Medical Xpress

Research proves that intestinal bacteria can be used to classify the effects of different diseases

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Two studies co-led by researchers from the University of Valencia and the Foundation for the Promotion of Health and Biomedical Research of the Valencian Community (FISABIO) prove, for the first time ever, that it is possible to quantify and classify the effects of different diseases on the activity of intestinal bacteria. The work has been published in the journals *Scientific Reports* and *ISME Journal,* of the Nature Publishing Group.

The studies show that different pathophysiologies —lupus, infectious diarrhoea and obesity— may be segregated based on the composition of the chemical species found in the gastrointestinal tract. This differentiation cannot be observed when microbial populations are analysed, as was the case so far.

Human intestinal flora, known as microbiota, can be considered as an additional organ in the body. It consists of millions of bacteria that interact with each other and with the body, thus affecting its functioning and health. It is known that many intestinal disorders such as Crohn's disease and ulcerative colitis, and diseases such as obesity, cancer and autoimmune diseases can cause changes in the composition of gut bacteria.

However, such changes were also found when examining healthy individuals with different age, geographic location, diet or antibiotic

treatments. Therefore, until now no one had clearly elucidated what diseases produce or not the same or different alterations in the altered microbiota and whether it is possible to classify different diseases on that basis. Moreover, it was unclear whether in the case of multiple diseases or pathophysiologies one of them dominates in inducing gastrointestinal changes. "Defining such changes is important because these may have an effect not only on the progression of the disease but also on our health", explains Professor of Genetics at the University of Valencia Andrés Moya.

Lupus is a dominant factor over obesity

For the first time, researchers have analysed the composition and diversity of chemical species produced by intestinal bacteria, which is known as metabolome, in various groups of patients. A first group consisted of patients with lupus, a systemic chronic rheumatic disease. A second group was made up of patients with infectious diarrhoea caused by the pathogenic bacterium 'Clostridium difficile'. Finally, a third group consisted of healthy individuals. To do this, researchers separated bacteria from faecal material and extracted and analysed bacterial metabolites by next-generation mass spectrometry.

The study suggests that in healthy people without any disease, body mass index, and thus obesity, is the differentiating factor "regardless of age or any other parameter. That is, a healthy thin person has a composition and diversity of bacterial chemical species that is very different from those of an obese person", researchers point out. The change in intestinal metabolism occurs at a value of BMI of about 25 kg/m2. This does not occur with patients with lupus. That is, they all have a gastrointestinal metabolic profile that is different from that in healthy individuals, regardless of their BMI and medical history.

Clearly, lupus erythematosus is a dominant factor over obesity as regards

its influence on the activity of [intestinal bacteria](#), explains researcher Moya, who is also a member of the Joint Research Unit of the University of Valencia and FISABIO. Consequently, a person with lupus who is thin and another who is obese have similar composition and diversity of bacterial chemical species, but this does not happen in healthy people. This could be the reason for people with lupus to have greater predisposition to the so-called metabolic syndrome.

Different intestinal pathogens produce various alterations

An analysis of patients with infectious diarrhoea later revealed that infectious diarrhoea is also associated with a specific gastrointestinal metabolic profile. For example, individuals with infectious diarrhoea caused by 'C. Difficile' have similar profiles regardless of their BMI and medical history. "We were able to demonstrate that the changes induced by this pathogen are different from those caused by other pathogens, such as 'Escherichia coli'", researcher María José Gosalbes remarks. In addition, changes when 'C. Difficile' produces toxins or not, which causes serious health damage, are also visible and markedly different.

New ways to study the effect of disease

Researchers showed that the changes imposed by different pathophysiology specifically affect the top of the functional hierarchy, at the level of chemical species. This is where changes become effective. These studies have found that different pathophysiologies —such as pathogenic bacteria infections, immune response or obesity, among others— can be segregated based on metabolic patterns, i.e., based on the composition of the [chemical species](#) found in the gastrointestinal tract, while they can't when intestinal microbial populations are analysed. This provides new opportunities related to the study of how the

heterogeneities that appear at lower levels of the functional hierarchy, for example at the level of bacterial populations, eventually end up in the same chemical pattern that is specific to different diseases.

More information: "Ranking the impact of human health disorders on gut metabolism: Systemic lupus erythematosus and obesity as study cases." *Scientific Reports* 5, Article number: 8310 DOI: 10.1038/srep08310

"Clostridium difficile heterogeneously impacts intestinal community architecture but drives stable metabolome responses." *ISME J.* 2015 Mar 10. DOI: 10.1038/ismej.2015.32

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