

Sportomics, Metabolic Health, and Utilization of Functional Medicine Testing

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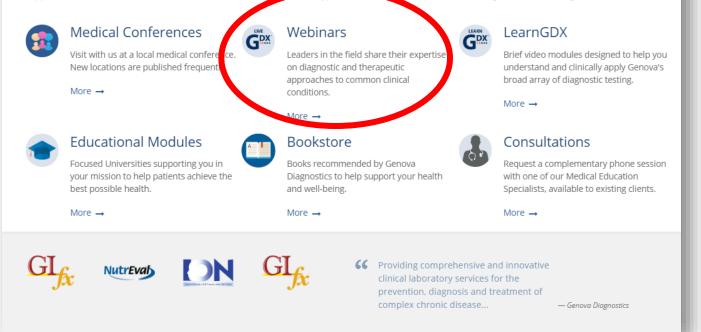
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Medical Education

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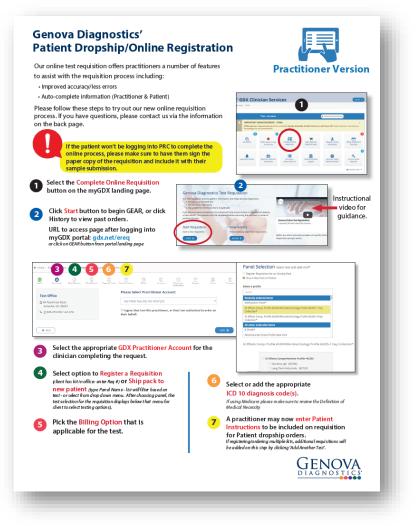
MY **GDX** – Order materials and get results





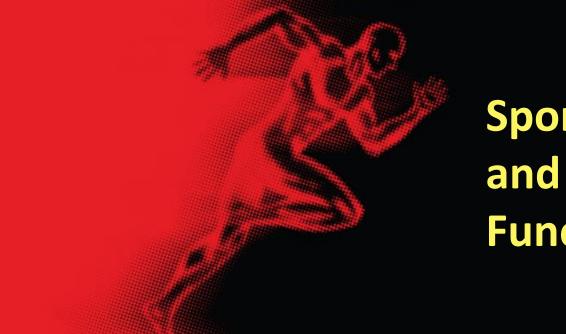
Patient Dropship/Online Registration

https://youtu.be/YHd0ID9GVG4









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Objectives for This Presentation

- At the conclusion of this program, participants will be able to:
 - Define Sportomics and its application to Exercise Performance and Metabolic Health
 - Identify and understand changes in metabolome and microbiome associated with exercise
 - Apply metabolomic and microbiome Functional Medicine testing to inform recommendations for improved exercise performance and metabolic health





OUTLINE

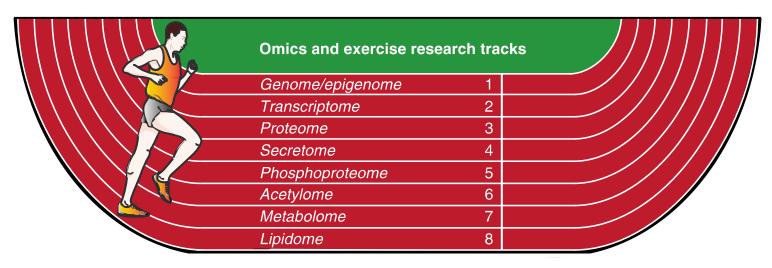
- Introduction to "SPORTOMICS"
- Exercise and Metabolome
- Exercise and Microbiome
- Sportomics and Exercise Performance

 Role of functional medicine testing
- Sportomics and Metabolic Health
 - Role of functional medicine testing



SPORTOMICS . . .

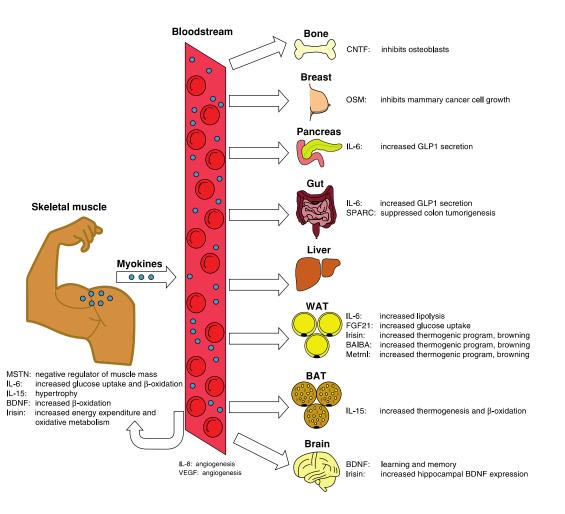
- Applies metabolomics to investigate the metabolic effects of physical exercise on individuals
- Works to advance knowledge in integrative physiology and the systems biology of movement with a goal to translate markers associated with metabolic challenges of training, or competition, to similar stresses of disease settings





SPORTOMICS: CLINCIAL RELEVANCE

- EXERCISE = Medicine
 - With a great "benefit to risk" profile
 - Three major clinically relevant questions:
 - What is "TIPPING POINT"?
 - Where/When/How does exercise become less health promoting?
 - Who are the "RESPONDERS" vs. "NON-RESPONDERS"?
 - How do you make a "NON-RESPONDER" a "RESPONDER"?
- EXERCISE = INVESTIGATIVE TOOL as a STRESSOR to systems biology and integrative physiology

