Microbiota and Lifestyle

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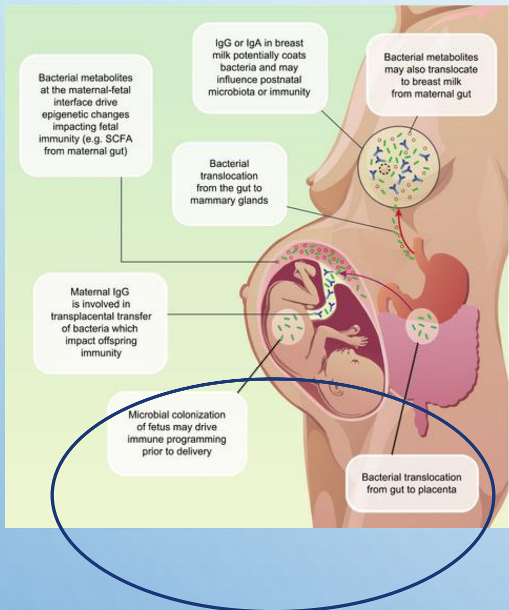
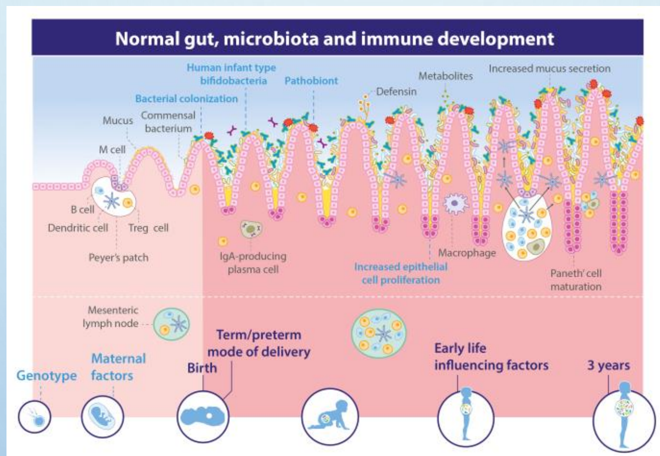
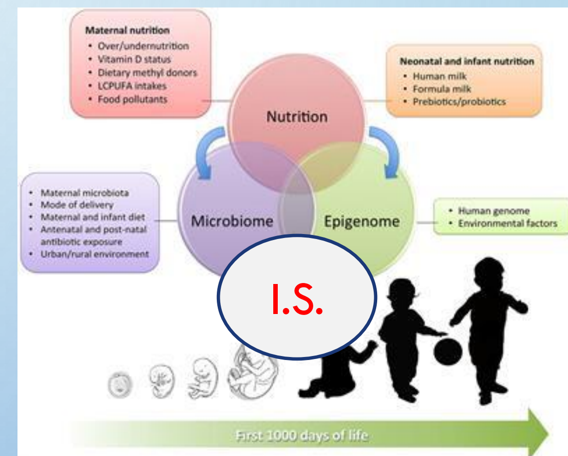
BIOMES

- Microbiota structure and diversity
- Microbiota Nutrition, Epigenetics
- Exercise, metabolics
- Gut brain, Fasting, Fasting Mimetics
- Aging
- Covid

DEVELOPMENT OF MICROBIOTA, I.S., AND EPIGENETIC SYSTEM, IMPRINTING

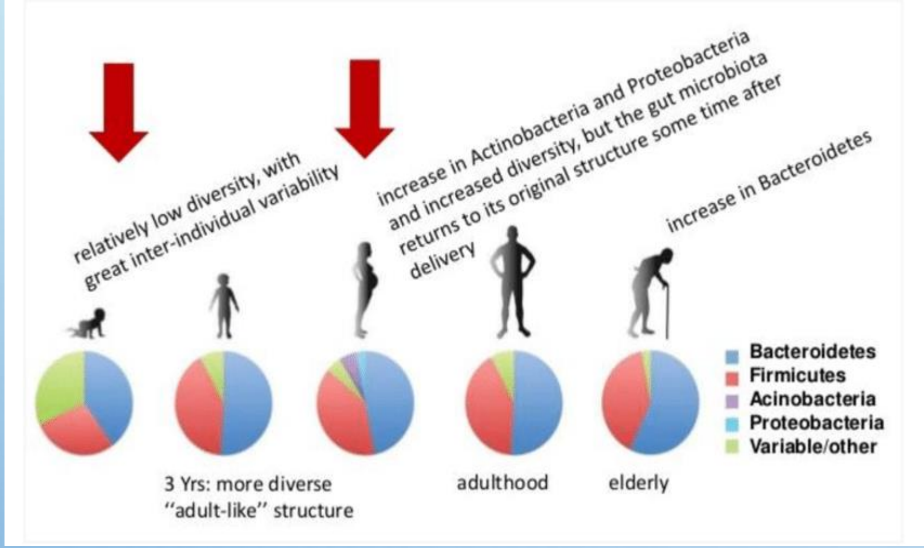


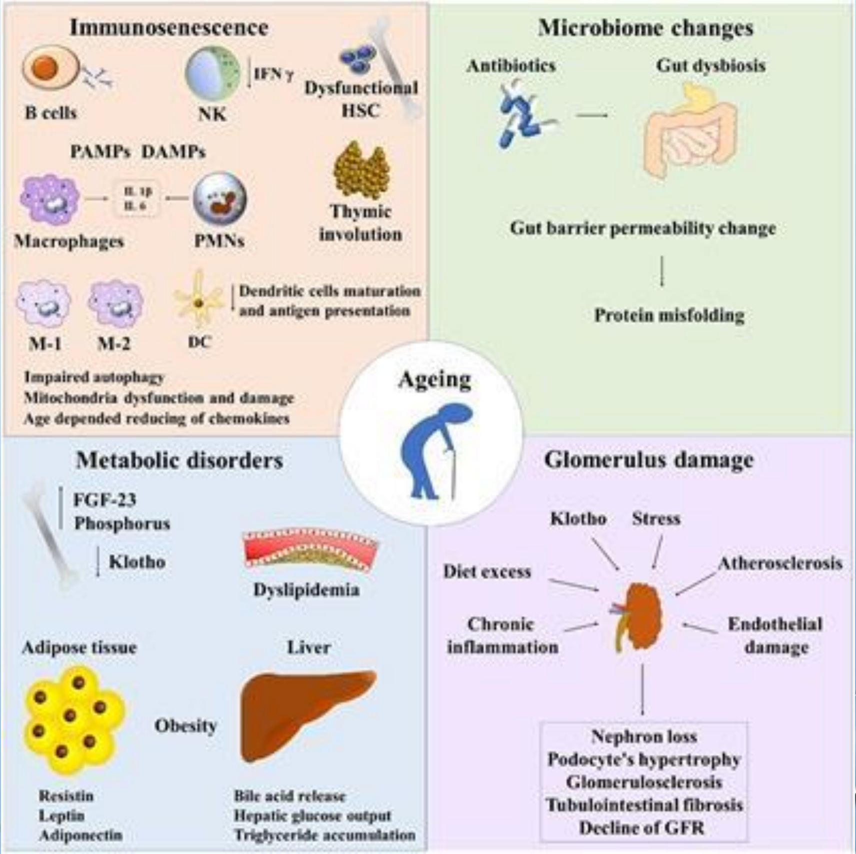




Development prenatal, Interaction with I.S., epigenetic maternal factors,
Diversity:delivery, breastfeeding, imprinting in 1000 days of life

INTERACTIONS MICROBIOTA DIVERSITY - I.S.- EPIGENETIC SYSTEM IN SENESCENCE



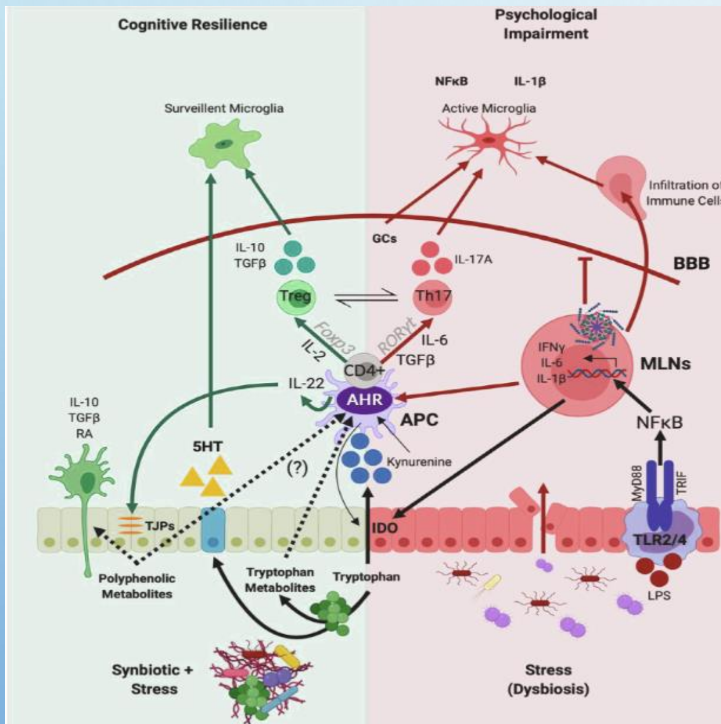


The Impact of the Microbiome on Immunosenescence

Daniel Amsterdam & Barbara E. Ostrov

Inflammaging

GUT BRAIN AXIS: MICROBIAL METABOLITES REGULATE TREG, TH17 BALANCE, IMPORTANT FOR COGNITIVE RESILIENCE



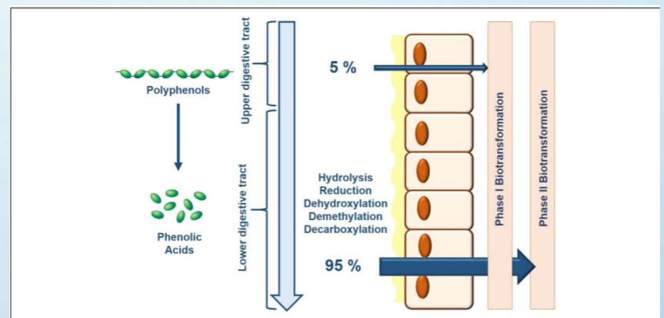
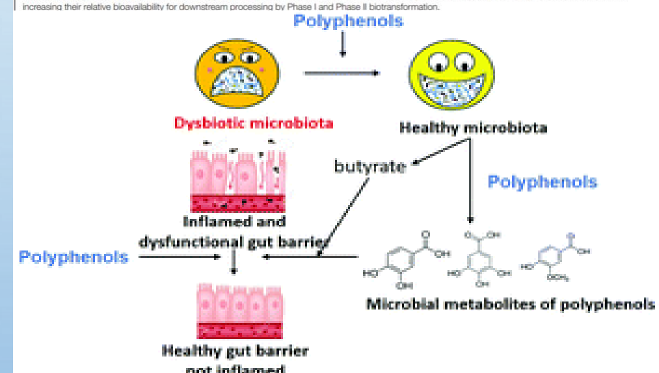
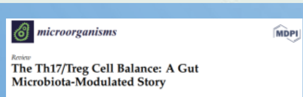


FIGURE 1 | Bioavailability of dietary polyphenols is primarily determined by the composition of the gut microbiota. As consumed, only 5% of dietary polyphenols are absorbed where consequently, Phase I and Phase II biotransformation takes place in the epithelial cells and liver which generates a limited battery of bioavailable metabolites. Upon reaching the lower colon, the gut microbiota breaks down the remaining dietary polyphenols through their endogenous enzymatic activity increasing their relative bioavailability for downstream processing by Phase I and Phase II biotransformation.



