Classifying Microorganisms
Sommerlund, Julie

Published in:
Social Studies of Science

Publication date:
2006

Citation for published version (APA):
ABSTRACT  This paper describes the coexistence of two systems for classifying organisms and species: a dominant genetic system and an older naturalist system. The former classifies species and traces their evolution on the basis of genetic characteristics, while the latter employs physiological characteristics. The coexistence of the classification systems does not lead to a conflict between them. Rather, the systems seem to co-exist in different configurations, through which they are complementary, contradictory and inclusive in different situations – sometimes simultaneously. The systems come into conflict only through the researchers' verbal articulations; in their application conflict is hardly present at all. This paper treats their relationship as the 'central tension of science' in reverse. Rather than comprising heterogeneous communities that need boundary objects to make cooperation and integration possible, the field of molecular biology seems to be overwhelmingly homogeneous, and in need of heterogeneity and conflict to add drive and momentum to the work being carried out. The paper is based on observations of daily life in a molecular microbiology laboratory at the Technical University of Denmark. It is thus a 'real time' and material study of scientific paradigms and discourses.

Keywords  classifications systems, laboratory studies, microbial ecology, molecular microbiology, multiplicity, research culture, scientific practices

Classifying Microorganisms:
The Multiplicity of Classifications and Research Practices in Molecular Microbial Ecology

Julie Sommerlund

Currently, microbiologists – and biologists at large – find themselves employing two systems for classifying organisms: a traditional, naturalist one concerned with the way organisms appear and act, and a more recent system based on the genetic code. My claim that these two systems are both used in the biological community stems from observational studies of a group of microbiologists working with molecular techniques and studying microorganisms in an ecological setting. However, before presenting the group, its work, and the double focus on molecular techniques and ecology, I will outline the theoretical debates with which this paper is concerned.

First and foremost is a theoretical debt, rather than debate: my paper studies work done in one specific laboratory, and in doing so it relies on the
tradition for performing laboratory studies, both methodologically and thematically. The tradition of laboratory studies started as a critical move against former investigations of science that focused on communities exterior to the laboratory. In turning attention to the laboratories and the people working there, science scholars turned towards ‘the place where the labor of science is performed’ (Lynch, 1985a: 4). Thus, a distinctive feature of this tradition is that it does not access science through endproducts, such as stabilized facts, but through studies (ethnographic and discourse analytic) of the laboratory work of stabilizing facts (Knorr Cetina, 1995). The focus is on ‘science in the making’ rather than ‘ready-made science’ (Latour, 1987: 4). This also means that science is not seen as a privileged system, which can be assumed to be rational, but as one epistemic system among many, in need of investigation as any other system. In this way, laboratory studies are essentially Kuhnian.

The tradition is marked out by the research agenda set up by Latour & Woolgar (1986 [1979]), Knorr Cetina (1981), Lynch (1985a) and others working in the 1970s and 1980s. Five monographs stand as landmarks within this tradition: Latour & Woolgar’s Laboratory Life (1986 [1979]), Knorr Cetina’s The Manufacture of Knowledge (1981) and Epistemic Cultures (1999), Michael Lynch’s Art and Artifact in Laboratory Science (1985a) and Sharon Traweek’s Beantimes and Lifetimes (1988). As noted by Knorr Cetina (1995: 147), each of these books presents an important approach to science studies: actor-network theory, constructivism, ethnomethodology and symbolic anthropology. As Knorr Cetina also notes, they are all constructionist: they see the work done in laboratory as constructing facts and realities rather than describing them. I have been inspired in various ways by these works, methodologically primarily by Latour & Woolgar and Traweek, and empirically by Latour & Woolgar (1986 [1979]), Lynch (1985b) and Knorr Cetina (1999), who all study biological laboratories.

Based in the tradition of laboratory studies, this paper addresses three sociological debates. The first is on classifications. Much of the work that has been done on classifications focuses on the instigation and implementation of one specific classification system at a time. For instance, Foucault (1970) analyses many different classification systems, but focuses on one at a time and analyses the succession of classification systems. Likewise, Bowker & Star (1999) analyse a range of classification systems in Sorting Things Out (including, for example, the South African classification of races during apartheid), and Latour (1995) analyses networks and scientific representation, including the classification of rainforest vegetation. Although these works have inspired the present study, my focus is different. I do not wish to tell the story of the rise (and fall) of one particular system of classification, or to analyse how classification systems follow each other in historical time, but to describe how two classification systems are simultaneously mobilized in the daily work of a group of researchers.

The second debate the paper addresses is concerned with the singular or multiple nature of phenomena, in this case, microorganisms. In science
studies, scientific knowledge has often been seen as an effect of the successful implementation of one system of classification, technology and rationality (see, for instance, Collins, 1985). Within more recent studies, singularity is not treated as something final, but as something that needs constant work, which will easily become visible in case of controversy (Latour, 1987). The present study indicates something slightly different: that scientific work in the research group in question is enabled rather than hindered by the multiplicity of classification systems.2

The third debate this paper focuses on has to do with the dominance of genetics. Contrary to most writings on genetics and genetic classification, I emphasize the multiplicity of classification work. The case of the naturalist and genetic systems is not a new one. The rise of genetics and genetic classifications within biology, and the parallel downfall of the naturalist paradigm (as well as the corresponding naturalist classification system), have been discussed extensively by Donna Haraway (1997), Evelyn Fox Keller (2000), Lily Kay (2000) and Richard Lewontin (2001). Each of them discusses the ascendancy of genetics within biology, although their focus differs. I agree with their argument that the genetic paradigm and the associated classifications are now totally dominant within biology. However, my paper differs by being firmly based in ethnography of practice and by considering the issue from a practical angle. Consequently, I do not consider the naturalist paradigm and the naturalist classification system to be a closed chapter, as Haraway, Keller, Kay and Lewontin, among others, claim (and sometimes lament). Rather, it seems to me that although the genetic paradigm and genetic classifications are dominant, the naturalist paradigm and corresponding classifications continue to play a role in, and have practical consequences for, day-to-day practices such as those I studied.

