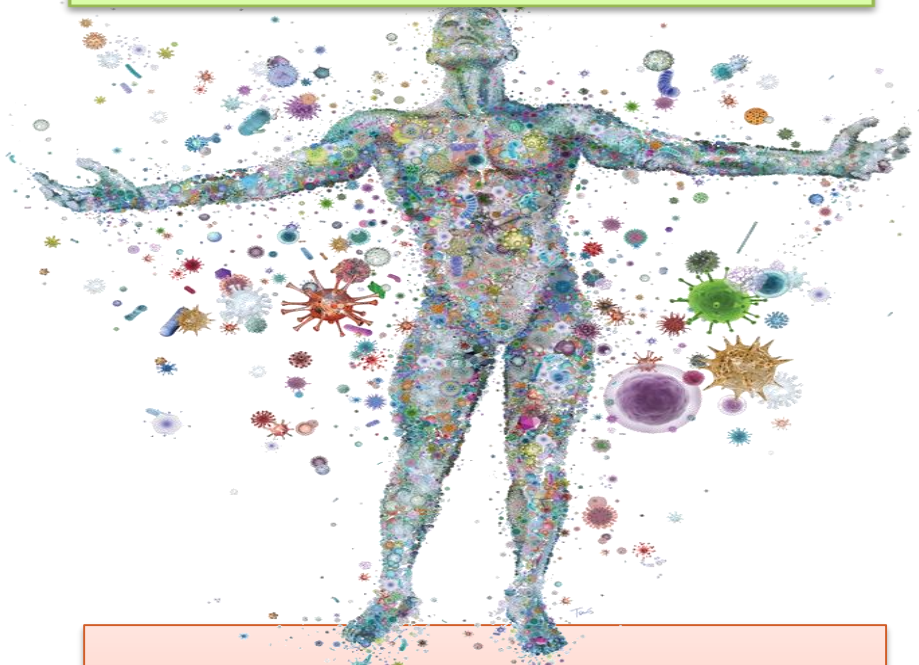
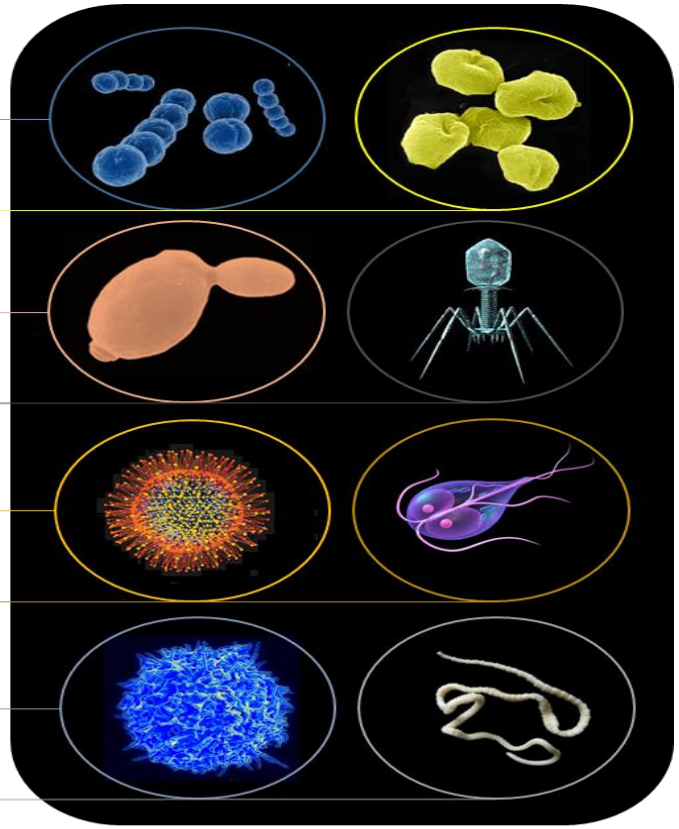
Our Microbiome

Human
~10 trillion cells
~23 thousand genes

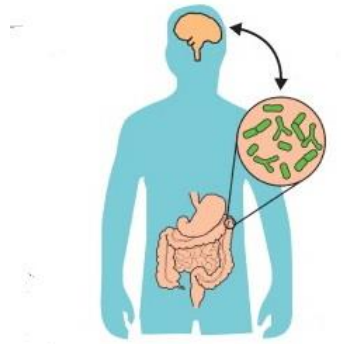


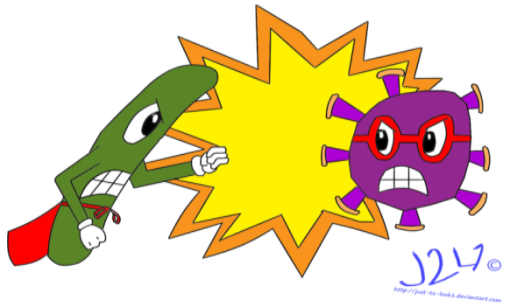
Microbiome
~100 **trillion c**ells
~3 million genes

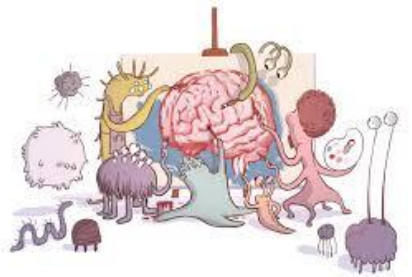
- Bacteriome
- Archaeome
- Mycobiome
- Phageome
- Euvirome
- Protozome
- Immunome
- Helminthome



Why do we study the microbiome ?

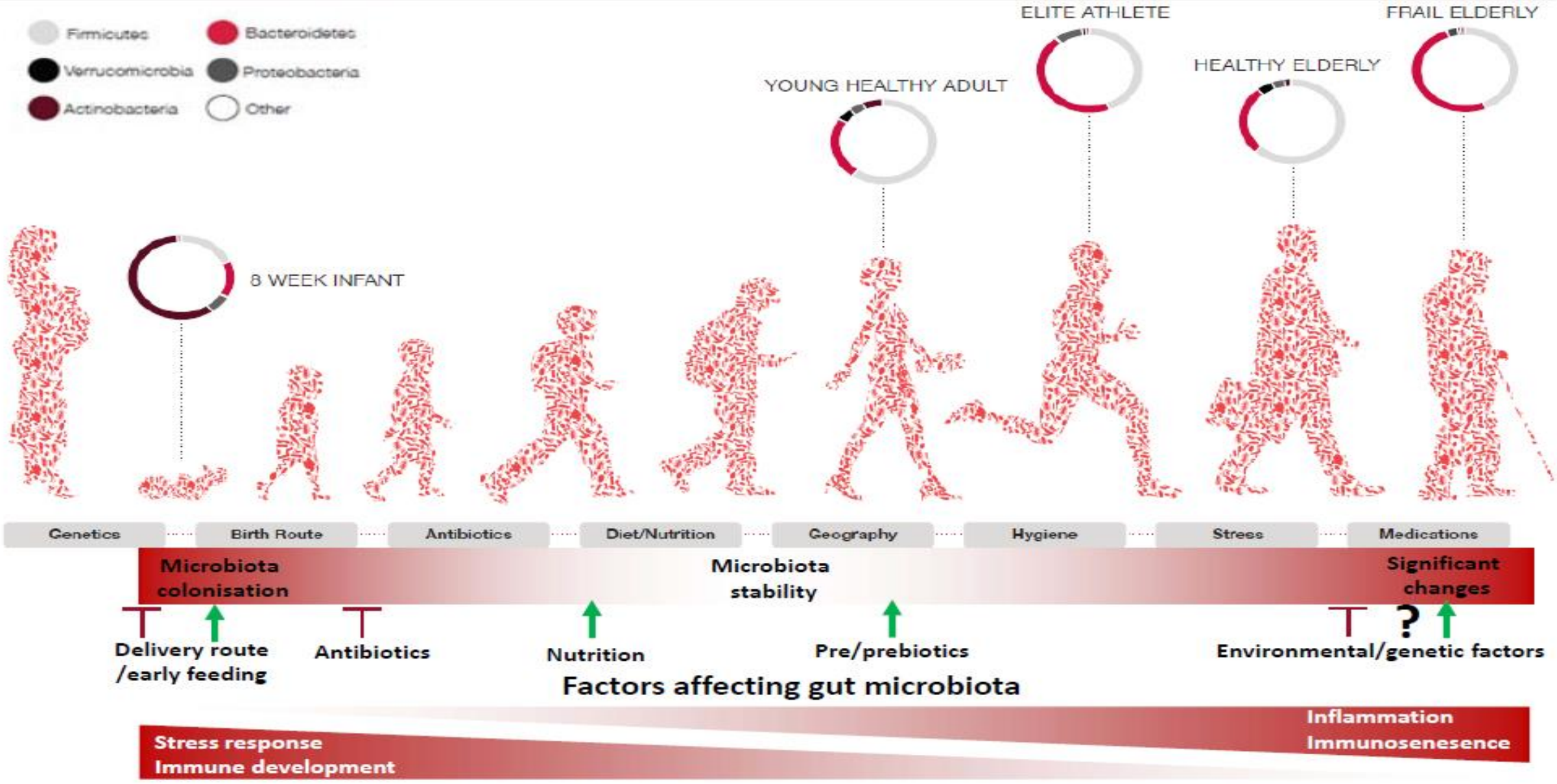






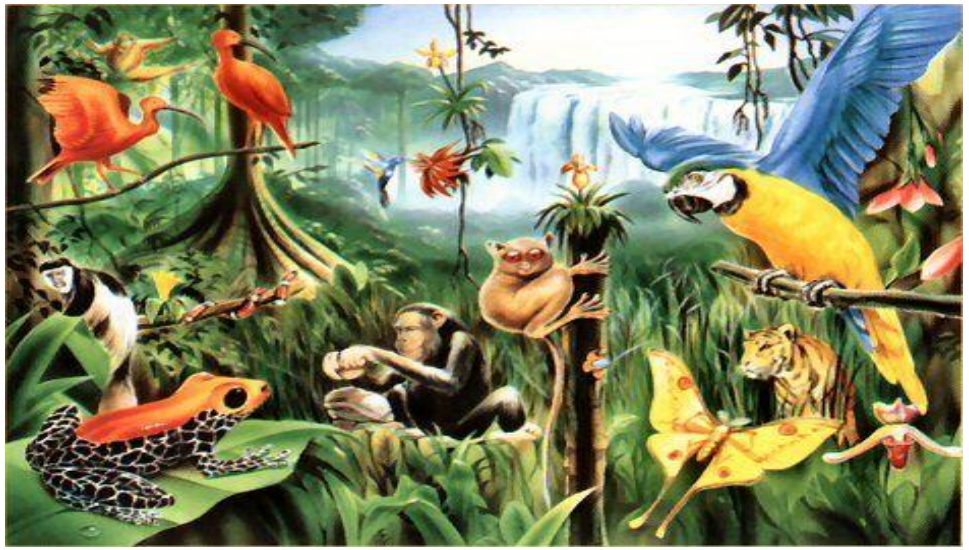
eagasc
Agriculture and Food Development Authority

Gut Microbiome over a lifetime



What is a healthy microbiome ?

