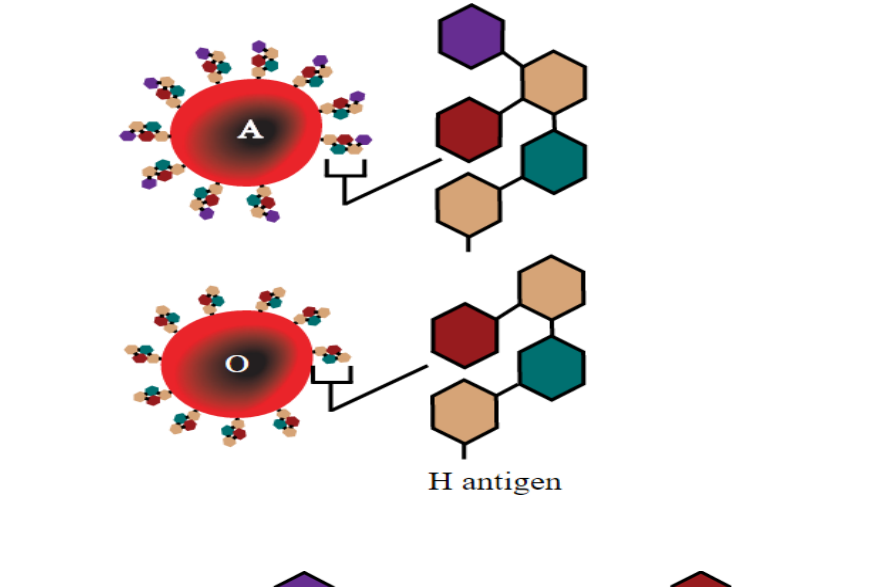
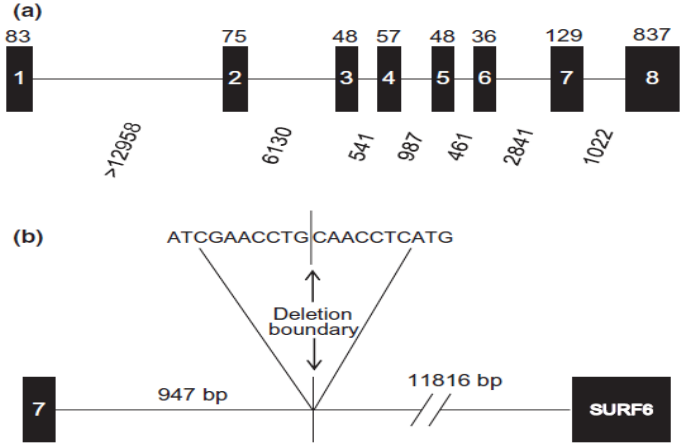
67th Annual Meeting of EAAP
Belfast UK, 29 Aug – 2 Sept 2016

The A0 blood groups effect on the porcine gut microbiota colonization

V. Motta, D. Luise, M. Colombo, P. Trevisi, P. Bosi

Porcine A0 Blood Group





Structure of the porcine A0 blood group gene allele A (a) and deletion junction involved in allele 0 (b)

From Nguyen et al. 2011

Blood Types and Glycomic

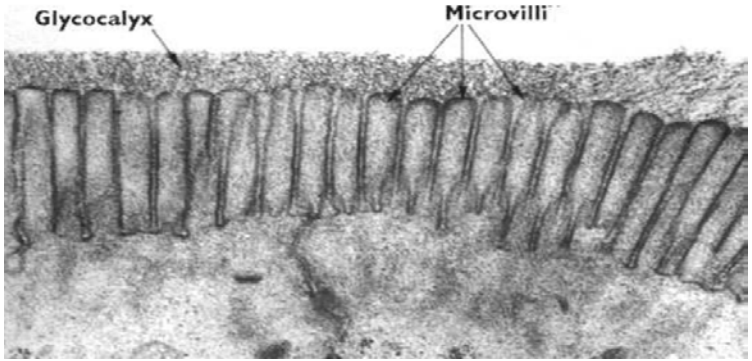
Mäkivuokko *et al. BMC Microbiology* 2012, **12**:94
http://www.biomedcentral.com/1471-2180/12/94