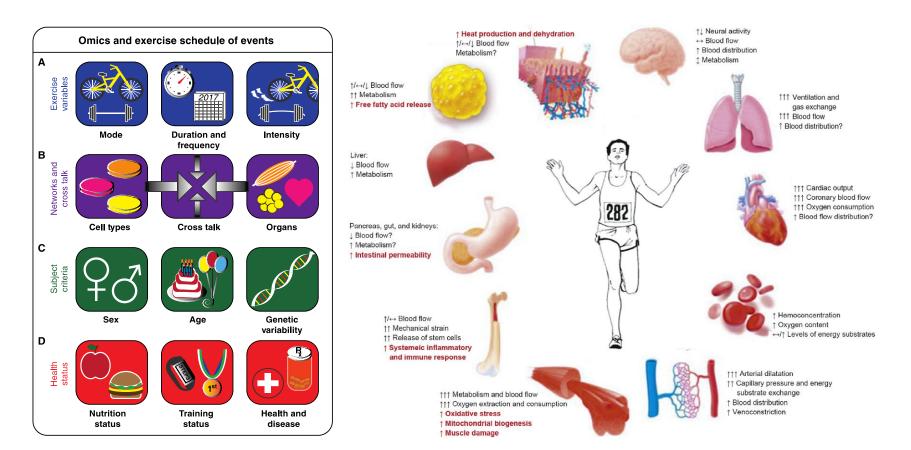




SPORTOMICS

MULTI-VARIATE

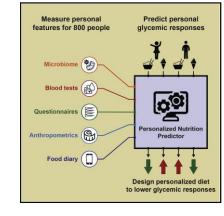
SYSTEMS BIOLOGY

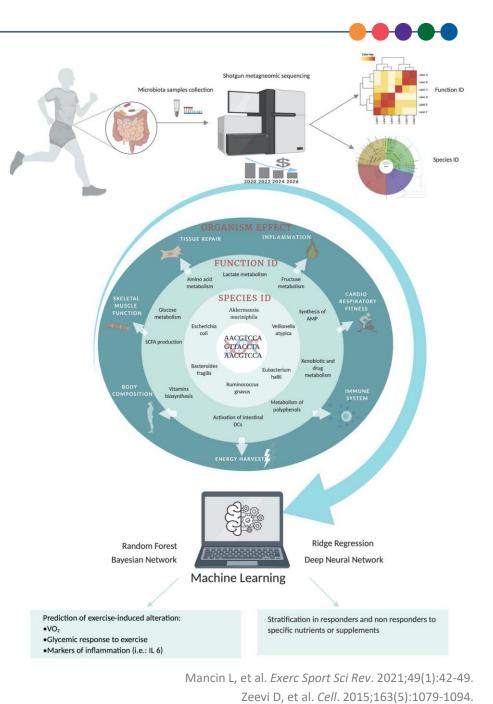




SPORTOMICS

- Must go beyond correlation/association studies
- Meta-omics and computational tools
- Potential for machine learning to predict exerciseinduce alteration and performance measures to distinguish responders and non responders
 - by Zeevi et al

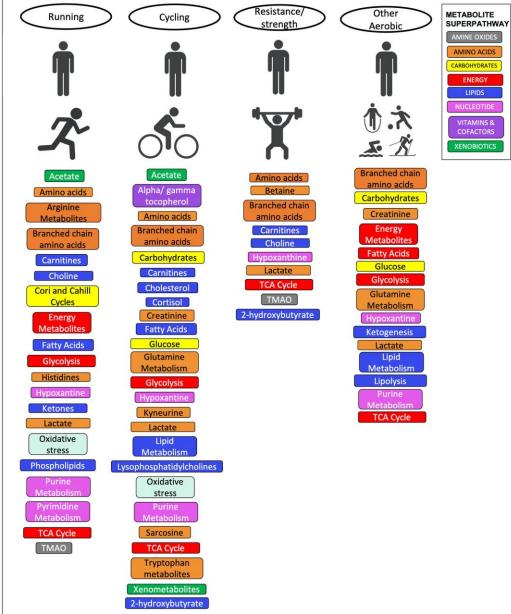






SPORTOMICS: METABOLOME

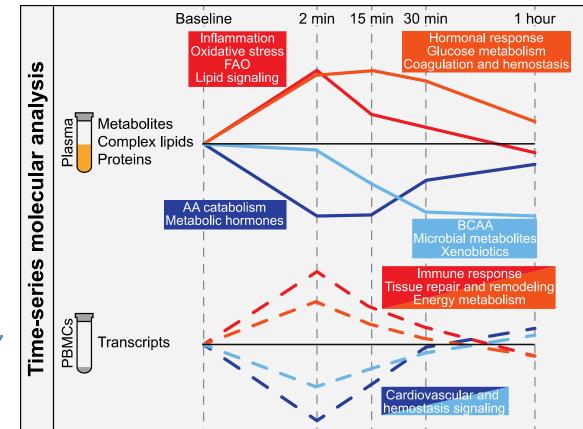
- SUMMARY:
 - Substantial heterogeneity of studies
 - Volume was biggest driver of changes
 - Generally short-lived response to acute exercise
 - However, changes are apparent in consistent movers
 - Multifactorial dose response relationship





SPORTOMICS: METABOLOME

- ACUTE EXERCISE:
 - Responses resolved minutes to hours later
 - Greater changes in less trained in response to marathon ¹
 - INCREASE:
 - Lactate, pyruvate, TCA intermediates, fatty acids, acyl-carnitines, ketone bodies ²
 - DECREASE:
 - Bile acids ²

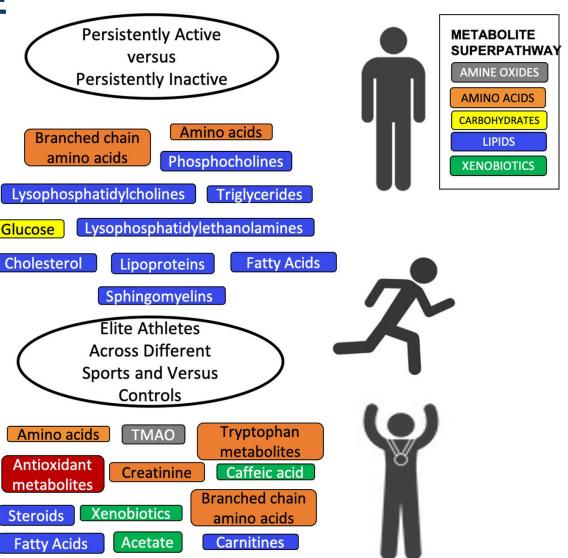


 Kelly RS, et al. *Biochim Biophys Acta Mol Basis Dis*. 2020;1866(12):1-17.
 Schranner D, et al. *Sports Med Open*. 2020;6(1):11. Contrepois K, et al. *Cell*. 2020;181(5):1112-1130.



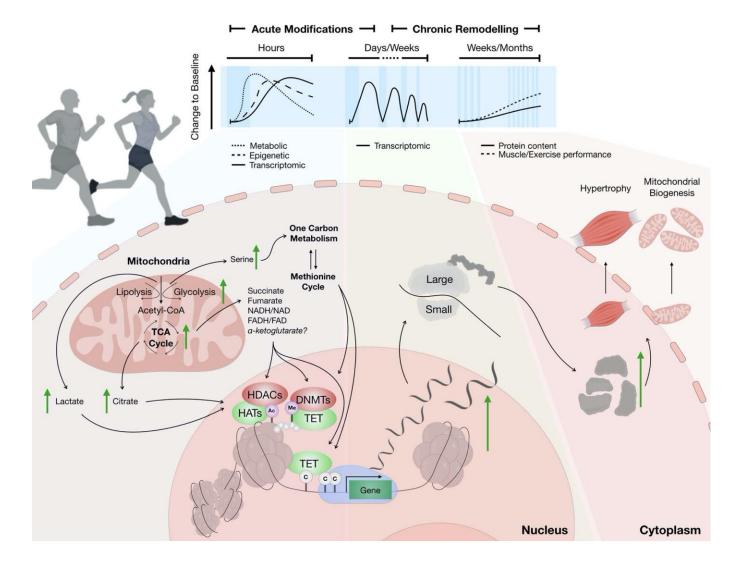
SPORTOMICS: METABOLOME & PERFORMANCE

- <u>CHRONIC EXERCISE</u>:
 - "Coherently healthier metabolic profile"
 - Lower amino acids (especially isoleucine)
 - Changes in several lipid metabolites
 - − Saturated \rightarrow polyunsaturated profile
 - Lower VLDL & TG and Higher HDL
 - Difference in intermediary metabolism, fuel substrate utilization, glucose transport, fatty acid oxidation, oxidative stress, steroid biosynthesis, insulin signaling
 - Epigenomic, Transcriptomic, & Proteomic studies are fewer but confirm gene changes