What ties together my treatment of these debts and debates is the question of how the coexistence of the classification systems is achieved on a practical level in the microbiological research group studied. In the words of John Law:

But now it appears that Natures are enacted in the plural ... And their relations are uncertain. Perhaps, sometimes they fit together nicely. Perhaps they contradict one another. Perhaps they pass each other without touching, like ships in the night. Perhaps they are included in one another. Perhaps they are deliberately kept apart, because any encounter would be a collision. Or perhaps their relations are a mix of these: Complementary, contradictory and mutually inclusive. (Law, 2004: 6)

The Molecular Microbial Ecology Group

The Molecular Microbial Ecology Group was established about 10 years ago. The work of the group combines experimental tools from molecular biology and microbial ecology for the new research area of biofilms – communities of bacteria living on surfaces protected by a layer of slime. The group has specialized in experimental setups that aim to be more
appropriate for the study of ecosystems than traditional test-tube experiments, and it has developed many new experimental tools that facilitate studies of bacterial activity in multi-species communities. Thus, the core research problems for the group have to do with methodology and representation: how to examine and represent multi-species communities, and how to generate and interpret data.3

The staff of the Molecular Microbial Ecology Group consists of about 17 researchers.4 I observed and interviewed the researchers in this group at different times over a period of 3 years.5 In studying the group, I used the ethnographic method of ‘following the actors’. I asked a number of researchers (about 10 – it is a little difficult to determine the precise number as the researchers often work closely together, attend meetings together, and insist that I notice and discuss their actions, as well as those of the ‘victim proper’) if I could shadow them, doing everything with them for a few days.

After making observations, I interviewed the researchers. However, it is important to note that observations were paramount, while the interviews served as backups and aids, and provided me with the opportunity to check whether I correctly understood what the interviewee had said earlier. Moreover, having the researchers go over arguments made in situ enabled me to incorporate their words and voices into my notes more closely.

Classification Work

When I first visited the Molecular Microbial Ecology Group, it struck me that everybody told me stories of conflict when they introduced me to their work. They told stories of historical conflicts (about earlier forms of science that had been difficult to get past) and stories of concurrent conflicts between traditions or paradigms that were still influential. These kinds of conflicts seemed very important to the researchers, presumably because their field is interdisciplinary, combining as it does molecular microbiology with microbial ecology. This relation to two major traditions seemed to engender a need to demarcate the group from both of them. But in spite of all the conflict stories, the group appeared to be a very harmonious and friendly unit; people seemed to like each other and to enjoy spending time with each other, professionally as well as socially.

Each of the two traditions – molecular biology and ecology – carries with it one of the two major classification systems: genetic and naturalist. When combining the two traditions, the researchers also attempt to combine the two classification systems. This leads to various dilemmas in their daily work. In the following sections, I examine some of these dilemmas: the debates surrounding a new category of microorganisms (VBNC – Viable But Not Culturable), the discussion of knowledge ideals, the construction of phylogenetic trees and the narrative figures used as resources in these debates. In each instance, I also discuss how the two systems interact.
VBNC

VBNC is a new category of microorganisms, which has emerged in the last decade. VBNC is an acronym for Viable But Not Culturable, meaning bacteria that are alive, but which cannot be cultured in the laboratory and hence cannot be studied by the researchers. Thus, the category is defined quite broadly and can encompass any species of bacteria, as it is focused on characteristics of the laboratory rather than the bacteria. Thus, the only defining characteristic of the organisms classified as VBNC is that they cannot live in the laboratory, but that researchers have a suspicion that they might exist anyway. This suspicion can arise in various ways. Here I will consider only the suspicions based in genetic techniques.

When the researchers talk about this category, the genetic and naturalist classification systems are described as conflicting. Paradoxically, however, in their daily practice the researchers seem to integrate techniques and arguments from the two systems without any major difficulty, thus pointing to a coexistence, rather than a contradiction between them.

One of the group’s research projects concerns microbial populations in drinking water. Traditionally, researchers examined drinking water by making plate counts: that is, they took a small amount of drinking water and spread it on a high-nutrition medium in a Petri dish. The Petri dish was then left in an incubator at 37°C for a period of 1 or 2 days. During this period, the single organisms left on the Petri dish would divide numerous times and form micro-colonies visible to the naked eye. If there were 10 micro-colonies on the plate, it was concluded that the drop of drinking water spread onto the plate had originally contained 10 organisms. They were then categorized by means of other techniques, for example, by growing them on different plates (plates with media mixed, for example, with different types of antibiotics, on which only some organisms can survive).

This type of experiment is connected to the logics embedded in naturalism and naturalist classifications. Naturalist classifications are part of a tradition that goes back to Linnaeus and Darwin. The goal within this tradition is to describe and classify organisms. It is based primarily on visual observations of morphological characteristics, as was usual for the endeavours within natural history in the 18th and 19th centuries. In the classical naturalist framework bacteria are defined by their lack of organelles, in contrast to reptiles, insects, mammals, copepods and so on. Thus, while animals and plants are classified according to their appearance – that is, whether they look alike or not – other physiological factors, such as metabolism, are important when describing and classifying bacteria.

