Does the host animal control the activity and composition of its gut microbiota?

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Content of the presentation

- Introduction
- Experimental design
- Hypotheses
- Data collected
- Preliminary results
- Concluding remarks

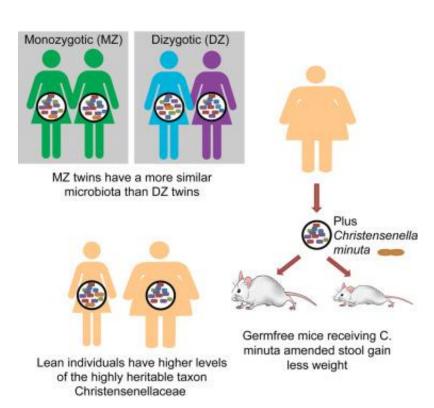


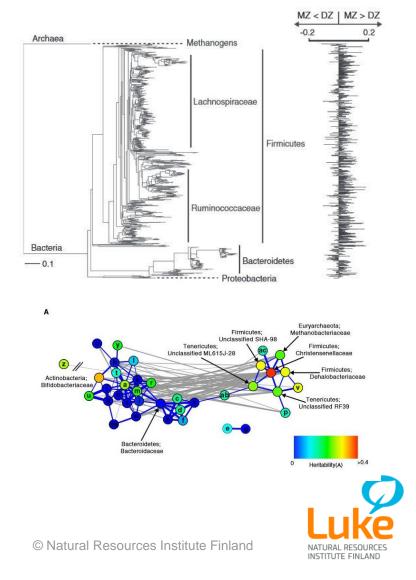
Human Genetics Shape the Gut Microbiome

Julia K. Goodrich,^{1,2} Jillian L. Waters,^{1,2} Angela C. Poole,^{1,2} Jessica L. Sutter,^{1,2} Omry Koren,^{1,2,7} Ran Blekhman,^{1,8} Michelle Beaumont,³ William Van Treuren,⁴ Rob Knight,^{4,5,6} Jordana T. Bell,³ Timothy D. Spector,³ Andrew G. Clark,¹ and Ruth E. Ley^{1,2,*}

21.10.2015

Cell 2014





Genetic and environmental control of host-gut microbiota interactions

Elin Org,¹ Brian W. Parks,¹ Jong Wha J. Joo,² Benjamin Emert,¹ William Schwartzman,¹ Eun Yong Kang,³ Margarete Mehrabian,¹ Calvin Pan,⁴ Rob Knight,⁵ Robert Gunsalus,⁶ Thomas A. Drake,⁷ Eleazar Eskin,^{3,4} and Aldons J. Lusis^{1,4,8}

Genome Res. 2015

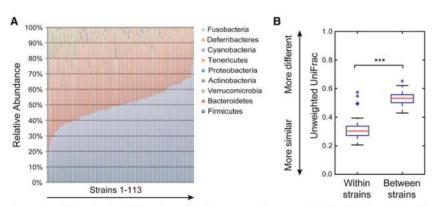
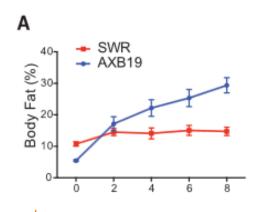
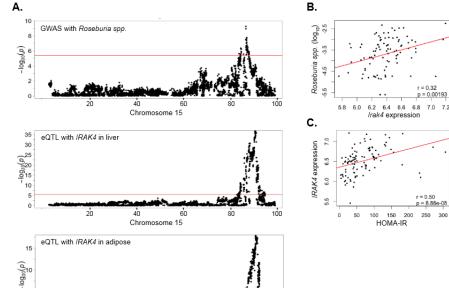


Figure 1. Phylum-level variability of gut microbiota composition across 113 inbred strains of mice. (*A*) Columns represent the relative abundance of microbial phyla in 113 strains (327 male and 297 female). (*B*) Box plot of β diversity distances between microbial communities obtained when comparing mice within and between strains. The specific distance metric used is indicated on the axes. (***) P < 0.001 for Student's *t*-test with 1000 Monte Carlo simulations. See also Supplemental Table 2.