SPORTOMICS: METABOLOME





SPORTOMICS: METABOLOME & PERFORMANCE & FUNCTIONAL TESTING

- 38yo year-round athlete
- In winter with significant XC and downhill skiing routine

Amino Acid		Refere	ence Range
Arginine	8		3-43
Histidine	212		124-894
Isoleucine	7		3-28
Leucine	15		4-46
Lysine	30		11-175
Methionine	4		2-18
Phenylalanine	21		8-71
Taurine		590	21-424
Threonine	51		17-135
Tryptophan	23		5-53
Valine	19		7-49
Nonesse	ential Protein A	mino A	cids
Amino Acid		Refere	ence Range
Alanine	17		63-356
Asparagine	38		25-166

Alanine	17	63-356
Asparagine	38	25-166
Aspartic Acid	đ	<= 14
Cysteine	21	8-74
Cystine	21	10-104
γ-Aminobutyric Acid	1	<= 5
Glutamic Acid	10	4-27
Glutamine	153	110-632
Proline	2	1-13
Tyrosine	27	11-135

Creatinine Concentration Reference Range 12.6 Creatinine + 3.1-19.5 mmol/L

Interm	ediary Metak	olites	
B Vitamin Markers		Refer	ence Ran
α-Aminoadipic Acid	12		2-47
α-Amino-N-butyric Acid	10		2-25
β-Aminoisobutyric Acid		217) 11-160
Cystathionine	18		2-68
3-Methylhistidine	95		44-281
Jrea Cycle Markers	3		
Ottom Him -			0000

Citru ll ine	2.3	0.6-3.9
Ornithine	5	2-21
Urea •	236	168-465 mmol/g creatinine

Range

Glycine/Serine Metabolites

Glycine	139	95-683
Serine	140	40-163
Ethanolamine	182	50-235
Phosphoethanolamine	6	1-13
Phosphoserine	a	3-13
Sarcosine	0.5	<= 1.1

Dietary Peptide Related Markers

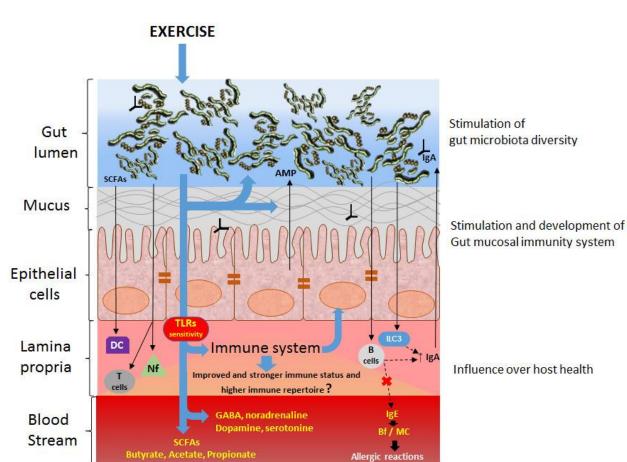
	ł	Reference Range
Anserine (dipeptide)	15.5	0.4-105.1
Carnosine (dipeptide)	8	1-28
1-Methylhistidine		1,377 38-988
β-Alanine	13	<= 22





SPORTOMICS: MICROBIOME

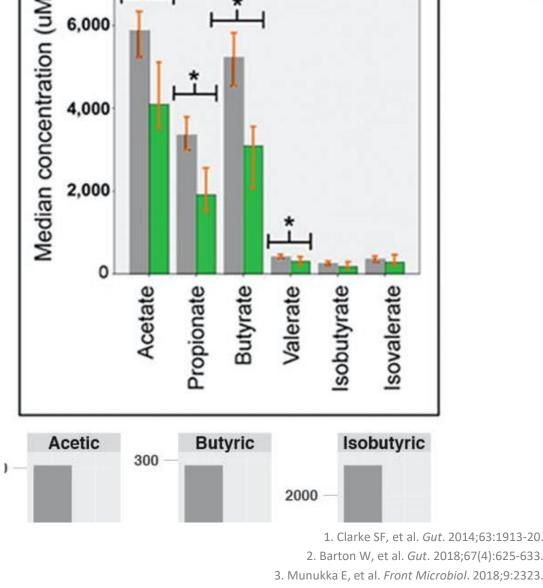
- 2014: 1st report of exercise increasing gut microbial diversity in humans
- Low BMI control and athletes with high BMI significantly higher proportions of Akkermansia muciniphila
- Greater microbiome diversity
 - HOWEVER, suggestion that exercise and protein intake were drivers of diversity



GENOVA

SPORTOMICS: MICROBIOME

- Greater diversity compared to nonathletes ^{1,2}
- Greater growth of certain species such as *Akkermansia muciniphila* ^{1,3,4}
- Relative increase in SCFA ^{2,5}
- Direct association between VO2max and F/B ratio ⁶



Bressa C, et al. *PLoS One*. 2017;12(2):e0171352.
 Estaki M, et al. *Microbiome*. 2016;4(1):42.

