ALMA MATER STUDIORUM - UNIVERSITY OF BOLOGNA

DEPARTMENT OF FOOD SCIENCE

Round Table

Do we know what we eat?

Introduction of M. Elisabetta Guerzoni

Do we know what happens when we deliberately and regularly introduce in our organism large and increasing amounts of probiotic microorganisms?

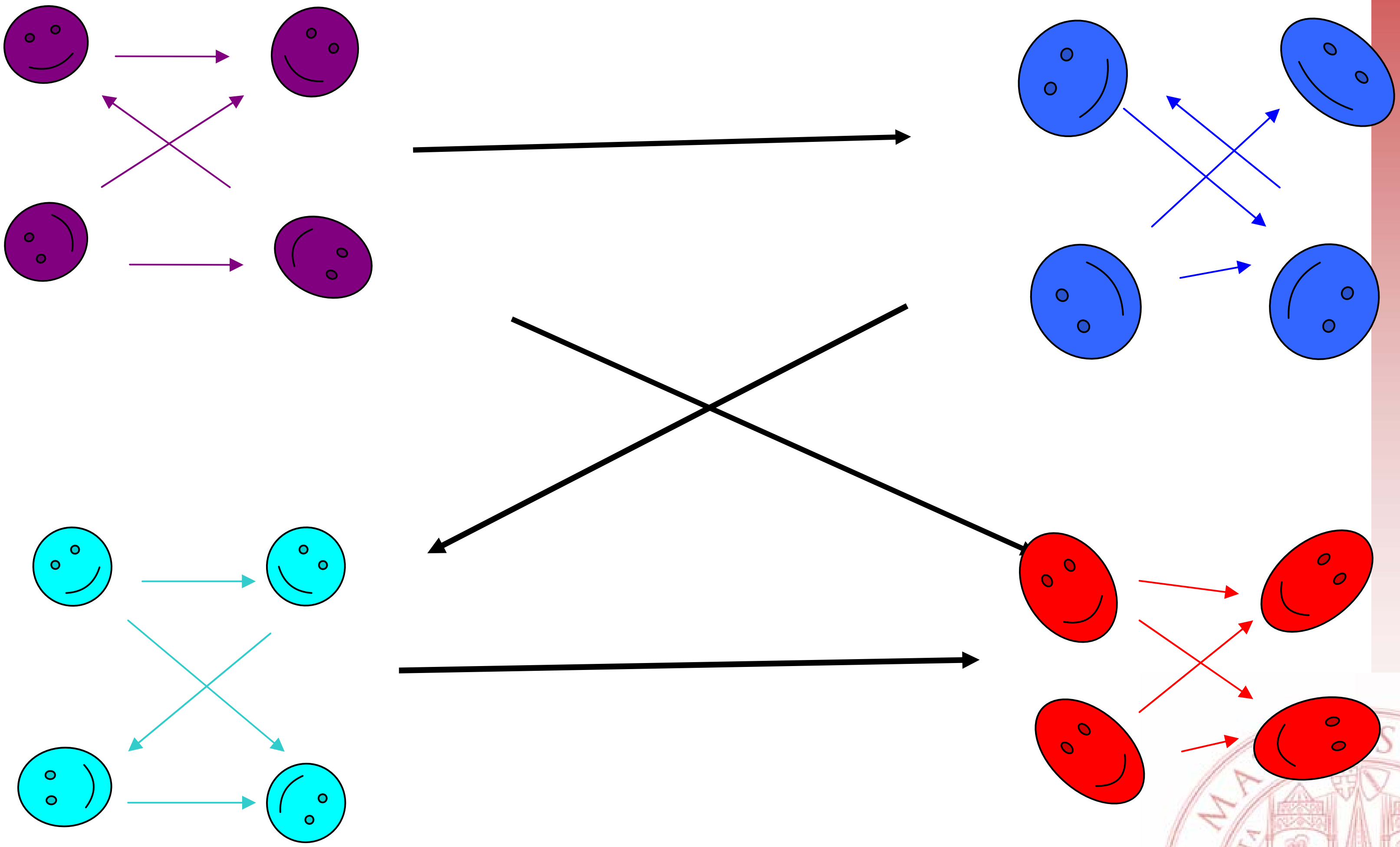
Probiotic “pandemonium”

The functional dairy drink market attained in 2007 3400 million Euro with a consumption reaching 999 million litres and a annual increase of 12% .

The European Commission, particulary through its 5th Framework Programme invested a substantial research effort in the intestinal microbiota, its interactions with host and methods to manipulate its composition and activity for the improvement of human health.

Eight interdisciplinary research projects covered a variety of topics required for the development of efficacious probiotics foods.