According to the researchers, there were numerous problems with this type of research. Most importantly, the organisms found by means of plate counts were not typical of aquatic environments: they were bacteria that thrived in environments with high levels of nutrition and high temperatures. Drinking water, in contrast, is characterized by low levels of nutrition and low temperature. Some types of bacteria that thrive under
low-nutrition and low-temperature conditions will not grow on high-nutrition plates at high temperatures. The experimental design of plate counts had created a completely misleading picture of the population in drinking water. The cell culture procedure is designed to model the internal environment of the human body, characterized by high levels of nutrients and temperatures of about 37°C. The strains that were assumed to be pre-potent in drinking water—because they grew rapidly on plates—turned out to be decidedly atypical of the population.

In the 1960s, the sequencing of nucleic acid became possible, leading to the classification by 16S rRNA analysis.10 The 16S sequence is a specific genomic sequence, i.e. a line of signs (bases), A, C, T and G, that is used to identify and categorize organisms instead of metabolism or appearance. The 16S sequence is very useful for identifying and categorizing bacteria, as parts of the sequence are the same in all bacteria while other parts always differ. In addition, 16S can be used to compare distantly related organisms (such as humans and bacteria). Finally, mutations in the 16S sequence are usually lethal to the organism and, accordingly, the 16S sequence changes very little from one generation to the next. 16S rRNA analysis introduced a new type of microbial classification with the potential to render older classifications obsolete. 16S makes it possible to take a drop of drinking water and develop a picture of the 16S gene sequences of all bacteria in the drop.11 ‘You put it into a computer, and it gives you total identification’, as one researcher said.12 This image is strikingly different from the one produced using the plate count technique.

I was told that a research group in Berlin had used 16S rRNA analysis on drinking water and found that only about 1% of the bacteria that live in drinking water appear on the plate.13 The typical water strains are ‘viable but not culturable’; in other words, they are alive but cannot be cultured, and cannot therefore be studied with the traditional laboratory method.

‘VBNC’ means that the researchers assume that there are bacteria that cannot be cultivated in the laboratory. Researchers can only be sure of bacterial characteristics such as energy sources, resistance to penicillin, growth patterns, and so on, if the bacteria can be grown and cultivated. Therefore, bacteria have traditionally been identified according to their reproductive activity, which can only be demonstrated if they reproduce in the laboratory. Since ‘VBNC’ is a category of bacteria, which by definition defies being studied in the laboratory when active, it challenges many of the traditional, ecological ideals of science. Why discuss something that we know nothing practical about?

Some researchers argue that these entities should be disregarded. For instance, the professor in the group said the category was troublesome because, ‘then you have to reconsider the question: what is life?’14 Microbiologists have traditionally used the test of reproduction to show microbial life, but if you cannot test the VBNC-bacteria—because they cannot live while being tested—how can you tell if they are alive, or even in existence? This line of argument implies rejecting both the use of the word ‘viable’ and the use of the word ‘culturable’: as long as viability is
connected to a test of activity, bacteria can only be ‘active’ or ‘non-active’ – as opposed to ‘viable’ or ‘non-viable’. Therefore, opponents of the VBNC category suggest the use of the words ‘active’ or ‘potentially viable’, instead of ‘viable’ and ‘non-viable’. Similarly, the use of the word ‘culturable’ is discouraged, as it implies that researchers have tried to cultivate the bacteria in all possible conditions and all possible media, which can never be the case.

The proponents of the VBNC hypothesis, on the other hand, object to a discursive shift from the term ‘alive’ to the term ‘culturable’. Furthermore, they argue that many organisms have been shown to be active (that is, they possess definite morphology and functioning metabolism), even if they are not reproducing. Certain cell types are assumed to have the ability to repress or block reproduction, or to be able to reproduce only under specific circumstances. Hence, researchers do not know whether these organisms will not or cannot reproduce under laboratory conditions, or whether they are dead. Moreover, as mentioned earlier, many bacteria thrive in environments very different from laboratory conditions, and a problem associated with 16S rRNA analysis is that gene sequence information tells researchers nothing about, for example, what type of environment a specific type of bacteria might prefer.  

But how does this affect laboratory practices? When the researchers I studied work on identifying the populations in a water sample, they use gene sequencing. One researcher told me that he found it very frustrating to name new species found by means of gene sequencing, when he knew absolutely nothing else about them. Within the ecological tradition, the practice of naming is connected to a test of characteristics, that is, what does it need for energy, what is lethal to it, what environment does it prefer … However, within the molecular tradition, naming is based on gene sequencing. Hence, the practice of naming the newly found organisms on the basis of gene sequencing is considered problematic within the ecological tradition, while not naming it, despite the gene sequence, would be considered non-scientific within the molecular tradition. A catch-22 situation therefore arises, although it should be mentioned that the researcher did in fact name his new gene-sequenced organisms, despite his reservations about doing so. Thus, the researcher was faced with the dilemma of having to choose between two strong and – in this case – conflicting systems that classify organisms in two different ways.

The issue of naming newly found bacteria on the basis of gene sequencing alone is connected to the VBNC category. The two classification systems have very different stances on this practice. The naturalist classification system is deeply concerned with the question of life and death, since it is critically important for establishing the practical difference an organism makes in its environment, whether it is alive or dead. This question is less important for the genetic classification system. If the aim is to create phylogenetic trees (see below) and to identify and classify all organisms on earth according to genetic sequences, then the critical question is not whether the specific organism is alive or dead, or whether
or not we know exactly how it lives, but rather, where it should be placed within the vast code/tree. Thus, the VBNC debate is directly connected to a tension between the two classification systems. The question of whether to place a certain bacterium in the categories of ‘viable’, ‘culturable’, ‘active’, and so on, is ultimately a question of privileging and mobilizing conceptual and methodological resources from one or the other programme. The classificatory tension turns on the basic of ontological classifications of ‘alive’ or ‘dead’, highlighting how classifications seem universal and natural, once they are in place, but also that ‘nature’ is different when classified in terms of different systems.