Diversity is Key

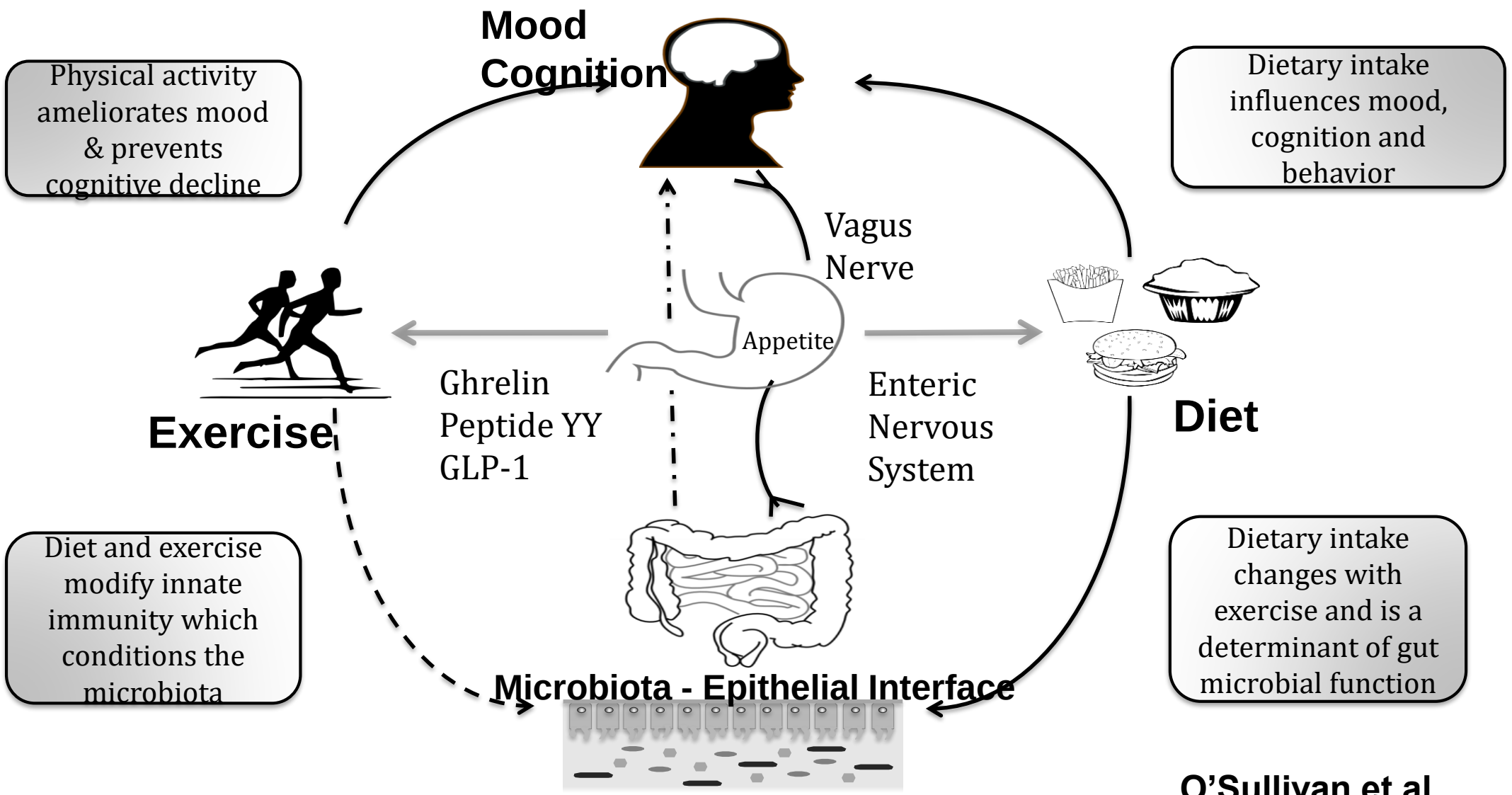


High Diversity

Low Diversity

Low total diversity within the gut microbiota is generally regarded as less desirable and has been observed in children that are more susceptible to allergies as well as sufferers of IBD, IBS and *C. difficile* infection (among others)

Exercise and the Microbiome



O'Sullivan et al., (2016)

Agriculture and Food Development Authority

Rugby Microbiome

Elite Athletes n=40
Control BMI <25 n=23
Control BMI >28 n=23

Data collected

- Fasting blood sample (metabolic & inflammatory markers)
- Clinical bloods (CHOL, TG, fasting glucose etc.)
- Diet (FFQ)
- Body composition (DXA and W:H measurement)
- Faeces (microbial sequencing)

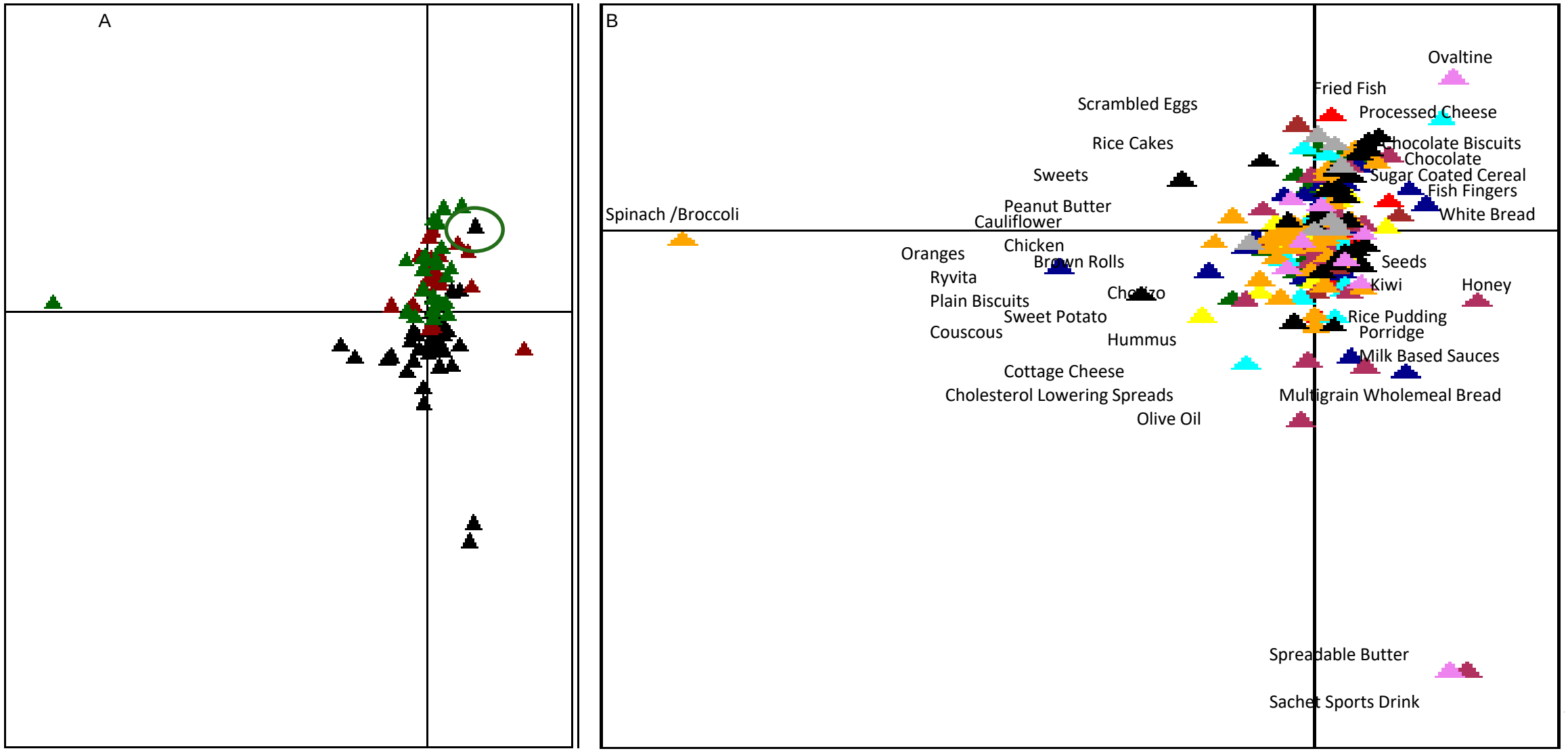
Editor's choice
Scan to access more free content

ORIGINAL ARTICLE

Exercise and associated dietary extremes impact on gut microbial diversity

Siobhan F Clarke,[1,2,3] Eileen F Murphy,[2,4] Orla O'Sullivan,[1] Alice J Lucey,[5] Margaret Humphreys,[6] Aileen Hogan,[2] Paula Hayes,[2] Maeve O'Reilly,[2,4] Ian B Jeffery,[2,3] Ruth Wood-Martin,[7] David M Kerins,[8,9] Eamonn Quigley,[2] R Paul Ross,[1,2] Paul W O'Toole,[3] Michael G Molloy,[10] Eanna Falvey,[10,11] Fergus Shanahan,[2,10,12] Paul D Cotter[1,2]

