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HAS HUMAN SOCIETY AN *mfDNA* AKIN TO THAT FOUND IN BIOLOGICAL COMMUNITIES?

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Abstract:

Scientific research and advancements in microbiome and bioinformatic field are providing new insights into the complex role of microbial communities and their interactions. Analyses of microflora deoxyribonucleic acid (*mf*DNA) represent an innovative approach also to an understanding of complex biological societies, including cooperation, synergy and antagonism within a human group.
Several hypotheses and answers may be examined to support the parallelism between microbial community and human society. We propose a new tool, the "social *mf*DNA", as a further model to approach human society, indicator of the properties, composition and dynamics. The ability of mathematical models can be to support and predict similar phenomena based on an integrated and parallel approach where microbial and human communities combine, determining an enticing synergy between sociological and microbiological issues. The achievements of ecological or genetic studies can help explain organizational structures or leadership. In conclusion, this new approach is introduced to show that it is just as complicated to measure any form of society and of predictable behaviour, as it is to measure an individual, living entity.

Keywords:

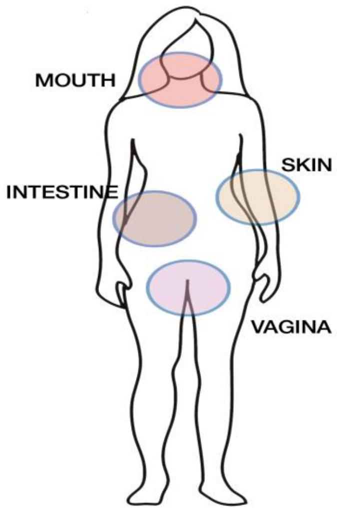
Sociology, Society, Community, Biology.

1. Introduction

Advancements in microbiomic research and bioinformatics are providing new insights to unravel the complex role of microbial communities and their interactions. Sampling and analyses of *microflora deoxyribonucleic acid* (*mf*DNA) represent an innovative approach to understanding complex biological societies, including phenomena such as cooperation, synergy and antagonism between different microorganisms actively present within a group (1) (2). This strategy outlines the structure and habits of a microbial community by sampling and analysing the genome of each single species collectively, "as a pool". Within this framework, the entire *mf*DNA complex becomes a marker by which to characterize communities and predict their evolution within a given environment. The laboratory and bioinformatics approach are based on quantitative (e.g. number and kinds of species) as well as qualitative (e.g. the respective representation in the pool) data. Several promising issues permit the characterization of a specific community, the possibility of comparing it *vs* others, or the prediction of its behaviour following the introduction of interfering factors (e.g. modification of the environment in defined ecological niches) (3).
Identification of biological fluids on crime scenes is one of the first applicative instances described for this method and one of the concrete uses, in forensic sciences (4). Other contexts include medicine, ecology or public health. The general principle is to treat the different genomes of a social group not as the mere sum of individual components, but as a kind of fingerprint or "meta-genome" of that particular biosocial group. In the light of this, a community is not considered as a "mosaic" of individual components, but as a complex and organic quasi-organism, consisting of a "social meta-genome" yielded by all the genomes present in the group's *mf*DNA pool. This perspective offers a new model and opens up a panorama of productive suggestions for sociology, providing possibilities by which to analyse very different kinds of populations, including human societies.
The development of scientific discoveries and progress in studies on human microbiome can open new perspectives for other disciplines, philosophy and humanities (5). Laboratory achievements allowed to explore identities and activities of the microbial communities in different ecological niches. If microbiologists hope to draw connections between microbiome composition, host genetics, and human health, sociology can pose new questions on possible indicators for communities' equilibrium and behaviours. The collection of trillions of microbes living in and on the human body, indeed, is not random, and scientists proposed that human microflora plays relevant roles in many basic life processes. In this context the *mf*DNA approach does not consist merely in gathering single genomes, but in obtaining information concerning their collective physiological/biochemical/genetic ability to adapt to that environment, or mutate, survive, grow, adjust and, finally, transmit the heritage thus acquired to the following generations, as members of the same dynamic society (6).
It is now possible to introduce an interesting hypothesis and provide several parallelisms between analyses of biological microflora communities and the dynamics of human societies, and also show how *mf*DNA can explain or monitor different social phenomena, including competition, recrudescence, symbiosis, parasitism, opening to different horizons related to social dynamics, economic implications, financial and agricultural interrelations, ancient and modern societies, or even virtual Internet-based communities (7).
The starting point is the question: "what is meant by human social *mf*DNA?"(5); and the final question can become is there an mfDNA-like indicator in human societies? Some answers and idea are proposed and several hints for further considerations are make available to the reader.