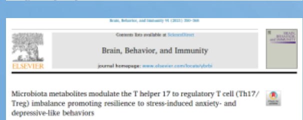

microorganisms

MDPI

Review

The Th17/Treg Cell Balance: A Gut Microbiota-Modulated Story

Hongyu Cheng, Xiong Guan, Dekun Chen * and Wentao Ma *


Contents lists available at ScienceDirect

Brain, Behavior, and Immunity

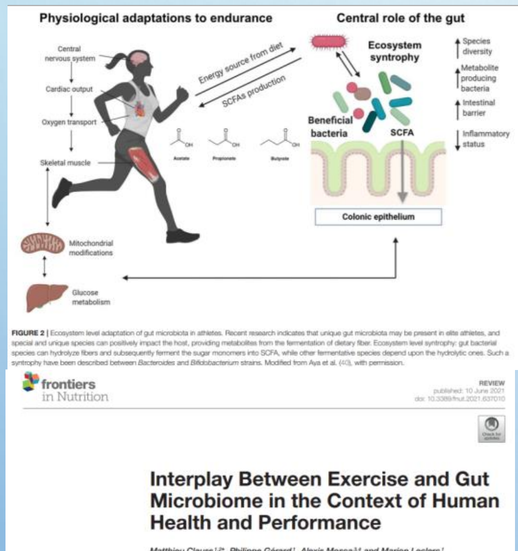
ELSEVIER

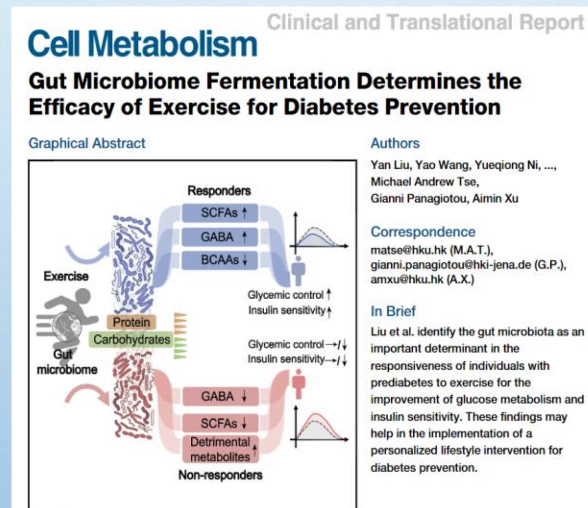
Microbiota metabolites modulate the T helper 17 to regulatory T cell (Th17/Treg) imbalance promoting resilience to stress-induced anxiety- and depressive-like behaviors

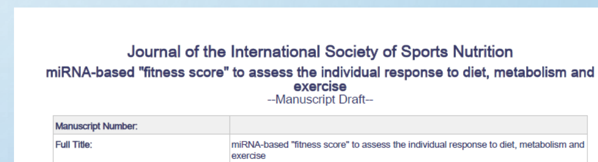
The gut brain axis: microbiota regulate bio-availability of polyhenol metabolites and their activity in neurological disorders,

***Giulio M Pasinetti**, Icahn School of Medicine at Mount Sinai, USA*

LIFESTYLE: EXERCISE MODULATES MICROBIOTA METABOLITES AND EPIGENETICS (MIRNAS)







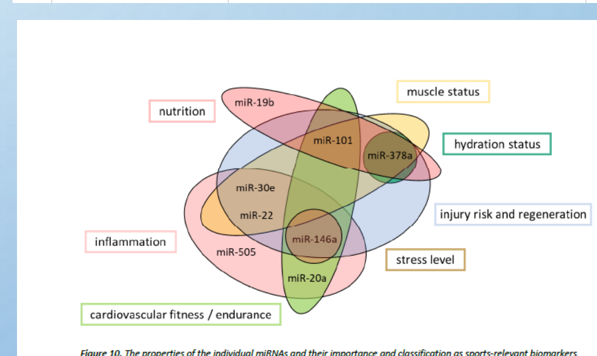
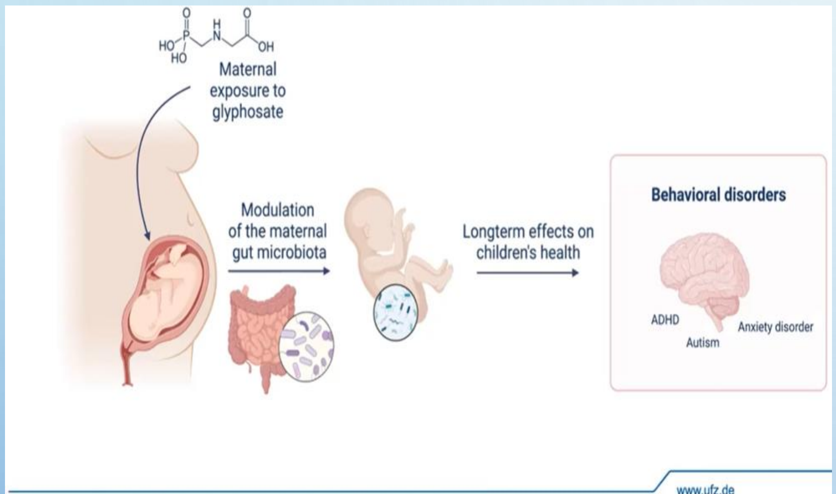
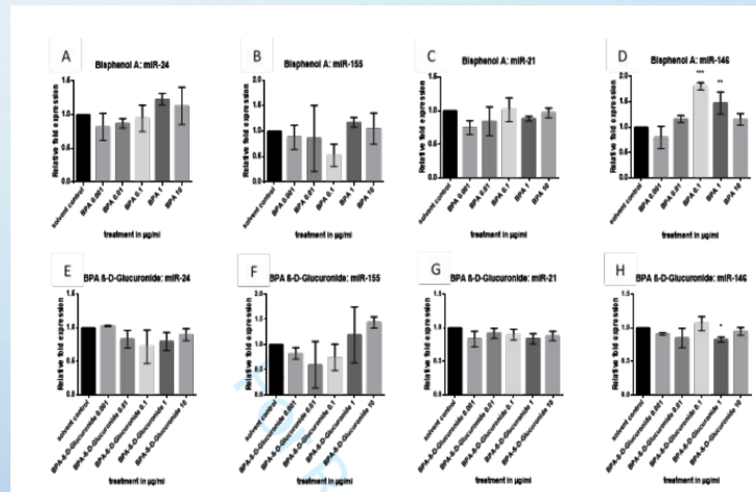


Figure 10. The properties of the individual miRNAs and their importance and classification as sports-relevant biomarkers.

Enhanced amount of SCFA producers by exercise ?
Production of metabolites decides effectivity of exercise against diabetes

TOXINS: GLYPHOSATE, BISPHENOLS, MICROBIOTA AND EPIGENETICS





*Lisa Buchenauer***, Helmholtz Centre for Environmental Research Leipzig, Germany**

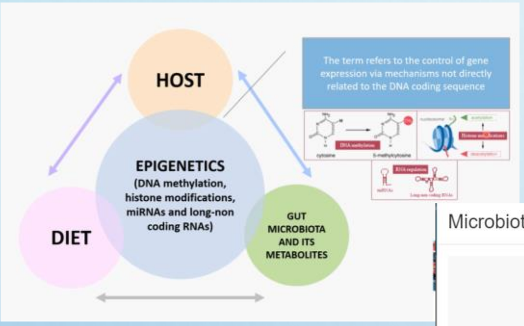
ENVIRONMENTAL EPIGENETICS

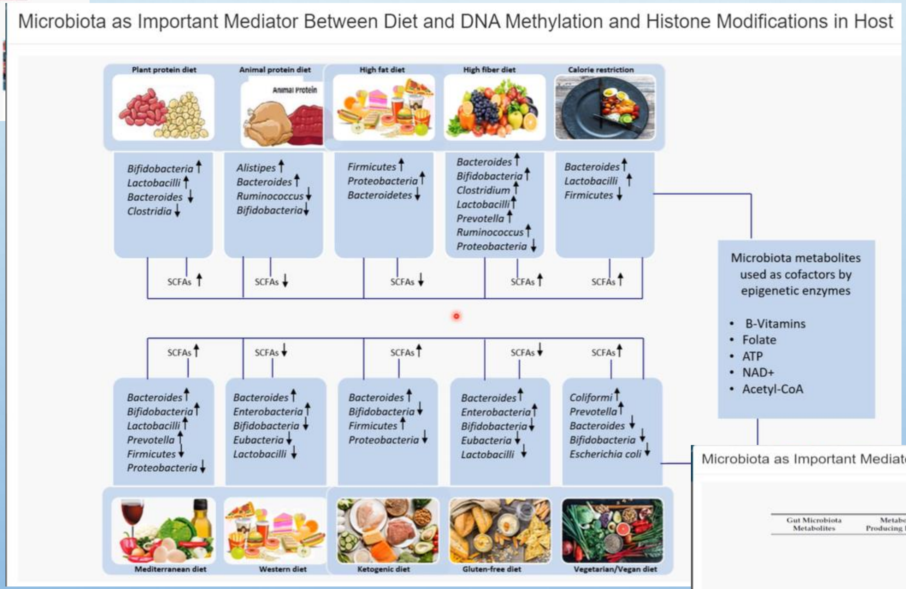
Different bisphenols including the metabolite BPA glucuronide induce non-monotonous changes in miRNA expression and CpG methylation in HLF and Caco-2 cell lines, a pilot study