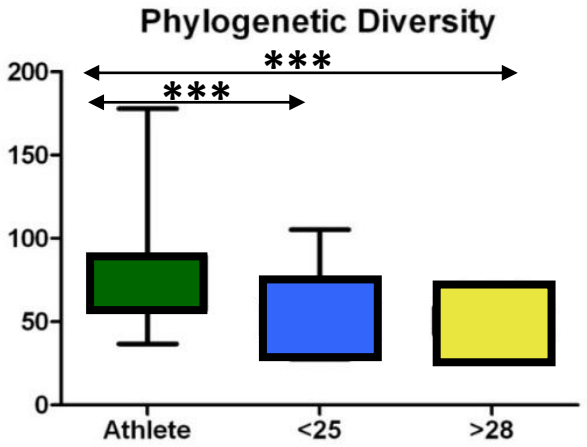
Diet -FFQ

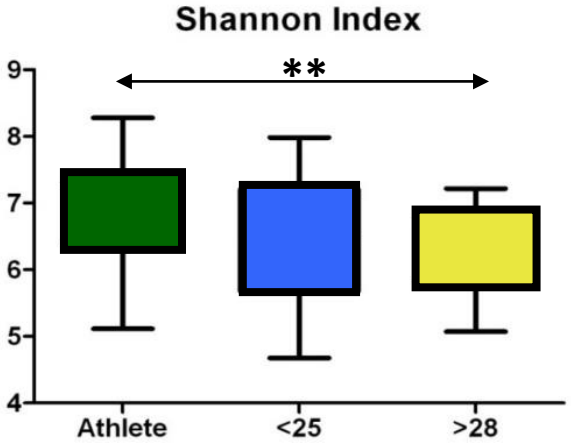


SC

Agriculture and Food Development Authority

Microbial Diversity



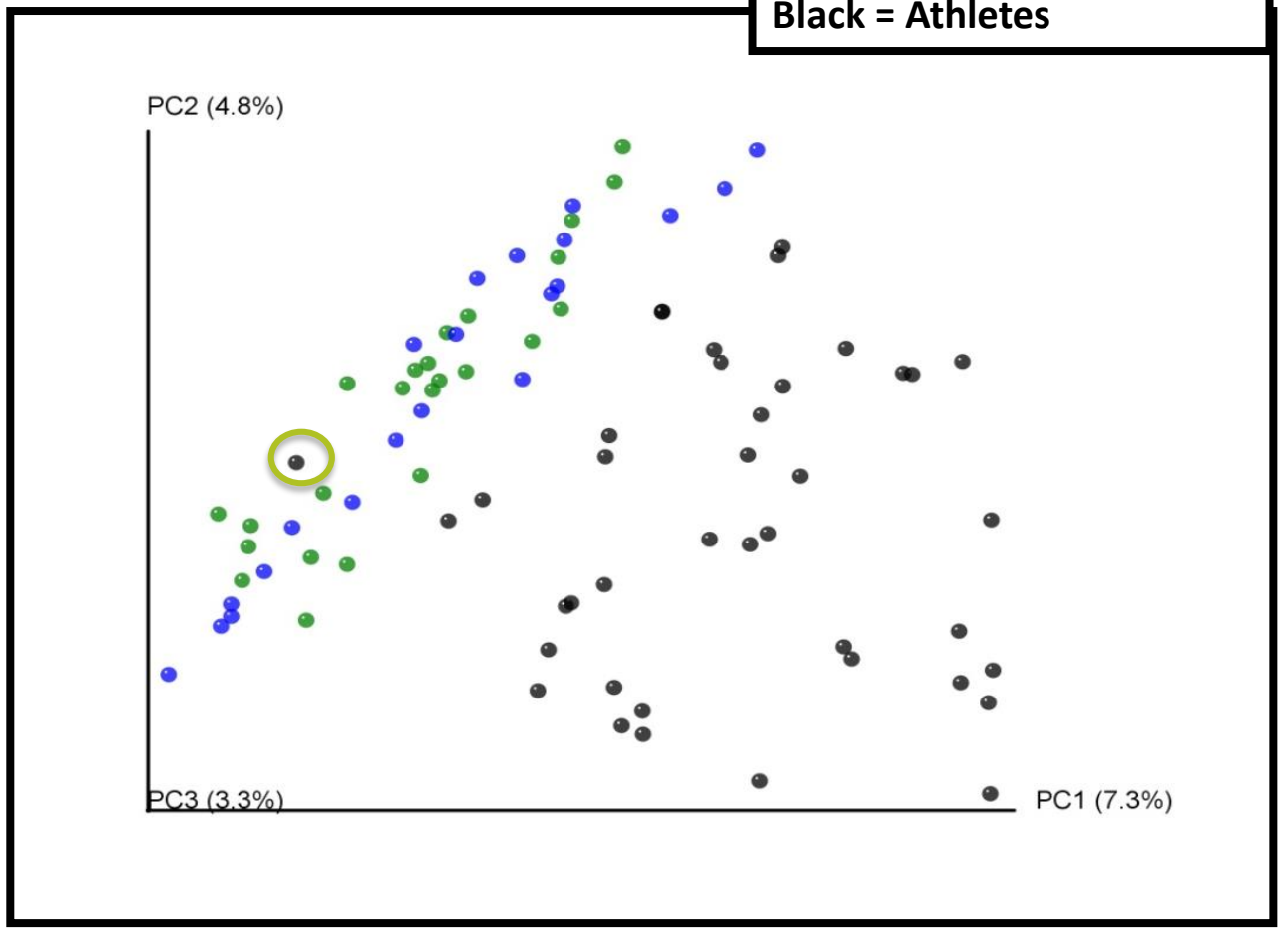


Unweighted Unifrac

Green = High BMI Controls

Blue = Low BMI Controls

Black = Athletes

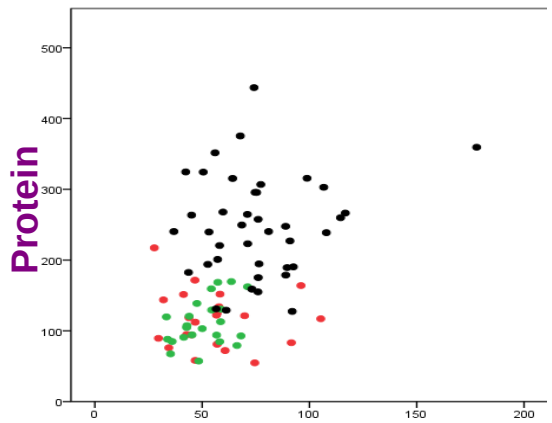


CK IU/L

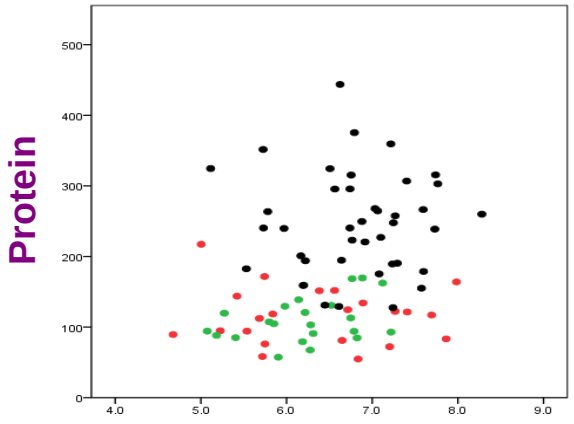
eagasc

ood Development Authority

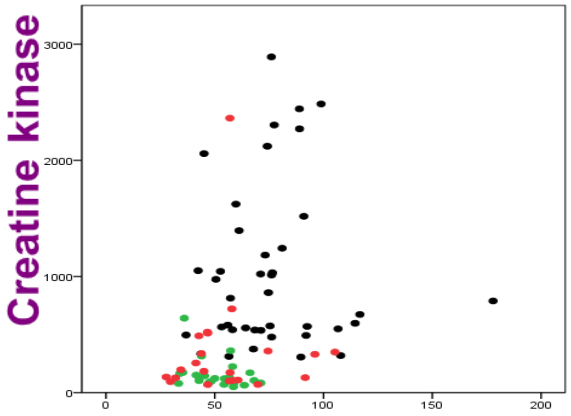
Correlation - microbial diversity/ protein/exercise



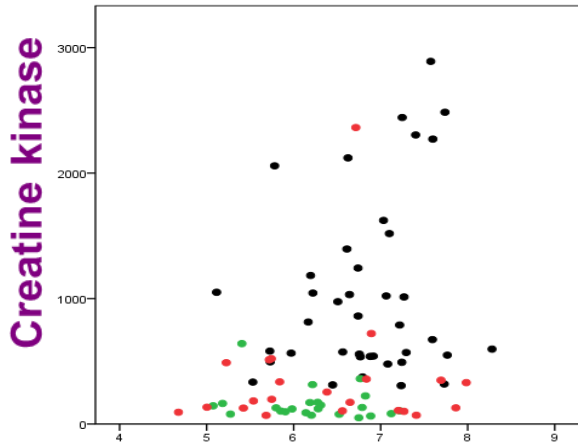
Phylogenetic diversity



Shannon index



Phylogenetic diversity



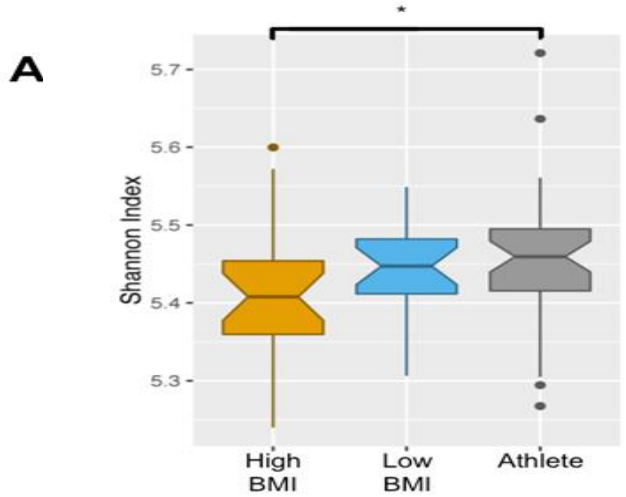
Shannon Index

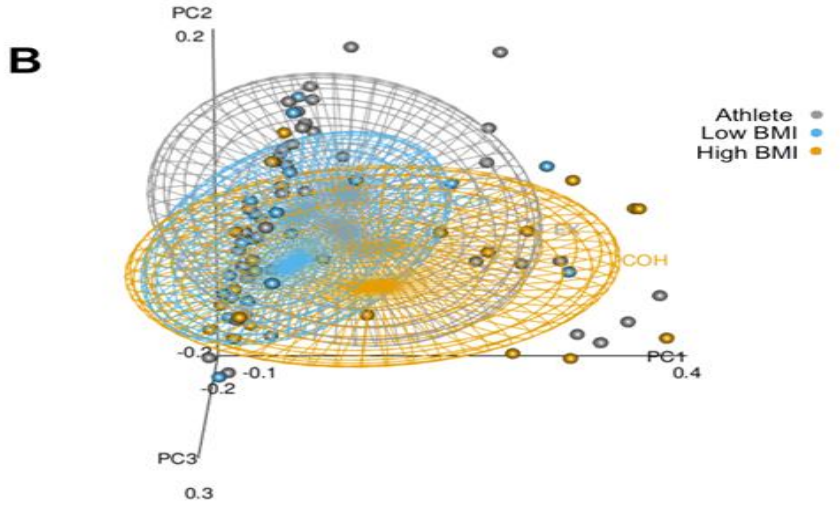
- Low BMI Controls
- High BMI Controls
- Athletes