6. Durk RP, et al. Int J Sport Nutr Exerc Metab. 2019;29(3):249-53.



Transit Time

a- Diversity

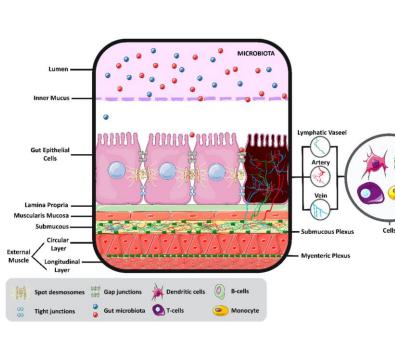
Butyrate Secretion

Tissue Permeabillity

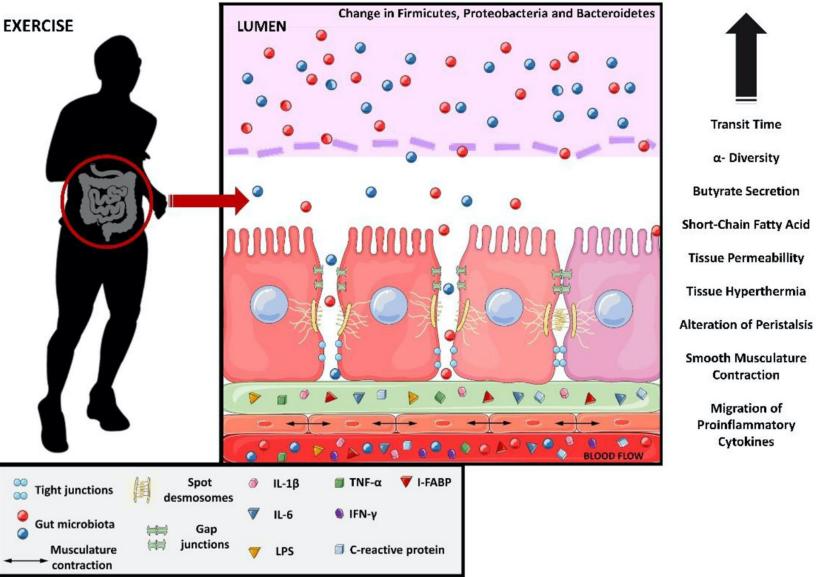
Contraction

Migration of Proinflammatory Cytokines

SPORTOMICS: MICROBIOME

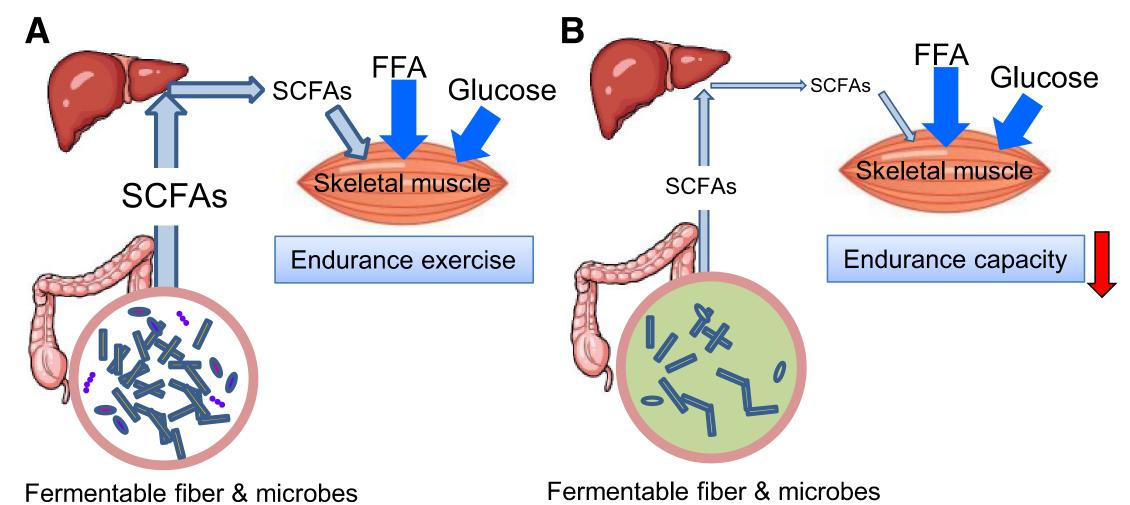




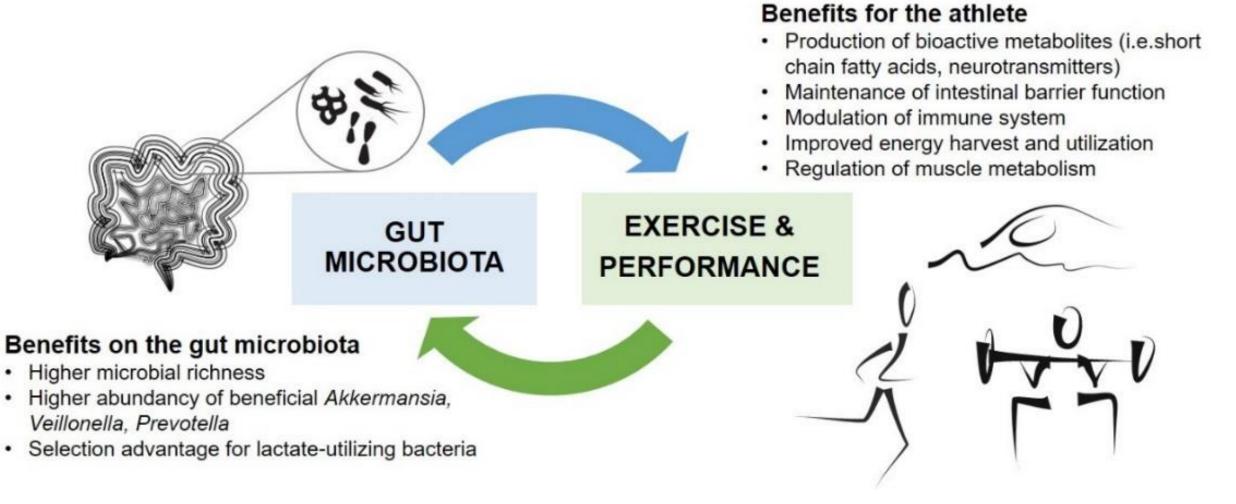


Ribeiro FM, et al. Front Nutr. 2021;8:627289.



