up our progress and understanding of microbial physiology and evolution.

The discovery of microbial communication through quorum sensing in the marine bacterium *Vibrio fischeri* has led to a new paradigm in microbial ecology and host-microbe interactions [9]. The understanding of the detailed molecular mechanism of cross-microbial species communication is challenged by the complexity of the respective microbiota. The detailed understanding of microbial cross-talk is expected to go a long way in understanding the formation of microbial communities in evolutionary perspectives. One of the future applications of such findings could be in developing microbial consortia for enhancing soil fertility and bioremediation.

Soil microbiology and geo-microbiology are very important sub-disciplines which have great potential in not only enhancing the soil fertility to improve agricultural productivity but also understanding how soil is formed through millinia. The nitrogen cycle in soils depends on the fixation of atmospheric nitrogen. Microorganisms are vital to the environment, as they participate in the geochemical cycles as well as fulfilling other vital roles in virtually all ecosystems.

Scientific perceptions of the microbial world and its “extreme” fringes have changed with increasing pace and with unforeseen consequences and lead directly toward the

grand research challenges for the future. Extremophiles have been isolated from rocks as much as 7 km below the earth’s surface. Extremophiles have been known to survive and multiply in temperatures as high as 130°C and as low as –17°C, pH less than 0 and up to 11, salinity- up to saturation, pressure: up to 1,000–2,000 atm, down to 0 atm for a prolonged time in a vacuum, and can be highly resistant to radiation, which may even allow them to survive in space [10].

Food microbiology is another important field of research and development. A variety of microorganisms are used in brewing, winemaking, baking, pickling and other food-making processes. Microbes are also responsible for food spoilage and several pathogenic microorganisms are also transmitted through food and food products. Therefore, developing tools and technologies to monitor food safety is very urgent need particularly in countries such as India.

Bio-energy is another exciting field in which microbiology can play important role. Microbes are used in fermentation to produce ethanol and in biogas reactors to produce methane. Scientists are exploring the possibility of the use of algae to produce liquid fuels and bacteria to convert various forms of agricultural and urban waste into usable fuels. Metagenomics and synthetic biology are expected to play a significant role in making bioenergy a feasible technology. A recent report of more than 27,000 putative carbohydrate metabolism genes from the metagenome of cow rumen fed with grass is to be seen in this light [11].

Biological warfare is another field which has become important in the era of terrorism and there are several pathogenic organisms which could be used as bio-terror agents. Anthrax is one such example. Pathogenic microorganisms are the cause of many infectious diseases of humans, animals and plants including agricultural crops. About 12 million people around the world die each year due to microbial diseases which could be prevented or cured through the use of vaccines or medication (World Health Organization). Approximately half of all deaths caused by infectious diseases each year can be attributed to just three diseases: tuberculosis, malaria, and AIDS. Besides very dangerous human pathogens HIV-AIDS, anthrax, tuberculosis, dengue, polio, cholera, etc., there are several crop and animal pathogens which have potential to disrupt food supplies and pose threat to food security of the country. Therefore, the pathogenic microbiology has been one of the most important branches of microbiology since the times of Louis Pasteur and Robert Koch. The recent emergence of bird-flu and swine-flu, besides SARS, Ebola, Hanta, have amply demonstrated the deficiencies in tackling such diseases. Emergence of drug resistance and non-availability of effective chemotherapeutic agents against

majority of the viral pathogens of humans and animals is an important area for enhancing global research and development efforts.

The past few decades have witnessed a quantum leap in our knowledge of microbes. Having said that, it is also quite fascinating how little this has helped in generating new vaccines for various infectious microbes or developing new therapies against multi-drug resistant bacteria. It is also astonishing how few viral infections have effective therapeutic agents or vaccines. This dichotomy clearly indicates that, although our excitement and hyperventilation about the new advances is well justified, we have a long way to go.

Microbes in amazing diverse forms and functions have helped in understanding the fundamentals of biology for over two centuries. Based on diverse spectrum of microbial activities, several distinct sub-disciplines of microbiology have emerged. The advances in molecular biology and development of new tools and technologies have created unprecedented opportunities for cross-talk amongst sub-disciplines of microbiology and allied biological sciences. The research in one sub-discipline has profound impact on other sub-disciplines. Hence it is important to catalyze and facilitate formation of multi-sub-disciplinary networks based on needs and emerging challenges of human and animal health, agriculture, environment, energy, biotechnology industry, etc. Keeping this perspective in view the Association of Microbiologists of India has rightly chosen “Recent Advances in Cross-disciplinary Microbiology: Avenues & Challenges” as main theme for 51st Annual Conference and International Symposium being organized here.

I hope that the International Symposium will provide ample opportunities to the scientists, teachers, students and biotech industry representatives from India and abroad to have cross-disciplinary interactions and exchange of ideas to address some of the challenges faced by the humanity. It will be good platform for developing collaborative linkages amongst microbiologists, researchers, scientists, academicians and industry. The International Workshop planned concurrently on rRNA sequencing, phylogeny and next

generation genome sequencing will provide young researchers, postdoctoral fellows, Ph.D. scholars an opportunity to have first hand insight into the next-generation sequencing technologies.

I would like to conclude with what Louis Pasteur said when he discovered that there are some good microbes which help in fermentation whereas there are some bad ones which can spoil the fermentation process.

Why, no one can tell that other kinds of small beings did a thousand other gigantic and useful and perhaps dangerous things in the world

-Louis Pasteur

References

- Guardino RF (2005) Early history of microbiology and microbiological methods. In: Miller MJ (ed) Encyclopedia of rapid microbiological methods, vol I. PDA Publications, USA, pp 1–27. www.pda.org/bookstore
- <http://nihroadmap.nih.gov/hmp/>
- Turnbaugh PJ et al (2006) An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature* 444:1027
- Barton ES et al (2007) Herpesvirus latency confers symbiotic protection from bacterial infection. *Nature* 447:326
- Qin et al (2010) A human gut microbial gene catalogue established by metagenomic sequencing. *Nature* 464:59
- Schloss PD, Handelsman J (2005) *Genome Biol* 6:229. doi: [10.1186/gb-2005-6-8-229](https://doi.org/10.1186/gb-2005-6-8-229)
- Venter JC, Remington K, Heidelberg JF, Halpern AL, Rusch D, Eisen JA, Wu D, Paulsen I, Nelson KE, Nelson W et al (2004) Environmental genome shotgun sequencing of the Sargasso Sea. *Science* 304:66–74
- Omsland A, Dale Howe D, Fischer ER, Virtanevac K, Sturdevant DE, Porcella SF, Heinzen R (2009) Host cell-free growth of the Q fever bacterium *Coxiella burnetii*. *Proc Natl Acad Sci USA* 11:4430–4434
- Miller MB, Bassler BL (2001) Quorum sensing in bacteria. *Ann Rev Microbiol* 55:165–199
- <http://en.wikipedia.org/wiki/Microorganism>
- Hess M, Sczyrba A, Egan R, Kim TW, Chokhawala H, Schroth G, Luo S, Clark DS, Chen F, Zhang T, Mackie RI, Pennacchio LA, Tringe SG, Visel A, Woyke T, Wang Z, Rubin EM (2011) Metagenomic discovery of biomass-degrading genes and genomes from cow rumen. *Science* 331:463–467