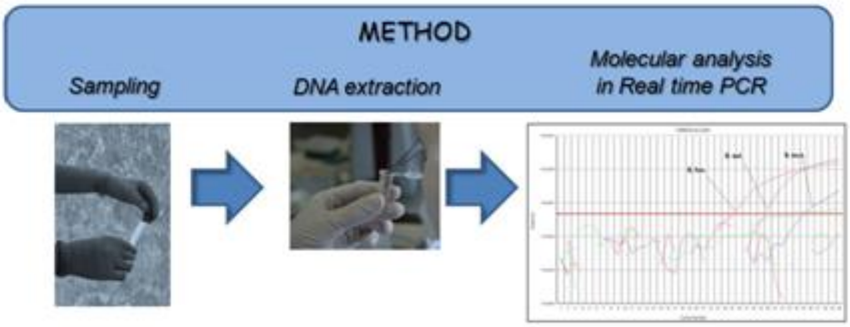
2. The social mfDNA: from the forensic approach to the sociological perspective

Recently, some our collaborative group published an article describing an innovative and easy method for the identification of body fluids (8). It is not difficult to foresee how useful this method may prove to be to different fields, and in particular to forensic medicine, where the solution of difficult cases can be based on body-fluid traces of dubious nature and origin, detected in a crime scene. The cause of the problem lies in the fact that body-fluid traces are hard to be identified by routine analyses, especially when a considerable length of time has passed, as in cold cases. The general principle is based on the fact that some not-sterile biological fluids are not only a made of water, salts, proteins, DNA or different chemicals, but also by microorganisms. A biological fluid can indeed be constitutively made of a typical microbial community. This is for example the case of mucosal fluids as saliva, or vaginal fluid or faecal. The technique used for the identification and classification of this microflora can be based on different methods, but presently the most successful approach adopted is the Real-Time Polymerase Chain Reaction (PCR) amplification, to obtain fast data, both qualitative and the quantitative, with high sensitivity and specificity. Evidently, given the exiguous number of the microflora DNA molecules present in the traces of body fluids, it was necessary to use the Polymerase Chain Reaction, a DNA amplification technique universally employed in various kinds of analyses, developed by the Nobel Laureate Kary Mullis during the ‘80. The choice fell on DNA as the reference molecule because of its ability to survive for a long time. By way of example, suffice it to recall the numerous studies carried out on ‘ancient DNA’ e.g. in anthropology, using traces of genome molecules belonging to organisms that died hundreds, even thousands of years ago (9). Protein and RNA (ribonucleic acid) molecules do not provide a similar opportunity since they are more easily destroyed by ubiquitous lytic enzymes (10). The analytical evidence provided by the authors have showed that it is possible to discriminate the biological fluids based on different, specific bacteria present on the oral, anal, intestinal, skin or vaginal biological fluids, that are not naturally sterile, but harbor a microflora:



The test was so specific that provided trustworthy markers of the body’s different kinds of biological fluids. The general principle described by the authors is based on analyses of the DNA, that is, the DNA of the fluid’s microflora, extracted as a whole and examined as a characteristic of the microbial community. The body fluid is consisted not only of water, salts, proteins, but also of the specific microflora it contained, as a whole (see *Fig I*), shown by traditional culture-based methods and new technologies based on DNA (4).