**Epistemic Ideals**

In the following, I will clarify the nature of the conflict expressed in regard to the VBNC category by broadening the discussion to include practices and concerns beyond those that can be linked directly to the VBNC category, as well as the epistemic ideals expressed by the researchers.

**Naturalism**

I was at the bench observing a researcher who was running a gel. However mysterious this procedure was to me, it was obviously a routine activity for the researcher. Running a gel takes time, but it does not demand much concentration from someone experienced with the procedure. The other researchers at the bench were joking or listening to the radio while performing their tasks, thus passing time while going through the motions of techniques that were presumably as routine to them as running a gel was to the researcher I was observing. He started to explain his project, the scope of it, how he had ended up working with it, and what it was that fascinated him about it. After some time his story touched upon the genetic classification tool of 16S rRNA analysis, and he discussed the kind of knowledge this technique produced and what kind of definitions of life it entailed. The researcher expressed a decidedly naturalist stance, and it was particularly interesting to hear him attribute dramatic fallacies and errors to genetic classifications, while at the same time he and the other researchers quietly performed routine genetic techniques in a relaxed, friendly and unbothered way. In a later interview, I asked the researcher to recap the discussion we had had in the laboratory. He recounted:

You can find new microorganisms everywhere. Because, especially with 16S, you’ll typically have 16,000 base pairs, and then, if you can find one base pair that is different between these two bacteria, well – then they’re different. But that’s – there are 16,000 base pairs, there are four combinations on each [ACTG], so really you have four to the 16,000th power, so that’s millions, a dizzying number, that’s how many species you could really find by looking at 16S. So if you don’t find ANY species that are the same . . . – but still you find out that there are some groups with similar characteristics, then you’ve like come a step further, instead of just saying, well describe some lakes and say, there are these and these and these, and they are not alike to any earlier described species. I mean – great!
anybody could find that out. Just go into the backyard, there are ten to the power of eight in every gram of soil, so you’ll be sure to find lots of bacteria that aren’t . . . There’s a pretty big chance that you won’t find any that have been described earlier. So really it’s more interesting if you can find one that HAS been described. That would make for a bigger success. But some people haven’t really figured that out yet.¹⁹

This statement describes an epistemic ideal close to that of naturalism, in which data that fail to reveal anything practical about bacteria are not interesting, even though the data might be correct and exact. This conception of data as interesting if they correct the picture of bacterial species, or if they reveal something practical about the bacteria, seems to be central for the researchers. I observed repeated use of such conceptions in different guises.

**Exactness**

The genetic classification system is connected to a different epistemic ideal: that of exactness. Accordingly, data that contain new information that corrects or specifies older data are considered important, regardless of their practical effects. The ideal of exactness was expressed in many different ways by the researchers. For instance, one researcher said the following during an interview:

> If you look at the sciences, there is this hierarchy – or in my head there is this hierarchy; and at the top you have like fundamental stuff, like fundamental particle physics and things like that, where you know that you have a photon, or you have a proton, and then you throw in a neutron, and then what happens? And from there, there is this spectrum to other things that are like . . . to sciences that are more descriptive, like examining how the natural sciences are communicated in Denmark, maybe something like what you are doing, which is very complex, and very difficult to tackle, there are a lot of factors that come into play. And there is this spectrum in the middle . . .²⁰

According to this researcher, sciences such as fundamental particle physics are perceived as the most exact and as being on top of a hierarchy of the sciences. What I was doing (in this case, conducting interviews with researchers – in other words, a form of social science) is placed at the bottom of this hierarchy.²¹ In this hierarchy, research in molecular microbial ecology is placed somewhere in the middle – not as exact as particle physics but more exact than social sciences.

The ideal of exactness is basic, not only for members of the Molecular Microbial Ecology Group, but also in the broader microbiological community. For instance, at the ISME conference that I observed (26–31 August 2001), I had to introduce myself frequently, as is customary at conferences. I briefly introduced my project and the concept of science studies, and the reply was almost inevitably, ‘But that’s not very scientific!’ When I asked what was unscientific about it, it was usually what appeared to the microbiologists as a lack of exactness with regard to measuring and producing data. According to the microbiologists, the fact that I had only
myself as a ‘measuring instrument’ presented a major problem. How could I presume to conduct exact scientific research that way? What is interesting about this anecdote is that the ideal of ‘exactness’ seems to be so deeply embedded in the way the researchers regard their work that it has become synonymous with ‘science’; their comment was not ‘that’s not very exact’, but rather, ‘that’s not very scientific’.

It is my claim that although naturalism is marked by a practical ideal, and genetics is influenced by the ideal of exactness, the relationships between research disciplines and epistemic ideals is complex. This complexity comes through in practice.

Naturalism and genetics were only mutually exclusive when the researchers explicitly talked about them. In practice, the researchers generally carried out their projects by using tools from the genetic platform, while using naturalist arguments when criticizing the knowledge produced by the genetics tools. Consequently, the systems did not always come into conflict. If a foreigner unfamiliar with the researchers’ language were to observe their practices, the systems might be viewed as complementary rather than conflicting. The complementarity and conflict of systems seemed to exist simultaneously: conflict in the articulation of science, complementarity in the practice of science. The verbally expressed conflict seemed to work as an engine, or perhaps energy source that fuelled discussions and arguments in the group. I will return to this point later.

Phylogenetic Trees

A central focus in identifying and categorizing bacteria, closely related to the naming of new strands mentioned in the previous section, is determining the evolutionary history, or phylogenetic history, of the bacteria. ‘Phylogenesis’ is a combination of two Greek words: ‘phylon’, meaning the hereditary line; and ‘genesis’, meaning ‘creation’ or ‘formation’. Phylogenetic history can be represented by phylogenetic trees, like the one below representing water bacteria (Fig. 1). Both naturalist and genetic classification systems used phylogenetic trees. During my observations in the laboratory it was quite hard to understand what the phylogenetic trees meant and how they were made. The following is the explanation given to me in a discussion I had with four researchers from the group.