Intestinal tract as a cocktail party according to the a free interpretation of the approach of the world's foremost expert in the new science of networks A. Laszlo Barabasi.



Cell to cell signaling: there is a whole lot of talking going on

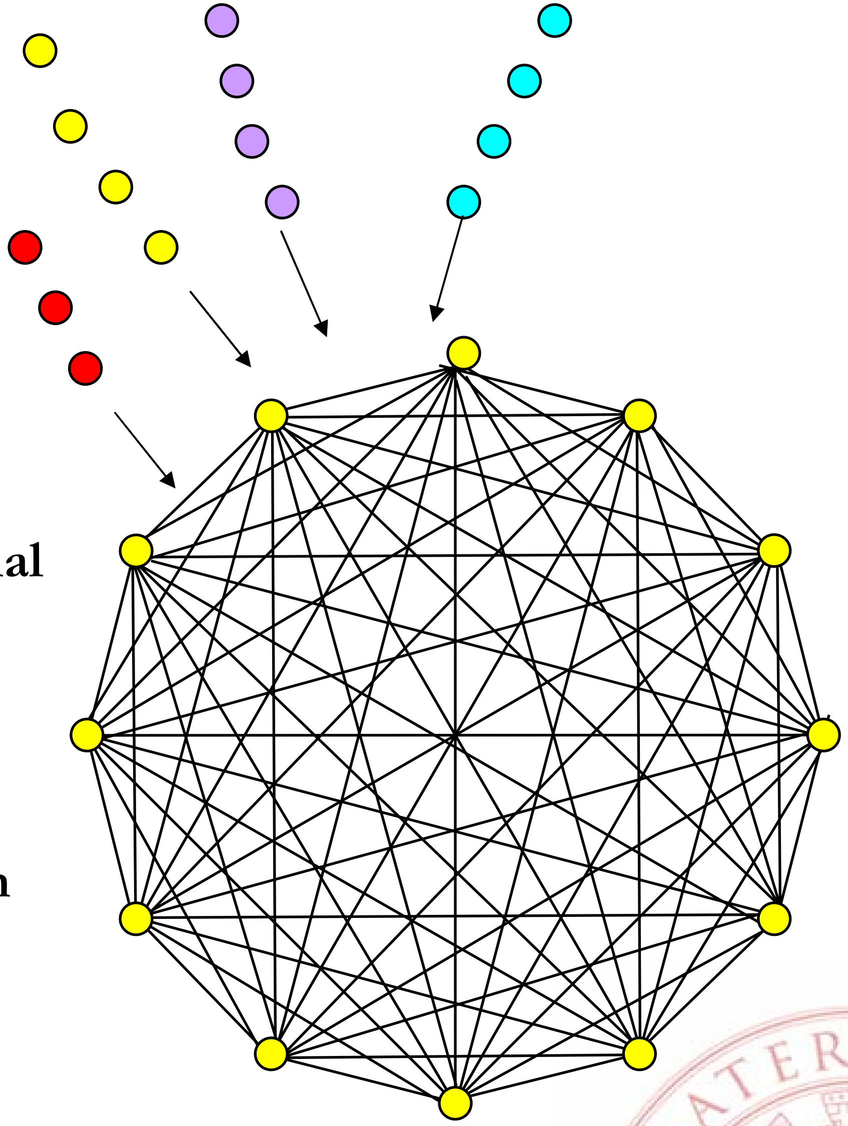
The guests or the bacteria are the nodes and the links are the metabolites or quorum sensing molecules