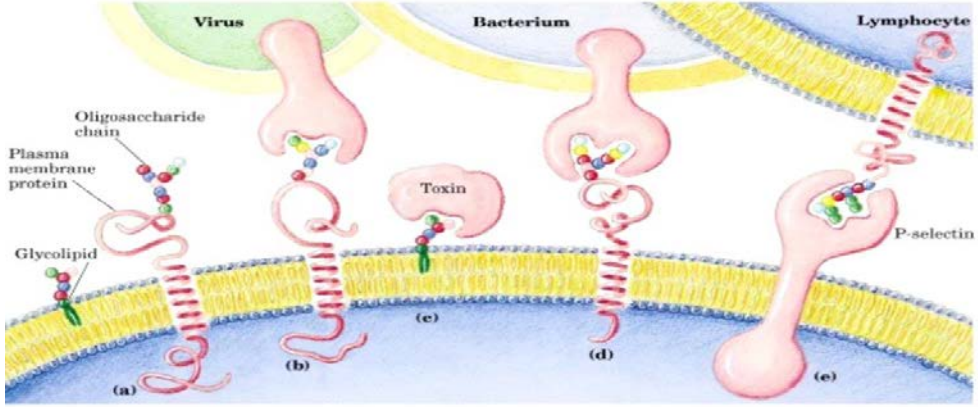
BMC Microbiology

RESEARCH Open Access

Association between the ABO blood group and the human intestinal microbiota composition

Harri Mäkivuokko[1*], Sampo J Lahtinen[2], Pirjo Wacklin[1], Elina Tuovinen[1], Heli Tenkanen[1], Janne Nikkilä[1], Marika Björklund[2], Kari Aranko[1], Arthur C Ouwehand[2] and Jaana Mättö[1]



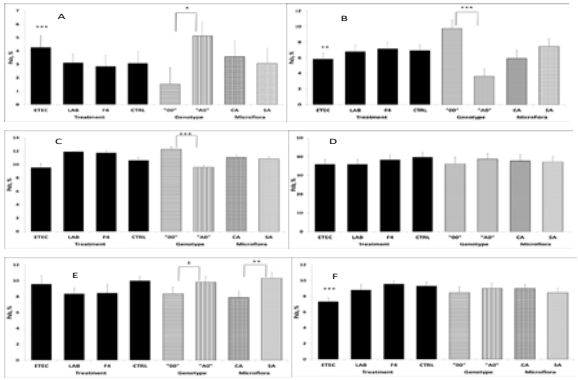


Our previous Study

The A0 blood group genotype modifies the jejunal glycomic binding pattern profile of piglets early associated with a simple or complex microbiota[1]

D. Priori,* M. Colombo,* S.-J. Koopmans,† A. J. M. Jansman,† J. van der Meulen,† P. Trevisi,* and P. Bosi*[2]

*Department of Agricultural and Food Sciences, University of Bologna, 40127 Bologna, Italy; and †Wageningen UR Livestock Research, P.O. Box 338, 6700 AH Wageningen, the Netherlands



Journal of Animal Science
The Premier Journal and Leading Source of New Knowledge and Perspective in Animal Science