Recently, genetic techniques have made it possible to set up phylogenetic trees in a new, very exact way. Earlier, when phylogenesis was based on phenotypic characteristics alone, biologists assumed, for example, that hippopotamuses were closely related to warthogs and other similar four-legged creatures. Hippopotamuses and warthogs were thus placed on branches close to each other on the phylogenetic tree. However, when genetic identification is used it becomes obvious that hippopotamuses are really much more closely related to whales than to warthogs. The assumption that hippopotamuses and warthogs were closely related was based on a kind of trompe l’oeil caused by the four legs. According to current
evolutionary doctrine, the four legs were not an evolutionary marker at all; they had evolved from two different lines and thus had no evolutionary significance whatsoever. Consequently, evolutionary history and nature can be represented differently in phylogenetic trees, in accordance with genetic or naturalist classificatory practices.

The Molecular Microbial Ecology Group constructed a phylogenetic tree in the following way: first, the 16S-sequence from an organism is isolated using the polymerase chain reaction (PCR). Then, the genetic material is sent to a commercial laboratory, which sequences the material. After the researchers get the specified 16S sequence back from the laboratory, either they upload the 16S sequence onto a website, which automatically constructs a phylogenetic tree based on the sequence, or
they use one of their own programs to do so. According to my inform-
ants, choosing between different websites and programs is difficult and
involves trade-offs between user-friendliness, computational power and
other matters.

The conceptual basis of these simple-looking programs is not simple at
all. A basic assumption behind the trees is that the distance between
bacteria in the tree structure is proportional to the number of different
base pairs in their 16S sequences. The trees are constructed using math-
ematical algorithms that contain assumptions about how far apart the
branches should be placed. A given map of evolutionary history thus
directly mirrors the genetic analysis, and trees generated using different
algorithms can look quite different from one another.

Heroes

When the researchers discuss the histories and heroes of their field,
inclusion is one of the key narrative themes. For example, members of the
Molecular Microbial Ecology Group included Carl Woese – an American
microbiologist who started working in the field in the 1960s – as an heroic
figure in their accounts of genetic classifications and the design of phylo-
genetic trees. My very first visit with the group started with a meeting with
the professor who was my primary contact. During this meeting the
professor told me a story to illustrate what the group’s work was all about.
Later, I heard the same story repeated by different people in many
different situations – and the fact that this story is repeated in so many
different contexts makes me regard it as being crucial to the group. The
story goes something like this:

It is assumed within biology that every living organism on earth has a
common ancestor, known as the ‘universal ancestor’. Unfortunately, no
fossils or other physical evidence of the universal ancestor have ever been
found. In order to be able to continue working without the physical
evidence that could prove the hypothesis, molecular biologists work with
phylogenetic trees, in essence towards establishing a phylogeny of all living
organisms. Within the phylogenetic trees, biologists work with one root
point that represents the missing universal ancestor.

Using the new technique of 16S rRNA analysis, Carl Woese began working
on the universal phylogenetic tree in 1966. In 1976 he made a major
discovery: life on earth was not – as previously assumed – divided into five
kingdoms, formulated by the famous 18th-century naturalist taxonomist
Linnaeus: plants, fungi, animals, bacteria and protists. In reality, there
were three major branches on the evolutionary tree: Bacteria, Archaea and
Eucarya. Analyses using 16S rRNA showed that Archaea and Bacteria did
not belong to the same group as hitherto assumed, since genetically they
were as far apart from each other as they both were from the Eucarya. This
group, on the other hand, included plants and animals that were more
closely related than hitherto assumed. Thus Woese fundamentally changed
the outlook on biology and overturned one of the basic biological dogmas.
His analytic approach – combining classic microbial taxonomy with techniques from molecular biology – has been broadly accepted in the scientific community, as have the three branches on his phylogenetic tree. In addition, Woese’s approach has made it clear that bacteria are genetically diverse; so diverse, in fact, that there are species of bacteria that share fewer genes with one another than do humans with oak trees.

The story seems central for the researchers in the Molecular Microbial Ecology Group, because it keeps reappearing in their attempts to explain the momentum of their work to an outsider, such as me. It includes, as a central point, the combination of traditions – microbial ecology and molecular biological techniques – that is the group’s raison d’être as well as its reason for dealing, on a daily basis, with the coexistence of the two classification systems.

Moreover, it bears the mark of a grand narrative of scientific progress – including such markers as: ‘before, researchers would . . .’, ‘but in reality . . .’. The story is a narrative that portrays one classification system as reflecting reality, while bracketing another system as not doing so. The five-kingdom taxonomy that Woese overthrows in the narrative is described as simply being untrue. This is interesting because the narrative stresses that the genetic classification system is (becoming) the dominant one. Still, if one’s primary interest is not genetic codes but rather physiological phenomena, it seems fair to suggest that two species of bacteria (even if their genetic codes differ dramatically) still appear to be quite similar to each other: both are microscopic, one-celled organisms without organelles or cell nuclei. The two bacteria look very much alike in a microscope, and the claim that they are ‘in reality’ more distantly related than humans and oak trees seems strange.

Woese himself made some interesting points about his ‘discovery’ – which I am currently treating as a narrative – that are worth taking into consideration. In an interview in the semi-popular online periodical BioWeb,32 Woese defines his story as an extension of one of the most persuasive narratives in the history of the sciences, namely Darwin’s The Origin of the Species. One effect of the connection to Darwin is that it lends legitimacy and grandeur to Woese’s narrative. Woese’s description of his own narrative as a fulfilment of the dreams contained in Darwin’s theory is a very powerful rhetoric device to further his own project – in this case, a genetic classification system.33 Darwin, of course, used the Linnaean taxonomy. And so, while Woese distances his classifications from the naturalist system, the two systems share common narrative roots. This constitutes a powerful common ground, which is important for understanding how the Molecular Microbial Ecology Group managed to use the two systems and discourses without apparent disruption.