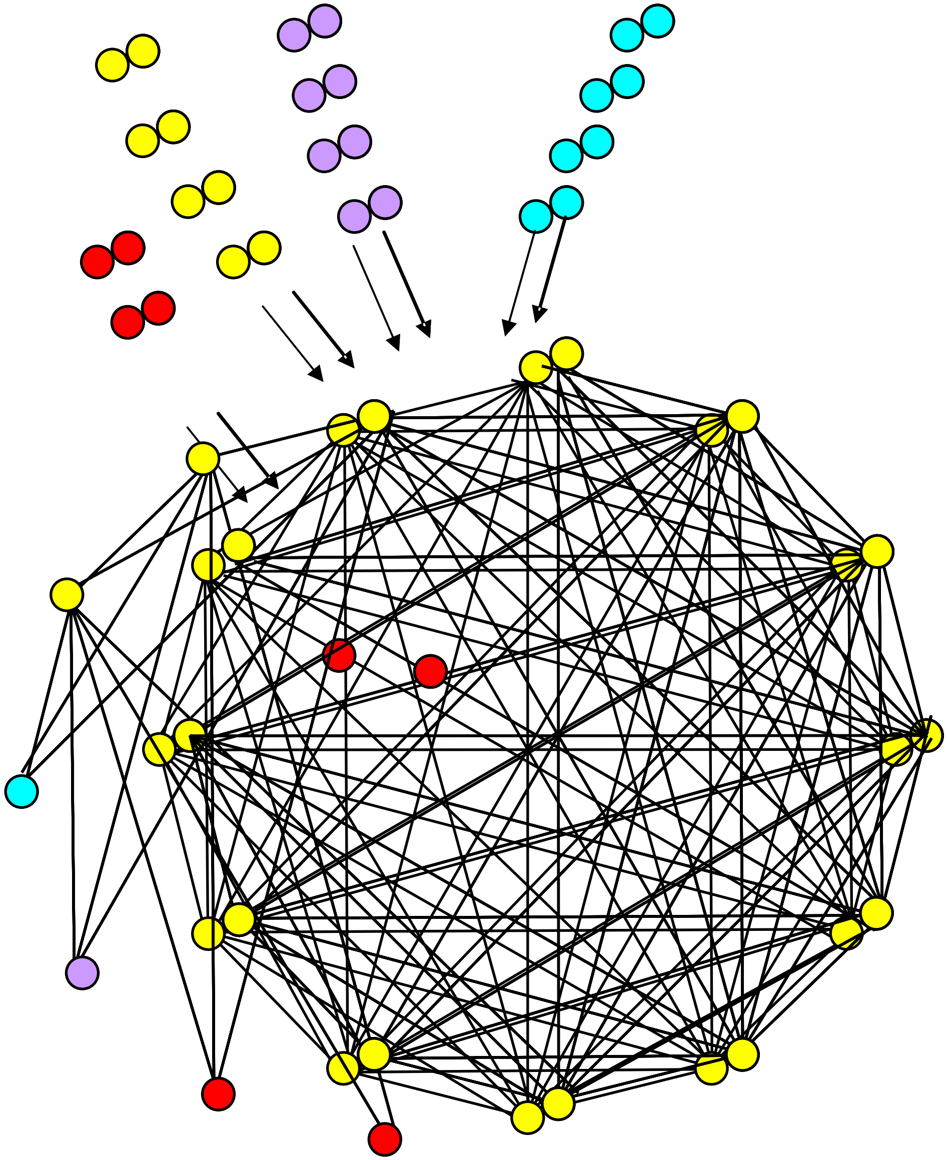
The main challenge in the giant network of the intestinal tract is to understand the complex cooperative metabolism that develops among the hundreds of different microbial species

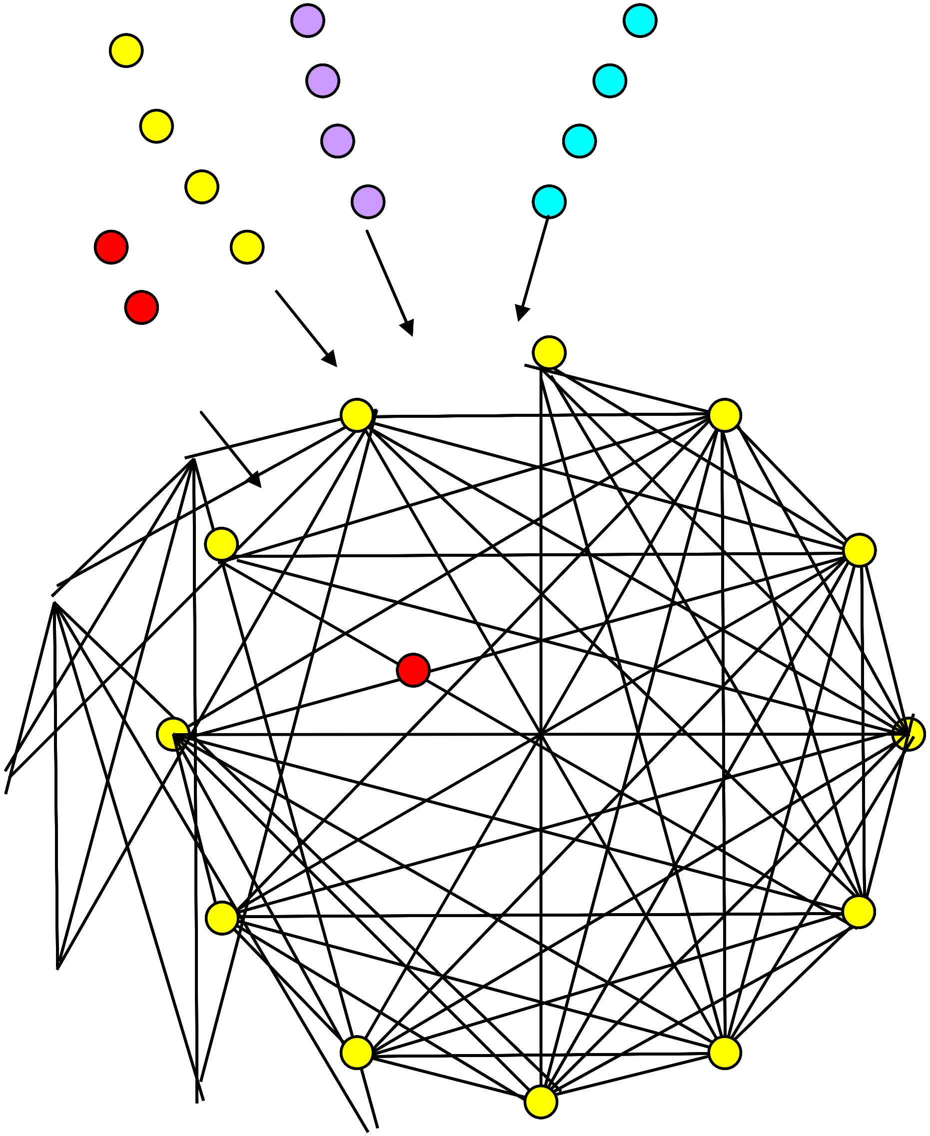
But much remains to be understood about the nature of the molecular interaction between “newly arrived” bacteria (probiotics) and resident microbial community members.