Fig I - The diagram is an example of the approach (8).



Besides the intrinsic significance in microbiology of this discovery and its useful applications in the field of

forensic medicine, it is interesting to extend its significance, by way of analogy, to a different kind of society, which is of great interest for different disciplines, including sociology: the human community/ies. This ought not to appear as a particularly audacious step. Even if a population of cells, such as the bacteria growing on a certain biological pabulum, is quite different from a community of human beings capable of making free and deliberate choices, one cannot exclude, however, that the natural forces that determine the composition and the characteristics of microbial populations bear a resemblance to the deep, unconscious and instinctive impulses that mark human inter-subjectivity and the parameters that underscore the dynamics of the equilibrium existing within different societies (11).
These similarities can be explained by four brief considerations. First it is known that the chemical composition of body fluids varies according to their origin and their biological function and, therefore, when they become nutrients for bacteria, it is not surprising that they should favour the growth of certain bacterial species to others. One might say that the relationship between the microflora and the fluid is so bi-univocal that, to some extent, the body fluid itself consists of a characteristic chemical solution plus equally characteristic microflora. Indeed, the nutritional requirements of bacteria can vary considerably from species to species, so that it may account for the differences between populations growing on them. Furthermore, heterogeneity of the microflora growing on a given medium secures the internal equilibrium of its ecological niche: the survival of each bacterial species also depends on the metabolic products of all the others. It is easy to find analogies with human social communities in which local populations are markedly dependent on the food and energy resources available on the spot and, in more general terms, on the various bi-products of the socio-economic sub-groups. So, even the physical aspect of single individuals, their life expectancy and their tendency to particular pathologies, mark entire populations, in clear dependence on the available natural resources. To prove the validity of a similar comparison, let us remember that human beings, unlike other living species, adapt themselves to their environment modifying it to meet their needs (12). If, therefore, human populations clearly depend on food and energy sources, this must mean that a similar dependence runs so deep that it is capable of conditioning the human ability to change his own environment (13).
Consequently, the second consideration concerns the fact that the bacterial colonies that express their dependence on nutrition sources and bacteria are relatively simple cells (prokaryotes). Their molecular architecture is less complex than that of more highly developed cells (eukaryotes) and their ability to survive is more closely connected with the environment. They tend to form colonies where the individuals are noticeably independent of each other but very connected with their habitat. The degree of complexity of their molecular architecture and functions is directly proportional to their ability to be independent of their vital medium. The degree of complexity of their molecular architecture and functions is directly proportional to their ability to be independent of their vital medium. This condition is very correlated with different classes of human populations or conditions, including children or nomadic society (14).
The third consideration regards some more specifically cultural aspects of human life. As profound as the material aspect and, to a certain extent, more evident than it, is the cultural tie which binds human populations to their specific sources of survival. Great civilisations arose and flourished close to rivers or in particularly fertile territories, which favoured the development of crop growing and animal husbandry. Once consolidated, these traditional aspects of a civilisation nurtured the subsequent spiritual growth of the individuals and favoured the development of new forms of culture. Cultural growth also needs to be nurtured by constantly new acquisitions capable of enhancing a people’s heritage. So, the development of single members of the community owes a two-fold debt: to the natural environment with its food, water and energy resources and to the human milieu comprising an unitary construct of meanings and values. It is not difficult to identify the peculiarities of these two sources, starting from the physiological and cultural traits of single persons, but the overall result is a totally new “meta-genome” with specific contours and properties, greater than the sum of the characteristics of single individuals.
The fourth consideration begins with the methodology used to analyse the DNA of the microflora. To make bacterial DNA suitable for analysis, the authors had to multiply the rare DNA molecules present in the original sample, while, at the same time, measuring their relative amount. This kind of qualitative and quantitative complexity is the very basis of microflora diversity. Therefore just as the amplification of the DNA tends to make the sample for suitable analysis also social habits and customs used by humans brings out some of the concepts already rooted in its spirit. All cultures and civilisations are endowed with organised structures, deliberately conceived to identify and promote the growth of certain cultural traits, tendencies, simple and profound needs, which, if not appropriately safeguarded, nourished and allowed to thrive, would risk being silenced or disappearing as in a biological selection process. Many social institutions