However, the common ground constituted by Darwinian theories does not mean that geneticists hold favourable views of naturalism today. In the BioWeb interview, Woese expresses little praise for researchers who still rely on naturalist classifications, as to some extent do some of the researchers who told me versions of the Woese story:
The problem as regards botanists and to some extent zoologists can be summed up in a phrase, ‘intellectual inertia’. These folks were brought up to classify in terms of gross morphological similarities and differences. The idea of doing so in terms of molecular sequence is a bit hard for many of them to swallow, particularly so the botanists. Since they are suspicious of using molecules as phylogenetic measures, it is understandable that they are reluctant to accept the resultant taxonomies. You get the feeling talking to some of them that if they can’t see a morphological difference, they can’t intuitively accept that profound phylogenetic difference exists.

Woese describes advocates of naturalist classification, especially those concerned with morphology, as blind and resistant to change. However, his arguments can easily be turned against him. Is the statement ‘if they can’t see a morphological difference, they can’t intuitively accept that profound phylogenetic difference exists’ inherently more ‘true’ than the statement: ‘if they can’t see genetic difference, they can’t intuitively accept that profound phylogenetic difference exists’? Both claims expresses equal dogmatic faith in one system over the other.

It is interesting to note that in the same interview from which I quoted above, Carl Woese shows a clear understanding of the definitive power of narratives and classifications, and the fact that the narrative’s capacity to convince people determines whether or not the associated classifications can claim to define reality: ‘So long as textbooks with the five-kingdom scheme are printed and accepted by school boards, then five kingdoms will persist.’ The stories and heroes point to the common ground used to include one or both of the two systems in the same narrative: the goal is the same, the opponents simply go about it the wrong way. Thus, the stories show how the two (conflicting) ways of mapping species through classification can be included in the same narrative.

Discussion and Conclusion

I have described different forms of coexistence between two classification systems in the daily life of the Molecular Microbial Ecology Group. Both naturalist and genetic systems were used for identifying and classifying the microbial population in drinking water, and both featured in the related debate over the VBNC category, in the construction of phylogenetic trees, and in the stories and heroes surrounding the two systems in relation to phylogenesis. The VBNC story was a story of vehement verbal conflicts that did not necessarily inscribe themselves into practical conflicts. The different stands and practices were conflicting or complementary, depending upon the context of discourse and practice.

The story of the design of phylogenetic trees was a simpler one, as the genetic system was more fully in command in this context. However, phylogenesis was still two very different things, depending upon whether it was a part of the naturalist or genetic system. When researchers were classifying in terms of naturalism, they considered organisms to be closely related when they resembled each other morphologically and/or physiologically, whereas such resemblances were irrelevant to classifications with
genetic system, for which only the genetic code matters. In contrast, the genetic code was irrelevant when seen from a naturalist perspective. This story was thus one of conflict.

Lastly, the Woese narrative was an example of how the two systems were included in one narrative that used common ancestors – Darwin and Linnaeus – to render the systems complementary rather than conflicting. At the same time, Woese repudiated the naturalist practice, even though it was used to an extent by some of the researchers who cited him as a ‘hero’ in a narrative that traced back to the common ancestors. All in all, the two classification systems were conflicting, complementary and inclusive – often at the same time.

But what does this multiplicity say about the scientific practice of the group studied? The multiple medical object described by Mol (2002) hinges on the distribution of practices. Here, however, we are dealing with one group, and hence no distribution. Where, then, does the multiplicity come from? And how can the researchers be actively involved in performing multiplicity without the group being torn by controversy?

The challenge of combining the two classification systems, traditions, and ideals of scientific knowledge held strong attractions to the researchers I studied. They did not want to choose the ‘right’ classification system with which to work. Rather, they wished to avoid choosing between the two. As one researcher put it: ‘it is about uniting rubber boots ecology and molecular biology’.34 The result is an intricate balancing act, related to what Star & Griesemer (1989) call ‘the central tension in science’: referring to scientific work as being inherently and necessarily heterogeneous, and at the same time in need of cooperation, integrity and generalizable findings.

This, I believe, is one explanation for why the researchers explicitly talk about controversies and conflicts that are hardly noticeable in practice; the controversies seem to work as incentives. In Star & Griesemer’s terms, the heterogeneity is inherent in scientific work, while boundary objects that can provide integrity and cooperation demand active engagements. Star & Griesemer examine work done between communities of practice and not within them, as I do. Still, scientific work was heterogeneous, a point consistent with Thomas Kuhn’s The Essential Tension (1977). In the group I studied, however, the heterogeneity that may be necessary to add momentum and drive to scientific work – to make, in effect, scientific work into science – was not automatically present. The researchers’ articulations attempted to instil heterogeneity in a field that is dominated by one frame of reference and classification system, namely, the genetic one. This is what I mean by describing the controversies as incentives: without the heterogeneity created by these controversies, one side of the central tension would be missing. There would be only homogeneity.

This conclusion may seem consistent with the idea of the dominance of the genetic system over the naturalist one, which I questioned at the start of this paper. Surprisingly, what seemed at first glance to be a conflict between two equal classification systems now seems to be the dominance of one system, albeit supplemented in different ways by the
other. Techniques (for instance, traditional plate count techniques) and narratives (for instance, Darwinian evolution) are borrowed from the practical, naturalist classification system, presumably to make the scientific work more like a conventional view of science and less like work. In addition, combining the two systems gives the group a distinctive scientific profile, demarcated both from the naturalist science of the past and the genetic mainstream of today.