Published February 12, 2016

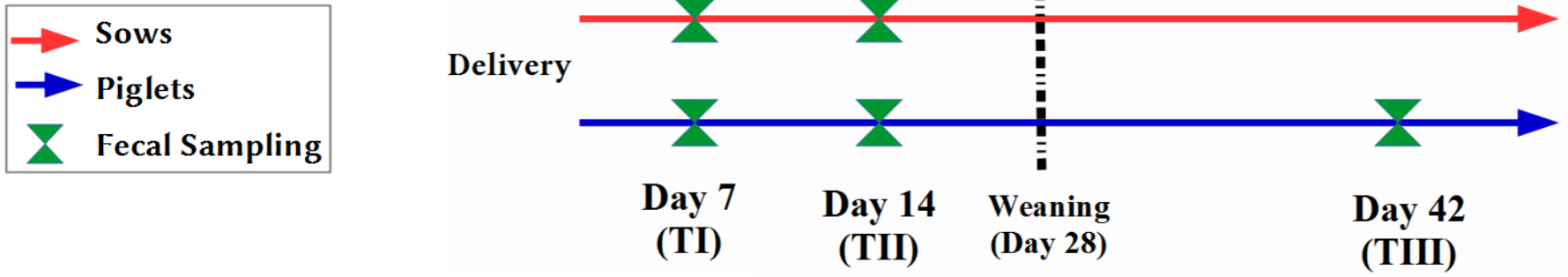
Material and Methods

2 sows A0 genotype

3 piglets A0 3 piglets A0

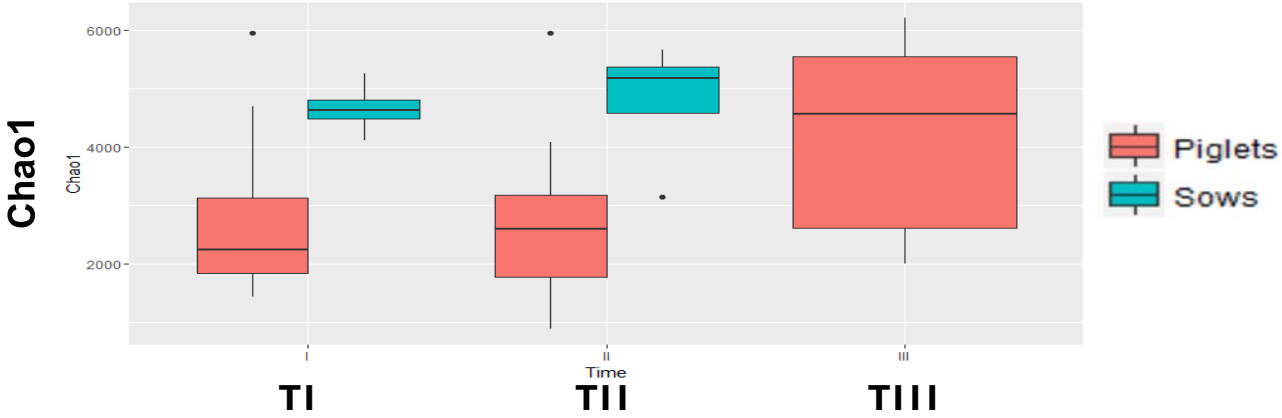
2 sows 00 genotype

3 piglets 00 3 piglets 00



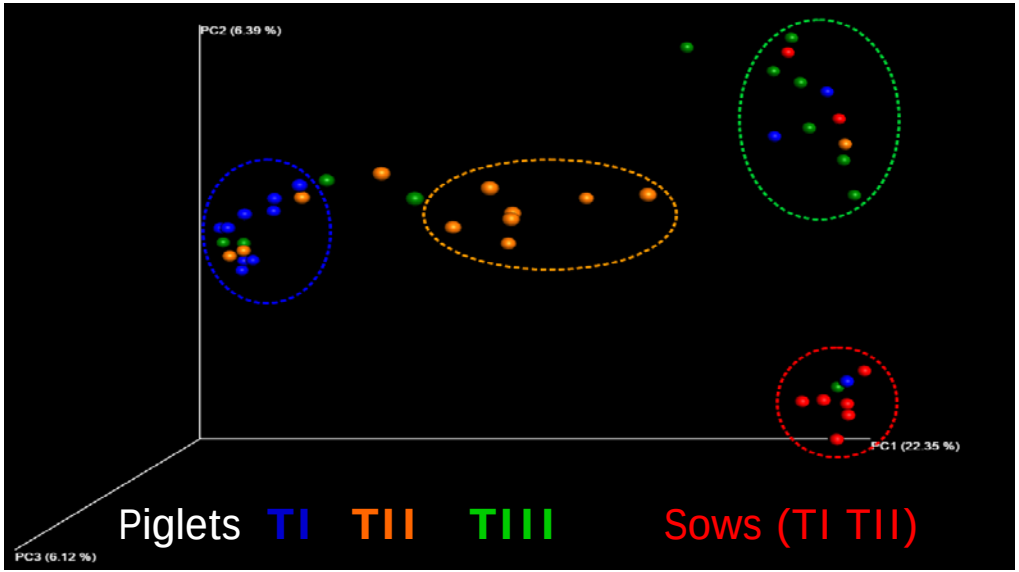
V3-V4 region 16S → illumina® → qiime Quantitative Insights Into Microbial Ecology