3 Julia Oldenburg*, Maria Fürhacker**, Christina Hartmann***, Philipp Steinbichl***, Rojin

4 Banaderakhshan**, Alexander Haslberger *

INTERACTIONS DIET MICROBIOTA AND EPIGENETICS, EXPERIENCE



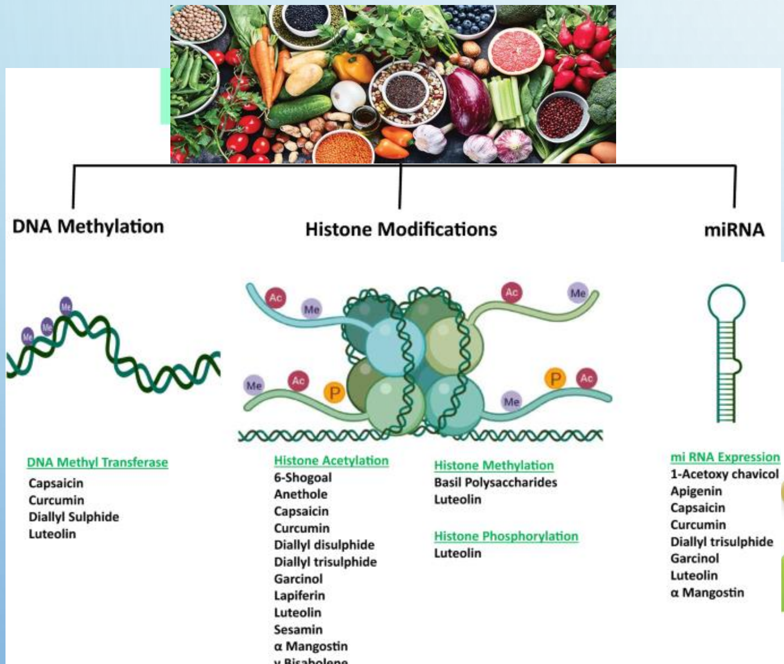


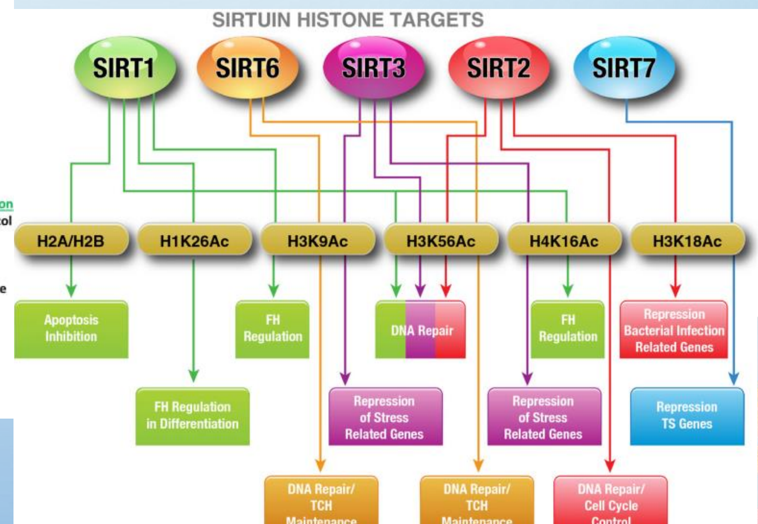
Microbiota as Important Mediator Between Diet and DNA Methylation and Histone Modifications in

Gut Microbiota Metabolites	Metabolite Producing Bacteria	Biological Functions of Metabolites	Metabolite-Induced Epigenetic Changes	Epigenetics-Associated Effects	Associated Diseases
Short-chain fatty acids (SCFAs): Acetate, propionate, butyrate, iso-butyrate, caproate, branched SCFAs (BCFAs), hexanoate, lactate, 2-methylpropionate, valerate, iso-valerate	*Lactobacillus, Eubacterium, Roseburia, Anaerostipes hadrus, Faecalibacterium, Coprococcus catus, Clostridia* (clusters IV and XIVa)	Regulation of: • fatty acid, glucose, and cholesterol metabolism • mucin synthesis • synthesis of AMPs • daily turnover of the epithelial lining and stem cell proliferation • gut integrity by TJs • neutrophil functions • differentiation and function of Th1, Th7, and regulatory T (T_{reg}) cells • intestinal macrophage activation and recruitment • dendritic cells in the induction of tolerance Suppression of pro-inflammatory cytokine secretion Improvement in insulin sensitivity and weight control Energy source for colonocytes	Inhibition of DNMT enzymes Decreased DNA methylation Inhibition of MBD2 Inhibition of HDACs Increased histone acetylation Activation of HAT Increased histone acetylation	Upregulation of FOXP3, β-defensin 2 and 3, ADIPOQ, RETN, Sp1/Sp3, BAK1, CDKN1A, CDKN1B, PPARγ, IFNγ, FAS, NOS2, CD36, IL-6, IL-8, IL-12B, ERRα, MHC class II, USF1, ACOT7, TAC1, LMNA, SCD5, HDAC7, IGF2BP, and SIRT1 genes LINE-1 DNA methylation Downregulation of NRP1, NF-kB, FTO, MC4R FOXD1, KCNIP4, SERINC3, MEF2A, and STAT1 genes	Inflammatory bowel disease, cardiovascular disease, ulcerative colitis, Crohn's disease, obesity, metabolic syndrome, colorectal cancer, type 1 diabetes, type 2 diabetes, nephropathy, autism spectrum disorders
Polyunsaturated fatty acid (PUFAs): Arachidonic acid, docosahexaenoic acid, conjugated linoleic acids, conjugated linoleic acids, linoleic acid derivative	*Bifidobacterium, Roseburia, Lactobacillus, Klebsiella, Enterobacter, Citrobacter, Clostridium*	Maintenance of intestinal barrier function Regulation of intestinal IgA production Improvement in insulin sensitivity Regulation of development and function of the central nervous system	Inhibition of DNMTs activity Decreased DNA methylation Decreased histone methylation and phosphorylation Increased SIRT1 deacetylation activity	Downregulation of EZH2 and CDK2 genes Upregulation of CDH1, PRKAA1, and IGFBP3 genes	Chronic systemic inflammation, hyperinsulinemia, depression, cognitive anxiety

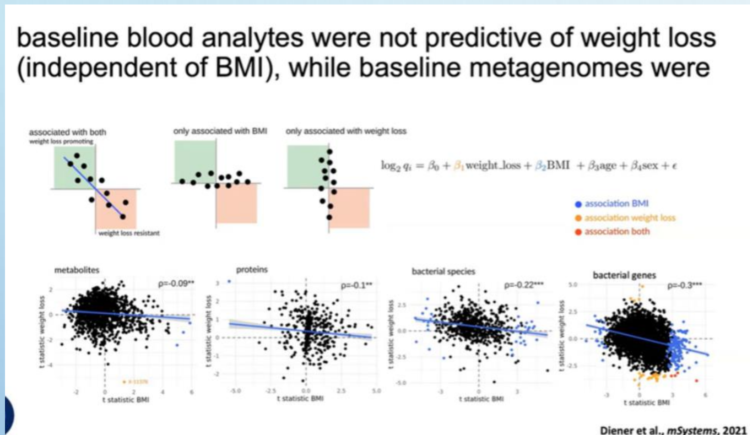
Dina Bellizzi, *University of Calabria, Italy* , ***Annalisa Terranegra***, *Sidra Medical and Research Center, Qatar*

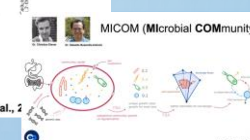
DIETARY INGREDIENTS AND MICROBIOTA DERIVED METABOLITES (SCFAS) ADDRESS ALL ELEMENTS OF THE EPIGENETIC SYSTEM

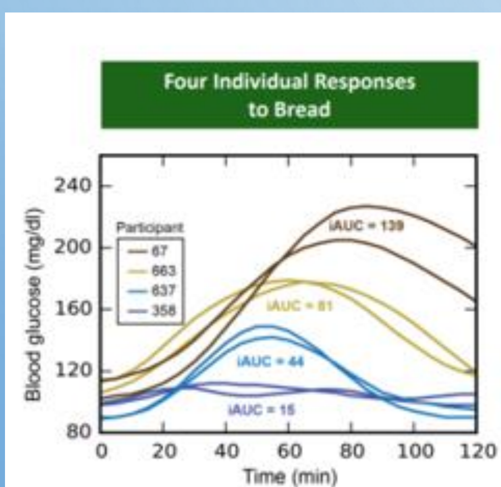


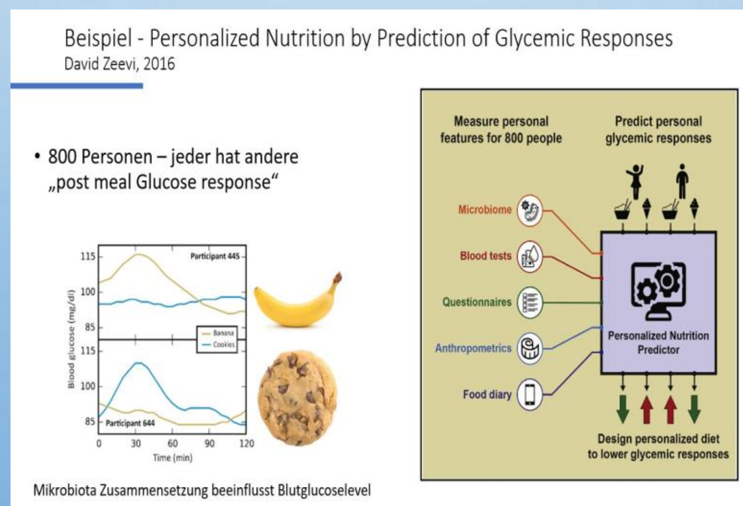


MICROBIOTA PREDICT PERSONAL RESPONSES TO DIETS



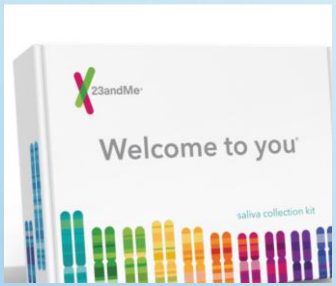


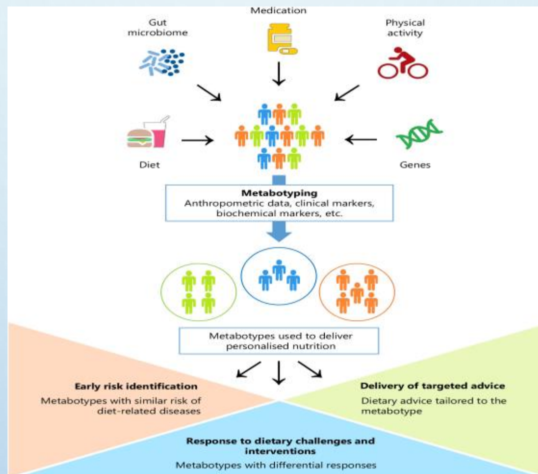


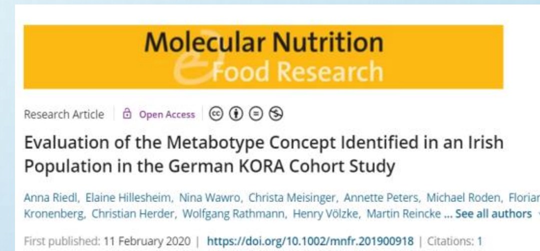


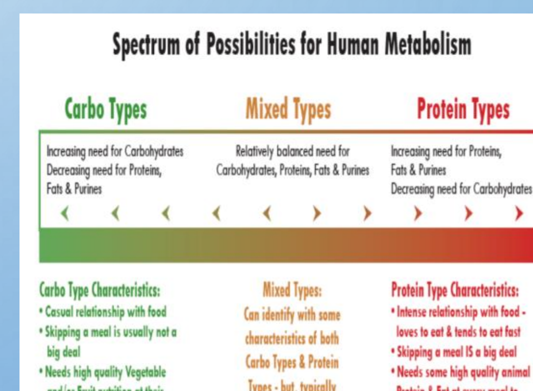
Eran Elinav and Eran Segal, Weizmann Institute of monitoring the blood sugar, diets, and other traits of 800 people, they built an algorithm that can accurately predict how a person's blood-sugar levels will spike after eating any given meal.
They also used these personalized predictions to develop tailored dietary plans for keeping blood sugar in check.