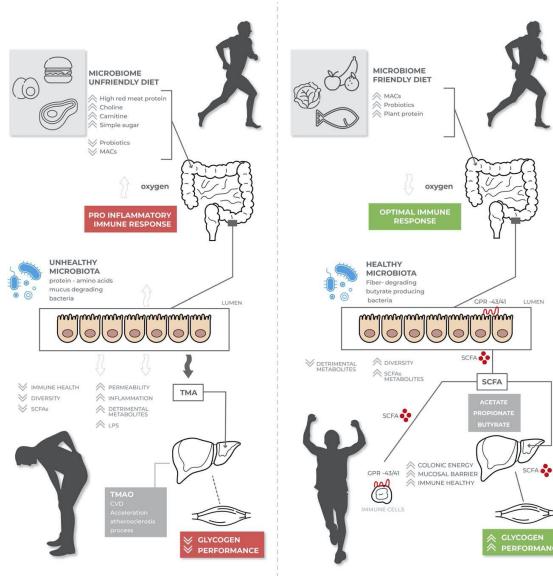




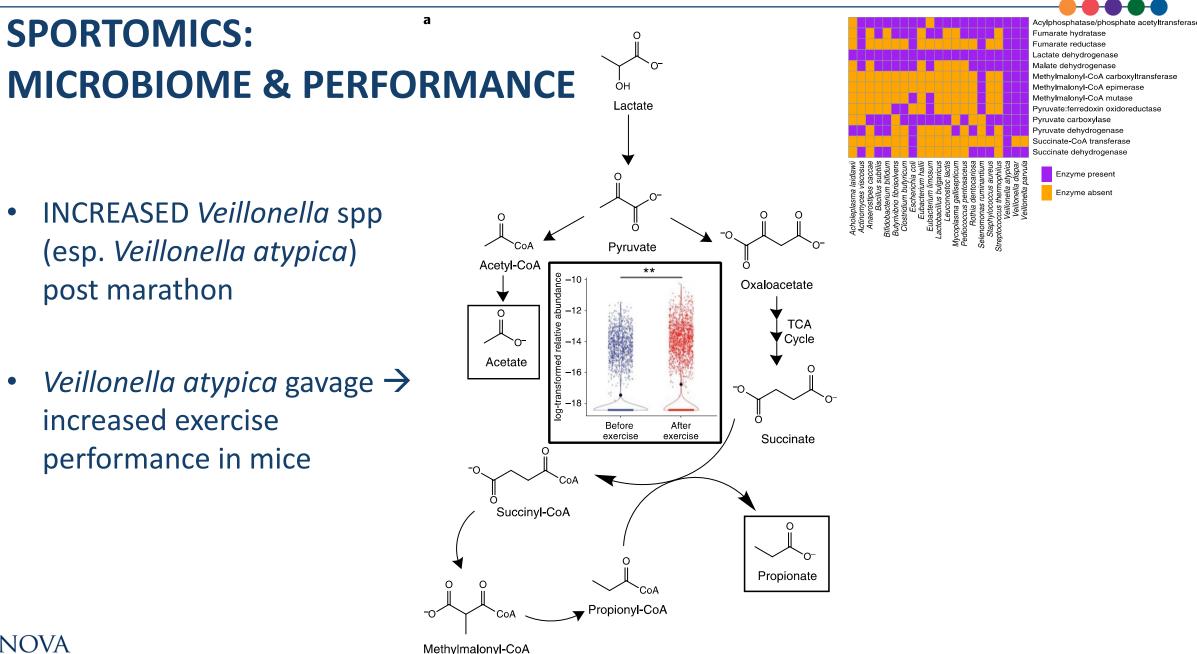








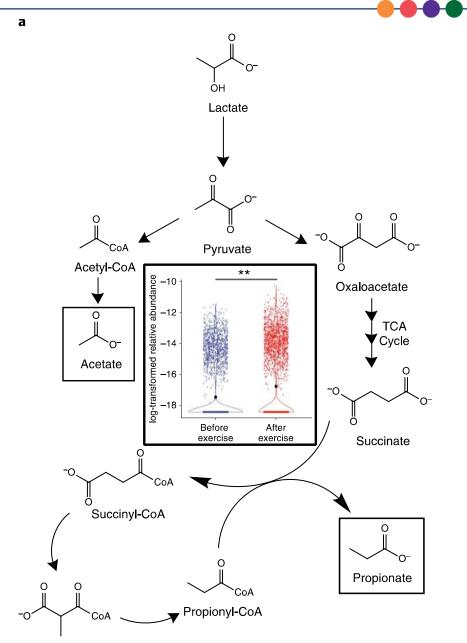






Scheiman J, et al. Nat Med. 2019;25(7):1104-9.

- IMPROVED EXERCISE PERFORMANCE in mice with *Veillonella atypica* gavage
 - PROPOSED MECHANISM OF ACTION:
 - LACTATE production and conversion into propionate

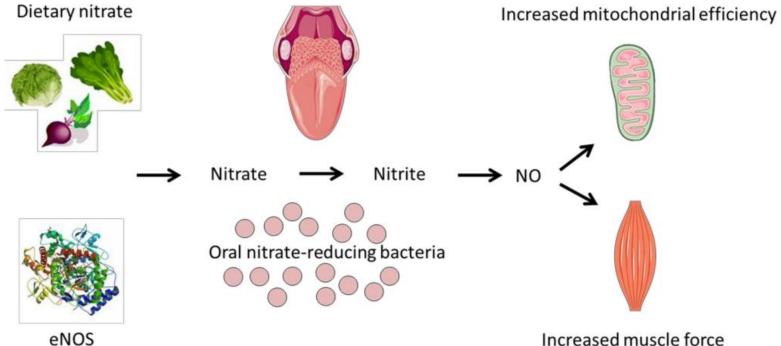




Methylmalonyl-CoA



- *Veillonella* spp. = oral nitrate-reducing bacteria
 - ADDITIONAL PROPOSED **MECHANISM OF ACTION:** Nitric oxide (NO) production by the oral microbiome



eNOS



SPORTOMICS: MICROBIOME & PERFORMANCE & FUNCTIONAL TESTING

Vethodology: DNA by PCR

emmeneel Restaria (ROR)	Result		
ommensal Bacteria (PCR)	CFU/g stool		nce Rang U/g stool
Bacteroidetes Phylum			
Bacteroides-Prevotella group	2.4 E8	→ + → + → 3.4E6	3-1.5 E9
Bacteroides vulgatus	1.2 E9	<=2.2	E9
Barnesiella spp.	3.6 E7	<=1.6	E8
Odoribacter spp.	7.1 E7	<=8.0	E7
Prevotella spp.	1.4 E8 H	⊢ + + + → 1.4E5	5-1.6 E7
Firmicutes Phylum			
Anaerotruncus colihominis	3.4 E7 H	← ← ← ← ← ← ← ← ← ← ← ← ← ← ← ← ← ← ←	E7
Butyrivibrio crossotus	5.0 E7 H	5.5E3	3-5.9 E5
Clostridium spp.	ICEB 2.1E8	► + + + + 1.7E8	8-1.5 E10
Coprococcus eutactus	1.0 E8	<=1.2	E8
Faecalibacterium prausnitzii	7.5 E8	5.8 E7	-4.7 E9
Lactobacillus spp.	1.6 E8	8.3E6	-5.2 E9
Pseudoflavonifractor spp.	3.0 E8 H	4.2E5	-1.3 E8
Roseburia spp. Lactate DEGRA	DER7.6E7 L	← · · · · · · · · · · · · · · · · · · ·	-1.2 E10
Ruminococcus spp.	1.9 E9 H	9.5 E7	′-1.6 E9
Veillonella spp.	1.5 E8 H	<u> </u>	-5.5 E7
Actinobacteria Phylum			
Bifidobacterium spp.	1.5 E8	← + + + + + < <=6.4	E9
Bifidobacterium longum	1.4 E8	<=7.2	E8
Collinsella aerofaciens	5.1 E8	⊢ ⊢ ⊢ ⊢ ⊢ ⊢ ⊢ ⊢ − − − 1.4E7	′-1.9 E9
Proteobacteria Phylum			
Desulfovibrio piger	8.7 E7 H	<=1.8	E7
Escherichia coli	1.3 E8 H	9.0E4	-4.6 E7
Oxalobacter formigenes	5.0 E7 H	<=1.5	E7
Euryarchaeota Phylum			
Methanobrevibacter smithii	1.4 E8 H		E7
Fusobacteria Phylum			
Fusobacterium spp.	2.3 E7 H	<=2.4	E5
Verrucomicrobia Phylum			
Akkermansia muciniphila	3.1 E7	>=1.2	E6
Firmicutes/Bacteroidetes Ratio			
Firmicutes/Bacteroidetes Ratio	11 L	12-62	_



SPORTOMICS: MICROBIOME & PERFORMANCE & FUNCTIONAL TESTING

 40yo with chronic fatigue syndrome, pain amplification syndrome and exercise intolerance – previously failed graded exercise program