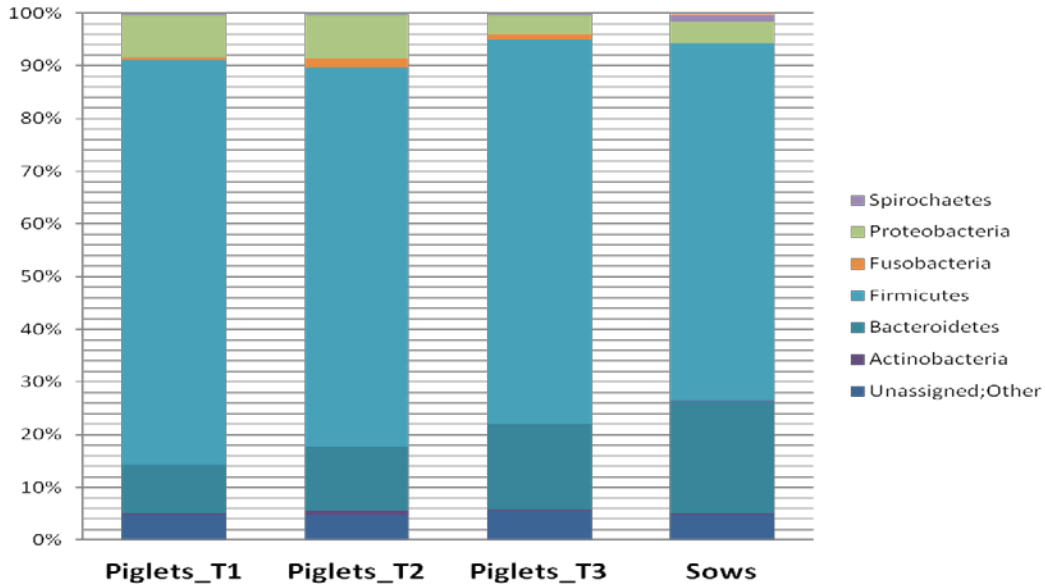
Results
Time Effect



- Greater α Diversity and stability in Sows (Adult Microbiota)
- In Piglets α Diversity increase After Weaning (T III)
- Correlation in α diversity between TI and TIII in piglets (r = 0.62 p = 0.02)