DEFINITION OF METABOTYPES FROM GENETIC-, MICROBIOTA- METABOLOMICS- BASED INFORMATION, METABOTYPING, FOOD4ME









Personalisation of Additives for Prevention: Monitoring basic hallmarks of health/aging. Use of mixes of supplements, functional foods which address specific mechanisms „Achilles Fersen Concept“

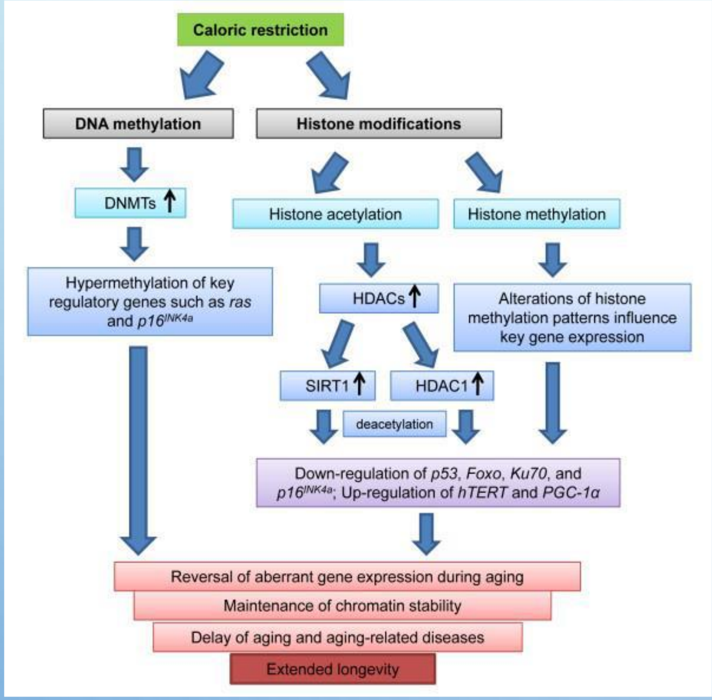
HealthBioCare GmbH

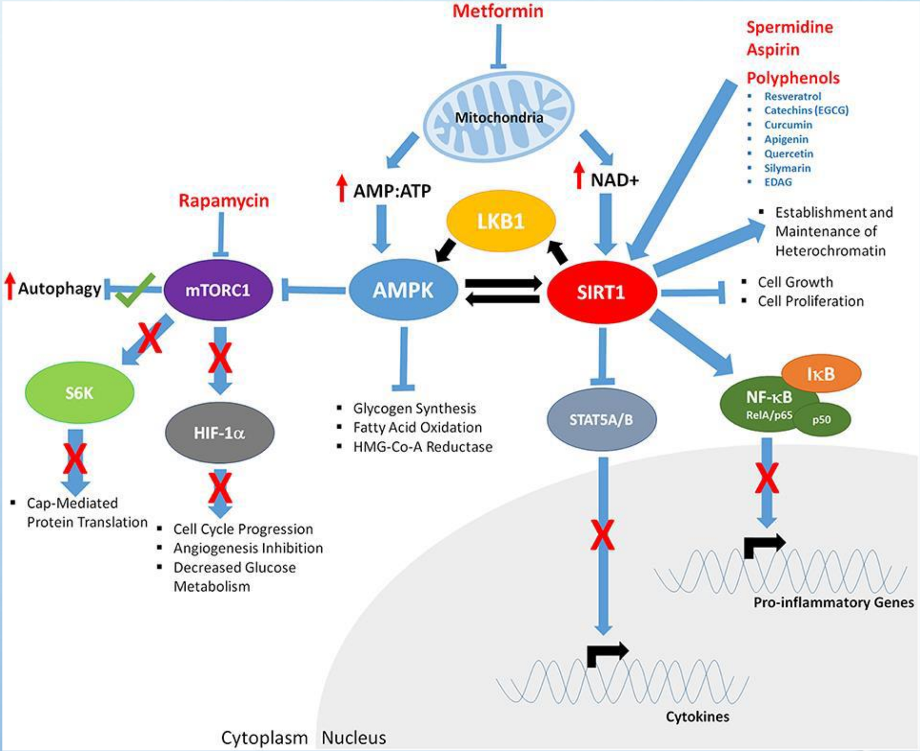
Precision Probiotics + Prebiotics with Viome's Gut Intelligence™ Test

For gut health

AG Haslberger

GUT HOST INTERACTIONS OF CENTRAL IMPORTANCE CASE STUDY: COMPARING CALORIC RESTRICTION : FASTING MIMETICS





CR, fasting: Fasting mimetics: AMPK, SIRT, TOR pathways similar, difference ketogenesis

STUDY DESIGN

STOFF	WIRKSTOFF	MENGE / 25ML	Wirkstoff
Blueberry Extract	Anthocyanins/ Anthocyanidin..	40 mg	14mg 10mg
Broccoli Extract	Sulpharapane, Glucoraphin..	30 mg	
Apfel extract	Phlorentin, Quercetin..	50 mg	
Citrus extract	Naringin..	40 mg	
Nikotinamid	Nikotinamid ribosid	24 mg	
Zinkgluconat	Zink	7.5 mg	

Wasser, Stevia, Erythrit

Buchinger Fasting < 120 kcal/day
n: 22 in Pernegg Monastery

Feces , blood spots, before and
After the end, first solid feces

Active (N. 131) Placebo (n: 30)
Intervention 3 months

Feces, Blood spots before, after 1,3 month

Illuminia sequencing, Line 1 methylation bisulfite qPCR,
HR-MCA, RNA, MiRNA RT QPCRi

BUCHINGER FASTING RESULTED IN A RISE IN THE DISTRIBUTION OF PROTEOBACTERIA, INCREASED MICROBIOTA DIVERSITY AND A SIGNIFICANT INCREASE IN CHRISTENSENELLA

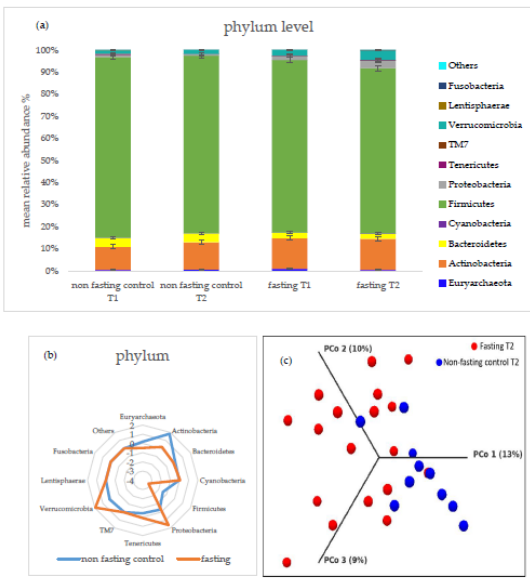


Figure 4. The dissimilarity of the microbiota composition of the non-fasting control and fasting group. (a) Bar charts of sequencing data given in mean +/− SD relative bacteria abundance in % at phylum level for non-fasting and fasting group. (b) Major differences between non-fasting and fasting groups at the phylum level. Values are given as the mean abundance of T2–T1. (c) PCoA based on Bray–Curtis dissimilarity index showing cluster for fasting and non-fasting group at T2. Permutational multivariate analysis of variance (PERMANOVA; $p = 0.00004$) was applied for the analysis.

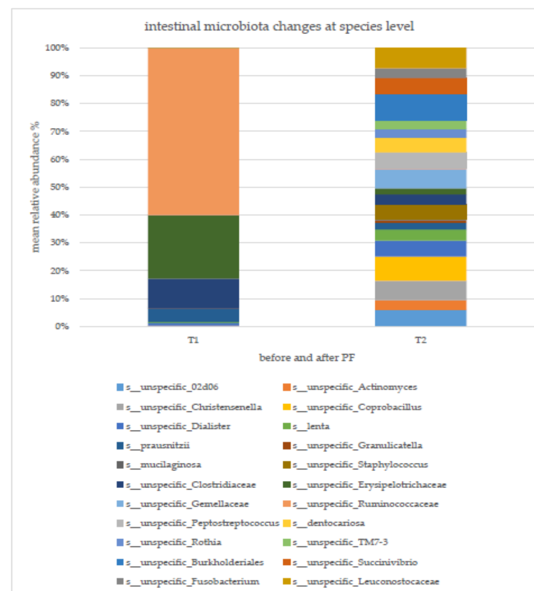


Figure 5. Microbial changes at species level before and after PF. Bar charts of all statistically significant changes of the sequencing data at species level given in mean relative bacteria abundance in % for the fasting group. Statistical significance was determined using paired *t*-test for parametric values and Wilcoxon test for nonparametric values and defined as $p < 0.05$.

3M SIRT INDUCING DRINK INCREASED *ACTINOBACTERIA*. FIRMICUTES/*BACTEROIDETES* RATIO DECREASED AND CORRELATED WITH BMI. ONLY FASTING INCREASED BUTYRATE SIGNIFICANTLY

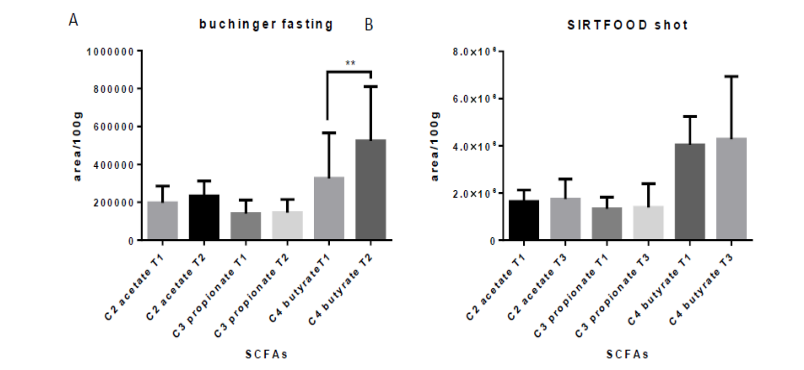


Figure 7: Amount of SCFAs produced given as area/100g stool for buchinger fasting (A) and SIRTFOOD shot (B) interventions. Statistical significance between timepoint 1 (T1) and end (T2 or T3) of the intervention was determined using paired t-test for parametric values and Wilcoxon test for nonparametric values.

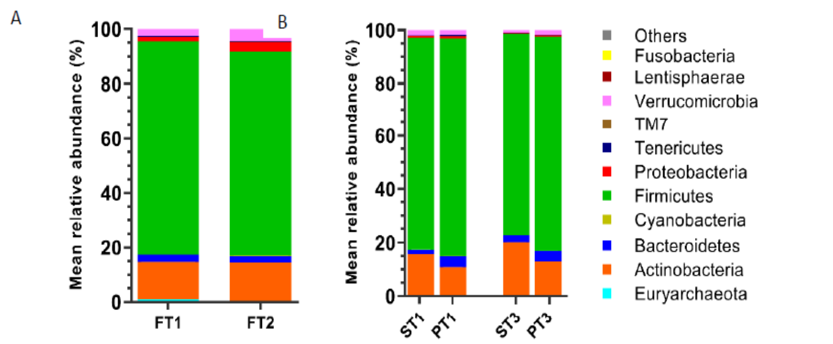


Figure 6: Abundance microbiota by phyla for fasting group (A), SIRTFOOD shot (ST1 vs ST3) (B) and placebo group (PT1 vs PT3) (B). Results are expressed in percentage of the mean of relative abundance for the different phyla. Statistical significance between timepoint 1 (T1) and end (T2 or T3) of the intervention was determined using paired t-test for parametric values and Wilcoxon test for nonparametric values.