80



40

Chromosome 15

60



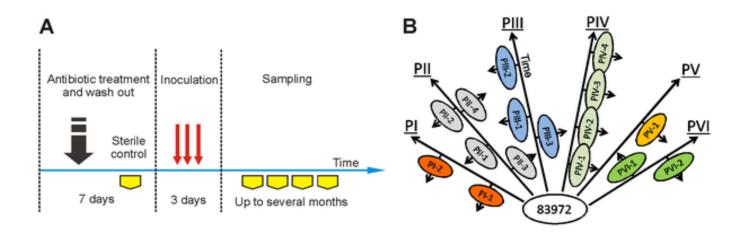
Host Imprints on Bacterial Genomes—Rapid, Divergent Evolution in Individual Patients

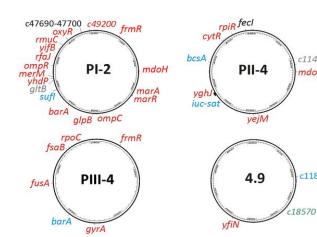
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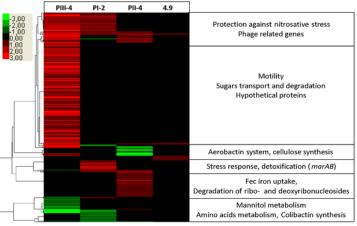
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Zdziarski J, Brzuszkiewicz E, Wullt B, Liesegang H, Biran D, et al. (2010) PLoS Pathog 6(8): e1001078.









How about ruminants?





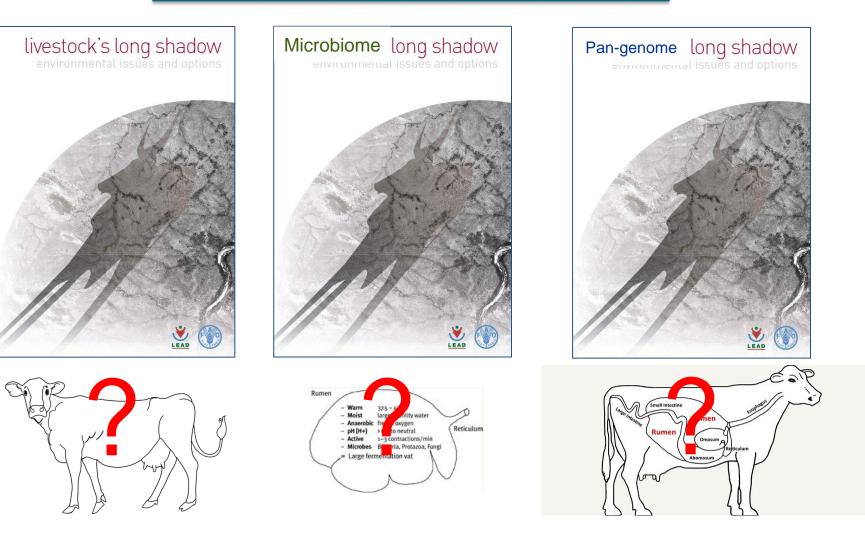


Some ruminants utilize feed more efficient than the others

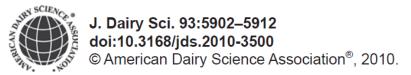
Some ruminants produce less methane even if they are fed the same diet



What are we dealing with?



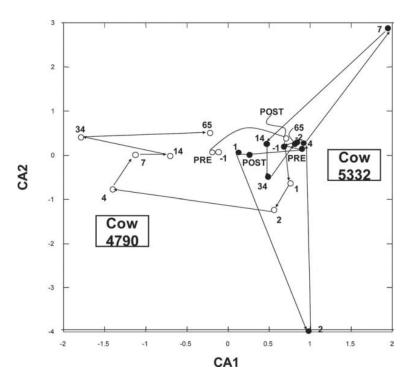




Host specificity of the ruminal bacterial community in the dairy cow following near-total exchange of ruminal contents¹

P. J. Weimer,*⁺² D. M. Stevenson,* H. C. Mantovani,[‡] and S. L. C. Man⁺

*USDA-ARS, US Dairy Forage Research Center, Madison, WI 53706 †Department of Bacteriology, University of Wisconsin–Madison, Madison 53706 ‡Departamento de Microbiologia, Universidade Federal de Viçosa, Viçosa-MG, 36571-000, Brazil