How do probiotics affect the functional properties of indigenous microbial communities?

Do they induce large scale changes in the microbial community functional repertoire?

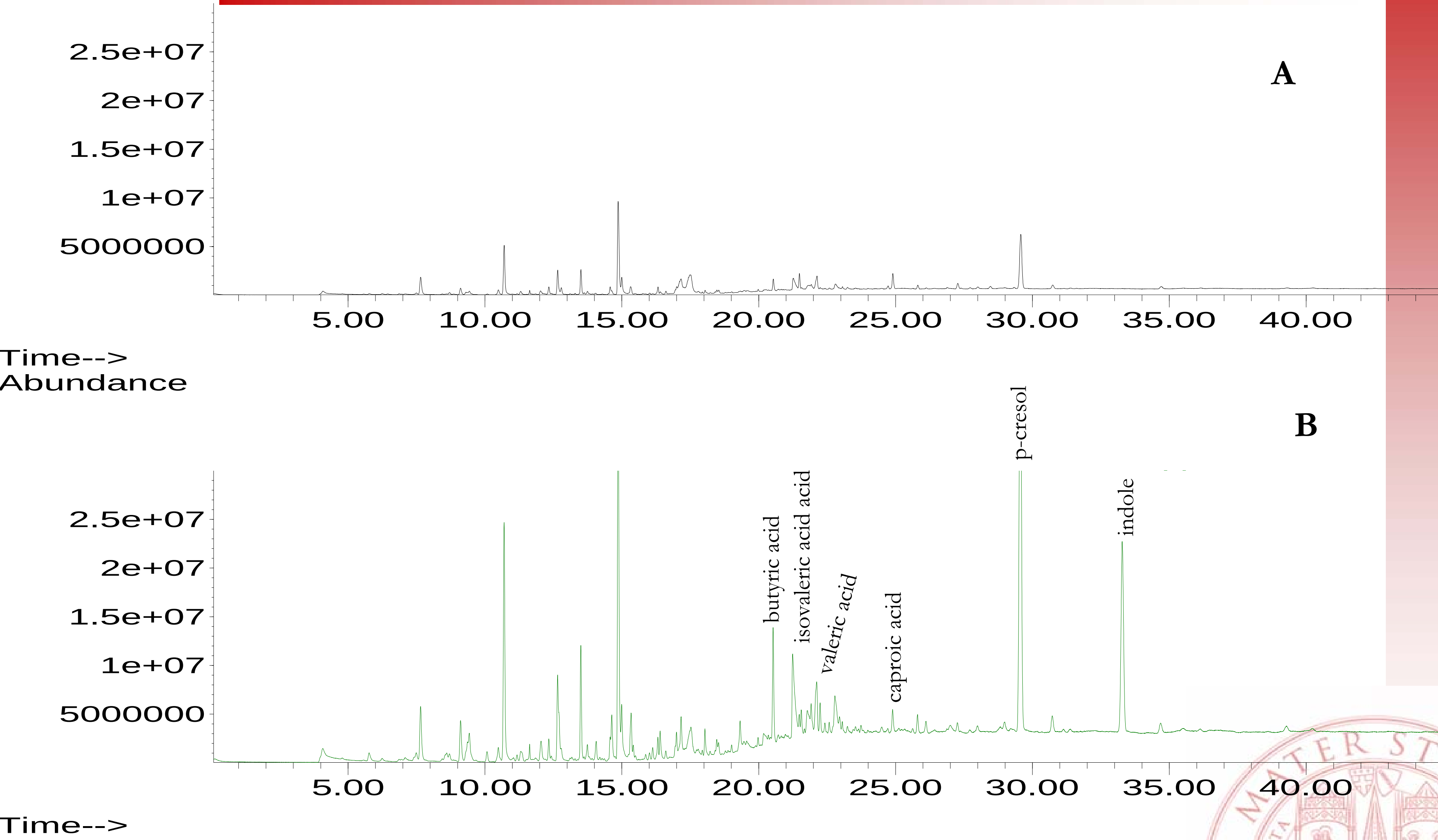






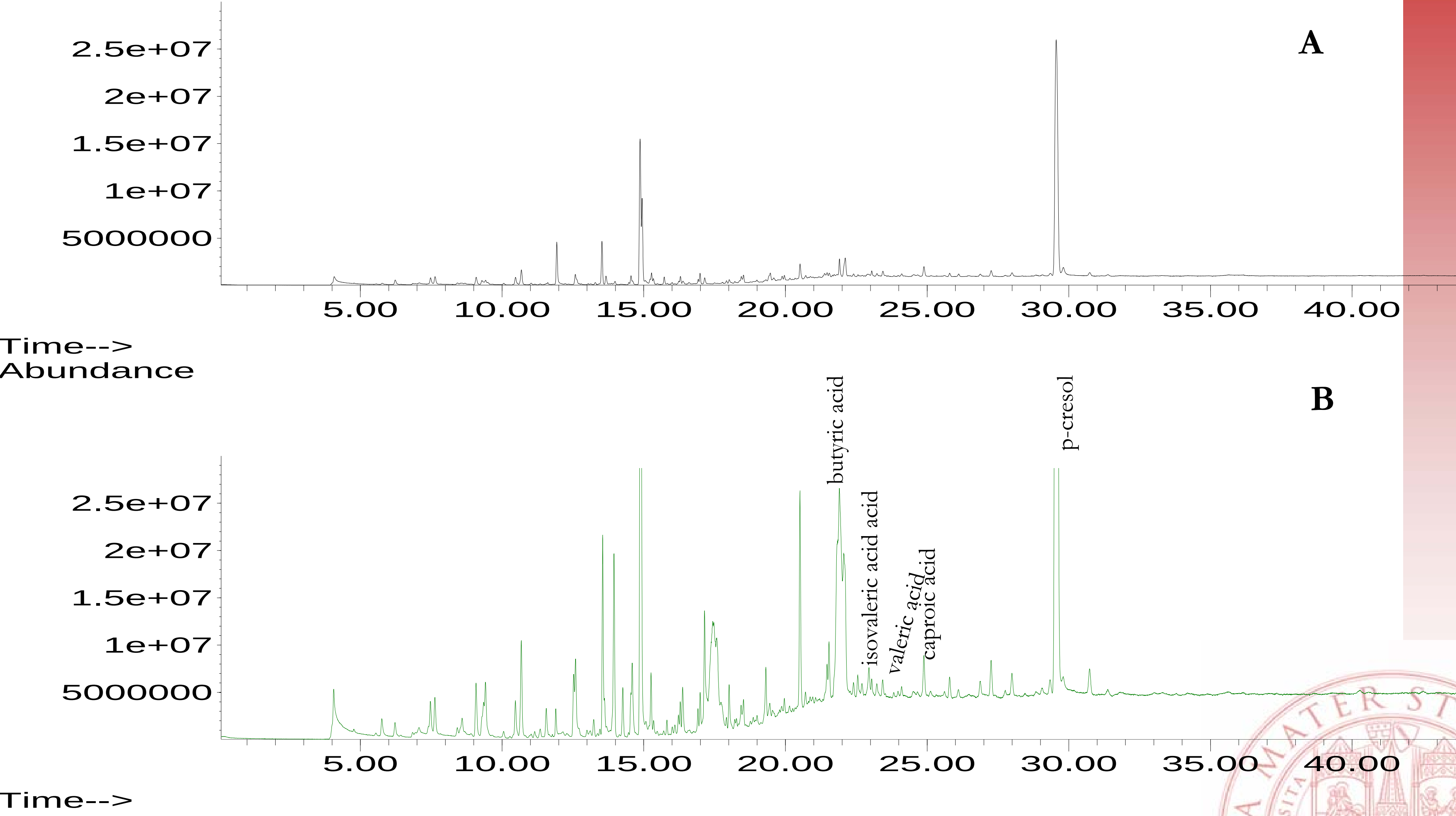
Metabolic profiles (GC-MS/SPME, gascromatography-mass spectrometry/solid phase microextraction) of faecal slurries of people characterized by a natural different level of probiotics before and after 1 month of supplementation with a cocktail of probiotics (*Bifidobacterium longum* and *Lactobacillus acidophilus*)