			1
	Gut Mic	crobiome Metabolites	
Metabolic			
Short-Chain Fatty Acids (SCFA) (Total*) (Acetate, n-Butyrate, Propionate)	3.1 L	+ + + + +	>=23.3 micromol/g
n-Butyrate Concentration	1.2 L	+ + + + +	>=3.6 micromol/g
n-Butyrate %	38.7 H	+ + + +	11.8-33.3 %
Acetate %	<dl l<="" td=""><td>• • • • •</td><td>48.1-69.2 %</td></dl>	• • • • •	48.1-69.2 %
Propionate %	60.8 H	F F F F	<=29.3 %
	1,063		368-6,266 U/g

Bacteroidetes Phylum Bacteroides Prevotella group Bacteroides vulgatus 2. Barnesiella spp. 1. Odoribacter spp. 7. Prevotella spp. 4. Firmicutes Phylum Anaerotruncus collihominis 9. Butyrivibrio crossotus Clostridium spp. 6. Coprococcus eutactus 3. Faecalibacterium prausnitzii 6. Lactobacillus spp. 1. Pseudoflavonifractor spp. 2. Roseburia spp.	Result FU/g stool 3E8 4E7 2E7 2E6 8E6 4E5 4E5 4E5 6E8 3E7 3E7				IDISTRIE 3rd	UTION 4th	Sth Sth Sth Sth Sth Sth Sth Sth Sth Sth		Reference Rang CFU/g stool 3.4E6-1.5E9 <=2.2E9 <=1.6E8 <=8.0E7 1.4E5-1.6E7 <=3.2E7 5.5E3-5.9E5 1.7E8-1.5E10 <=1.2E8 5.8E7-4.7E9 8.3E6-5.2E9
Bacteroidetes Phylum Bacteroides Prevotella group 1. Bacteroides vulgatus 2. Barnesiella spp. 1. Odoribacter spp. 7. Prevotella spp. 4. Firmicutes Phylum 9. Butyrivibrio crossotus 9. Clostridium spp. 6. Coprococcus eutactus 3. Faecalibacterium prausnitzii 6. Lactobacillus spp. 1. Pseudoflavonifractor spp. 2. Roseburia spp. 3.	.3E8 .4E7 .2E7 .2E6 .8E6 .4E5 .0L L .8E8 .8E5 .0E7 .6E8 .3E7				•				3.4E6-1.5E9 <=2.2E9 <=1.6E8 <=8.0E7 1.4E5-1.6E7 <=3.2E7 5.5E3-5.9E5 1.7E8-1.5E10 <=1.2E8 5.8E7-4.7E9
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	.3E7 L				•	I	+	-	4.2E5-1.3E8
		+					+		1.3E8-1.2E10
Ruminococcus spp. 5.	.2E7 L	•					+	-	9.5E7-1.6E9
Veillonella spp.	<dl l<="" td=""><td>•</td><td></td><td></td><td></td><td>I</td><td>+</td><td>-</td><td>1.2E5-5.5E7</td></dl>	•				I	+	-	1.2E5-5.5E7
Actinobacteria Phylum									
<i>Bifidobacterium</i> spp. 2.	.1E7	+				I	+	-	<=6.4E9
Bifidobacterium longum	<dl< td=""><td>•</td><td></td><td></td><td></td><td> </td><td>1</td><td>-</td><td><=7.2E8</td></dl<>	•					1	-	<=7.2E8
Collinsella aerofaciens 1.	.7E8			♦		I	+	-	1.4E7-1.9E9
Proteobacteria Phylum									
Desulfovibrio piger 8.	.6E5	-					•	-	<=1.8E7
Escherichia coli	<dl l<="" td=""><td>•</td><td></td><td></td><td></td><td>I</td><td>+</td><td>-</td><td>9.0E4-4.6E7</td></dl>	•				I	+	-	9.0E4-4.6E7
Oxalobacter formigenes 1.	.9E6	ŀ				⊢ ◆	+	-	<=1.5E7
Euryarchaeota Phylum									
Methanobrevibacter smithii 6.	.4E6					+ +		-	<=8.6E7
Fusobacteria Phylum									
<i>Fusobacterium</i> spp. 1.	.1E4				•		1	-	<=2.4E5
Verrucomicrobia Phylum		l						_	
Akkermansia muciniphila 1.	.4E7		-	•		+		-	>=1.2E6

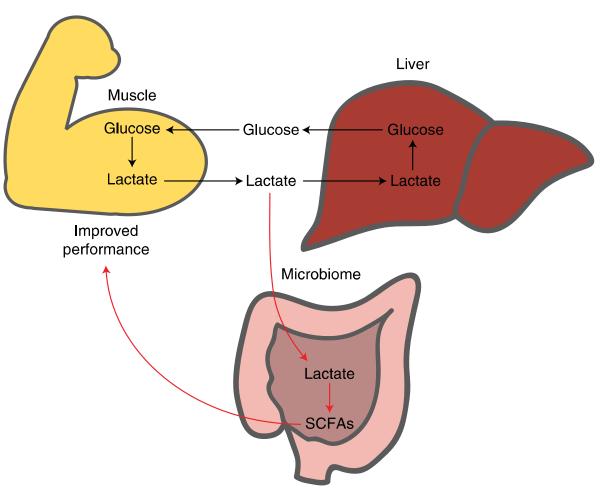


- LOW cardiorespiratory fitness independent predictor of cardiometabolic disease and mortality¹
- Exercise capacity more powerful predictor of mortality from cardiometabolic disease than other established risk factors²
- VO2max is highly correlated with skeletal muscle mitochondrial capacity ³



Wei M et al. JAMA. 1999;282(16):1547-53.
 Myers J, et al. N Engl J Med. 2002:346(11):793-801.
 van der Zwaard S, et al. J Appl Physiol. 2016;121(3):636-45.

- METABOLIC FLEXIBILITY
 - Ability to appropriately adjust substrate oxidation relative to substrate availability
- LACTATE SHUTTLE:
 - Lactate = gluconeogenic precursor
 - Increased with increased energy expenditure or reduction in energy from aerobic oxidation