had and continue to have this function. As far as the Middle Ages are considered, one need only think of the work of the monasteries (15); the main purpose of which was that of identifying and sustaining the demand for religion which, although it resided in the human heart, might well have been overwhelmed by other interests and habits unless given particular attention. The same may be said of strictly cultural institutions, like universities and schools (16). The germ of culture also appears small and fragile when compared to the numerous stimuli, needs and interests that fill human life, and to the economic or juridical bonds which may either maintain and sustain its vital, dynamic balance, or suffocate and overpower it. It is the task of social structures to devise positive stimuli and help them grow in an operative way akin to what is found in the bacterial communities that constitute the various kinds of microflora. Human communities and their history, can represent an extremely complex evolution of the dynamic equilibrium developed in a very particular kind of "macroflora". In this case, the *mf*DNA-principle would not at all represent the DNA analysis of a genetic meta-property of the community, also because all individuals would belong to the same species, but would represent instead a kind of indicator of their role in maintaining community dynamics by belonging to groups.

2.1. Biological and social developments

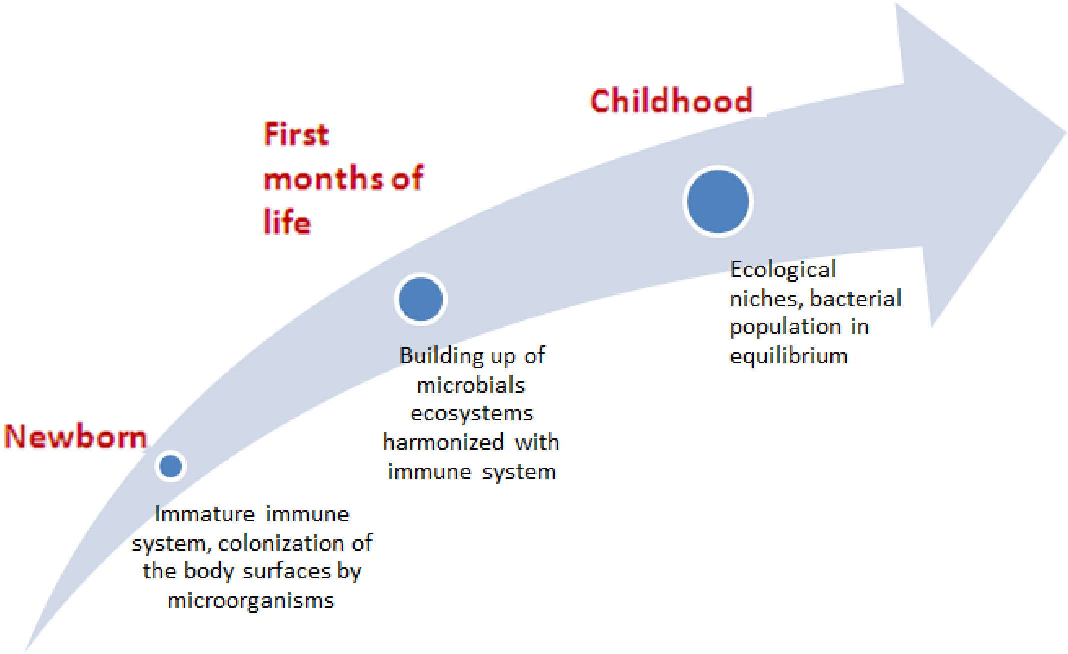
The *mf*DNA approach can explain in a rational and innovative perspective the thesis and provide several parallelisms between analyses of biological microflora communities and the dynamics of human societies, and also show how the *mf*DNA principle can explain or help in monitoring different social phenomena.

