Microbiota and stability

The microbiome is the last great ubiquitous organ of the human body to be investigated. In recent years, we have witnessed a plethora of studies that have allowed us to know the composition and function of microbial communities harboured in different parts of the body and whose alteration (or **dysbiosis**) is associated with pathology. Members of this team have been involved, funded by different projects and in close cooperation with different groups of domestic and foreign research, in the study of some of them, such as Crohn's disease [11,12], irritable bowel syndrome [13] obstructive pulmonary disease, colitis by *Clostridium difficile* (CD) and alterations by treatment with antibiotics [14,15], lupus [16], obesity [16, 17], [18], AIDS [19], etc. However, although there is no doubt that certain diseases, such as intestinal ones, imply changes in the microbiota, it is unclear if **it is a cause or consequence**. Much of the problem comes from the fact of not being able to figure out what is or what is a healthy microbiota. The microbiota, against any disturbance, can remain unaltered (**resistance**), return to the initial state after disappearing the disruptive effect (**resilience**), or even change in composition but not in function when that effect disappears (**functional redundancy**). These three concepts suggest that the microbiota is stable while the nature of the effect does not go beyond a certain threshold, which delimits its ability to restore or not, in composition or function. In fact, the concept of threshold could be the combination of a set of systemic variables descriptive of the community that would allow us to diagnose it. The effect can become so disturbing that the microbiota would change to a new state, abnormal or pathological. A key element to distinguish properly between the two microbiotas is **time**, that is, the possibility to examine the nature of the changes over time and extract, as discussed, some sort of descriptive variables. That is what we have investigated: we have tried to identify in time series from several published studies of microbiota, including those carried out in our own team [13.20-24], the existence of some kind of parameter (s) allowing the discrimination between **microbiota with capacity to stabilize compared to others that do not**. Such parameters would be global descriptors of the state of the community, i.e. descriptors of the microbiotas that would allow separate states of health (**healthy microbiota**) against disease (**sick microbiota**). What we have discovered, a finding that we consider very important, is the existence of two parameters, estimated from the relative species composition, which allow define whether the microbiota is stable or not (Marti et al., submitted). We note in particular that the dynamics of the microbiota fits well with the **Taylor’s power law** [25]. This law gives us clues to understand the aggregations in communities composed of species with different relative abundances, and where any given taxon in a metagenome shows a power ratio between the relative abundance of the considered taxon and its dispersion. The two parameters that characterize this law are **the same amplitude of fluctuation**, V, and **the index of the power law**, β. What we have observed is that certain values of both coefficients draw a healthy microbiota window, while others, who are out of that window, are usually associated with pathology.

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