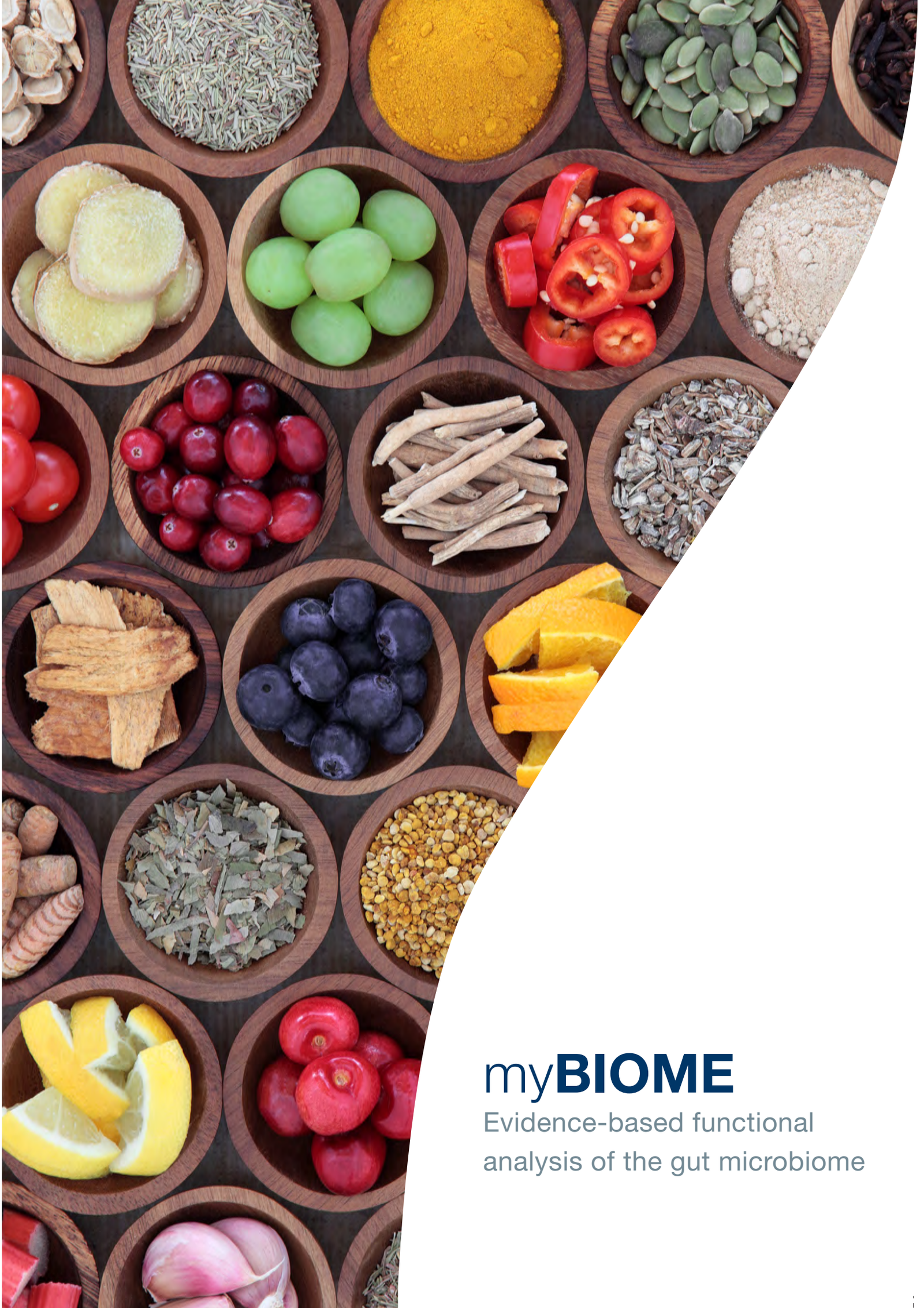


myBIOME

Evidence-based functional analysis of the gut microbiome

myBIOME CAN TELL US ABOUT:

MICROBIAL DIVERSITY: This is determined through the Shannon index, a measure of diversity used by members of the scientific community to compare results over time and reflects the **different types and number of bacterial species** that make up our intestinal microbiota. **High microbial diversity or within the range of normality is associated with good health.** A varied diet rich in plant-based foods such as fruits, vegetables, whole grains and nuts can help increase that diversity.

IMPORTANT SPECIES: Identification of **potentially beneficial or pathogenic** bacteria with scientific soundness.

DIGESTIVE POTENTIAL: The analysis provides information on the potential to **digest components** such as fiber and protein.

SAMPLE COMPOSITION: Most of the DNA in the stool (~99%) comes from microorganisms, while only a small amount (~1%) is human DNA. myBIOME provides information on the percentage of the **major groups of microorganisms living in the gut** (bacteria, archaea and eukaryotes (fungi and parasites)), as well as novel (unidentifiable) DNA and human DNA contained in the sample. More than **4% of human DNA can be an indirect marker of intestinal inflammation.**

MICROBIAL METABOLITES: The bacterial functional genes are quantified to provide the metabolic potential to produce or consume metabolites involved in the **development of certain diseases or metabolites associated with beneficial health effects**. Metabolites that may be key in the prevention of such diseases (health indicators, neuroendocrine, short chain fatty acids (SCFA) and vitamins) are determined on the basis of functional genes.

EUKARYOTIC MICROORGANISMS: It reports the presence of **fungi, archaea, yeasts and parasites** important for health.

NUTRITIONAL RECOMMENDATIONS: The report provided includes **personalized dietary recommendations** based on the results obtained.