Notes

I would like to thank the staff at the Molecular Microbial Ecology Group at the Technical University of Denmark for treating me with courtesy and great hospitality. For insightful readings and comments, I would like to thank Signe Vikkelsoe, Leigh Star and Torben Elgaard Jensen, as well as the anonymous reviewers at Social Studies of Science. Finally, Michael Lynch’s efforts and comments have been invaluable. The research for this paper was made possible by a grant from the Corrit Foundation (Danish Technical University) and an internal grant from Copenhagen Business School.

1. It is not possible to loyally represent the body of work encompassed in this tradition. I refer to Knorr Cetina’s comprehensive review of laboratory studies for a fuller discussion (Knorr Cetina, 1995).

2. This argument shares certain points with the line of reasoning presented by Annemarie Mol (2002) in her book The Body Multiple. Mol describes a medical object, atherosclerosis, as resulting from distributed and multiple work, without a centre of focus that aligns the different types of technology and arguments used to produce it. In this sense, atherosclerosis is seen as ‘more than one’ (non-singular) and ‘less than many’ (non-fragmented) (Mol, 2002: 55). My finding that science is performed as multiple (although in this case hardly distributed) rather than singular work is surprising, even when based on the arguments Mol sets forth. She points out that it has often been noted (especially within the sociology of science of the 1960s and 1970s) that when scientific data (or classification systems) presented by different research groups contradict each other, there will be controversy and conflict, ending when one side has ‘won’ (Mol, 2002: 88–89). Accordingly, she sees science as being different – or being treated differently – from the hospital she explores. However, in common with the staff at the hospital, the research group in the scientific laboratory I studied also exhibits the performance of multiple rather than singular objects.

3. The group’s members also work with outside parties, for instance, with hospitals working on medical interventions against cystic fibrosis (caused by biofilm in the lungs); with environmental research units, examining the microbial populations of drinking water; and with the food industry, researching probiotica for dairy products.

4. The group includes one professor (tenured), two associate professors (tenured), four laboratory technicians, two assistant professors, two post-docs, seven PhD students and three research assistants. However, only the three tenured researchers and the four laboratory technicians are stable members of the group. The other members change continuously. Thus, the numbers presented here represent the average number of group members during the period when I was making observational studies.

5. The professor in the group had explicit ideas of the work I should do at their facility. I was put to work on an experiment, part of a much larger experiment, in which the main goal was to construct a microbial community that was able to degrade the organic solvent toluene. My job was to modify two species of bacteria genetically, and find out if their metabolic systems were activated by benzylalcohol and natrium-benzoat respectively. I was given the very best treatment, starting many days with a 1-hour crash course in molecular microbiology taught by the professor, followed by a day in the laboratory, supervised by a very capable laboratory technician, who made sure I did everything by the book, and asked me questions to check if I understood what was going on.

7. The techniques are still in use in spite of the past tense of the story. For further information see Bergey’s *Manual of Systematic Bacteriology* (Garrity, 2001), the classic key to bacterial taxonomy used for identification of bacteria in the traditional naturalist way.

8. The visual bias and basis of this classification system was not inevitable. Other attempts at defining classification systems for all living things were made in the same period. For further discussions see Ritvo (1997) and Foucault (1970: 125–65).

9. For instance, the water was taken from the waterworks, as if there were no aftergrowth during the transport through water pipes to taps. However, water pipes are large real-life biofilm systems, and researchers know that this means plenty of aftergrowth. In addition, different water pipes have different populations depending on the material, length and structure of the system.

10. DNA can only be found in the core of the cell. However, the information contained in the DNA is transported out into the rest of the cell by different types of RNA: first, messenger RNA (mRNA) is created through a process called ‘transcription’, in which double-stranded DNA is ‘rewritten’ as single-stranded RNA. The mRNA codes are further used to produce proteins through a process called translation. This happens in the ribosomes (protein plants of the cell), which are themselves created from ribosomal RNA (rRNA). It is this RNA – rRNA – which is used as a basis of 16S-sequencing.

11. The researchers carry out sequencing of, for example, populations in water, using a technique called PCR; the starting point for PCR is a ‘target sequence’ – that is, a gene, or a segment of DNA. In this case, the target sequence would be the 16S DNA sequence. DNA consists of two interconnected helixes, hence the name ‘the double helix’. The two helixes separate when heated to 95°C. The researchers put the target sequence (usually contained in a small tube) into a small incubator. The tube containing the target sequences also contains *primers* (two small pieces of synthetic DNA, each complementing a specific sequence at one end of the target sequence; the primers are made commercially). After the incubator has been heated to 95°C the double helixes of the target sequence divide, the temperature is reduced and DNA polymerases (a DNA *polymerase* is a naturally occurring enzyme that facilitates the formation and repair of DNA and that starts an activity that is basic to all living organisms – the production of new DNA) start working at each primer and copy the sequence of that strand. Within a short time, exact replicas of the target sequence have been produced. The process is repeated numerous times: the researchers program the incubator to bring the temperature up and down between, for example, 30 and 95°C, a certain number of times within 1 hour. Thus, double-stranded molecules of both the original DNA and the copies are separated in subsequent cycles; primers again attach to complementary sequences and the polymerases replicate them. When the researchers have sufficient amounts of target DNA (16S), it is sequenced. This is done ‘out of house’ and what the researchers get back is a sequence of the signs A, T, G and C. For further reading on PCR, see Rabinow (1996).

