# Metaorganism

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## Synonyms

Superorganism Microbial community system

### Definition

A metaorganism is the community of interacting biological entities that is indicated by a metagenome. A variety of highthroughput and other techniques are used to understand the role metaorganismal interactions play in host physiology and local and global biogeochemistry.

## Characteristics

From one point of view, metagenomics is straightforwardly a technique that provides access to otherwise inaccessible microbial communities. However, another evolutionarily and ecologically informed line of thought underpins and ultimately drives metagenomics. The latter is a perspective that is built on the idea that metagenomes are communal resources and that the entity to which the resource is available is a coordinated, developing and multifunctional 'multicellular' organism (e.g., Committee on Metagenomics 2007; Turnbaugh and Gordon 2008). This entity, the metaorganism, is usually composed of large numbers of cells of different lineages and capabilities, and is able collectively to regulate the functions of its constituting entities. Traditionally conceived individual organisms, from this viewpoint, are interacting components of the more fundamental collective. The metaorganism, the more basic form of life, is the entity that interacts with the environment and enables the reproduction of the different parts that constitute it. It is, however, a very flexible organization of parts and processes and for this reason, appears less cohesive to many biologists than does a conventionally theorized monogenomic organism.

Metaorganisms refer to both microbial systems in geochemical environments and mixed microbial-macrobial systems. The metaorganism concept attempts to capture the ways in which microbes survive and flourish in a remarkable range of diverse environments, and how such entities may, in fact, be crucial to understanding the adaptability and diversity of microbial life. Metagenomic inventories and analyses are increasingly directed towards gaining sophisticated understandings of the structure as well as the dynamics of these metaorganismal entities (Mueller et al. 2010; Egert et al. 2006). The highthroughput analysis of

the human microbiome is rapidly becoming a classic exemplar of metaorganismal research. A major focus of this strand of research is the gut microbial community and its interactions with the host organism, the human, in a quest to understand systemically health, illness and basic biological functioning (NIH HMP Working Group 2009; Gill et al. 2006). Microbiomic research encourages the conceptualization of any multicellular organism as a composite of all three domains (bacteria, archaea and eukaryotes) and the fundamental genome as a metagenome of microbial and other DNA (Gill et al. 2006; Turnbaugh et al. 2007). It is even suggested that humans and other animals could be regarded as 'advanced fermenters', the main role of which is to house, nourish and assist the reproduction of an enormous array of microbes (Nicholson et al. 2005). The original human genome sequencing projects were, from this perspective, about only a tiny and unrepresentative complement of our genes, but this limitation is rapidly being remedied by the human microbiome project (Turnbaugh et al. 2007; NIH HMP Working Group 2009).

What the concept of metaorganism suggests, therefore, is that the fundamental activity of cells, beyond self-organization and maintenance, is to form collaborative associations in a plurality of forms. Whether prokaryotic or eukaryotic, microorganismal or macroorganismal, cells work together in a great variety of ways, collectively structuring their activities through numerous mechanisms. Cellular life-forms can thus be understood as fully functional only when cooperating with other cells. But concomitantly, this claim has implications for all the acellular entities that are of such evolutionary and functional importance (e.g., viruses, plasmids, prions). They too accomplish their life-associated functions in cooperation with other cells. Although there is little doubt that competition and selection have been essential to the evolutionary process, it may be that the main mode in which organisms or cells have competed has been with respect to their ability to collaborate in populations or multi-species communities that can generally be understood as metaorganisms.

From this more inclusive point of view, interactors (the differential survival of which leads to the differential proliferation of replicators) are best understood as complex associations that involve the collaboration of highly diverse lineage-forming entities. Units of selection are not, therefore, usually monogenomic entities, but the cooperative collaborations of many different lineage-forming entities (Doolittle and Zhaxybayeva 2010; O'Malley and Dupré 2010). Entities such as fungi, plants, animals or biofilms are not exclusively monogenomic units of selection, because all the lineages that constitute a communal capacity for survival have to be considered together. This sort of interactor is a fundamental unit of selection and it filters the selection of other units, such as organisms and genes. Going beyond evolution to the nutrition, development, immune response and other functions of paradigmatically multicellular organisms, also requires an

acknowledgement that the relevant system is a broad one that includes many genomically different [polygenomic] kinds of cells. Indeed, as is often noted, the majority of cells in the systems we think of as humans are actually microbial rather than conventionally understood human cells (Turnbaugh and Gordon 2008). These growing insights, many of them being developed through metagenomic analysis, are understandably beginning to excite not only medical practitioners but also ecologists with their interests in biodiversity and bioremediation.

One possible concern of metaorganismal thinking is that it might lead ultimately to a biosphere-level approach, which may evoke Gaia-like concepts of the world and thereby raise questions about the value of the metaorganism as an ontological category (Committee on Metagenomics 2007). In today's systems biology, however, whether it is practised from the top-down or bottom-up, quantitative, mathematical representations of systems do not presume homeostasis or optimal adaptation as was so often the case in the most fullblown and notorious theoretical incarnations of the superorganism. And so far, the metaorganism concept has not been extended to the planet as a whole to encompass the totality of ecosystems. Thus, all the entities or processes considered to be metaorganisms are also potential units of selection, and they can collaborate with and compete against other such entities.

A final point about metaorganisms is that they are paradigmatically dynamic entities as are all biological systems. Genomes, cells, and ecosystems are in constant interactive flux, subtly different in each iteration, but similar enough to constitute a distinctive process. Dynamically self-organizing self-sustaining systems are very different from machine-like ones in that in the former, causation can be seen to run not merely upwards from part to whole [upward causation], but also downwards from whole to part [downward causation]. The behaviour of individual cells, for instance, whether in multicellular eukaryotes or microbial aggregates, is in fundamental respects determined by the features of the system of which it is part. The emergence of the concept of the metaorganism is closely linked to the emergence of systems biology: without systems approaches, the metaorganism would not be a tractable research entity.

The flow of interactions in such systems entails an importantly pluralistic conclusion to this discussion of metaorganisms. Because the analysis of biological systems into entities is not determinate, then for some purposes of inquiry a monogenomic organism is the most appropriate, whereas for others, the appropriate focus is on polygenomic systems. Answering the question, 'What is an organism?', requires seeing that there is a great variety of ways in which cells and other biological elements, sometimes genomically homogeneous, sometimes not, combine to form integrated biological wholes. The organism should therefore

be placed in the group of biological categories for which there is a plurality of interpretations (e.g., species, genes). From a metagenomic point of view, genomes, cells, organisms and lineages are all assemblages of constantly changing entities, maintained by dynamic, self-sustaining and self-repairing processes. This pluralistic, process-oriented ontology is the consequence of thinking further about metaorganisms and their underlying approach of metagenomics.

#### **Cross-references**

Metagenomics Monogenomic Bottom-up Top-down Highthroughput Self-organizing Homeostasis Systems biology Systems Dynamic Downward causation Upward causation

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