eagasc

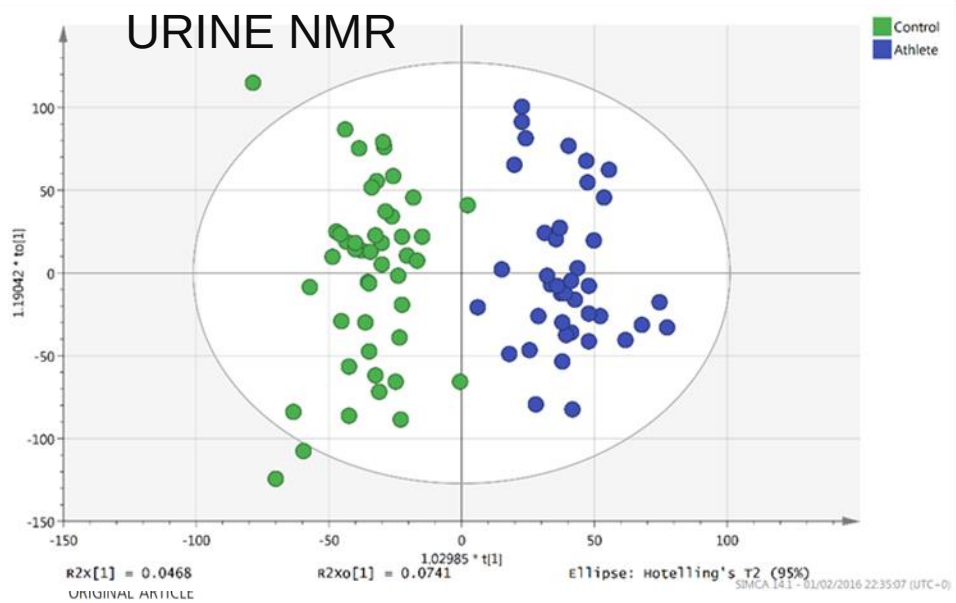
ood Development Authority

Functional Diversity

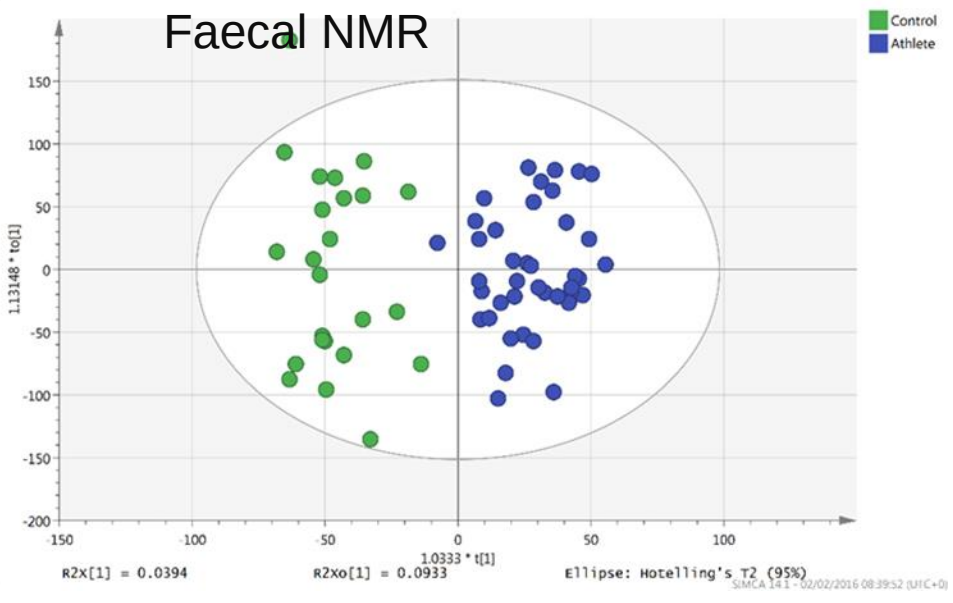




URINE NMR



Faecal NMR



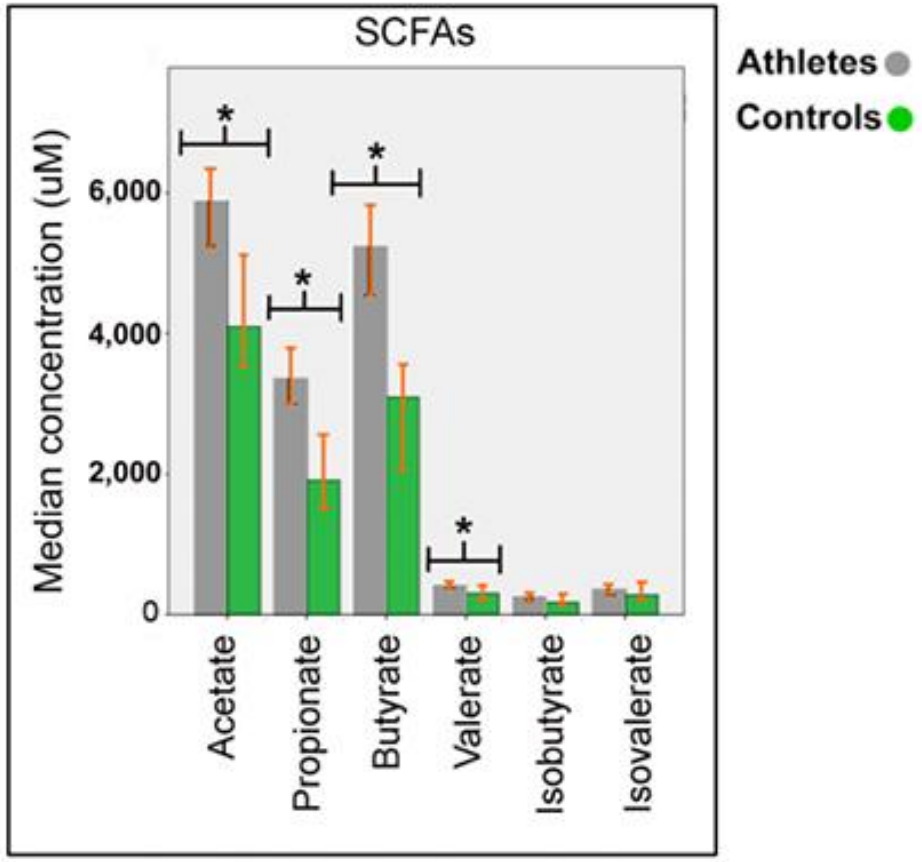
ORIGINAL ARTICLE

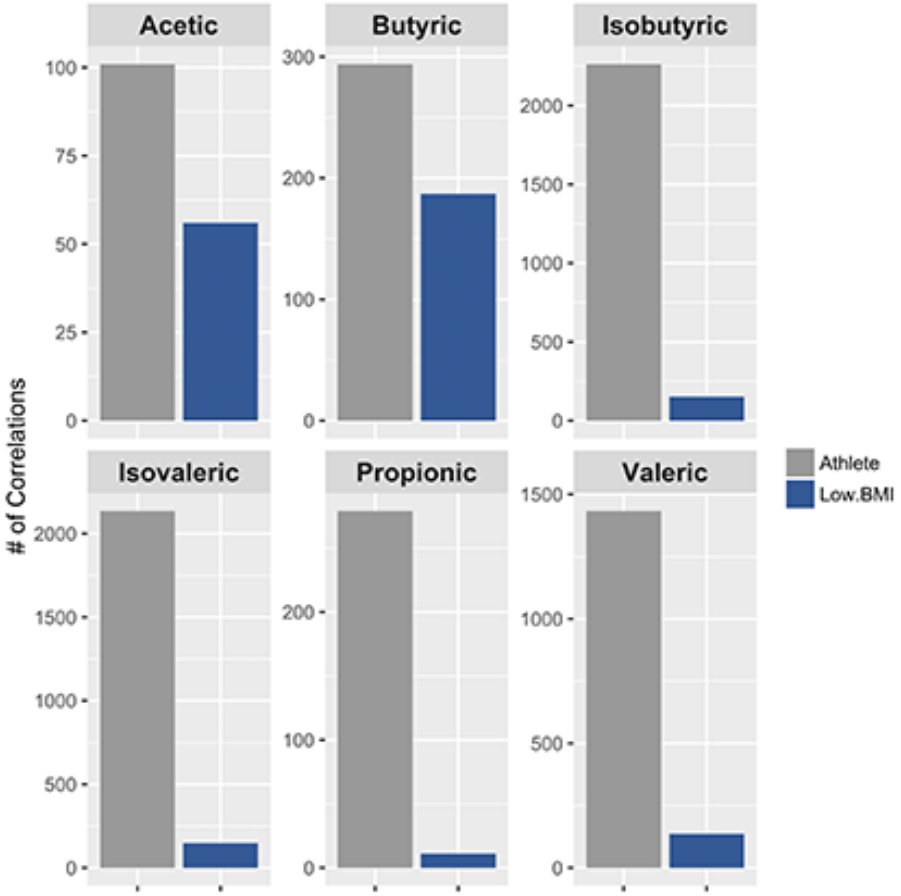
The microbiome of professional athletes differs from that of sedentary subjects in composition and particularly at the functional metabolic level

Wiley Barton,[1,2,3] Nicholas C Penney,[4,5] Owen Cronin,[1,3] Isabel Garcia Perez,[4] Michael G Molloy,[1,3] Elaine Holmes,[4] Fergus Shanahan,[1,3] Paul D Cotter,[1,2] Orla O'Sullivan[1,2]

teagasc
Agriculture and Food Development Authority

SCFA Profile is Unique to Cohort





Agriculture and Food Development Authority

Metabolomics highlights

- Athletes ↑ in by-products of protein metabolism
  - TMAO
  - Carnitines
  - Trimethylamine
  - 3-hydroxy isovaleric acid

- Athletes ↑ in metabolites of muscle turnover
  - creatine
  - 3 methylhistidine

- Athletes ↑ in metabolites of vitamins and recovery
  - Glutamine
  - Lysine
  - 4-pyridoxic acid

Can we “train” our gut microbes?

8 weeks

- Exercise (n=25)
- Exercise + protein (whey; n=27)
- Whey protein (n=22)

Data collected

- Fasting blood sample (metabolic & inflammatory markers)
- Clinical bloods (CHOL, TG, fasting glucose etc.)
- Diet (FFQ)
- Body composition (DXA and W:H measurement)
- Faeces (microbial sequencing)

eagasc
Agriculture and Food Development Authority

Exercise improves health !!!!

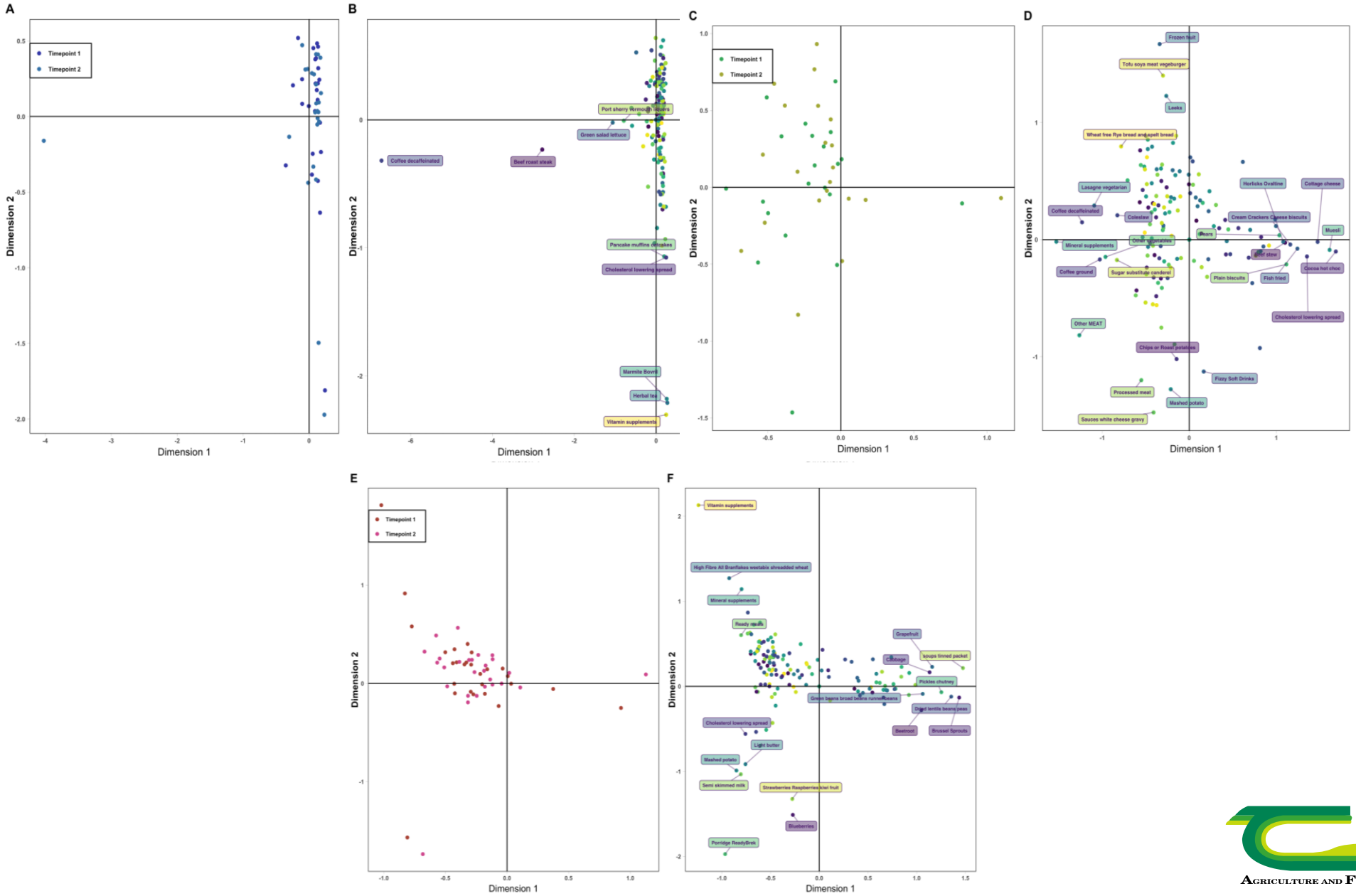
	Exercise (E) Group (n=25)	Exercise + Protein (EP) Group (n=22)	Protein only (P) Group (n=27)	p-value
Weight (kg)	-0.9 (-2.6, 0.9)	-0.8 (-1.6, 0.1)	-0.5 (-1.3, 0.6)	0.549
BMI (kg/m^2)	-0.3 (-0.9, 0.2)	-0.2 (-0.6, 0)	-1.1 (-0.4, 0.2)	0.419
Resting heart rate (BPM)	-5 (-16, 6) ∞	-5 (-9, 3) Ψ	4 (-3, 10)	**0.005***
Systolic BP (mmHg)	-8 (-12, 1)	-8 (-16, 0)	-4 (-11, 0)	0.545
Diastolic BP (mmHg)	-5 (-12, 1)	-6 (-9, -2)	-5 (-8, 0)	0.785
Waist:Hip ratio	-0.01 (-0.03, 0.01)	-0.02 (-0.04, 0.01)	0 (-0.01, 0.04)	0.07
Body fat (%)	-1.3 (-2.4, -0.5) ∞	-0.8 (-1.7, -0.5) Ψ	0.5 (-0.2, 1)	**<0.001***
Fat mass (kg)	-0.9 (-1.5, -2.7) ∞	-0.8 (-1.2, -0.4) Ψ	0.4 (-0.5, 0.9)	**<0.001***
Fat mass (trunk) (kg)	-0.5 (-1, 02) ∞	-0.6 (-0.8, -1) Ψ	0.1 (-0.4, 0.6)	**0.001***
Lean tissue mass (kg)	0.7 (0.3, 1.8) ∞	0.5 (-0.4, 1.1) Ψ	-0.2 (-0.9, 0.3)	**0.001***
Weekly PA (METS)	1,159 (712, 1,964) ∞	1,265 (434, 2,487) Ψ	111 (-244, 634)	**<0.001***
Weekly PA (kCals)	1,442 (818, 2,628) ∞	1,789 (571, 3,289) Ψ	184 (-418, 800)	**<0.001***
Sitting time (hours per week)	-5 (-17, 2)	-12 (-30, 1)	-5 (-18, 1)	0.407
Motorized transport (hours per week)	0 (-3.3, 2.8)	0 (-1, 1.3)	0.1 (-0.4, 5)	0.519

Between-group differences in post-intervention changes were compared using Kruskal-Wallis tests (p-values shown). When significantly different a Mann-Whitney U test was applied to determine between which groups the difference existed.