×2

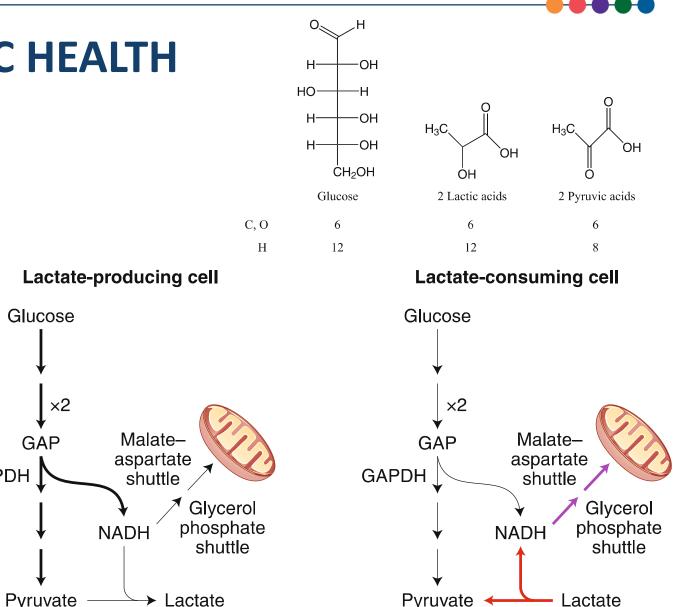
LDH

GAP

GAPDH

LACTATE

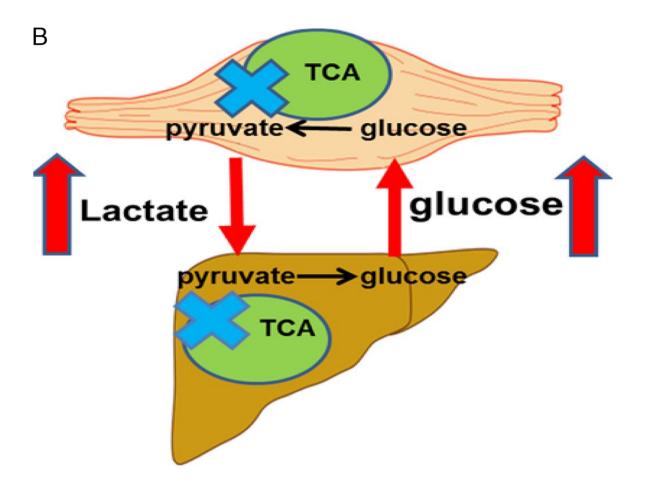
- Glucose as specific fuel and lactate as universal fuel¹
 - Lactate as a substrate for generating fuel
 - Radiolabeled lactate \rightarrow labeling of TCA intermediates greater than radiolabeled glucose²





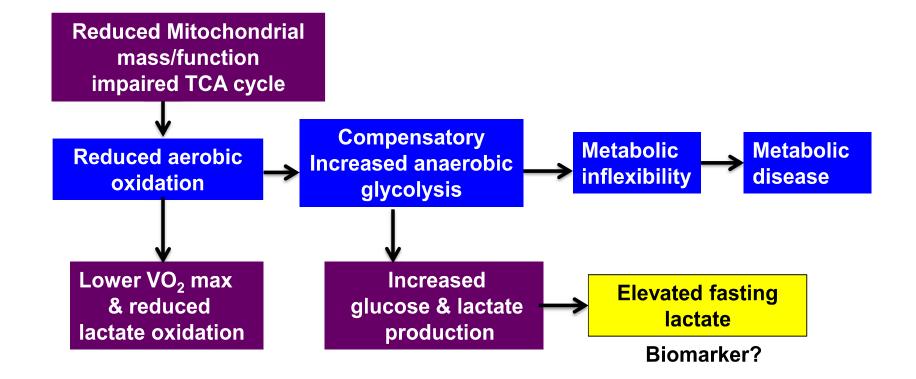
LDH

- Metabolic Disease
- Obesity
- Insulin Resistance
 - With OBESITY/INCREASED VAT:
 - Skeletal muscle tissue minimally increases glucose oxidation with insulin and preferentially partitions it with net lactate release ¹
 - "VISCIOUS CORI CYCLE"²
 - Due to impaired pyruvate oxidation





- Metabolic Disease
- Obesity
- Insulin Resistance





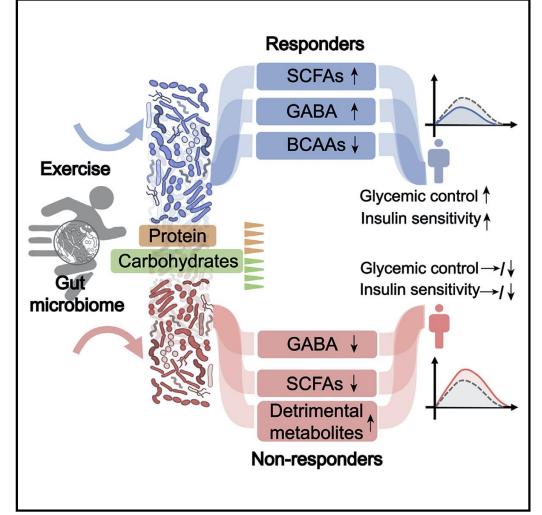


SPORTOMICS: METABOLIC HEALTH & FUNCTIONAL TESTING

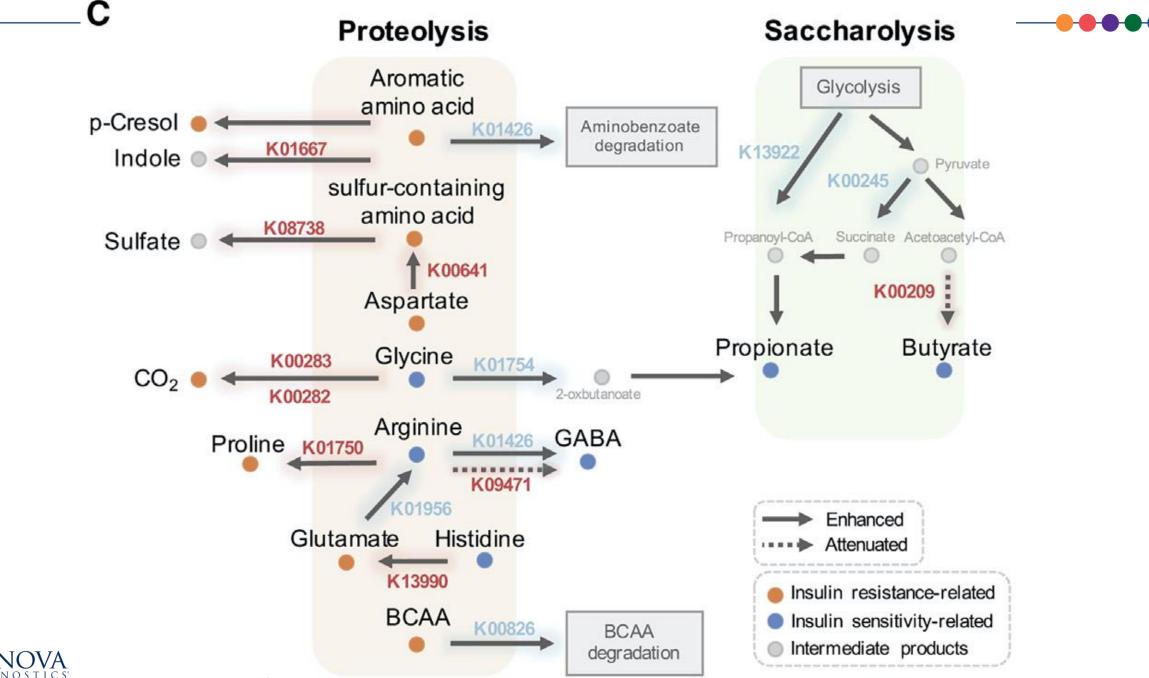
- EVIDENCE of "Vicious Cori Cycle" and impaired metabolic health
 - ELEVATED Lactic Acid (especially relative to Pyruvic Acid)
 - LOW Citric acid
 - Often seen in severe obesity
 - LOWER TCA intermediates ¹
 - Labeled by some as "hypometabolic state" or "mitochondria retraction"
 - +/- HIGHER Malic Acid/Succinic Acid