However, also interactions between microflora and society can be considered, showing the complex role of all species interacting in a wider ecosystem. The clearest example to understand these parallels is the condition of newborn baby that receives a special type of imprinting due to its mother's bacterial flora (17). This initial "contamination" is implemented by the vagina. The baby is delivered after a number of hours' contact with the mother's vaginal canal. In the case of delivery unhindered by technological intervention, the mother, immediately after birth, brings her baby spontaneously to her breast, not to feed it but to look at it. This is a profound kind of contact, caused by a specific endorphin hormonal *cocktail* to which mother and child are subject during this phase: this process is called *bonding*. Immediately afterwards, the baby, finding itself close to its mother's breast, responds to its own innate reflexes by rotating its head, groping, extruding its tongue. It then begins to suck at the breast.

In the case of home births, the contamination continues thanks to the bacteria belonging to the "family" and to the closest social circle. Most modern societies, however, tend to separate the mother and child at birth and replace colostrum and milk with artificial product (18).

When children are born they are composed only of their own cells (there is, however, a subsequent transmission of maternal bacterial flora, after birth, however). The immune system is immature and, therefore, the individual is open to acquisition of many elements. And so, various microorganisms begin to develop on and in the child's body. In actual fact, the human child, from the moment of its conception begins a relationship with another subject: his/her mother with an intense and not random exchange and selection of microorganisms. Even the infant-mother relationship and the adult-child bonds can be considered as symbiotic. This kind of ever-growing symbiosis ensures that the *link* thus established will become increasingly mutual and imitative, something extremely useful during the early learning and socialisation phases of development. One must consider the fact, however, that it is not so much a question of one type of microorganism as of a microfloral milieu (micro meaning small but also microbic) colonising various parts of the body. The same may be said of human relations during the early stages of life (see *Fig II*): a striking compound of interpersonal, linguistic and behavioural exchanges take place, together with habits that begin to crystallise and consolidate to become a kind of bedrock which will be very difficult to undermine or change later on in life.

Fig II - Microbes-human relations during the early stages of life: newborn, first months, childhood.



This is true, for example, of natural biodegrading processes where pollutants trigger off series of procedures on the part of microbes, minuscule worms and other tiny metazoans, which transform them into polluted liquids and purify them: which is exactly what happens to fluvial sediment or the active sludge treated by urban waste purification plants. In these environments, too, what might be deemed a microfloral community, classifiable as the genome of those particular contexts, springs into action.

At human level, transformations occur as the result of a number of key-interventions which bestow direction on the life of an individual, causing him/her to change course due to conviction or as the result of conscious and autonomous choice, although, later on, it is not possible to establish what are the results of a significant influence.

In addition, it should be noted that specific microfloral elements are capable of adapting themselves to some very peculiar environments and connected example, with volcanic or sulphurous contexts. It is important to keep in mind, however, that outside of certain environments and ecological niches some microfloral components would be unable to survive. The opposite also holds because the microflora in and on our bodies would be unable to resist in volcanic or sulphurous conditions. Therefore, one can say that microfloral elements are endowed with a specific and well-known degree of both adaptability and complexity. The microflora of the oral cavity differs from that of the mouth and that of the faeces (of which it is a relevant component, weighing about one fifth of the whole). Its structure, however, is extremely diversified and, in this, might be compared to complex and differentiated social communities. In the case of human society, variability is even more far-reaching and varied and presents characteristics shared by a given group, but also found in distant and not necessarily similar contexts. Above all, one trait of human society needs to be underlined explicitly and clearly: the society of people is always associative and collective, with a constituent and distinctive profile of its own.

