

## Case Report

# From the Single Bacterial Cell to the Microbial Community: A Round Trip to better understand the Secrets of Complex Microbiological Ecosystems

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## Abstract

There is increasing evidence of the difficulty in understanding the “biological functioning” of some complex microbial communities. Complex microbial communities exist everywhere in nature, and the interactions among their constituent microorganisms are a crucial aspect that influences their development. The ability of microorganisms to colonize an environment includes their ability to interact with other species in the same ecosystem, as well as their ability to adapt and integrate into the evolving community. The interactions among microorganisms and not just their numbers, or the presence of different species, biotypes, and variants, in many cases, seems to become a decisive factor in understanding and analyzing the development of microbial ecosystems and the biological function of the individual microbial entities that are part of them.

After working to isolate individual microbial cells and study the mechanisms of their functioning and development, it is time to embark on a backward journey “from the small to the complex” for a better understanding of complex microbial ecosystems and their application potential. The purpose of this brief contribution is to further the development of the understanding of the role of microbial communities in nature and the mode of their development and evolution.

## Introduction

There is increasing evidence of the difficulty of understanding the ‘biological functioning’ of certain complex microbial communities, characteristic of different environmental systems. The study of their microbial cells has gone as far as a detailed understanding of the differences between species, biotypes, and variants. In this context, the results obtained in recent years have enabled advances in knowledge that we can describe as astounding. Nevertheless, something still seems to elude us, particularly if we try to reconstruct from single selected cells the complexity of the systems from which these cells were isolated. For this reason, it appears of great interest to discuss and understand the biological value of complex microbial communities and their application potential.

There is much evidence of how these varied populations, frequently consisting of different microbial species and biotypes, condition the functioning of different environmental

ecosystems. The interactions between microorganisms in complex ecosystems are probably the key factor defining their survival. Indeed, the individual cell finds its metabolic significance in these systems not only as a cellular unit but also, perhaps above all, in its ability to communicate and interact with other microbial cells in the ecosystem. Some microbial biotypes, for example, only survive and multiply within a population. Indeed, in numerous studies, it has been possible to observe how an important part of the biotypes present in different complex ecosystems is unable to multiply if placed to grow in pure cultures after isolation. The biological role of these non-culturable bacterial cells within microbial ecosystems remains much debated and needs further investigation for its exact understanding. The presence in the same microenvironment of different isogenic variants, i.e. genetically identical cells expressing different phenotypes, also has a specific significance in the survival and adaptability of the ecosystem. In particular, in complex ecosystems, the phenotypic heterogeneity present in biotypes of the same species can favor the persistence of the microbial community

## More Information

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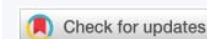
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in environments subject to frequent changes in abiotic characteristics. The development of mutants can also favor the evolution of a culture and its ability to adapt to hostile environmental factors. The sum of these factors favors the resilience of the ecosystem and could explain its survival and ability to perpetuate and adapt over time. In short, following the principles dictated by Darwin, cells capable of surviving the stresses that characterize a given ecosystem adapt to become dominant. In short, the individual microorganisms in the complex ecosystem would be trapped in deep networks of interdependence, both evolutionary and ecological [1-8].

### Food ecosystem

In the agri-environmental and food sector, there is growing evidence that understanding the biological functioning and survival of certain complex ecosystems cannot be done without understanding the role and interactions of and between the microorganisms that populate them.

Fermentation of many foods provides a fitting example of how a microbial community can grow and evolve. During food fermentation, stimulatory and/or inhibitory interactions among microorganisms can help maintain the viability of a portion of the microbial population and promote the ability of the microbiota to adapt to frequent and varied changes in the “food environment,” including those resulting from the metabolic activity of the microorganisms themselves.