- EXERCISE & DIABETES PREVENTION
 - Overweight, prediabetic treatment-naïve males
 - Identified responders to exercise intervention (improved glucose metabolism & insulin resistance)
 - Increased capacity for increased SCFA synthesis
 - Increased capacity for BCAA catabolism
 - FMT of responders improved mice response to exercise
 - Through machine learning then predicted glycemic response to exercise in additional 30 subjects





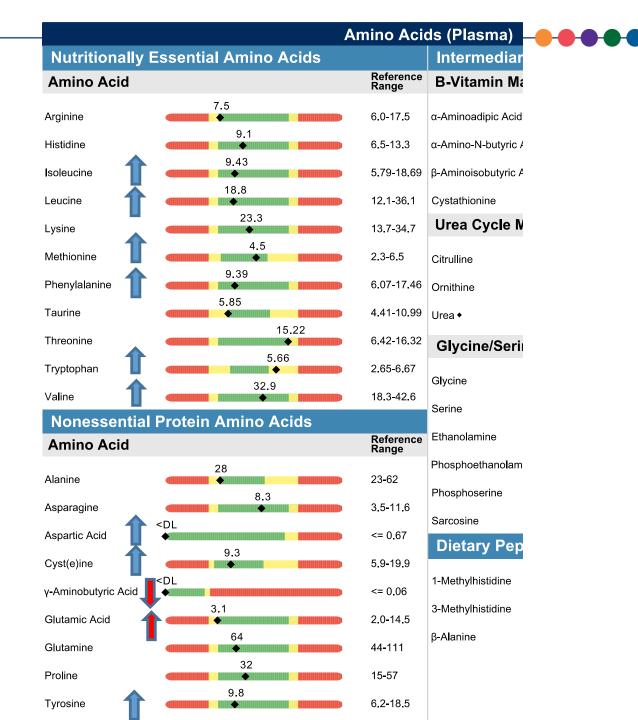


DIAG

Liu Y, et al. Cell Metabolism. 2020:31(1):77-91.

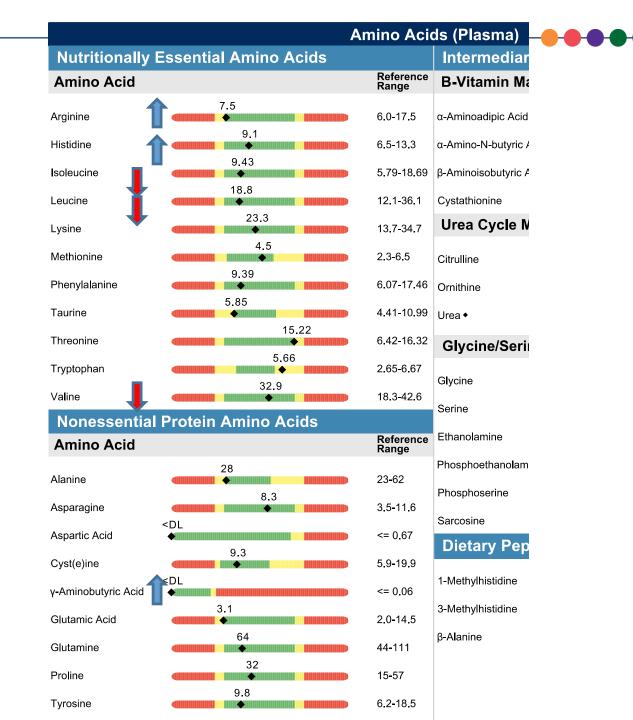
SPORTOMICS: METABOLIC HEALTH & FUNCTIONAL TESTING

- ASSOCIATED w/INSULIN RESISTANCE
 - LOW butyrate (GI Effects)
 - ELEVATED aromatic amino acids (tryptophan, tyrosine, phenylalanine)
 - ELEVATED sulfur-containing amino acids (cysteine, methionine) & aspartate
 - ELEVATED branched chain amino acids (isoleucine, leucine, valine)
 - ELEVATED glutamate with LOWER GABA



SPORTOMICS: METABOLIC HEALTH & FUNCTIONAL TESTING

- ASSOCIATED w/INSULIN SENSITIVITY
 - ELEVATED SCFAs (GI Effects)
 - ELEVATED histidine, arginine, GABA
 - LOWER branched chain amino acids (isoleucine, leucine, valine)







SPORTOMICS: METABOLIC HEALTH & FUNCTIONAL TESTING

- FUNCTIONAL MEDICINE TESTING INFORMED RECOMMENDATIONS for metabolic health & insulin resistance
 - IF EXERCISING & METABOLIC DISEASE
 - POTENTIAL NON-RESPONDER WITH ...
 - Elevated BCAAs and AAAs; Elevated glutamate and Decreased GABA; Elevated cysteine & methionine
 - PROBABLE RESPONDER WITH ...
 - Increased Firmicutes & SCFAs; Increased lactate utilizers // (absence of non-responder characteristics)
 - IF NOT EXERCISING & AT RISK FOR METABOLIC DISEASE
 - POTENTIAL RESPONDER WITH ...
 - Elevated Bacteroides // Elevated GABA
 - IF NON-RESPONDER OR POTENTIAL NON-RESPONDER
 - Work to elevate SCFAs (fiber, resistant starches, fermented foods/probiotics, butyrate)
 - Decrease exercise volume/intensity



THANK YOU FOR YOUR TIME AND ATTENTION

Jeffrey B. Kreher, MD, FAAP, IFMCP CMO and Co-Founder wellstead, LLC

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Presenter

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We look forward to hearing from you!

Questions?

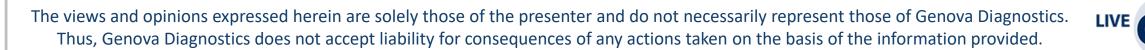


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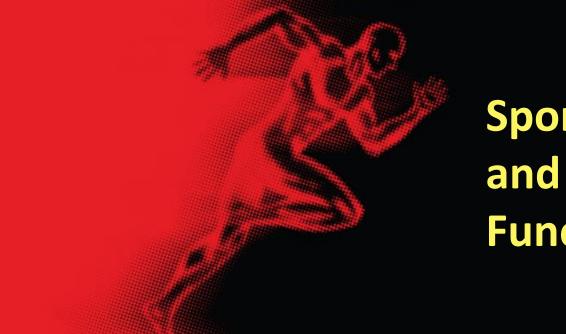
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Sportomics, Metabolic Health, and Utilization of Functional Medicine Testing

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