POSITIVE CORRELATION OF THE ABUNDANCE OF BUTYRATE-PRODUCING *BACTEROIDETES* WITH MIR125, SIRT-1 EXPRESSION, TELOMERE LENGTH

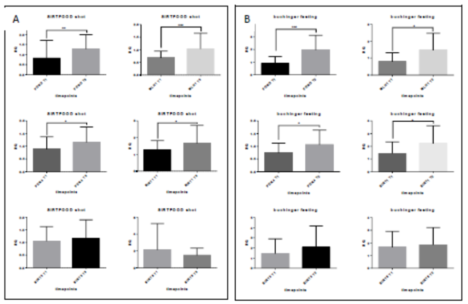


Figure 4: RQ selected mRNA gene expression (*FoxO1, MLH1, PDK4, SIRT1, SIRT3, SIRT6*) SIRTFOOD shot and buchinger fasting. The results are expressed as mean +/- SD. Statistical significance between timepoint 1 (T1) and end (T2 or T3) of the intervention was determined using paired t-test for parametric values and Wilcoxon test for nonparametric values.

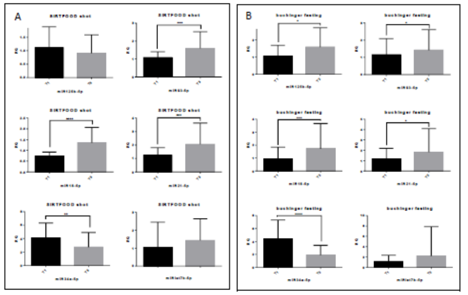


Figure 5: RQ selected miRNA gene expression (*miR125b-5p, miR93-5p, miR16-5p, miR21-5p, miR34a-5p, miRlet7b-5p*) SIRTFOOD shot and buchinger fasting. The results are expressed as mean +/- SD. Statistical significance between timepoint 1 (T1) and end (T2 or T3) of the intervention was determined using paired t-test for parametric values and Wilcoxon test for nonparametric values.

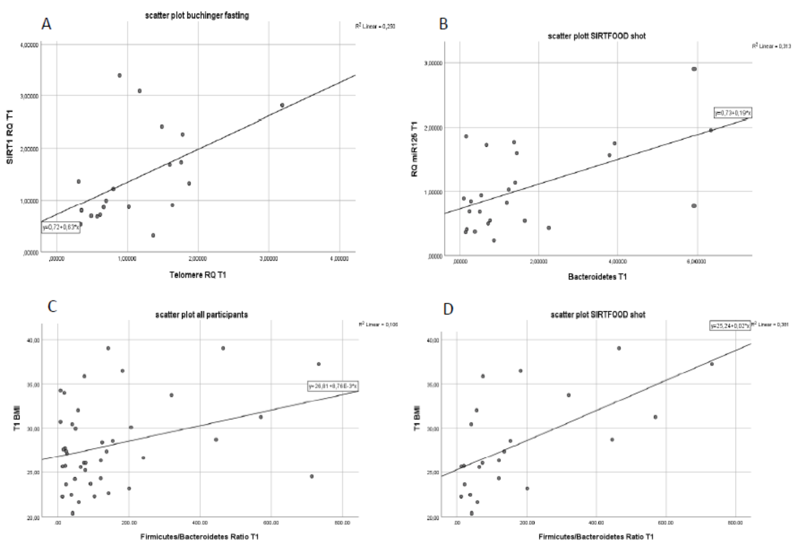


Figure 8: spss output scatter plots. (A) shows a positive correlation between telomere length and SIRT1 expression for buchinger fasting at baseline. Bacteroidetes and miR125b-5p positively correlated in the SIRTFOOD shot intervention at baseline(B). For all participants the ratio of Firmicutes/Bacteroidetes increased with higher BMI (C), which was also seen for the SIRTFOOD shot intervention Discussion (D). Statistical significance was defined as $p < 0.05$.

CONCLUSIONS

In conclusion fasting and to some extend fasting mimetics result in beneficial modulation of microbiota (e.g diversity, SCFA, BHP) and metabolism (e.g SIRTS, mtDNA, telomer length)

Microbiota structure seems to interfere with the expression of Sirtuins and metabolism relevant miRNAs

Hindawi
Oxidative Medicine and Cellular Longevity
Volume 2020, Article ID 4793125, 13 pages
https://doi.org/10.1155/2020/4793125

Hindawi

Research Article

Epigallocatechin Gallate Effectively Affects Senescence and Anti-SASP via *SIRT3* in 3T3-L1 Preadipocytes in Comparison with Other Bioactive Substances

Stephanie Lilja,[1] Julia Oldenburg,[1] Angelika Pointner,[1] Laura Dewald,[1] Mariam Lerch,[1] Berit Hippe,[2] Olivier Switzeny,[2] and Alexander Haslberger[1]

International Journal of *Molecular Sciences*

MDPI

Article

Five Days Periodic Fasting Elevates Levels of Longevity Related *Christensenella* and Sirtuin Expression in Humans

Stephanie Lilja [1], Carina Stoll [1], Ulrike Krammer [1], Berit Hippe [1], Kalina Duszka [1], Tewodros Debebe [2], Ingrid Höfinger [3], Jürgen König [1], Angelika Pointner [1] and Alexander Haslberger [1,*]

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Functional Foods in Health and Disease

Home Editorial Team Iss

Home > Vol 10, No 10 (2020) > Lilja

Fasting and fasting mimetic supplementation address sirtuin expression, miRNA and microbiota composition

Stephanie Lilja, Hanna Bäck, Kalina Duszka, Berit Hippe, Lucia Suarez, Ingrid Höfinger, Tewodros Debebe, Jürgen König, Alexander Haslberger

Bioactive Compounds in Health and Disease 2021; 4(4): 45-62 BCHD Page 45 of 62

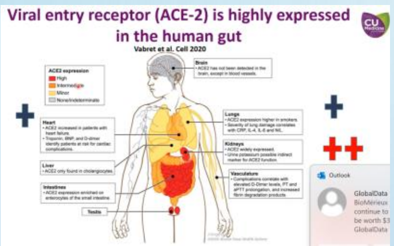
Research Article **Open Access**

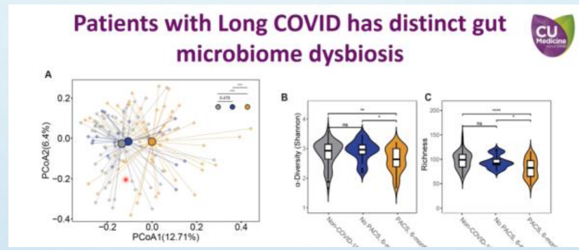
BCHD
Bioactive Compounds in Health and Disease

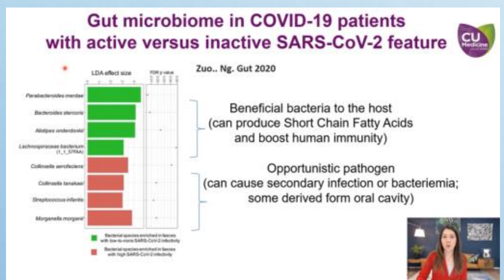
Increased Sirtuin expression, senescence regulating miRNAs, mtDNA, and bifidobacteria correlate with wellbeing and skin appearance after Sirtuin- activating drink

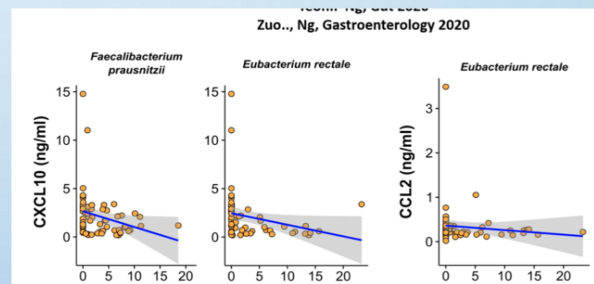
Stephanie Lilja, Hanna Bäck, Carinna Stoll, Anna Mayer, Angelika Pointner, Berit Hippe, Ulrike Krammer, Alexander G. Haslberger*

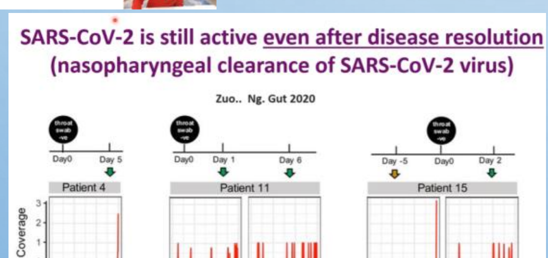
COVID, LONG COVID, MICROBIOTA AND EPIGENETICS





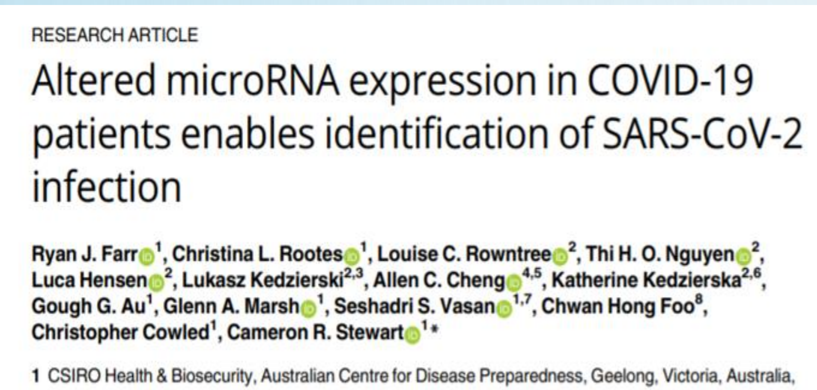






The Promise of Microbiota Modulation during COVID-19 Pandemic
Siew C Ng, *University of Hong Kong, Hong Kong*

3 MIRNAS MONITOR SARS-COV-2 INFECTION, MIRNAS MONITOR ANTI-VIRAL IMMUNE-RESPONSES

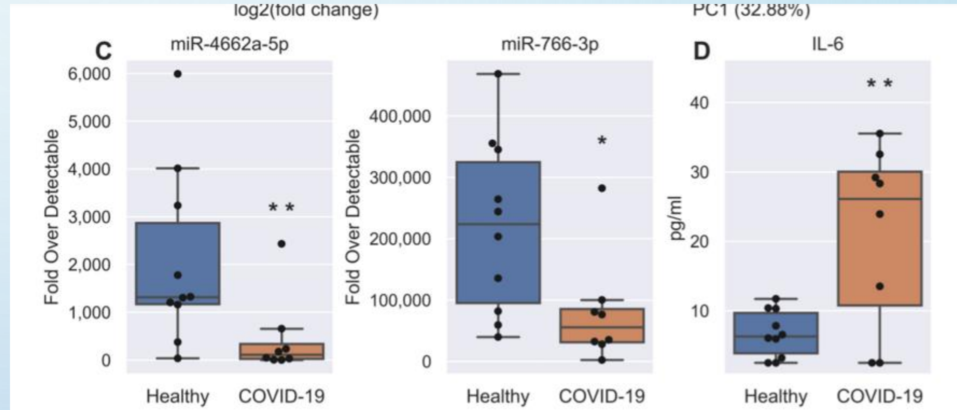


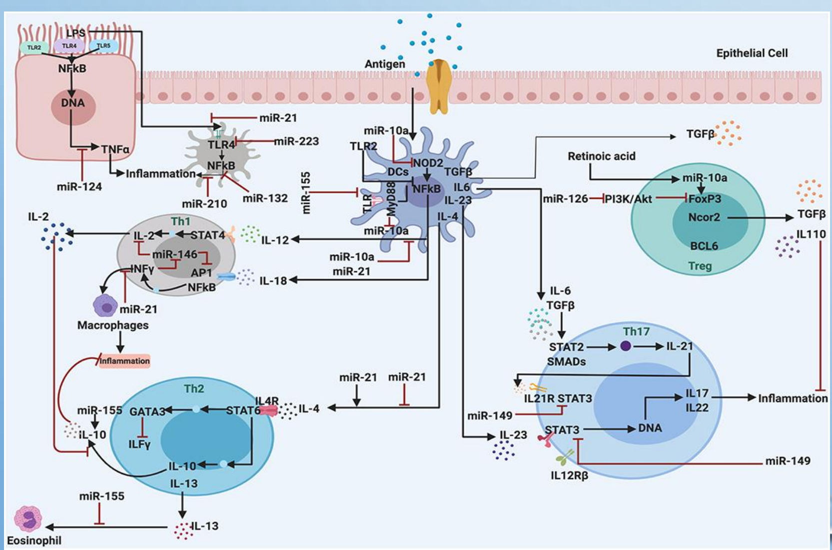
RESEARCH ARTICLE

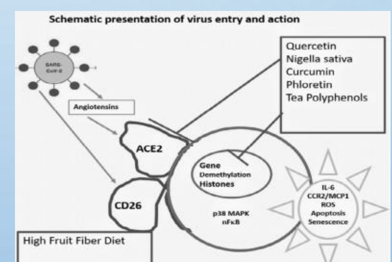
Altered microRNA expression in COVID-19 patients enables identification of SARS-CoV-2 infection