The use of metagenomic sequencing together with the interpretation of the findings that this state-of-the-art technology offers, makes **myBIOME the reference test for the analysis of the intestinal microbiota**, providing an exhaustive differentiation and characterization of the microorganisms that compose it, in addition to providing nutritional recommendations that allow a healthy balance to be achieved.

Key points

- The only test that performs a **metagenomic analysis** of the entire genes of the bacteria residing in the gut.
- Offers a **better informed taxonomic classification** both at the qualitative and quantitative level.
- Is capable of detecting bacteria, archaea, eukaryotes (fungi, archaea, yeasts and parasites).
- It measures the potential for **bacteria present in the intestine to produce metabolites and vitamins** with key health functions.
- Provides personalized nutritional recommendations based on specific **bacterial needs of each individual.**

What is my**BIOME**?

my**BIOME** is a metagenomic sequencing test that allows an **in-depth, objective and actionable study of the gut microbiome**, providing detailed information on the microorganisms that inhabit the gut and their functionality, the impact they have on health and how to achieve a balance through personalized nutritional recommendations.

Scientific evidence

my**BIOME** performs an analysis of the gut microbiome by metagenomic sequencing. Through NGS technology (Next-Generation Sequencing), the entire genetic material (DNA) from the microbial communities that reside in the intestine is sequenced, thus **allowing the study of collective genomes and obtaining sequences of all the microorganisms that make up the intestinal ecosystem.**

THE MOST ADVANCED TECHNOLOGY
TOGETHER WITH PERSONALIZED RECOMMENDATIONS, MAKE myBIOME** A UNIQUE TEST IN THE MARKET**

Why choose my**BIOME**?

METAGENOMIC SEQUENCING myBIOME	16S ARNr/PCR SEQUENCE
It analyzes **all the genetic material (DNA)** in the sample, allowing a more sensitive strain of the microorganisms that make it up.	**It selects and amplifies** a small portion of the 16S ribosomal RNA present in bacteria.
Detects all species with a relative abundance **greater than 0.01%.**	**16S rRNA:** can detect very few microorganisms at the species level.
High resolution and coverage: taxonomic identification of all present microorganisms down to the species level.	**16S rRNA:** low resolution, taxonomic identification down to genus level. Does not detect species/strains. **PCR:** high resolution but limited coverage by detecting pre-established target organisms.
Can identify **previously unknown new species.**	Does not detect new species.
Can detect **bacteria, archaea, fungi, and protists.**	**16S rRNA:** only detects bacteria. **PCR:** can detect bacteria, fungi, protists and viruses in a targeted manner.
Identifies functional potential of microorganisms **(according to gene abundance).**	Does not provide information about the **functionality of present microorganisms.**
Allows the definition of personalized dietary patterns to counteract **altered microbial functions.**	It does not allow the determination of microbial functions.

Advantages

The use of metagenomic sequencing for the analysis of the gut microbiota **offers a number of advantages** over those based on 16S gene sequencing or RT-PCR/culture.

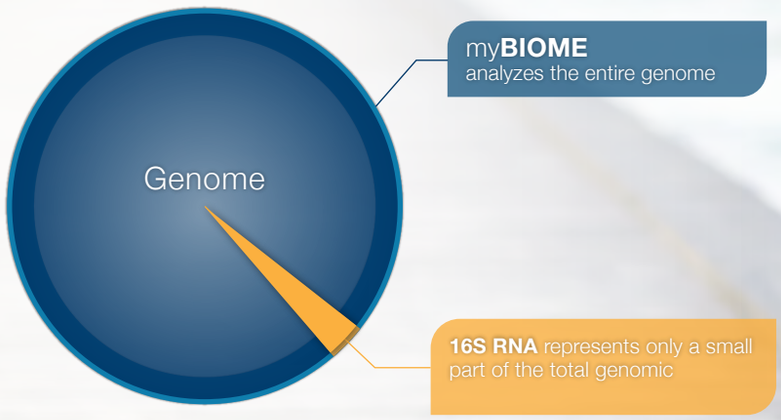
METAGENOMIC STRATEGY:

The conventional analysis of bacterial populations by amplification of the **ribosomal 16S RNA gene** (16S rRNA), is based on the amplification of hypervariable regions of the 16S rRNA gene by means of primers that amplify this fragment in most of the bacteria present in a sample. The sequences of the amplified gene are then compared and the phylogenetic relationships between the detected organisms are established. Although this technique has been extensively refined, **it cannot detect microorganisms that have undergone changes at the site of attachment of the primers[1] so that these bacteria are technically "invisible" and escape analysis[2].**

Apart from this limitation, the 16S rRNA gene represents only a small part of the entire genome of a bacterium, which makes any kind of analysis beyond phylogenetic classification difficult.

Compared to conventional studies of the microbiota based on 16S rRNA analysis, my**BIOME allows the detection of all the genes present in the microorganisms in the sample thanks to the use of metagenomic sequencing techniques**, thus avoiding amplification bias and facilitating a complete sampling of all the genes present in the organisms[3]. **This strategy allows a great depth of analysis, providing not only information on the totality of bacteria present up to the taxonomic level of species and strain**, but also on other microorganisms present in the sample such as **fungi, archaea, yeasts and parasites.**

In addition to identification, metagenomics allows the characterization and quantification of functional genes, which provides information on the functions of the microorganisms present in the sample.



HIGH RESOLUTION:

Another differentiating feature of the technology used in myBIOME is the **high resolution** compared to conventional 16S rRNA gene amplification analysis. This is because different bacterial species may have similar or even identical 16S regions, which makes the 16S gene amplification unable to discriminate between them[4]. **This limitation implies a significant loss of information**, since different species of the same genus can have very different functions[5]. The massive sequencing of the entire genome using myBIOME **is currently the technique with the highest resolution for the identification of microorganisms and the detection of their functional genes.**