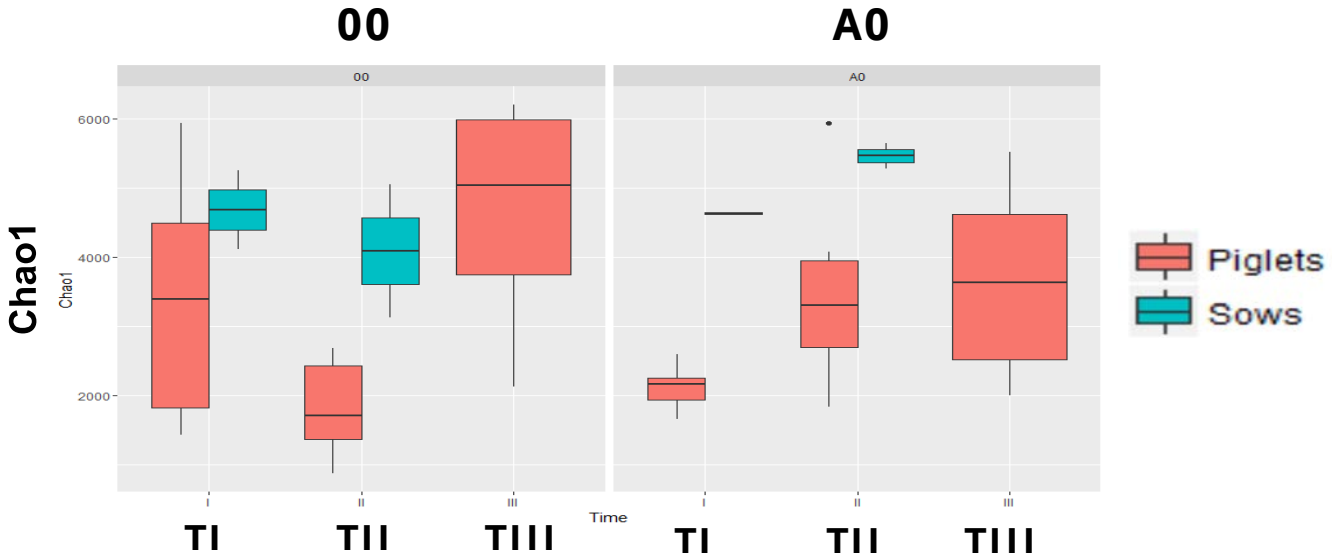
Results
Time Effect





Gradual change over time in diversity and taxonomic composition

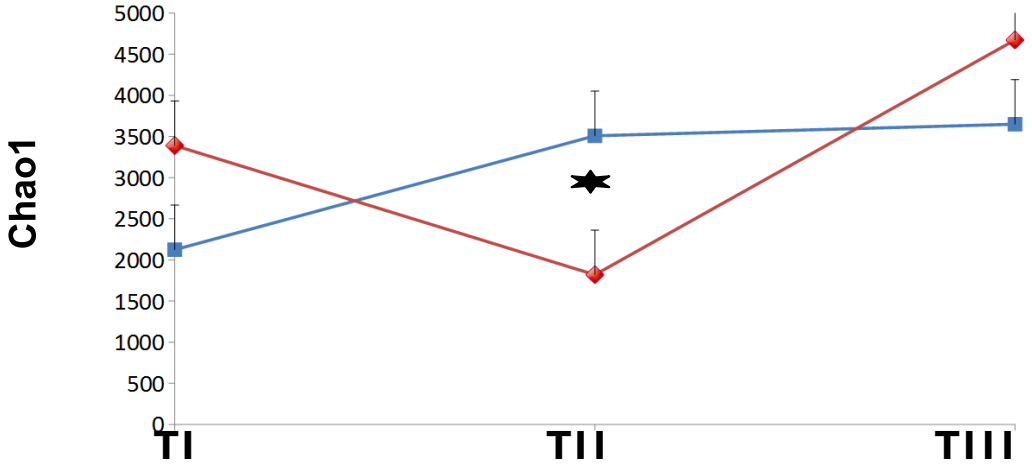
Results
A0 Genotype Effect



No difference in α, β Diversity and taxonomic composition in "Adult Microbiota" (Sows)

Results

Genotype effect in pre-weaning period in piglets

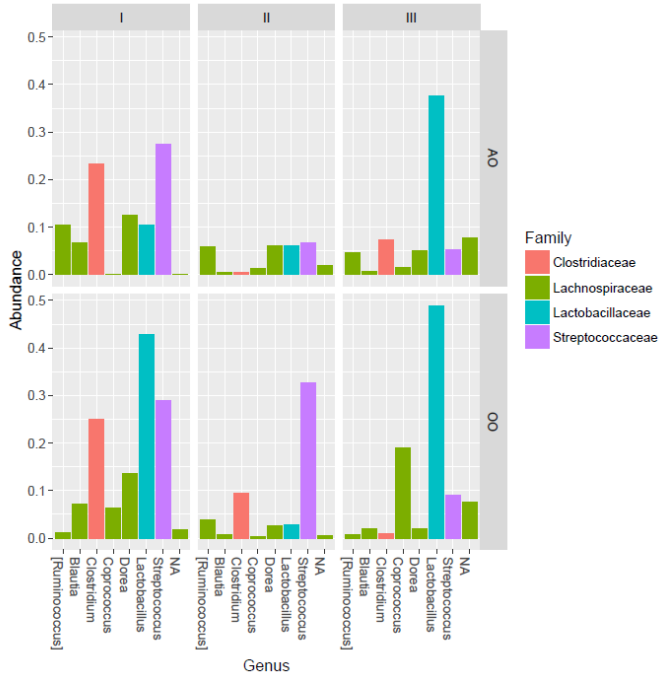


★ P<0.05

Chao1 (Mixed Model)				
Factor	**DF num**	**DF den**	**F Value**	**p**
Time	2	30	6.61	0.0042
Genotype	1	30	0.13	0.7204
Time x Genotype	2	30	6.32	0.0051