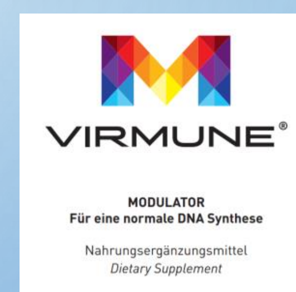
Ryan J. Farr[1], Christina L. Rootes[1], Louise C. Rowntree[2], Thi H. O. Nguyen[2], Luca Hensen[2], Lukasz Kedzierski[2,3], Allen C. Cheng[4,5], Katherine Kedzierska[2,6], Gough G. Au[1], Glenn A. Marsh[1], Seshadri S. Vasan[1,7], Chwan Hong Foo[8], Christopher Cowled[1], Cameron R. Stewart[1]*

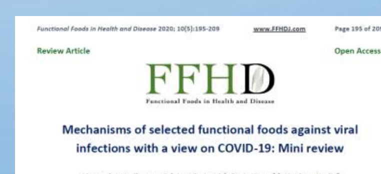
1 CSIRO Health & Biosecurity, Australian Centre for Disease Preparedness, Geelong, Victoria, Australia,











Functional Foods in Health and Disease 2020; 10(5):195-209 www.FFHDJ.com Page 195 of 209

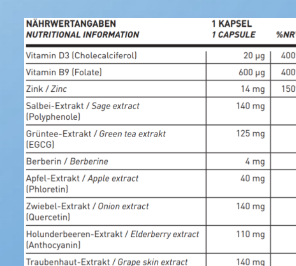
Review Article Open Access

FFHD

Functional Foods in Health and Disease

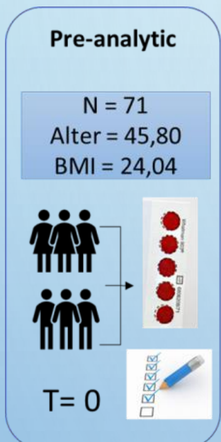
Mechanisms of selected functional foods against viral infections with a view on COVID-19: Mini review

Alexander Haslberger G.[1], Ursula Jacob[2], Berit Hippe[3,4], Heidrun Karlic[5]

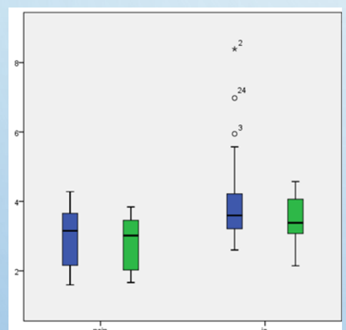


NÄHRWERTANGABEN *NUTRITIONAL INFORMATION*	1 KAPSEL *1 CAPSULE*	%NRV
Vitamin D3 (Cholecalciferol)	20 µg	400%
Vitamin B9 (Folate)	600 µg	400%
Zink / *Zinc*	14 mg	150%
Salbei-Extrakt / *Sage extract* (Polyphenole)	140 mg	
Grüntee-Extrakt / *Green tea extrakt* (EGCG)	125 mg	
Berberin / *Berberine*	4 mg	
Apfel-Extrakt / *Apple extract* (Phloretin)	40 mg	
Zwiebel-Extrakt / *Onion extract* (Quercetin)	140 mg	
Holunderbeeren-Extrakt / *Elderberry extract* (Anthocyanin)	110 mg	
Traubenhaut-Extrakt / *Grape skin extract* (Resveratrol)	140 mg	

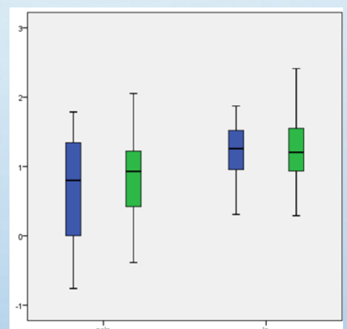
MODULATION OF I.S. -, AND VIRAL INFECTION RELEVANT MIRNAS AND INFLAMMATION RELATED NFKB AFTER 2 M



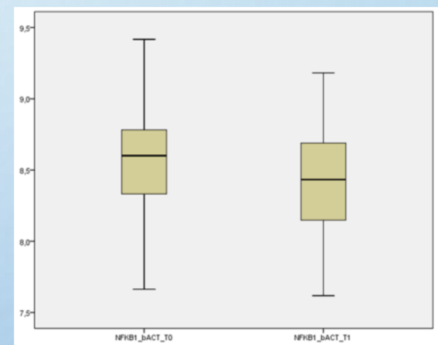
miRNA30e5
p= 0,01



miRNA101
p= 0,014



NFkb mRNA
p= ,050



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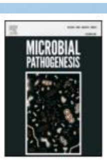

Gga-miR-30d regulates infectious bronchitis virus infection by targeting USP47 in HD11 cells

Hao Li, Jianan Li, Yaru Zhai, Lan Zhang, Pengfei Cui, Lan Feng, Wenjun Yan, Xue Fu, Yiming Tian, Hongning Wang, Xin Yang*
Key Laboratory of Bio-Resource and Eco-Environment of Ministry of Education, Animal Disease Prevention and Food Safety Key Laboratory of Sichuan Province, College of Life Sciences, Sichuan University, Chengdu, 610065, Sichuan, PR China

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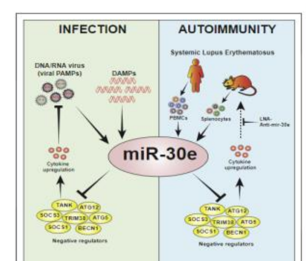
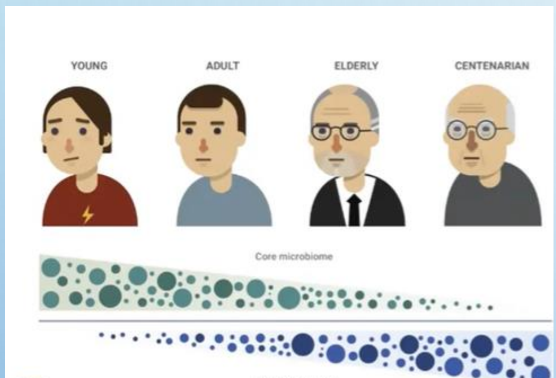
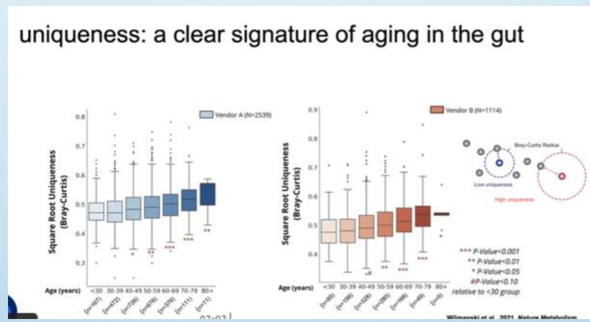
Article

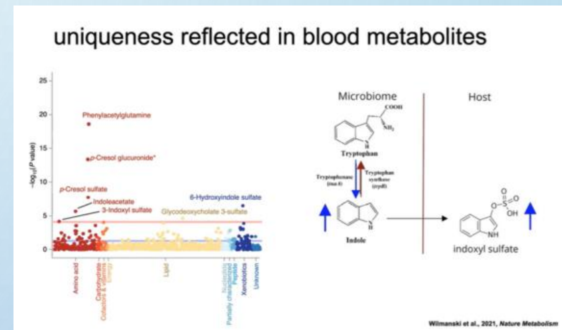
MicroRNA-30e-5p has an Integrated Role in the Regulation of the Innate Immune Response during Virus Infection and Systemic Lupus Erythematosus



AGING, BACTERIAL DIVERSITY, UNIQUENESS AND HEALTH





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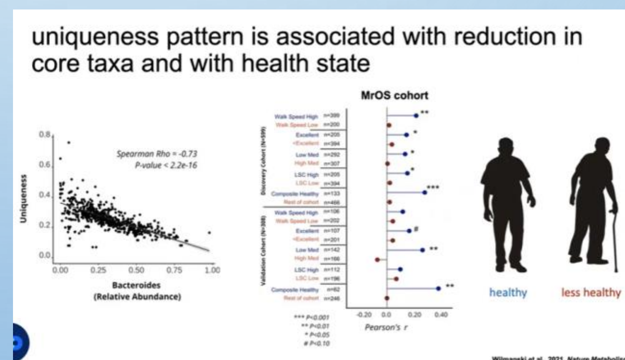
Combined PCR-DGGE fingerprinting and quantitative-PCR indicates shifts in fecal population sizes and diversity of *Bacteroides*, bifidobacteria and *Clostridium* cluster IV in institutionalized elderly

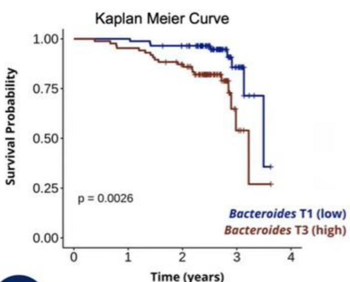
Jutta Zwielehner [a], Kathrin Liszt [a], Michael Handschur [a], Cornelia Lassl [a], Alexander Lapin [b], Alexander G. Haslberger [a,*]

[a] Department of Nutritional Sciences, University of Vienna, Austria
[b] Sozialmedizinisches Zentrum Sophienspital, 1070 Wein, Apollogasse 19, Austria



BACTEROIDETES DECIDE UPON HEALTHY AGING ?