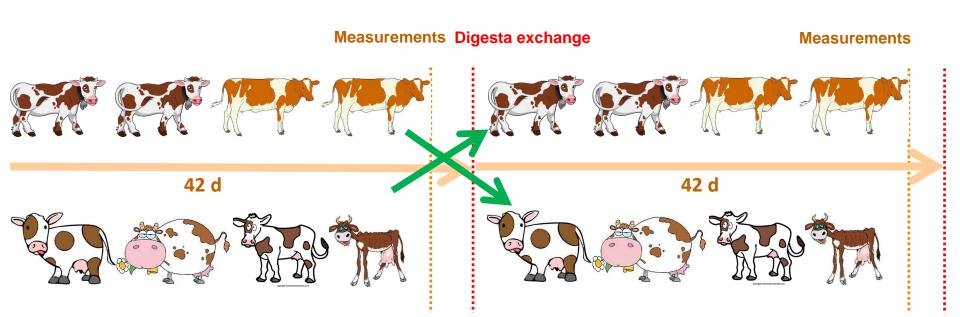


Following exchange of ruminal contents, ruminal pH and total VFA concentration returned to their pre-exchange values within 24h.

Ruminal bacterial community composition displays substantial host specificity that can re-establish itself with varying success when challenged with a microbial community optimally adapted to ruminal conditions of a different host animal.



Experimental design



Rumen sampling at exchange and in weekly intervals



Experimental design



Identical twins were created by splitting embryo into 2 parts and implanting them back to their mother



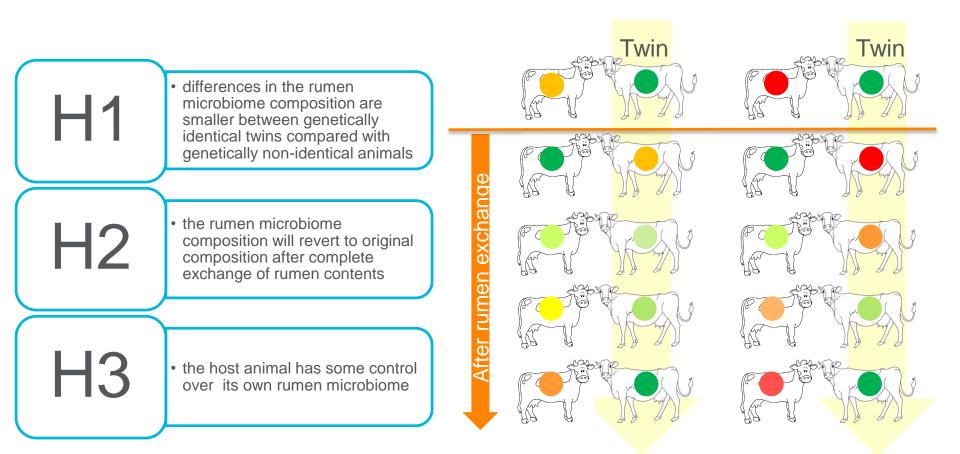
Several pairs of twins were born in Luke barn



Animals were kept in the same barn, fitted with cannulae and recruited to the experiment

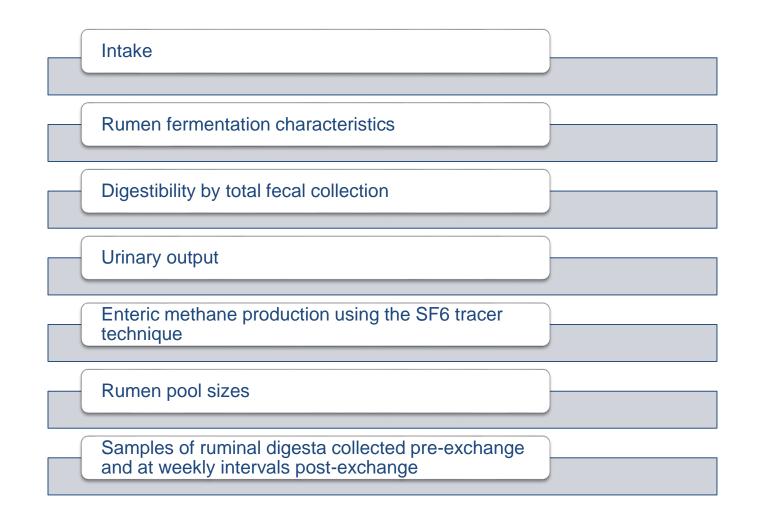


Hypotheses





Data collected





Rumen sampling design

Rumen sampling

Rumen sample processing

DNA extraction

Amplicon library preparation (bacteria, archaea, ciliates, fungi)