∞ indicates a difference between E and P groups, Ψ indicates a difference between EP and P groups (All

Agriculture and Food Development Authority

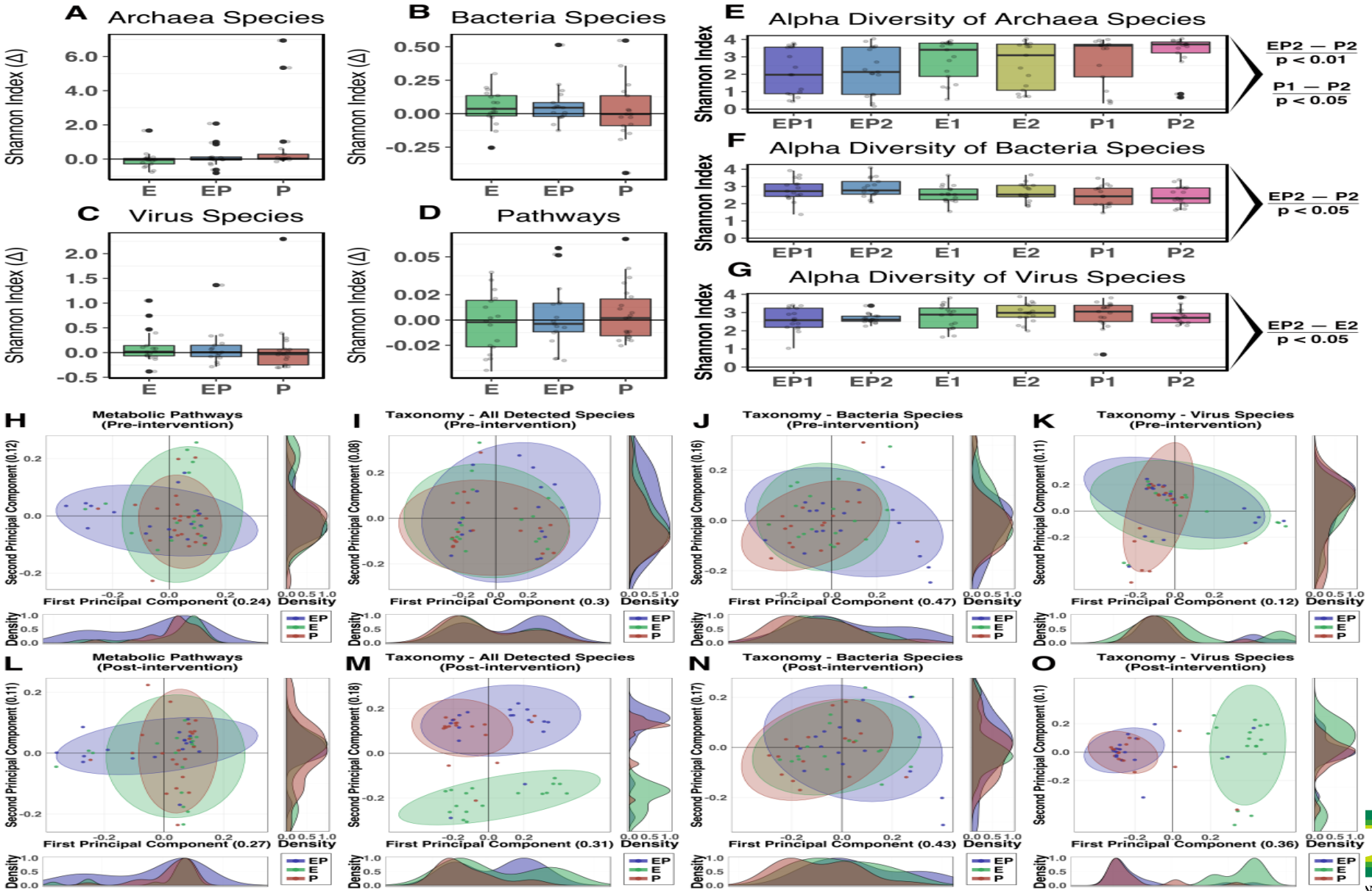
Diet



eagasc

Agriculture and Food Development Authority

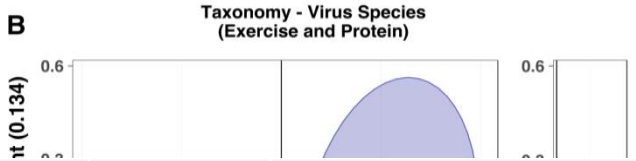
Subtle Changes in Microbiome



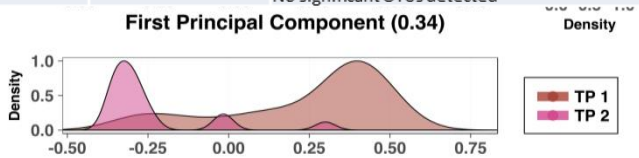
eagasc

AND FOOD DEVELOPMENT AUTHORITY

Viral Diversity



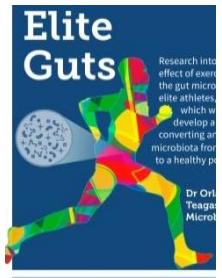
1. Group	Domain	ANCOM Detected Features (FDR = 0.05)	Pre-treatment RA	Post-treatment RA	Whey Powder RA	Supplement Control RA
Exercise and Protein (EP)	Virus	s__Lactococcus_phage_Tuc2009	0.000499917	0.002095861	0.002071575	0
		s__Lactococcus_phage_TP901.1	0.000166639	0.0015426	0.000980502	0
		s__Lactococcus_phage_340	0.008536341	0.243830028	0.003362651	0.000596659
		s__Lactococcus_phage_jm2	0.008406096	0.037533828	0.001866694	0
		s__Lactococcus_phage_jm3	0.006220945	0.03575589	0.001139854	0
		s__Lactococcus_phage_P680	0.015701368	0.140042772	0.001845555	0
		s__Lactococcus_phage_phi7	0.008339229	0.036861977	0.001156114	0.000596659
		s__Streptococcus_phage_Alq132	0.001808553	0.009054736	0.08402562	0.005966587
		s__Streptococcus_phage_Sfi19	0.002491731	0.004525762	0.054496732	0.002386635
		s__Streptococcus_phage_DT1	0.008555464	0.019793861	0.207416043	0.010143198
		s__Streptococcus_phage_7201	0.003592347	0.009275997	0.158168168	0.007159905
		s__Streptococcus_phage_Abc2	0.003863716	0.015320872	0.123153022	0.008353222
		s__Lactococcus_phage_SK1	0.000892074	0.008264603	0.000349599	0
		s__Lactococcus_phage_bIL170	0.005030033	0.041632521	0.001048796	0.000596659
		s__Lactococcus_phage_P008	0.002543755	0.040451612	0.001121968	0
		s__Lactococcus_phage_712	0.001866797	0.018814728	0.001808157	0
		s__Lactococcus_phage_jj50	0.001058712	0.013484408	0.000403258	0
		s__Lactococcus_phage_bIBB29	0.006197035	0.038155223	0.000832533	0
	Bacteria	s__Vibrio_anguillarum	6.43857E-06	1.32543E-05	2.00236E-06	5.00103E-06
		s__Fervidobacterium_pennivorans	6.73413E-06	1.07671E-05	0	1.25026E-06
		s__Streptococcus_thermophilus	0.000742779	0.001276861	0.309245576	0.000563866
		s__Lactococcus_lactis	0.000161433	0.000344833	0.299223083	0.000635131
	Archaea	No significant OTUs detected	NA	NA	NA	NA