It must be pointed out that society on the whole, like microflora, is no mere mosaic comprising many tesserae but a structure in its own right, enclosed, one might say, in a particular environment necessary to its effective functioning. However, the components of the structure do not remain confined forever within this reference frame, but may be expelled, ousted, ejected (similarly to how each individual can expel the bacteria). The tiny structural parts will stay in their niche, carry out their functions and grow together. Equally, a given social group will remain within a given territory, characterise, define, colonise and transform it (19). A further concept concerns the variation within the microfloral milieu, including the pathological condition. For example, an excessive quantity of pathogen bacteria in the mouth can cause periodontal disease. If a single component develops too much, this imbalance will alter the microenvironment of all the other elements, so that the person whose mouth hosts this altered microflora will suffer pain and discomfort. It may also occur that, in the absence of one element, all the others may readjust. In brief, the members of a microfloral community are inter-related and the imbalances produced impact on

the host, on the ecological niche, on the surrounding environment, bi-unequivocally. This is exactly what one finds in human social groups or communities (20). The “suffering”, the discomfort, of a single member has an impact on the rest of the group, so that consequences, changes and effects of all kinds are produced. If a social actor wields excessive power, this fact produces change within the relative social framework. All the other members of the group perceive this power as authoritarian and as an imposition, different, in any case, from the normal flow of the social “fluid”, that is, of the social lymph, the “amniotic” liquid, which guarantees the survival of all social beings.
Craig Venter’s examination of the microorganisms present in the Sargasso Sea (21), where the microflora presents an amazing morphological, genetic and functional variety of microbic species, as found, besides, in other natural matrices, like soil, water, debris. But the Sargasso Sea would not possess the singular characteristics it does without its particular microflora, taken as a dynamic whole, like other microfloral complexes. Some fluids, however, in order to avoid serious danger, need to be sterile, like cerebrospinal fluid or sperm and even blood itself; all of these are devoid of microflora, at least when the body enjoys normal good health. From this it may be deduced that it is not useful to consider single elements independently of all the others, but that it is necessary to focus on the community as a whole. In other words, it is opportune to study the group in order to grasp the relationships existing between the individual and the community as well as between the group and its single members.

2.2 The liquid society and mfDNA

Some authors define the society such as liquid (22) (23), which witnesses the liquefaction of the solid structures of the past. Lack of employment, the end of job security and the increased mobility of individuals, due to globalisation processes, have created conditions favouring unwonted and persisting flexibility (for the moment, at least). The individual and the social are interlinked more, perhaps, than ever before, just like the DNA microflora clings almost inextricably to the human body. But an unexpected event may cancel a job, creating instability; in the same way, the action of a human being and/or of an external, environmental biological factor can undermine the bond existing between a DNA microfloral reality and the body that hosts it. What is most intriguing is, however, the fact that the ejection of even a sole microbe from its community produces effects that cannot be underestimated. One needs, of course, to discover the reasons for the separation, the motives, the independent variable that favoured it. The theory of situational determinism advanced by Lucy Suchman (24), with its “situated cognition” and “situated action”, considers the environment as a part of the cognitive and operative process; it holds that knowing is linked to doing and belongs to social, cultural and physical frameworks. It is a fact, however, that today there is a marked tendency to come to terms with a kind of modernity where no solid, tendentially static, protective, sheltering, safeguarding haven exists any longer. In actual fact, we are now obliged to renounce many certainties and allow ourselves to be assailed by myriad existential worries of all kinds. The stabilisation of a community is no longer a given. Work placement is an increasingly recurring worry. Bankruptcy and redundancy loom on the horizon which draws closer and closer. The socio-economic crunch is no longer a marginal issue that concerns only the few. Instability and flexibility are practically the norm fixed in time and space. All told, as Bauman writes, jobs in consolidated workplaces appear today as a memory from the past; no special skills or experiences exist which, once acquired, are capable of guaranteeing a permanent and, above all, lifetime job (25). The same may be said of the liquid elements present in some of the body’s cavities: they are not guaranteed to last in time, exposed as they are to environmental degradation, to interaction with others and with other bacterial communities which come into contact with the oral, intestinal and vaginal mucous areas of the body. These biological fluids, once they enter the environment, are subject to ulterior modification, caused by various agents including other microorganisms. The *microbial signature* determined by residues of mfDNA does not last very long either and yet, although no longer vital, it can, nonetheless, permit us to recognise its origin. This is true too of social individuals, whose origins are hard to conceal for various reasons (from the language they speak to the colour of their skin, from their somatic traits to their cultural attitudes and behaviour). Vestiges of ancient civilizations, documents, ruins and architectural remains, which survive the ravages of time and destruction, tell far more than the story of their specific original function, reflecting, as they do, the complexity, history and roots of the society that produced them. Similar information is by no means static, therefore, but its traces assume a dynamic and complex significance in the light of the original texture that gave birth to it.