Metabarcoding sequencing

Sequencing data analysis









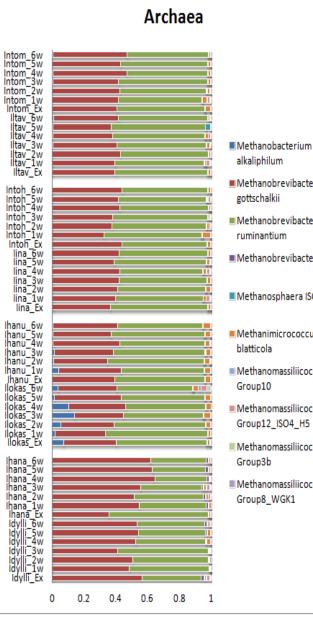
Milk yield

Rumen fermentation

Digestibility

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Methanobrevibacter Methanobrevibacter Methanobrevibacter RT

Methanosphaera ISO3_F5

Methanimicrococcus

Methanomassiliicoccaceae

Methanomassiliicoccaceae Group12_ISO4_H5

Methanomassiliicoccaceae

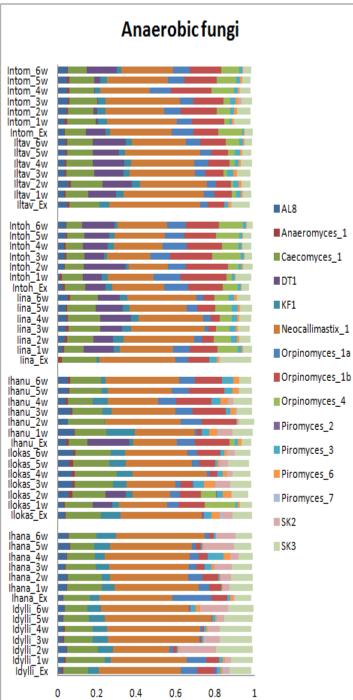
Methanomassiliicoccaceae Group8_WGK1



			(Cili	iate	pro	tozo	ba
Intom_6w Intom_5w Intom_4w Intom_3w Intom_2w Intom_1w								
Intom_Ex Iltav_6w Iltav_5w								Dasytricha_unc
Iltav_4w Iltav_3w Iltav_2w	÷.							Diplodinium_u
Iltav_1w Iltav_Ex	÷							Entodinium_lor
Intoh_6w Intoh_5w								Entodinium_un
Intoh_4w Intoh_3w								Isotricha_spL
Intoh_2w Intoh_1w								Isotricha_uncu
Intoh_Ex lina_6w lina_5w								Metadinium_m
lina_4w lina_3w								Ophryoscolex_
lina_2w lina_1w lina_Ex								Polydiniella_m
lhanu 6w								Polyplastron_u
Ihanu_5w Ihanu_4w								Trichostomatia
Ihanu_3w Ihanu_2w								
lhanu_1w								
Ihanu_Ex								
llokas_6w llokas_5w								
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Ihana_3w								
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Idylli_6w Idylli_5w								
Idvlli 4w								
Idylli_3w Idylli_2w								
ldylli_2w								
ldylli_1w								
Idylli_Ex								
	0	0.2	0.4	4	0.6	0.8	1	

d
Dasytricha_uncultured
Diplodinium_uncultured
Entodinium_longinucleatum
Entodinium_uncultured
Isotricha_spLDK_2011
Isotricha_uncultured
Metadinium_minorum
Ophryoscolex_uncultured
Polydiniella_mysorea
Polyplastron_uncultured
Trichostomatia_uncultured