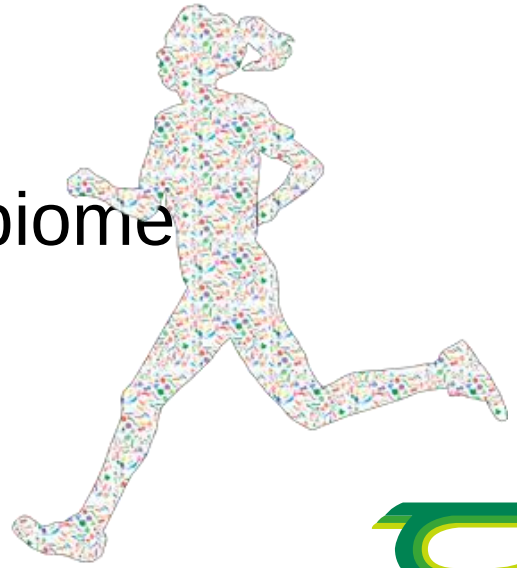


eagasc
Agriculture and Food Development Authority

Summary- ExMET

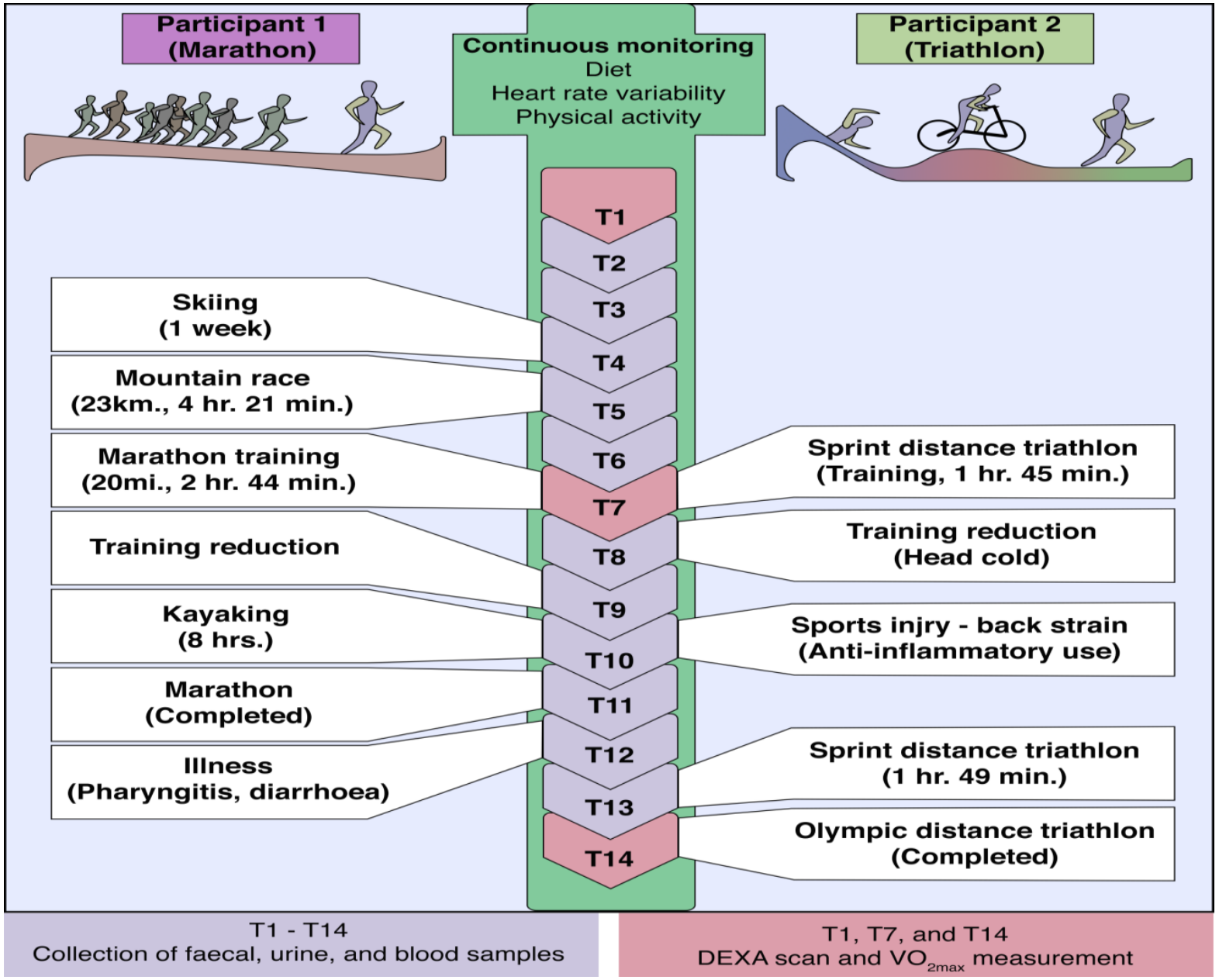
- Exercising groups had increased fitness and reduced body fat
- Does not induce significant alteration in gut bacterial and archaea diversity : too short an intervention ???
- Virus carry-over with whey protein
- **Athlete** microbiome ≠ **Exercise** microbiome





Agriculture and Food Development Authority

A STEP TOWARDS PERSONALIZED MEDICINE FOR ATHLETES

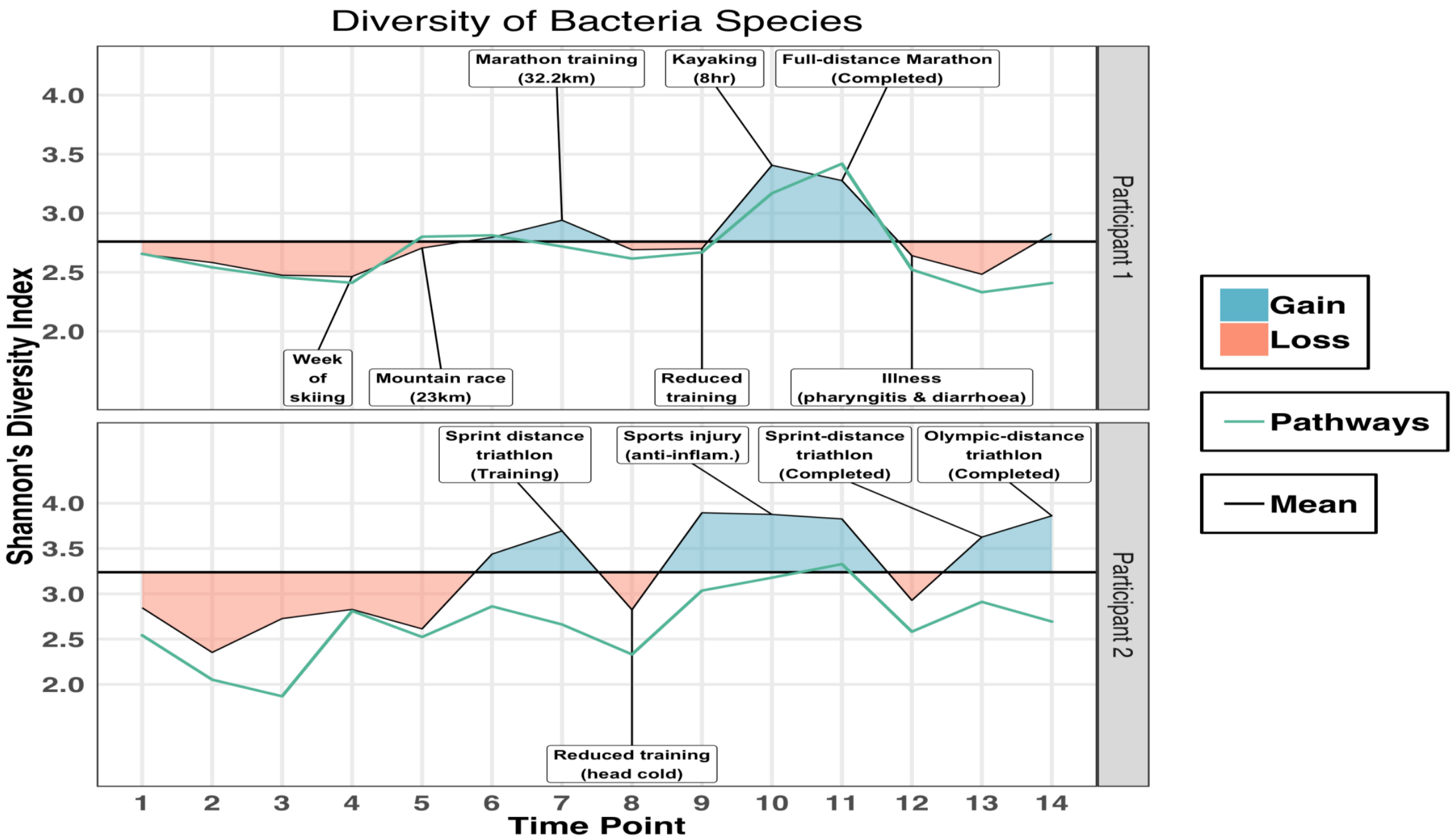


teagasc
Agriculture and Food Development Authority

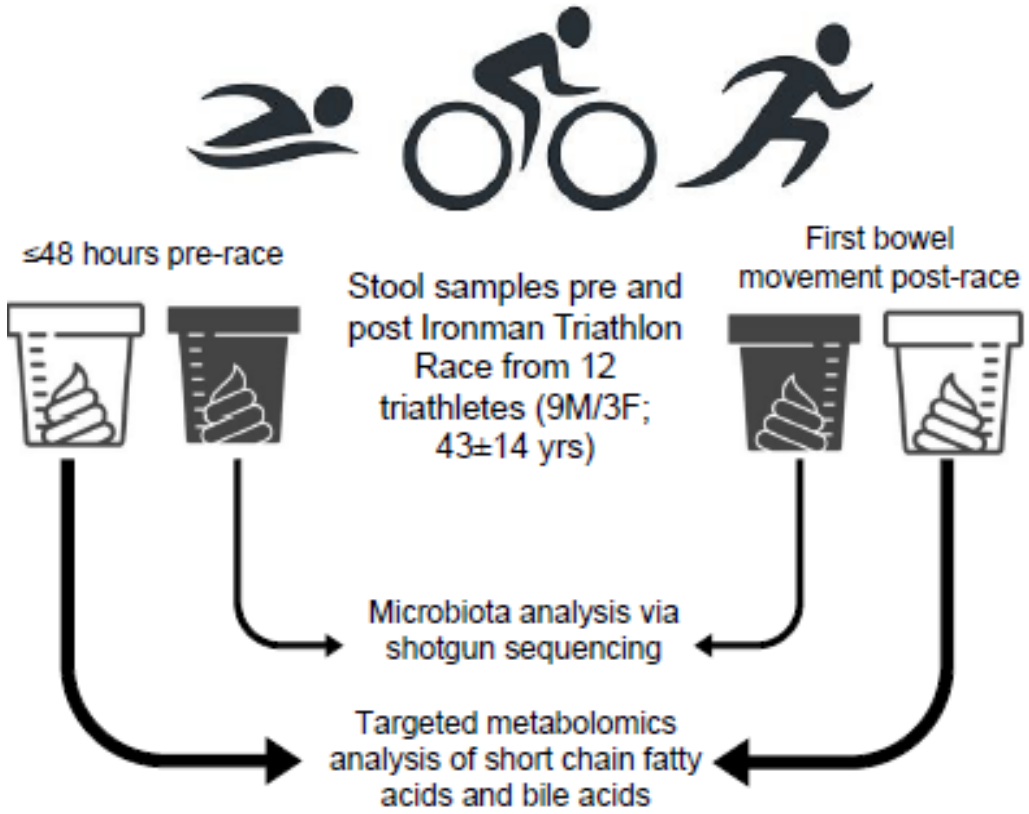
Improved body composition

Improved cardiorespiratory fitness

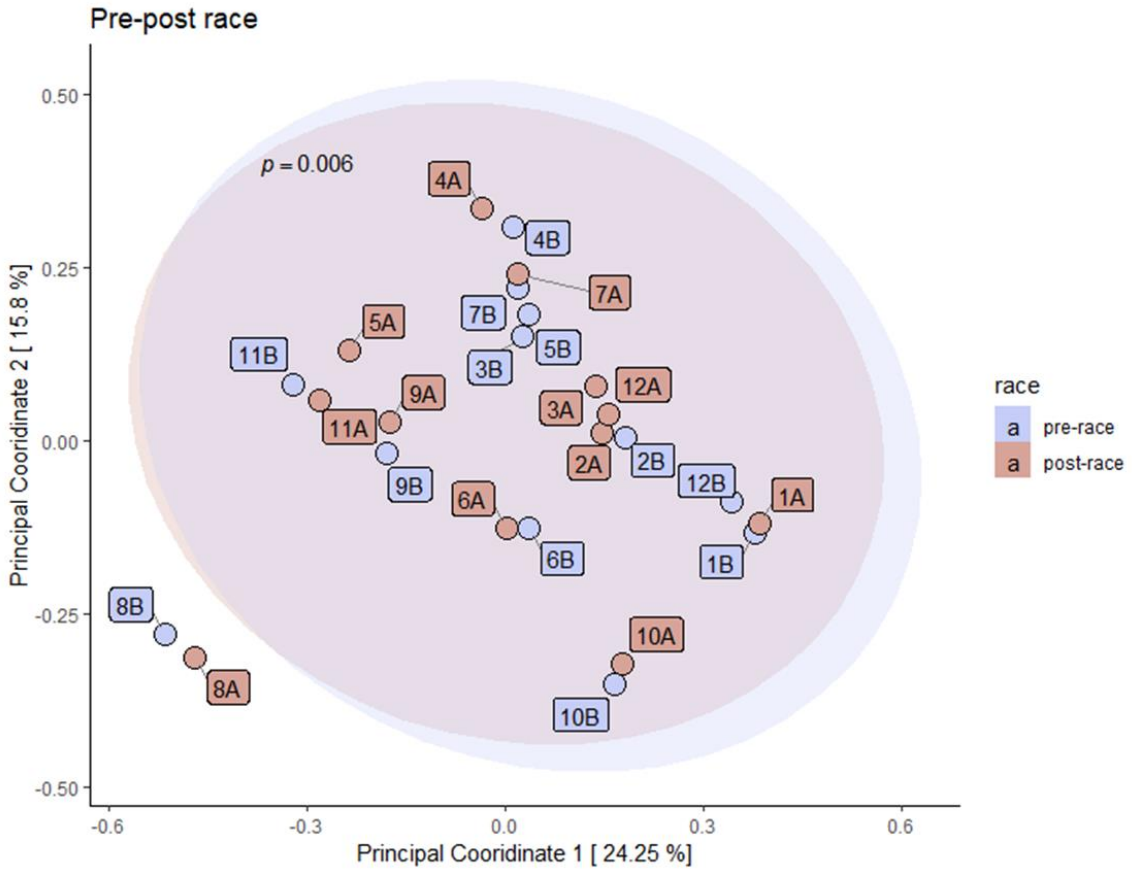
Patient characteristics	Values					
	Participant 1 (Marathoner)			Participant 2 (Triathlete)		
	T_0	T_{14}	Δ	T_0	T_{14}	Δ
Age (years)	30	—	—	33	—	—
Height (cm)	181	—	—	182	—	—
Weight (kg)	93.8	89.2	**-4.6**	104.9	103.4	**-1.5**
BMI (kg/m^2)	28.6	27.2	**-1.4**	31.7	31.2	**-0.5**
Waist:Hip ratio	0.92	0.92	**0.0**	0.95	.91	**-0.04**
Body fat (%)	25.6	21.7	**-3.9**	34.7	34.5	**-0.2**
Fat mass (kg)	23.9	19.4	**-4.6**	36.3	35.7	**-0.6**
Fat mass (trunk) (kg)	14.8	11.7	**-3.1**	20.9	20.4	**-0.5**
Lean tissue mass (kg)	65.6	65.9	**0.2**	64.97	64.2	**-0.7**
Estimated VO_{2max} (mls/kg/min)	41.1	46.6	**5.5**	33.6	38	**4.4**
Max HR (bpm)	183	179	**-4**	196	179	**-17**
Resting HR (bpm)	69	50	**-19**	58	72	**-2**
Systolic BP (mmHg)	122	116	**-6**	128	127	**-1**
Diastolic BP (mmHg)	77	75	**-2**	87	72	**-15**
Weekly PA (IPAQ, METS)	891.5	—	—	646.5	—	—
Weekly PA (IPAQ, kCals)	1,393.7	—	—	1,130.3	—	—