Bacteroides abundance predicts survival in 4 year follow-up of MrOS subjects



Cox Proportional Hazards Regression models

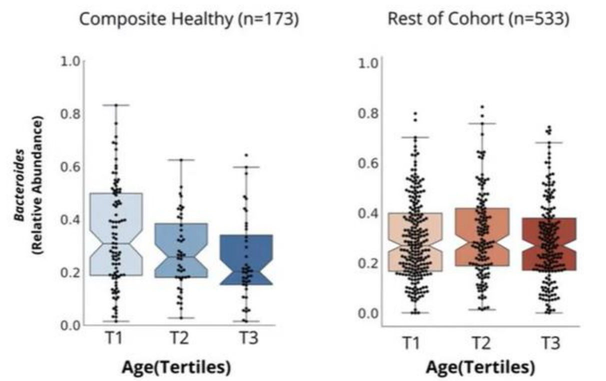
	Unadj. HR (95%CI)	Age, Clinical Site, & batch Adj. HR (95%CI)	Multivariable Adj. HR (95% CI)*	
Relative *Bacteroides* Abundance	1.21 (0.95-1.53)	1.30 (1.01-1.67)	1.28 (1.00-1.64)	Community dwelling participants all ages (N=706)
Uniqueness (Bray-Curtis)	1.17 (0.92-1.48)	1.1 (0.86-1.40)	1.11 (0.87-1.42)	
Relative *Bacteroides* Abundance	1.70 (1.25-2.31)	1.88 (1.35-2.62)	1.90 (1.37-2.64)	Community dwelling Participants 85+ years old only (N=257)
Uniqueness (Bray-Curtis)	0.76 (0.54-1.07)	0.69 (0.49-0.99)	0.70 (0.50-0.99)	

Wilmanski et al., 2021, *Nature Metabolism*

Bacteroides declines with extreme age in healthiest subjects, but not in the less healthy subjects

MrOS cohort

78-98 years old



Wilmanski et al., 2021, *Nature Metabolism*


Article | Published: 18 February 2021

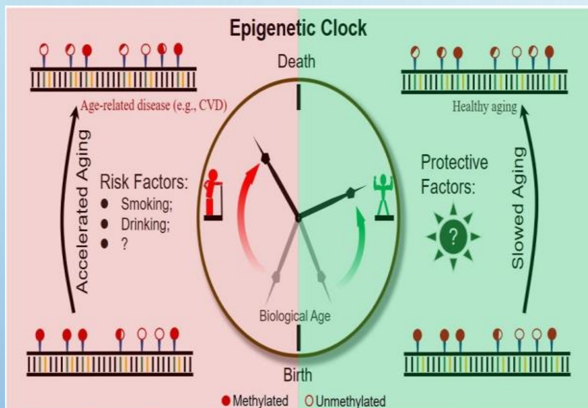
Gut microbiome pattern reflects healthy ageing and predicts survival in humans

Tomasz Wilmanski, Christian Diener, Noa Rappaport, Sushmita Patwardhan, Jack Wiedrick, Jodi Lapidus, John C. Earls, Anat Zimmer, Gustavo Glusman, Max Robinson, James T. Yurkovich, Deborah M. Kado, Jane A. Cauley, Joseph Zmuda, Nancy E. Lane, Andrew T. Magis, Jennifer C. Lovejoy, Leroy Hood, Sean M. Gibbons, Eric S. Orwoll & Nathan D. Price

Nature Metabolism 3, 274–286 (2021) | Cite this article

The identified microbiome pattern of healthy ageing is characterized by a **depletion of core** genera found across most humans, primarily Bacteroides. Retaining a high Bacteroides dominance into older age, or having a low gut microbiome uniqueness measure, predicts decreased survival in a 4-year follow-up

AGING AND DIETS ARE REFLECTED IN THE EPIGENETIC CLOCK, CPG- DNA METHYLATION; PERSONAL TYPES OF AGING CAN BE SEEN IN AGEOTYPES




www.aging-us.com AGING 2017, Vol. 9, No. 2

Research Paper

Epigenetic clock analysis of diet, exercise, education, and lifestyle factors

Austin Quach[1*], Morgan E. Levine[1*], Toshiko Tanaka[2*], Ake T. Lu[1], Brian H. Chen[2], Luigi Ferrucci[2], Beate Ritz[3,4], Stefania Bandinelli[5], Marian L. Neuhouser[6], Jeannette M. Beasley[7], Linda Snetselaar[8], Robert B. Wallace[8], Philip S. Tsao[9,10], Devin Absher[11], Themistocles L. Assimes[9], James D. Stewart[12], Yun Li[13,14], Lifang Hou[15,16], Andrea A. Baccarelli[17], Eric A. Whitsel[12,18], Steve Horvath[1,19]

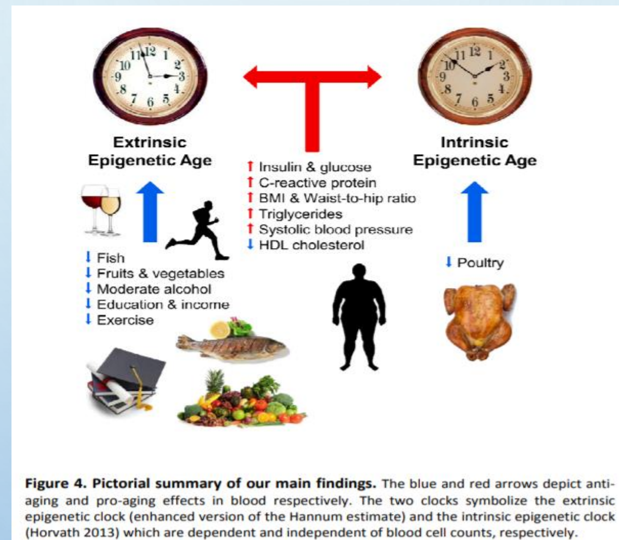
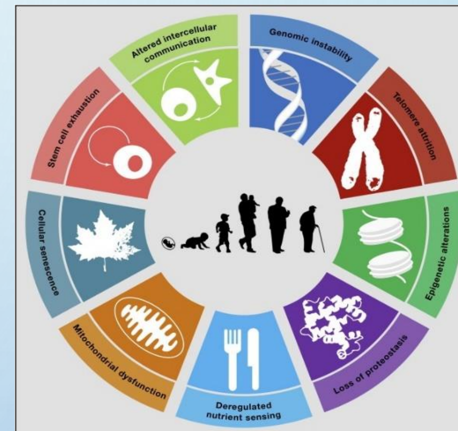


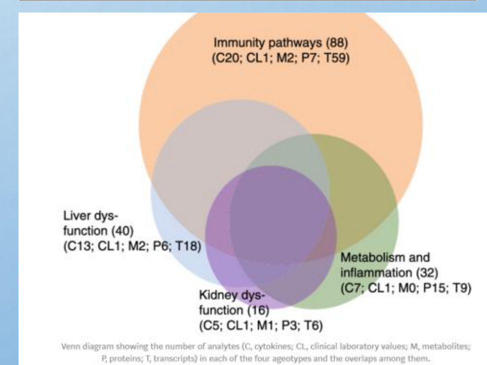
Figure 4. Pictorial summary of our main findings. The blue and red arrows depict anti-aging and pro-aging effects in blood respectively. The two clocks symbolize the extrinsic epigenetic clock (enhanced version of the Hannum estimate) and the intrinsic epigenetic clock (Horvath 2013) which are dependent and independent of blood cell counts, respectively.


nature medicine FOCUS | LETTERS
https://doi.org/10.1038/s41591-019-0719-5

Personal aging markers and ageotypes revealed by deep longitudinal profiling

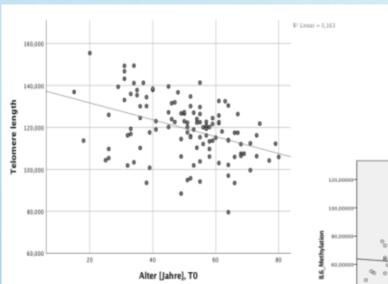
Sara Ahadi[1,2], Wenyu Zhou[1,2], Sophia Miryam Schüssler-Fiorenza Rose[1], M. Reza Sailani[1], Kévin Contrepois[1], Monika Avina[1], Melanie Ashland[1], Anne Brunet[1] and Michael Snyder[1*]



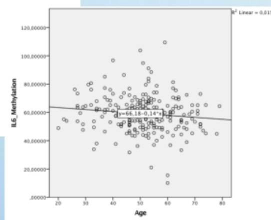


Venn diagram showing the number of analytes (C, cytokines; CL, clinical laboratory values; M, metabolites; P, proteins; T, transcripts) in each of the four ageotypes and the overlaps among them.

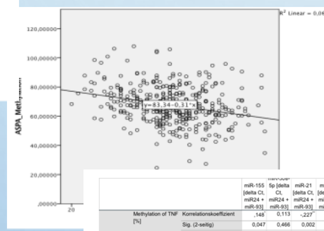
FACES OF PERSONAL AGING: CORRELATIONS OF AGE WITH TELOMERS, CPG-METHYLATION, INFLAMMATION, MIRNAS(N>500)



Correlation age with telomere-shortening



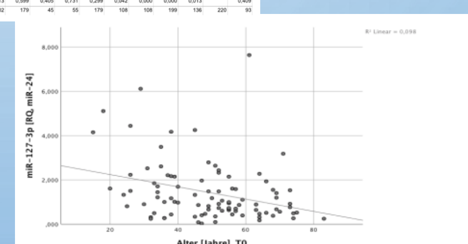
Correlation age with CPG methylation ASPA



Correlation age with CPG methylation IL6

		miR-155 [delta Ct, miR24 + miR-93]	miR-30e-5p [delta Ct, miR24 + miR-93]	miR-21 [delta Ct, miR24 + miR-93]	miR-19 [delta Ct, miR24 + miR-93]	miR-26b [delta Ct, miR24 + miR-93]	miR-106 [delta Ct, miR24 + miR-93]	miR-155 [delta Ct, miR24]	miR-30e-5p [delta Ct, miR24]	miR-127 [delta Ct, miR24]	miR-21 [delta Ct, miR24]	miR-151a [RQ, miR-24]	miR-328_3p [RQ, miR-24]	Methylation of TNF [%]	Methylation of IL-6 [%]	Methylation of Line-1 [%]	Interleukin 6 [Serum], T0
Methylation of TNF [%]	Korrelationskoeffizient	,148*	0,113	-,227**	-,217*	0,026	-0,066	,199**	0,148	-,378**	-,171*	-0,191	-,377**	1,000	-0,165	,265**	-,252*
	Sig. (2-seitig)	0,047	0,466	0,002	0,030	0,795	0,516	0,007	0,339	0,005	0,021	0,050	0,000		0,072	0,000	0,016
	N	182	44	182	100	99	100	182	44	54	182	106	106	203	120	199	91
Methylation of IL-6 [%]	Korrelationskoeffizient	0,020	-,439*	,232*	0,035	,258*	,368**	0,068	-,443*	0,146	,232*	-0,034	,288*	-0,165	1,000	,211*	0,100
	Sig. (2-seitig)	0,839	0,025	0,015	0,791	0,044	0,003	0,483	0,023	0,435	0,015	0,788	0,020	0,072		0,013	0,461
	N	109	26	109	61	61	61	109	26	31	109	65	65	120	138	136	56
Methylation of Line-1 [%]	Korrelationskoeffizient	-0,034	-0,183	-0,082	-0,175	0,031	0,101	-0,040	-0,127	-0,047	-0,078	-,196*	-,365**	,265**	,211*	1,000	0,087
	Sig. (2-seitig)	0,648	0,229	0,278	0,079	0,755	0,313	0,599	0,405	0,731	0,299	0,042	0,000	0,000	0,013		0,409
	N	179	45	179	102	101	102	179	45	55	179	108	108	199	136	220	93