Comparison of metabolic profiles of faecal slurries of a subject having a natural low level of bifidobacteria and lactobacillus before (A) and after a month of daily of probiotics (*B. longum* and *L. acidophilus*) intake



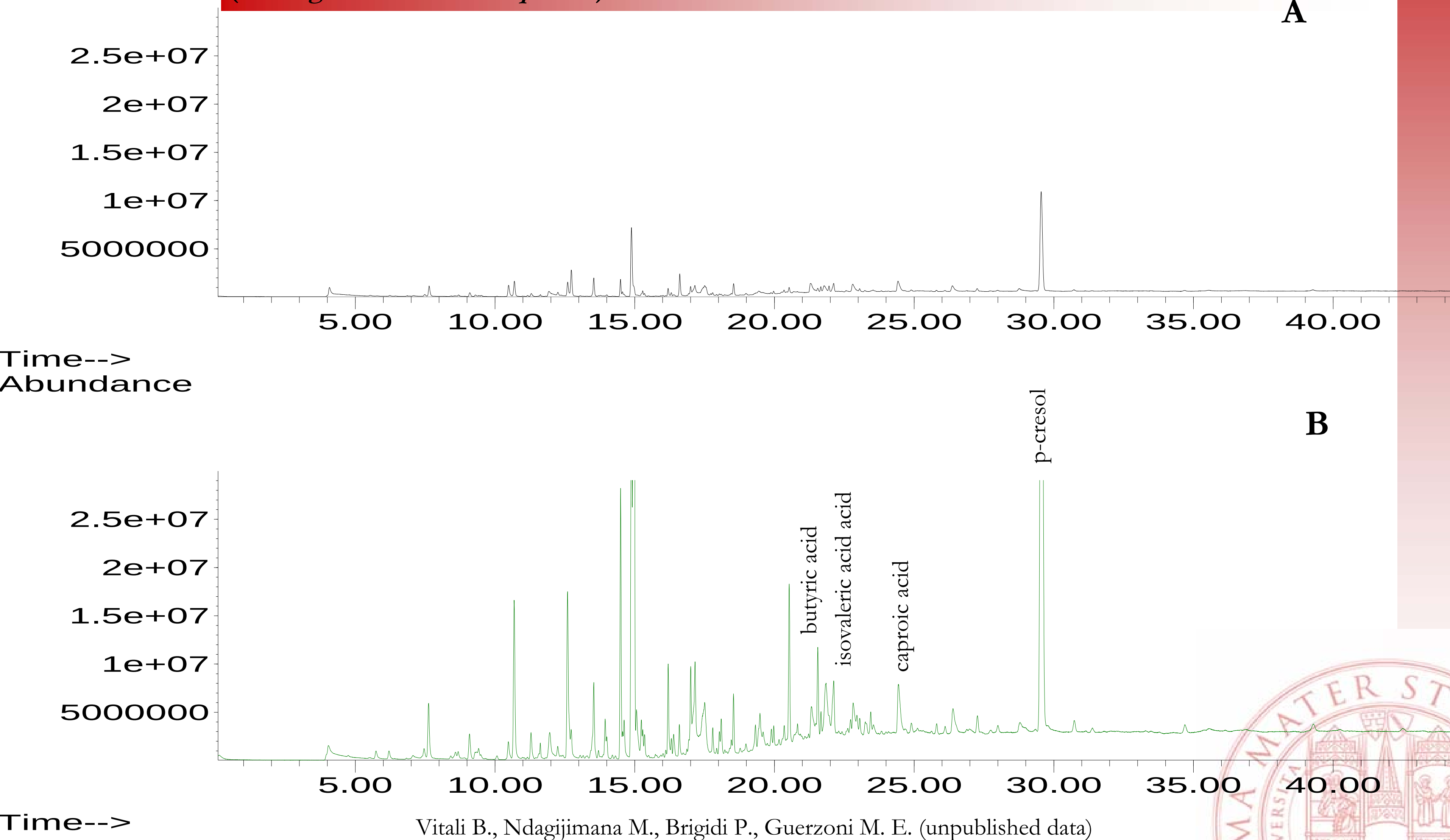
Vitali B., Ndagijimana M., Brigidi P., Guerzoni M. E. (unpublished data)

Comparison of metabolic profiles of faecal slurries of a subject having a natural mean level of bifidobacteria and lactobacillus before (A) and after a month of daily of probiotics (*B. longum* and *L. acidophilus*) intake