The liquid form is also the means by which to escape from the solidity of power, however it may be expressed, and enter mobility, flexibility and free circulation. Post-modern liquid society seems to provide increasingly broader degrees and ranges of freedom, though instability weakens existing bonds. And that is now membership of communities dwindles and leads to the affirmation of individuals without ties. In more explicit terms, Bauman holds that solidity is a curse, as is the case with every other form of persistence, because the latter is a sign of dangerous inability to adapt to a world which changes in rapid and unforeseeable manner, to the opportunities it unexpectedly offers and to the speed at which yesterday's resources become tomorrow's burden (25). In reality, what the idea of individualisation brings with it is emancipation from the unwritten, inherited determinism innate to its social character (24). The individual can no longer count on a haven in which to seek refuge. There is no further security.
In conclusion, it is possible to introduce a new perspective, driven by the mfDNA approach and biology, and suggest a wider context capable of improving our understanding of the role of individuals within societies. We propose a new tool, the "social mfDNA", as an interior indicator of the properties, composition and dynamics of human society. The ability of mathematical models can be to support and predict similar phenomena based on an integrated and parallel approach where microbial and human communities combine, determining an enticing synergy between sociological and microbiological issues. The achievements of ecological or genetic studies can help explain organizational structures or leadership, and vice versa (26).

2.3 Leadership and mfDNA

Microflora composition and interaction within an ecological niche can be plotted by undertaking analysis of the mfDNA. The presence of a dominant species can be detected by the relative representation of its genome. Microbial communities may, indeed, be considered as organisations, and as beings following a "boss-less" model. Each component acts independently and in the interest of the collectivity. The leader binds the individual species to the organisation, providing each one with a task and/or assigning it to a metabolic site. The microfloral hierarchical pyramid may even appear to be inverted compared to the classical human social model; here the leader appears as the dominant factor in proportion to the service it provides to the community. In certain physiological circumstances, in an ecological niche or in a biological fluid, the leading species characterises and governs the microbial community. This kind of leadership is achieved through access to the substrata and activation of the metabolic process, as well as by inducing environmental modification. The leading species is characterized by its active and massive presence in the biochemical process. For example, in oral saliva fluid, the *Streptococcus salivarius* may be considered as the leading organism. It is the most frequently found when sampling different fluids and is also present in the greatest quantity when analysing the mfDNA of specific samples. The same may be said of the *Lactobacillus* found in vaginal fluid or of the *Escherichia coli* found in faeces, and other species.
The leader influences the definition of the structure of the microflora fingerprint and the surrounding environment. This regards present and possible future projections. It possesses higher probabilities of replicating and maintaining the power to survive within that ecological niche and of conditioning balancing processes. It also acts as a kind of a dominant component, capable of protecting the community from foreign aggressors by supporting stable metabolic pathways or by competing for nourishment with possible contaminant microorganisms. So, the leading species is the most frequently and massively represented within a given microbial society, and not the less represented. In a certain sense, it is at the service of the other species, which may be weaker or in need of the support of other microorganisms in order to be able to resist within that biochemical chain and inside its specific metabolic slot.
In keeping with this evolutionistic view (27) of the leadership role (28), the general rule is that, in healthy conditions, a boss-less model may be appropriate. On the contrary, the prevalence of a leading species, independently of its representation and service to the community, permits minorities, characterized by the imposition of new environmental parameters, to remain. These microfloral patterns are reported in biological fluids in pathological conditions, such as paradontal disease, vaginitis and enteritis. In similar conditions, a different kind of balance is established, either in the entire region or in a sub-district. Independently of its extension, it is based on the traditional pyramidal structure and formal power flow where a hierarchical organisation is imposed, following a top-down scale. In these microfloral conditions, the microbial leader may even destroy the community's organisation. This may occur by reducing the influence of the natural/physiological leader or even by extinguishing some of the bacteria which perform a minor role, especially if they are highly dependent for survival on the previous general structure and biochemical chain.