Diversity of Bacteria Species
Shannon's Diversity Index
4.0
3.5
3.0
2.5
2.0
Marathon training (32.2km)
Kayaking (8hr)
Full-distance Marathon (Completed)
Week of skiing
Mountain race (23km)
Reduced training
Illness (pharyngitis & diarrhoea)
Participant 1
Sprint distance triathlon (Training)
Sports injury (anti-inflam.)
Sprint-distance triathlon (Completed)
Olympic-distance triathlon (Completed)
Reduced training (head cold)
Participant 2
1
2
3
4
5
6
7
8
9
10
11
12
13
14
Time Point
Gain
Loss
Pathways
Mean

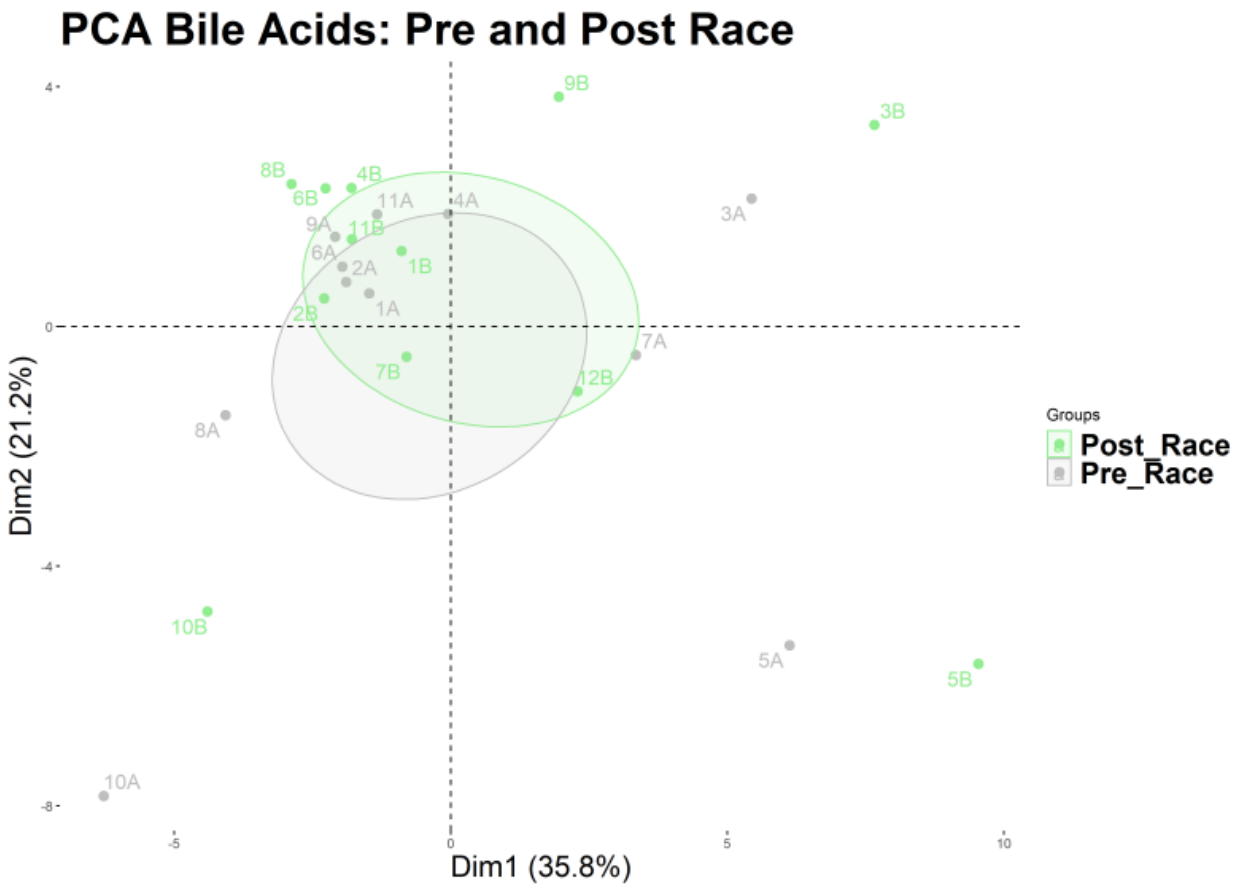
Impacts of an Ironman on gut health

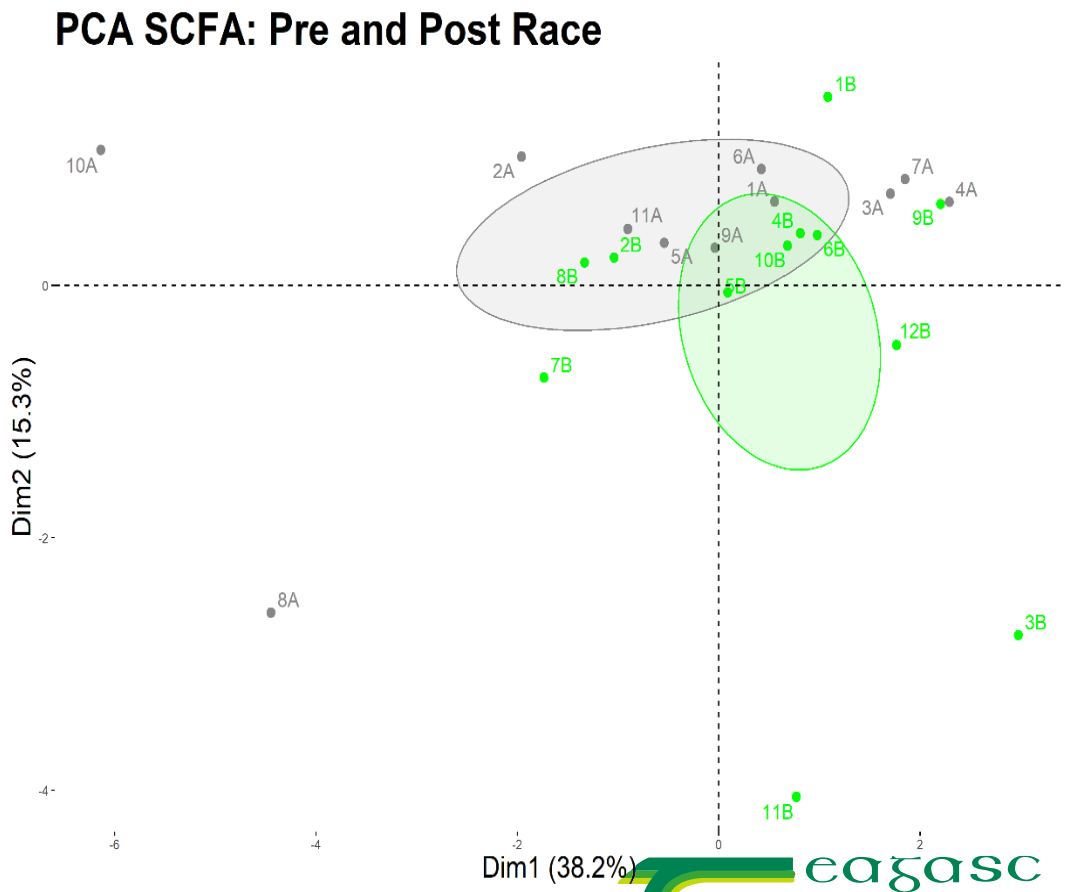


Intra- and inter-individual diversity of bacterial species were unaltered following race completion

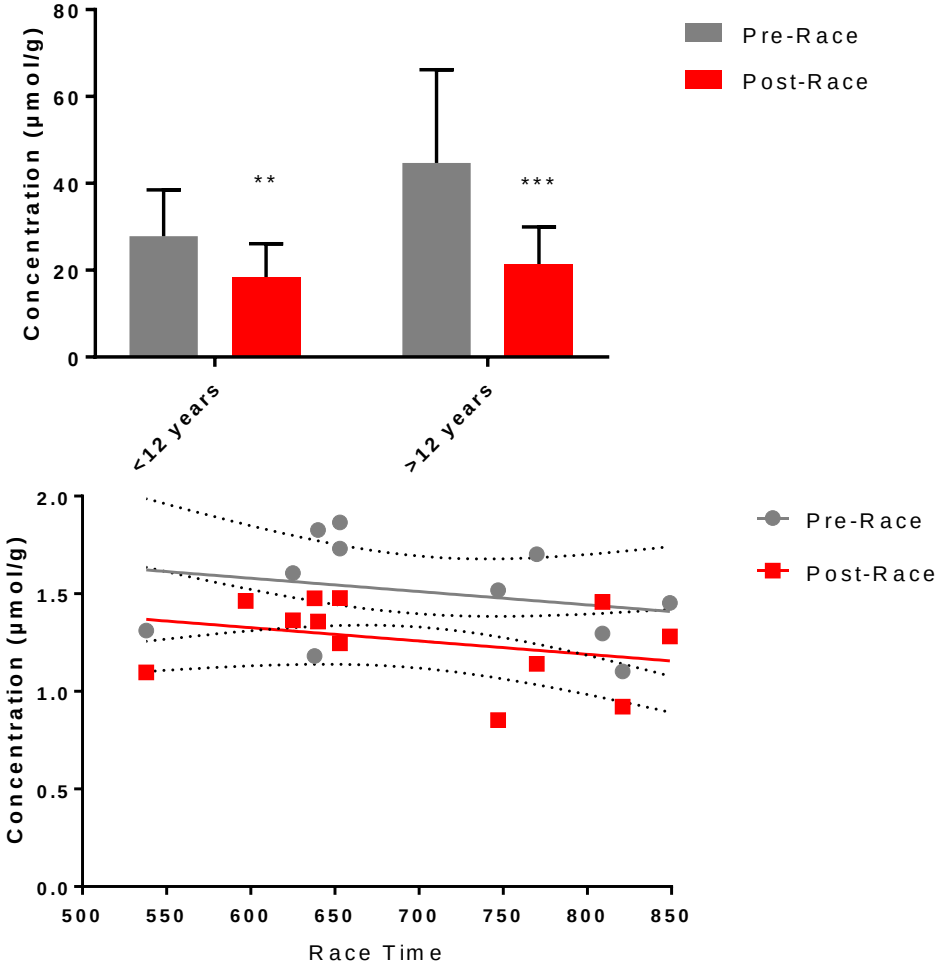


Changes in pre- to post-race bile short chain fatty acids and bile acids including reductions in secondary and free bile acids and reductions in butyric and pivalic acids