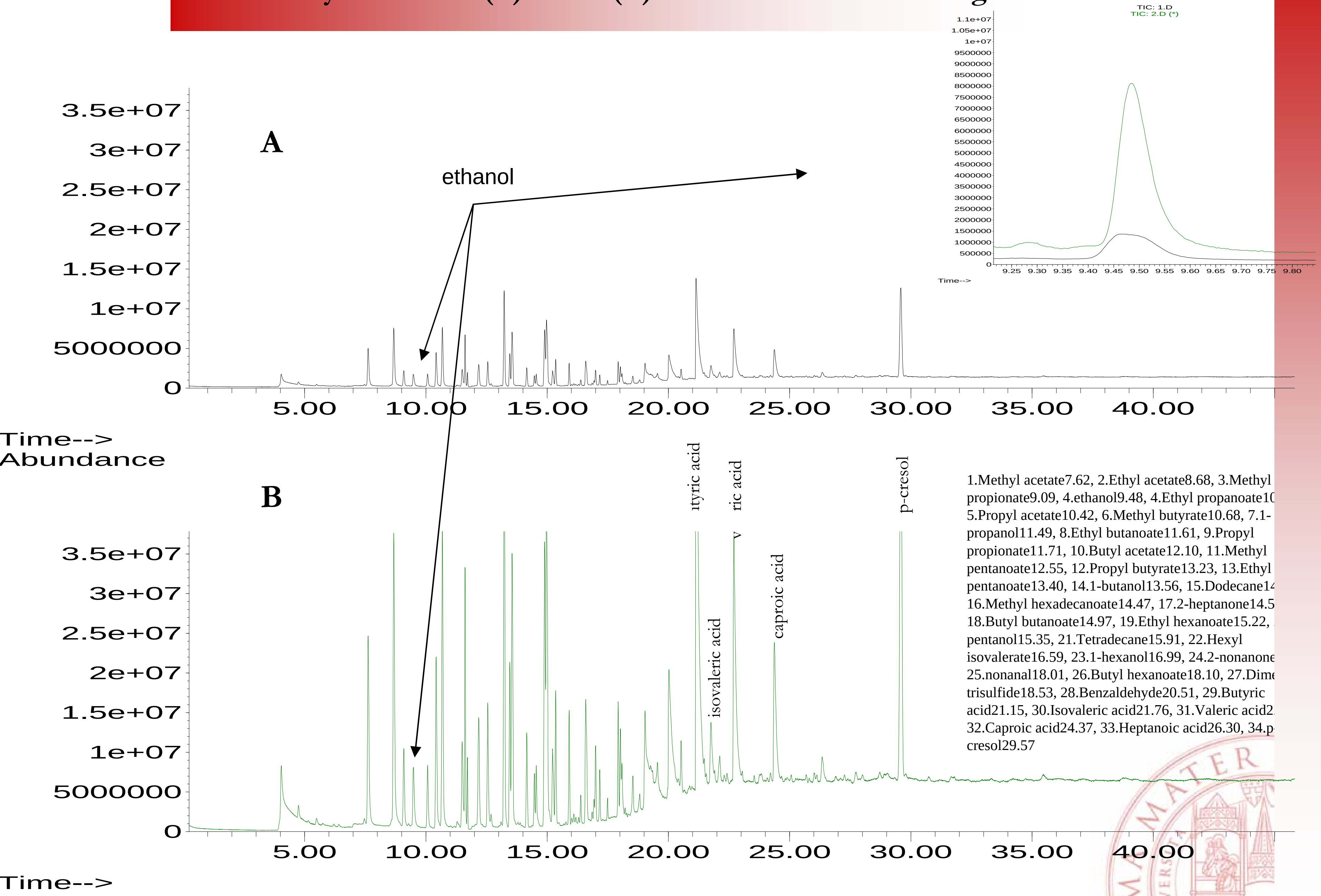
Vitali B., Ndagijimana M., Brigidi P., Guerzoni M. E. (unpublished data)

Comparison of metabolic profiles of faecal slurries of a subject having a natural high level of bifidobacteria and lactobacillus before (A) and after a month of daily of probiotics (*B. longum* and *L. acidophilus*) intake