Orpinomyces_4

Piromyces_2

Piromyces_3

Piromyces_6

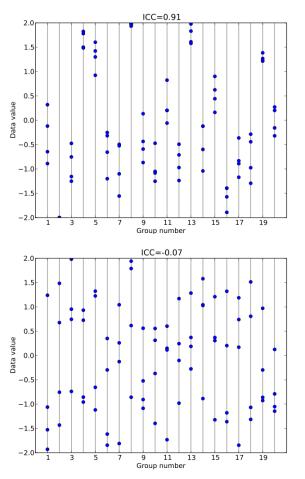
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Bacteria											
Intom_6w					163	1 64					
Intom_5w					166	181					
Intom_4w Intom_3w			_								
Intom_2w					191	193					
Intom_1w					196	197					
Intom_Ex					207	208					
lltav_6w lltav_5w				_	214	216					
lltav_4w					217	222					
lltav_3w					226	227					
lltav_2w					229	253					
lltav_1w											
Iltav_Ex					354	357					
Intoh 6w					360	417					
Intoh_5w					418	419					
Intoh_4w					421	426					
Intoh_3w					448	449					
Intoh_2w Intoh_1w		_			450	453					
Intoh_Ex											
lina_6w					458	460					
lina_5w					462	466					
lina_4w lina_3w					469	470					
lina_3w					472	490					
lina_1w					492	493					
lina_Ex					494	495					
Ihanu_6w					497	498					
Ihanu_5w											
Ihanu 4w					504	506					
lhanu_3w					508	521					
Ihanu_2w					524	526					
Ihanu_1w Ihanu Ex					555	570					
llokas_6w					576	584					
Ilokas_5w					596	601					
Ilokas_4w					608	629					
Ilokas_3w Ilokas_2w											
llokas_2w					657	671					
Ilokas_Ex					695	700					
					705	775					
Ihana_6w					796	813					
Ihana_5w Ihana 4w					815	836					
Ihana_3w					840	845					
Ihana_2w					901	908					
Ihana_1w											
Ihana_Ex Idylli_6w					918	949					
Idylli_5w					950	960					
Idylli_4w					976	984					
Idylli_3w					992	997					
Idylli_2w Idylli_1w					1002	1003					
IdyIII_IW					1010	1011					
					- 1012						
	0 0.2	0.4	0.6	0.8	1 1015						

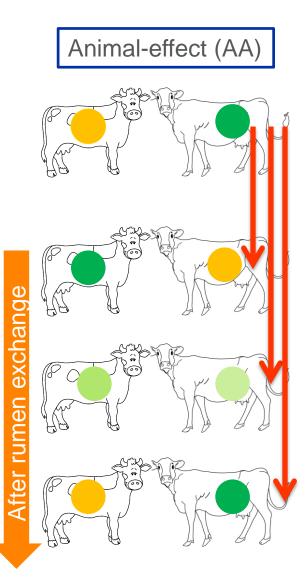


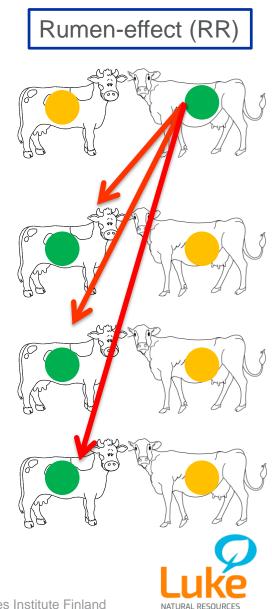
Intraclass correlation coefficient

(ICC) describes how strongly individuals within a group resemble each other in terms of a particular trait (rumen microbiota)

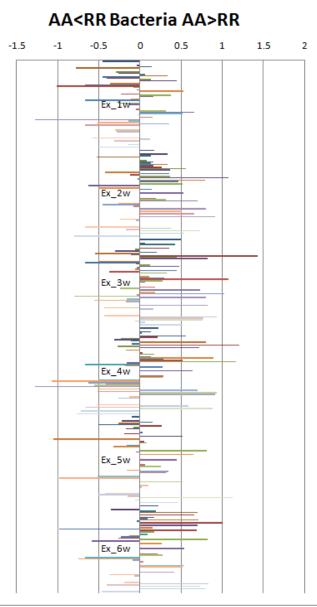


https://commons.wikimedia.org/wiki/File:ICCexample2.svg#/media/File:ICC-example2.svg





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Concluding remarks

Rumen microbial composition in twins is not identical

High between animal variation as a response to rumen content exchange

There are indications that the host ruminant may exert genetic control on some of the microbiota in the rumen - microbial group specific

An interval of 42 d may be too short to fully evaluate the adaptation of the rumen microbiome to rumen perturbation



Thank you!