In this sense, interesting cases for understanding the efficiency of such complexity are the natural starters used in the production of many fermented foods [9-11]. These are often complex cultures with great practical efficiency, and they can cope with the various selective pressures characteristic of food production processes. Natural starter microbial community endowed with the ability to adapt to artisanal, non-standardised production, and to evolve into food in the course of its production. For resilience and good performance, these microbial community seems to include dominant and other non-dominant microorganisms, which alternate and work together to ensure good technological performance. For these reasons the natural starters are difficult to replace from selected starters. Obviously, in different ecosystems, microbial populations can play roles of differing significance. Again, it is the interactions that define how the microbiota and the ecosystem of which the microbiota is an integral part survive, develop, and function technologically.

### Gut ecosystem and intestinal microbiota

In the human field, an excellent example of complex microbial communities is certainly the gut microbiota [12-14]. The human gut microbiota is a complex entity that lives within us and affects our health, sustenance, and well-being. These microorganisms, whose numbers roughly equal that of human cells, form a mutually beneficial relationship with their host. Various research suggests that a balanced and diverse gut

microbiota can be considered a key indicator of health. The gut microbiota functions as an additional organ that utilizes nutrients from the diet, influencing human health through the release of harmful or beneficial metabolites and regulating the immune system [12-15]. Diet can modulate the functionality of the gut microbiome, which utilizes nutrients from ingested foods, releases harmful or beneficial metabolites, and regulates the immune system [15-20].

Little is still known about the actual number of different species and biotypes that make up the gut microbiota. Several questions remain open. What are the specific roles of the different microorganisms present? Which microorganisms are actively involved in the interaction between microbiota and physiological or pathological states of the individual? How many microorganisms live, or survive, within the microbial ecosystem only through interactions with other microorganisms, whereas taken individually they would not be able to develop or express certain metabolisms relevant to our health? Can the eukaryotic cells that make up the surface of the gut in turn “communicate” with the microbiota, defining its aptitude for colonization? I believe that every human being is characterized by a peculiar “gut ecosystem” system, often evolving due to the same factors that condition the microbiota (age, health, diet...). These aspects may underlie the reasons why some probiotic preparations work in a way that is not always similar in the different individuals who use them. Only the study and understanding of the gut ecosystem as a whole, and thus of the interactions that regulate it, will provide definitive answers in this regard.

### Discussion and future perspective

If the primary ‘purpose’ of micro-organisms is to survive and multiply, complex microbial communities can therefore be considered as the most effective survival systems. Some recent research has emphasized how useful it would be, to understand their nature and secrets, to study and think of complex microbial ecosystems as multicellular organisms [3]. Understanding and managing these microbial ecosystems would thus lead to considering them almost as ‘super-organisms’, consisting of single unicellular units (mostly prokaryotes) that interact and communicate [1-3]. The network of interactions and communication would be the key aspects in the development of the system [3-8].

This is a model of interpretation that develops and looks in the opposite direction to the approach of research over the past decade. Research that is rightly dedicated to the study of individual cell units and the pursuit of the ‘smallest’, its ecological significance, and its characterization. Study, therefore, of individual microbial cell units, discriminating them from the system that contained them and to which they belonged. It was a necessity, rightly so, because it was also useful to delve beyond the boundaries of biodiversity and to find practical applications (e.g. selected cultures) where



the management of complex cultures was more problematic and less performing than expected. Now, also in light of the knowledge that has developed, I believe that going backward and considering the complexity of systems and their effect on the cellular entities that compose them is also possible, necessary, and useful. Microbial communities should therefore be studied in terms of biological function as well as composition. In this context, complex populations can be understood as collectivities that become fundamental units of life [7,8].

## Conclusion

There is still much work to be done to understand these complex systems. It is better to know them well before drawing hasty conclusions. Simplifications in this field, while necessary in some cases for understanding, may favor superficial and unreliable conclusions.

The fact remains that after devoting useful time and effort to understanding individual microbial cells and the mechanisms of their functioning, perhaps it is time to take a journey back “from the small to the complex.” A necessary journey to better understand the microbial world, complex microbial ecosystems, and their importance to our lives.

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