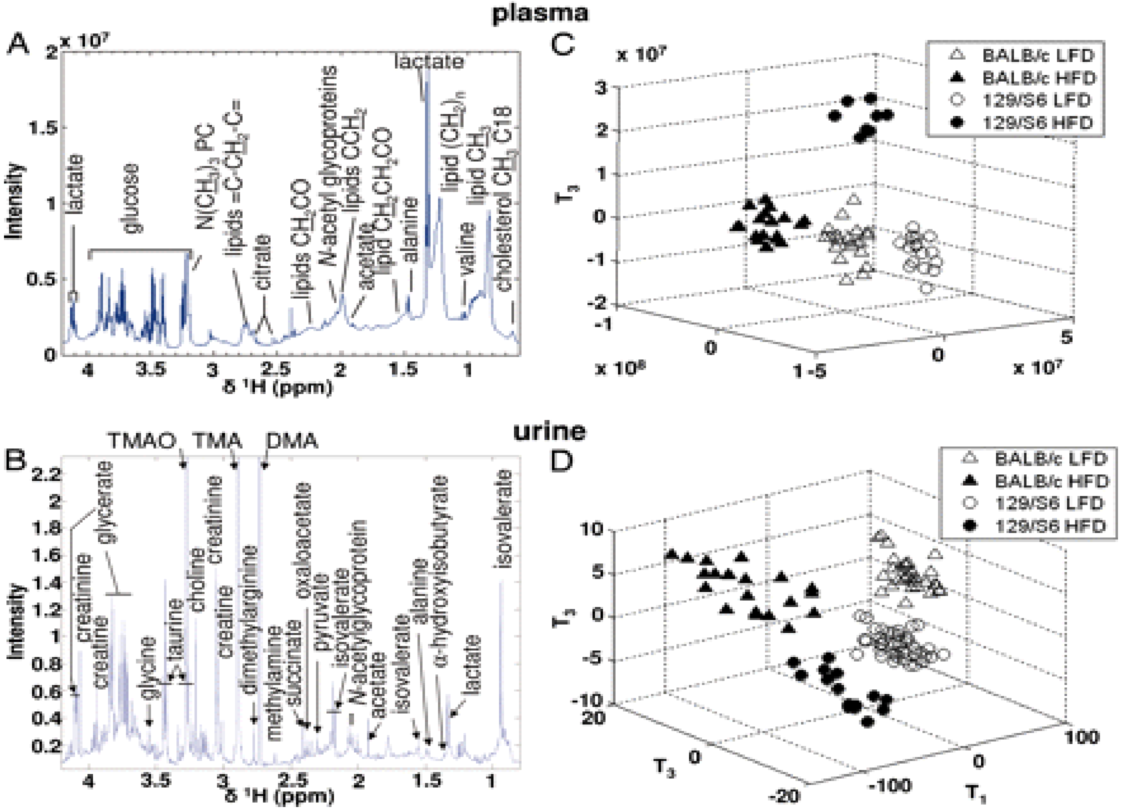
Vitali B., Ndagijimana M., Brigidi P., Guerzoni M. E. (unpublished data)

Faecal slurry inoculated (A) or not (B) with *Bifidobacterium longum*



1.Methyl acetate7.62, 2.Ethyl acetate8.68, 3.Methyl propionate9.09, 4.ethanol9.48, 4.Ethyl propanoate10 5.Propyl acetate10.42, 6.Methyl butyrate10.68, 7.1-propanol11.49, 8.Ethyl butanoate11.61, 9.Propyl propionate11.71, 10.Butyl acetate12.10, 11.Methyl pentanoate12.55, 12.Propyl butyrate13.23, 13.Ethyl pentanoate13.40, 14.1-butanol13.56, 15.Dodecane14 16.Methyl hexadecanoate14.47, 17.2-heptanone14.5 18.Butyl butanoate14.97, 19.Ethyl hexanoate15.22, pentanol15.35, 21.Tetradecane15.91, 22.Hexyl isovalerate16.59, 23.1-hexanol16.99, 24.2-nonanone 25.nonanal18.01, 26.Butyl hexanoate18.10, 27.Dime trisulfide18.53, 28.Benzaldehyde20.51, 29.Butyric acid21.15, 30.Isovaleric acid21.76, 31.Valeric acid2 32.Caproic acid24.37, 33.Heptanoic acid26.30, 34.p-cresol29.57

Other techniques such as high resolution 1H Nuclear Magnetic Resonance Spectroscopy of biofluids and tissues coupled with multivariate statistical methods are regarded as well established tool for metabolic profling. (Dumas et al. 2006).



Metabolic profiling associated with appropriate and new statistical methods can be a key or a tool to understand the effects of food intake on the changes of the gut microbiota

“The food supply has evolved. The composition database containing a variety of components is a powerful tool for a great number of user groups” *B. Burlingame* (Parma, today).

Moreover the food components introduced with the diet manipulate the intestinal tract microbial community (Hooper et al. 2002).

In turn the same gut microbiota

can affect the host physiology and food assimilation and conversion with more or less desirable effects such as increased extraction of calories from the diet, reduced serum lipid levels, increased absorption of mineral, etc.

A knowledge based calibration of food formulation and processing can direct the production of new type of food or multifuctional probiotics and prebiotics able to effectively manipulate the gut microbiota functional repertoire