In this case, the mfDNA changes, and a complex analysis of the microflora is not required. The pathogen is actually present as an invading, virulent element and is easily detected by simply applying a qualitative method. Any other species, if still detectable, will assume satellite significance. This is the case of an infectious disease. In this case, the leader is to be found in the pathogen and the complexity of the mfDNA is lost, reduced or rendered meaningless.

On the contrary, in normal physiological conditions, the leading species is part of the complex and plays a main role in assuring continuity to that society and re-creating the particular history of that community for the future.

The complexity of the mfDNA of a microbial society is based on the qualitative heterogeneity and the relative quantitative representation of the different components. From this perspective, the minorities are not the weakest, but form a part of a whole. The leader contributes by interconnecting the peripheral components to the central asset. As in the case of human societies, different parameters describe these interactions as degrees of freedom, trust and loyalty. As an indicator of microfloral communities, mfDNA can testify to the degrees of social freedom and potential of that population. In the case of bacteria these are not based on legal, economic or cultural rules, but on biochemical, ecological and natural laws.

The comparison of human and microflora societies and the integration of respective approaches may provide useful suggestions and open up interesting perspectives capable of providing greater understanding of leadership mechanisms or other social issues.

3. Conclusions

Scientific research in the genetic field seeks to study DNA, that is, the specific genome of each individual. Just as each human being has his/her specific genome, so too every living subject has its own DNA or genome, within which, in a certain manner, the constitutive characteristics are recorded. Inanimate objects as such have no DNA, unless they contain parts of living organisms: a simple sheet of paper has no its own genome, but if the page was an Egyptian Papyrus it had traces of the DNA typical of the plant, from which it derives; if it is a piece of vellum taken, for example, from the skin of a sheep, naturally, it preserves the DNA of the animal in question. In short, the presence of organic matter provides the possibility of tracing the source of its DNA. In the case of microflora, to be considered as a living whole, the DNA extracted is not unitary but heterogeneous and found in each component part.

A further aspect needs to be kept well in mind and that is the parasitic and lethal rapport existing between the microorganism and the environment or organism hosting it. For example, some viruses, like Ebola, are highly transmissible and lethal, although their infective action can be intermittent and limited, due to lack of carriers. In fact, one must hypothesise the existence of a “healthy” container for the virus, probably an animal capable of living alongside it while bringing it into accidental contact with human beings. Therefore, much depends on the more or less constant relationship between the healthy carrier and the parasite, between symbiosis and parasitism, between opportunism and virulence, the degree of lethality and survival.

Once more it appears that much of what occurs in nature and in society is contingent and depends on links, ties, which actually form a network. All this appears to happen by chance but, in reality, an effect is produced due to the greater or lesser constant probability of the occurrence of an event and its consequent impact on the other members of the community. It is the mother who transmits microbes to the child and the mother, yet again, who conveys messages of a behavioural type to the child too, during the early phases of socialisation, from which process the father could be extraneous, unlike other members of the family circle, who, on the whole, create the environment within which the individual and social personality of the newborn develops. Finally, communities of living beings are greater than the sum of their component parts and, paradoxically, every single member comprises not only the community of the cells which developed from his/her zygote/embryo, but also a community of extraneous cells, that is, his/her microflora. When all comes to all, we all form a part of an interconnected living texture (as individuals and as societies), which goes beyond the individual, so that we can hypothesize the existence of a kind of “community DNA”, whose profile is defined by elements both of a qualitative and a quantitative nature, and of social nature.

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