12. Field notes, 14 September 1999.


15. On 26–31 August 2001, I accompanied the researchers to a conference in Amsterdam, ISME (Interactions in Microbial Ecology). Interestingly, one of the sessions at the conference was on the VBNC category – at least, the researchers I was with referred to it as the ‘VBNC session’ – although it was called ‘Active but not Culturable Microorganisms’. If we assume that the conference represents the state of the art in the research community, then the community is in the middle of the debate signalled by oppositions between the terms ‘active’ versus ‘viable’, and ‘culturable’ versus ‘not culturable’. The conference can be viewed as an attempt to reach a compromise, by making the VBNC category into a boundary object that would help make the systems work in a complementary, rather than conflicting, fashion. It remains to be seen whether this attempt will succeed.


17. Field notes, 5 March 2001. ‘Running a gel’ – or gel electrophoresis – means producing a graphic/material representation of DNA: fragments of the target DNA obtained by enzyme treatments or from in vitro synthesis (PCR) are separated according to their
size (numbers of base pairs) on a pore-containing gel made of polysaccharides. At one end, slots are cut into the gel. An electric voltage is applied to the gel, creating a negative and a positive pole on either side of the gel. Pieces of DNA, along with a dye, are added to the slots at the ‘top’ of the gel with a pipette. The pieces of DNA carry a net negative charge (DNA is an acid), and they will therefore migrate towards the positive pole. The shortest pieces of DNA travel fastest through the pores of the gel, whereas larger fragments move slower. It is in this way the well-known pin code-like size distribution of DNA fragments is produced. For further discussion of gel electrophoresis, see Amann & Knorr Cetina (1988). Analyses of visualizations (such as Amann & Knorr Cetina’s) constitute an important discussion in the tradition of ethnographies of laboratories. See for instance Lynch (1985b), Cambrosio et al. (1993, 2005), Keating & Cambrosio (2000) and Sommerlund (2003).

18. These ‘routine techniques’ are much more complicated than suggested here when considered more closely. See for instance: Amann & Knorr Cetina (1988), who consider gel electrophoresis; Paul Rabinow (1996), who analyses the invention of PCR, a technique that reproduces genetic material, making it abundant and available for laboratory experimentation; and Jordan & Lynch (1992), who analyse the ‘plasmid prep’, a constitutive genetic technology in molecular biology.

21. According to Sharon Traweek (1988: 79), this hierarchy is perceived in a similar fashion within the physicist community: ‘Particle physicists share the assumption that this spearhead [particle physics] has a shaft behind it; after chemistry and engineering comes biology, followed perhaps by the social sciences and humanities.’
22. In Laboratory Life, Latour and Woolgar write: ‘[Our observer] was painfully aware of the enormous distance between the apparent solidity of his informants’ constructions and his own. In order to study half a gram of brain extract, they had at their disposal tons of material, millions of dollars, and a large group of some forty people; in order to study the laboratory, our observer was alone’ (1986 [1979]: 256).
23. The clash between the ideals of exactness and practicality is not restricted to microbiology. Keating, Cambrosio and MacKenzie point to a parallel conflict within immunology: ‘while avidity [a concept referred to as obsolete in the scientific community] was given a somewhat shaky epistemic status (“a function of techniques used in its measurement”), its existence seemed to be secured by its clinical imports (antigens of clinical interest being most of the time complex) compared with the idealized conditions under which the notion of affinity would apply (“the term affinity is most accurately applied to interactions involving simple, uniform determinants”). In other words, it seemed possible to summarize the matter by pointing to a gap between “pure science” and “applied (clinical) science”’ (Keating et al., 1992: 317).
25. The researchers studied typically used a German company called GATC.
27. The Ribosomal Database Project at Michigan State University has a service that can generate phylogenetic trees, but according to the researchers I studied, it uses a relatively simple algorithm (which, presumably, is not very good) as this does not require as much computer power.
28. Field notes, 3 September 1999.
29. The five kingdoms were further categorized into two overall groups: Eukaryotes (animals, plants, and other organisms that have cells with a nucleus) and Prokaryotes (bacteria and other organisms without cell nuclei). ‘Eukaryotes’ is a word shaped by combining two Greek roots: ‘eu’ meaning good and ‘karyote’ meaning kernel. Eukaryotes are organisms with cells that contain a nucleus. Analogously, ‘prokaryotes’ is a combination of two Greek words: ‘pro’, meaning before and ‘karyote’ meaning kernel. Thus, prokaryotes are organisms made up of cells that do not contain a nucleus.
30. Archaea are tiny organisms living in extreme environments without oxygen; they were earlier believed to be pre-historic bacteria types and were classified as bacteria.
31. Plants and animals.
32. The BioWeb was an online periodical, which has now unfortunately been taken off the web. At the 15 October 2001 I found the interview that I refer to on the following url: <www.hbcollege.com/lifesci/bioweb/depts/interviews/woese.html>

33. For further discussion of the alliance between the Darwinian narratives and modern genetics, see Haraway (1997).

34. Interview, 5 March 2001.

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**Julie Sommerlund** is Assistant Professor at the Copenhagen Business School. She holds a Masters degree in Modern Culture & Cultural Dissemination from University of Copenhagen and a PhD degree from Copenhagen Business School. The paper presented in this issue of *Social Studies of Science* is based on her PhD work, which consisted of extensive observational studies of a group of microbiologists.

**Address:** Department of Organization, Copenhagen Business School, Solbjerg Plads 3, 2000 Frederiksberg, Denmark; fax: +45 38152828; email: jso.ioa@cbs.dk

**Appendix**

**Data**

Notes from observations:
Laboratory of the Molecular Microbial Ecology Group:
1 September 1999 – 1 October 1999
1 February 2000 – 1 April 2001
Notes from ISME conference, Amsterdam:
26–31 August 2001
Notes from meetings, seminars, conversations, and so on:
September 1999 – September 2001

Interviews:
Research Assistant, 16 February 2001
Postdoctoral Student, 5 March 2001
Graduate Student, 21 February 2001
Associate Professor, 6 March 2001
Graduate Student, 16 February 2001
Graduate Student, 5 March 2001