Correlation age with miRNA-127

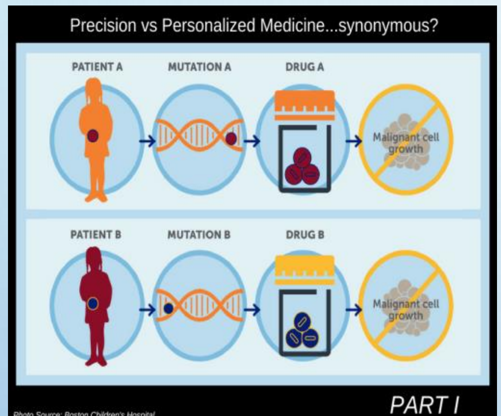


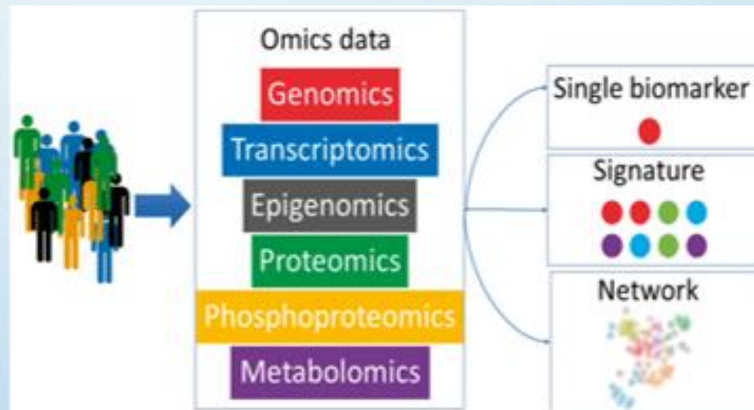
AGE DEPENDENT EPIGENETIC MARKERS: IN THE METABOLIC DISEASE GROUP (MD) CORRELATIONS ARE DISRUPTED, N>300

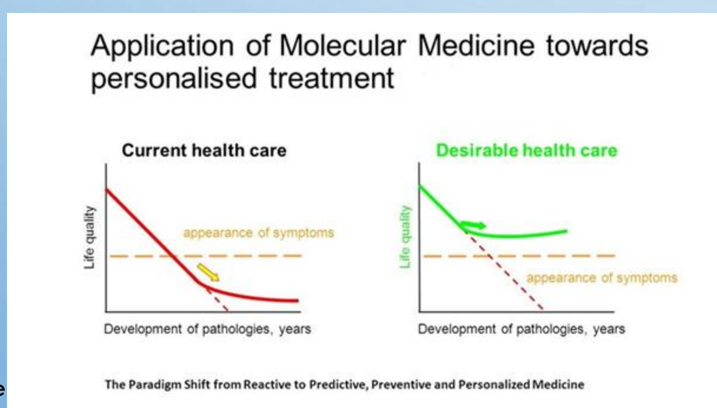
Marker	correlation analysis			age group comparison			direction
	All	HC	MD	all	HC	MD	
ASPA							--
IL6							--
TNF							--
miR-19b							--
miR-let-7a-5p							++
miR-877							++
miR-151a							++
miR-127							-+
miR-30e-5p							--
miR-150							
miR-21							
miR-101							

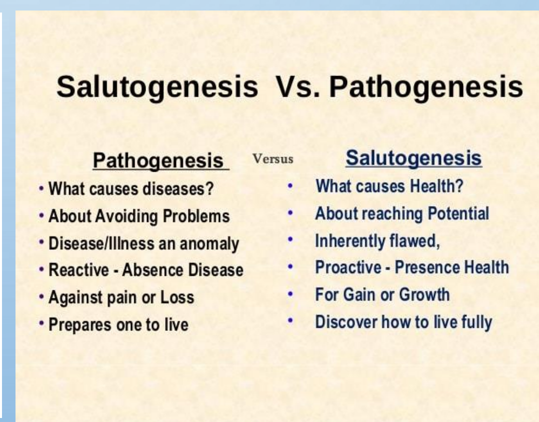
	correlation			Age Group			
	All	Healthy controls	Metabolic disorders	All	Healthy controls	Metabolic disorders	
ASPA	<0,001	<0,001	<0,001	p=0,000, korr. R2=0,185	0,001, korrR2 =0,207, überall 9<0,001, außer zwischen 40:59 zu 60-79:0,013	korrR2 = 0,140, 20-39:40-59: p = 0,041; 20-39:60-79: p=0,002	ANOVA Univariat
IL6	Trend (pearson: -0,127, p=0,079)	Pearson -0,73, p=0,412	Pearson -0,201, p=0,108	Sign. (20-39:60-79, p= 0,029) korr R2=0,026	Trend means	Trend means	ANOVA Univariat
TNF	Trend (spearman -0,054, p=0,384)	spearman -0,053, p= 0,491	pearson -0,105, p=318	Trend means	Trend means	Trend means	Kruskal Wallis
miR-19b	Linear regression: p= 0,018; (spearman -0,298**, p=0,005)	Linear regression: p= 0,027 (spearman -0,352** p=0,008)	spearman -0,174, p=0,341	Sign. 20-39:40-59 p=0,047	Trend p=0,06		Kruskal Wallis
miR-let-7a-5p	Linear regression: p= 0,028 (pearson 0,236*, p=0,028)	Linear regression: p= 0,001 (pearson 0,445** p=0,001)	pearson -0,085, p=0,613	Trend means	sign. (20-39:40-59: p=0,023); sign. (20-39:60-79: p=0,028) korrR2 = 0,162	sign. (20-39:40-59: p=0,027) korrR2 = 0,145	ANOVA Univariat
miR-877	Trend (spearman 0,207, p=0,058)	Trend Linear regression: 0,054 (spearman 0,288*, p=0,047)	spearman 0,105, p=0,544	X	Trend means	X	Kruskal Wallis
miR-151a	Trend (spearman 0,151, p=0,166)	Linear regression: [illegible] (spearman 0,295* p=0,039)	spearman 0,059, p=0,727	X	Trend means	X	Kruskal Wallis
miR-127	Trend (pearson 0,288, p=0,055)	pearson 0,196, p=0,336	Trend pearson 0,444, p=0,057	Sign. (40-59:60-79, p= 0,016) korr R2=0,133	Sign. (40-59:60-79 p=0,046) korrR2= 0,167	X	ANOVA Univariat
miR-30e-5p	Trend (spearman -0,246, p=0,163)	Trend spearman-0,436, p= 0,055	spearman 0,048 p =0,869	Trend means	Trend means	Trend means	Kruskal Wallis
miR-150	Trend (pearson -0,114, p=0,522)	pearson 0,082, p=0,731	pearson -0,416, p=0,139				
miR-21	Trend (pearson, -0,091, p=0,153)	pearson -0,094, p=0,233	pearson -0,098, p=377				
miR-101	Trend (pearson: -0,228, p=0,195)	Trend: pearson -0,317, p=0,173	pearson -0,074, p=0,803				

DISCUSSION: PERSONALISED (PRECISION) PREVENTION, MEDICINE, NUTRITION SALUTOGENESIS ?









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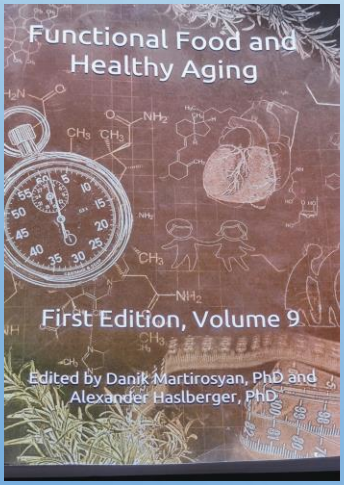
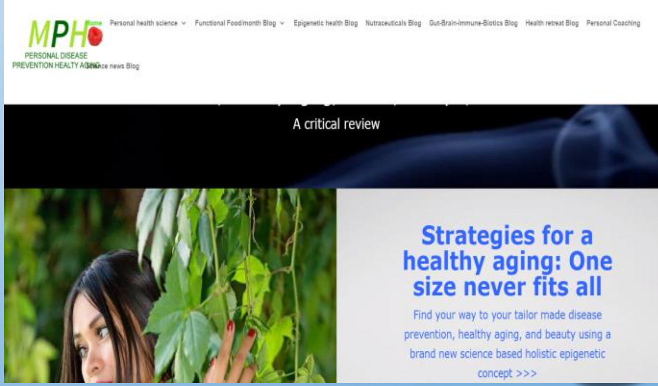


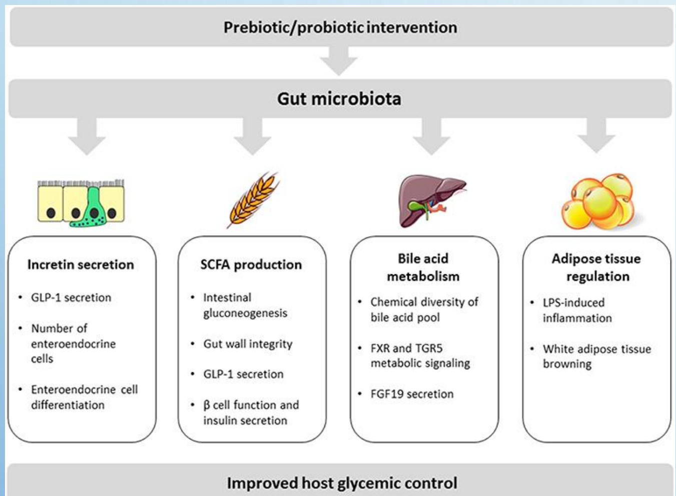
<u>Slides and materials:</u>

www.My-Personal.Health

Alexander.haslberger@univie.ac.at



MICROBIOTA AND METABOLIC DISORDER, INSULIN DEPENDENT DIABETES



Nutrients. 2021 Mar; 13(3): 836 PMCID: PMC7999932
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***Akkermansia*, a Possible Microbial Marker for Poor Glycemic Control in Qataris Children Consuming Arabic Diet—A Pilot Study on Pediatric T1DM in Qatar**

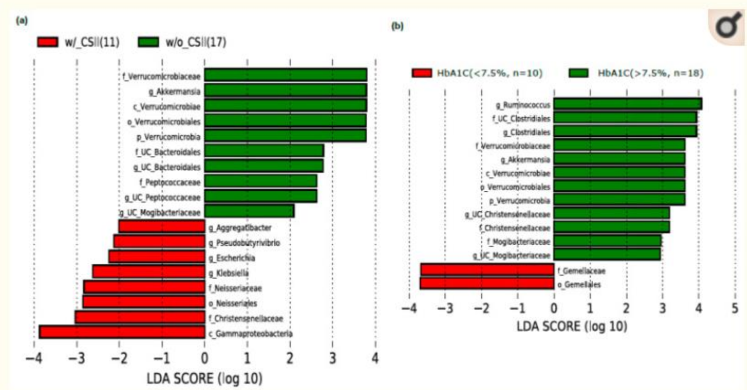

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Figure 2

Effect of CSII therapy and HbA1C level on the gut microbiome composition in the T1DM subjects. The LEfSe analysis showed (**a**) significant enrichment of *Akkermansia* in the subjects without CSII therapy and (**b**) significant enrichment of *Akkermansia* in the subjects with HbA1c level of more than >7.5% and <7.5% LDA cutoff value >2.0. Note: g_UC, genus_unclassified.