Results
Taxonomic Composition

Taxonomy						OTUs	Statistical significance (p)		
Phylum	Class	Order	Family	Genus	Species	ID	Time	Genotype	Interaction
Firmicutes	Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus		703741	0.029	0.313	0.398
			Streptococcaceae	Streptococcus		533277	0.022	0.209	0.144
						349024	0.019	0.678	0.046
	Clostridia	Clostridiales	Clostridiaceae	Clostridium		New_Ref. OTU216	0.043	0.941	0.653
			Lachnospiraceae			708680	0.024	0.897	0.807
				Ruminococcus	**gnavus**	294219	0.173	0.005	0.156
				Blautia	**producta**	696563	0.019	0.757	0.988
				Coprococcus		804526	0.004	0.028	0.006
				Dorea		564188	0.41	0.015	0.837
				Dorea		562376	0.003	0.418	0.303



significant differences for 10 Firmicutes OTUs belonging to 4 Families and 9 Genera

Results
Taxonomic Composition

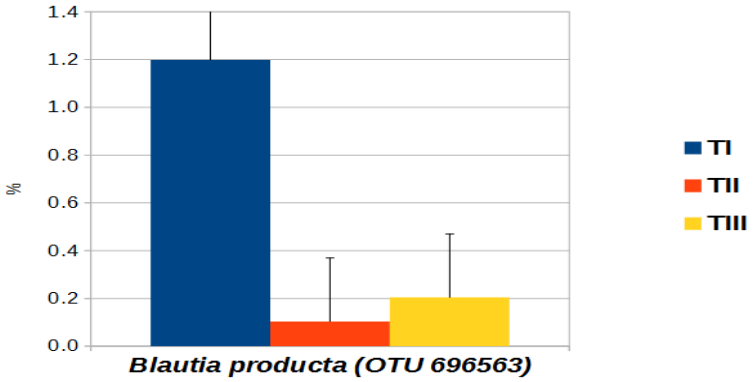
Science AAAS

RESEARCH ARTICLE

Gut bacteria that prevent growth impairments transmitted by microbiota from malnourished children

Laura V. Blanton[1], Mark R. Charbonneau[1], Tarek Salih[1], Michael J. Barratt[1], Siddarth Venkatesh[1], Olga Ilkaveya[2], Sathish Subramanian[1], Mark J. Manary[3,4], Indi Trehan[3,5], Josh M. Jorgensen[6], Yue-mei Fan[7], Bernard Henrissat[8,9], Semen A. Leyn[10], Dmitry A. Rodionov[10,11], Andrei L. Osterman[11], Kenneth M. Maleta[4], Christopher B. Newgard[2,12], Per Ashorn[7,13], Kathryn G. Dewey[6], Jeffrey I. Gordon[1,*]

Improves growth and metabolic abnormalities in recipient animals (mouse model)



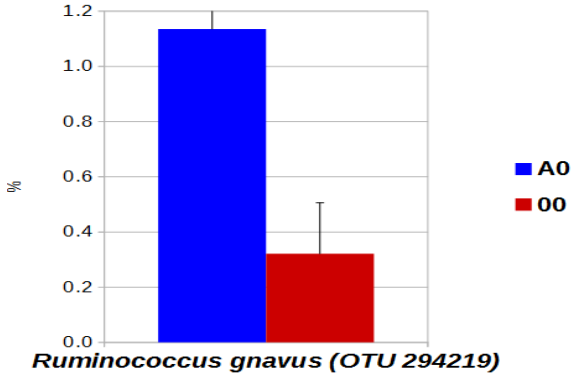
Blautia producta (OTU 696563)

gut microbes

Human intestinal microbiota: Characterization of a simplified and stable gnotobiotic rat model

Natalie Becker, Julia Kunath, Gunnar Loh & Michael Blaut

Related to a high-fat diet causing obesity in a mouse model



Ruminococcus gnavus (OTU 294219)

Conclusions

- The Blood group Genotype does not appear to influence the fecal bacterial communities in adults (supported also by data from a parallel study of our group)
- The microbiota of suckling pigs is affected by the Genotype
- The data confirms a progressive modification of the microbiota composition during piglet life

Thank You For Your Attention

This data are based upon work from COST Action FA1401, supported by COST (European Cooperation in Science and Technology)