Fecal Butyrate Following an Ironman Triathlon

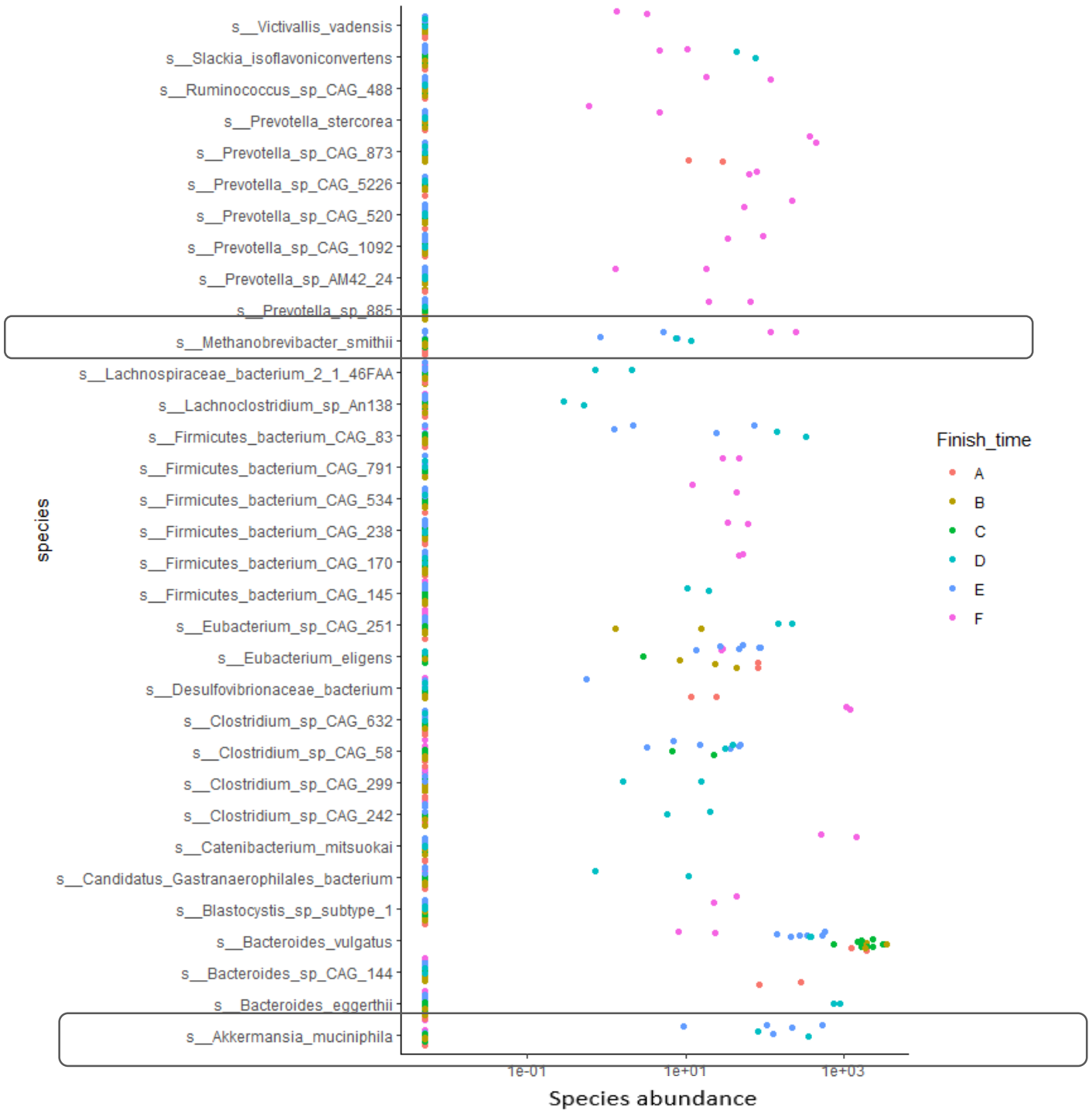


Butyrate is elevated in veteran triathletes & associated with race time

Certain microbial taxa are associated with race finish time

- 79 bacterial species
- *M. smithii* (14hrs)
- *A. muciniphila* (12hrs)

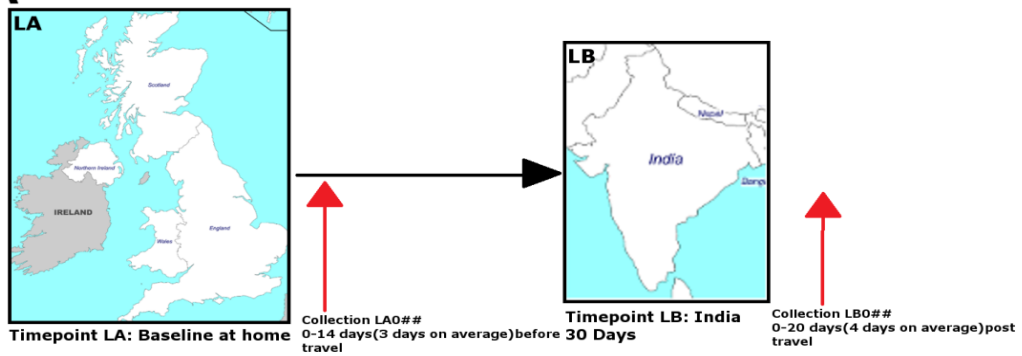
A = 9 hours
B= 10 hours
C= 11 hours
D= 12 hours
E= 13 hours
F= 14 hours

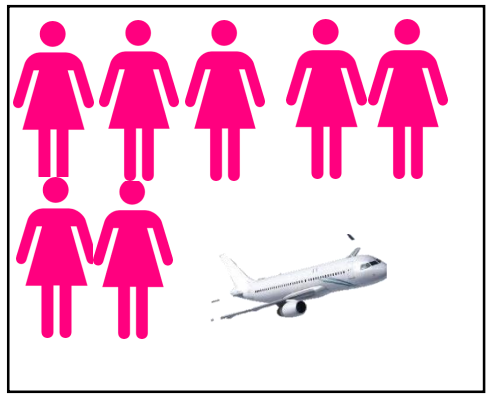


The Travelling Athlete

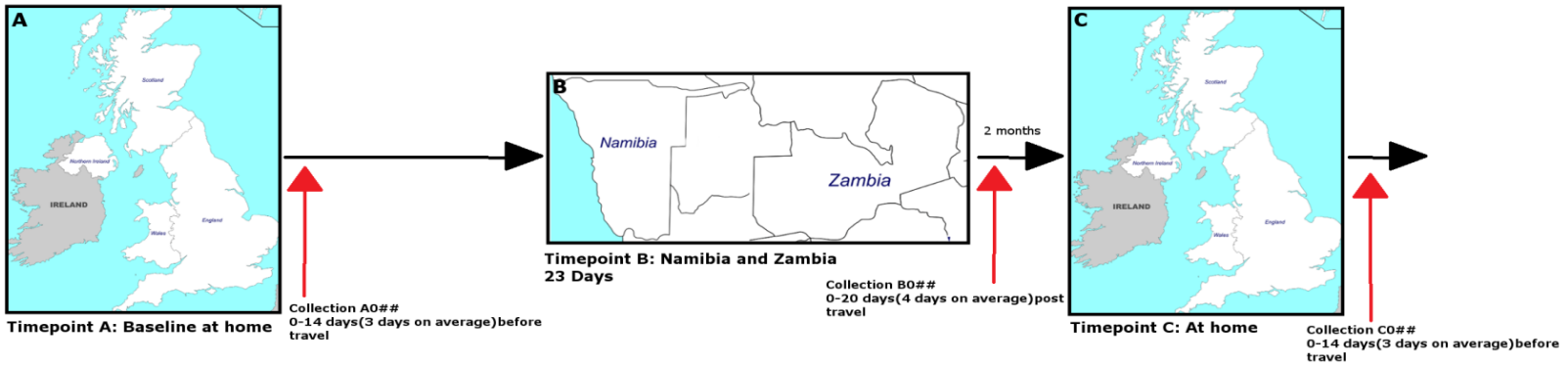
CRICKET IRELAND

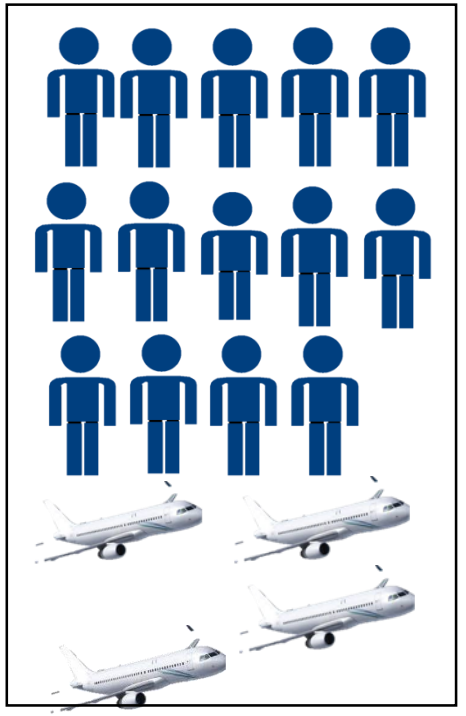
A

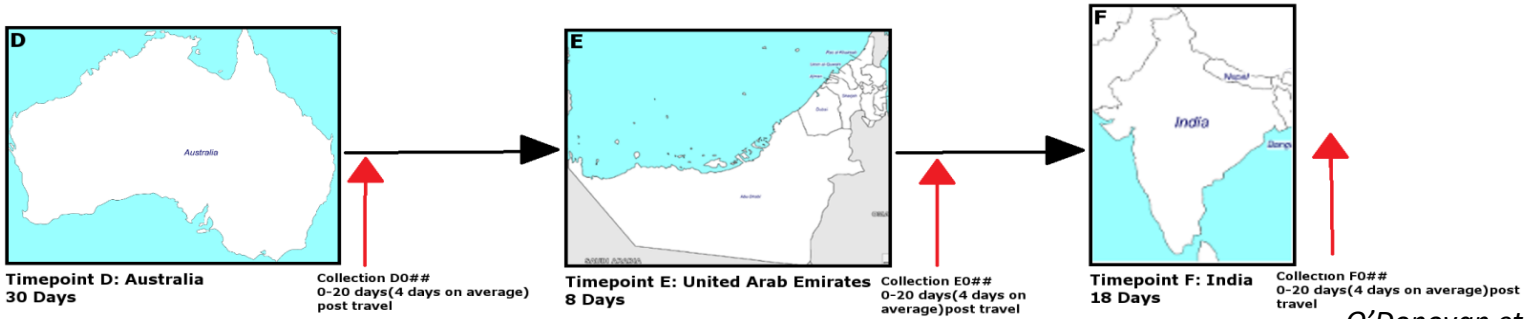




B

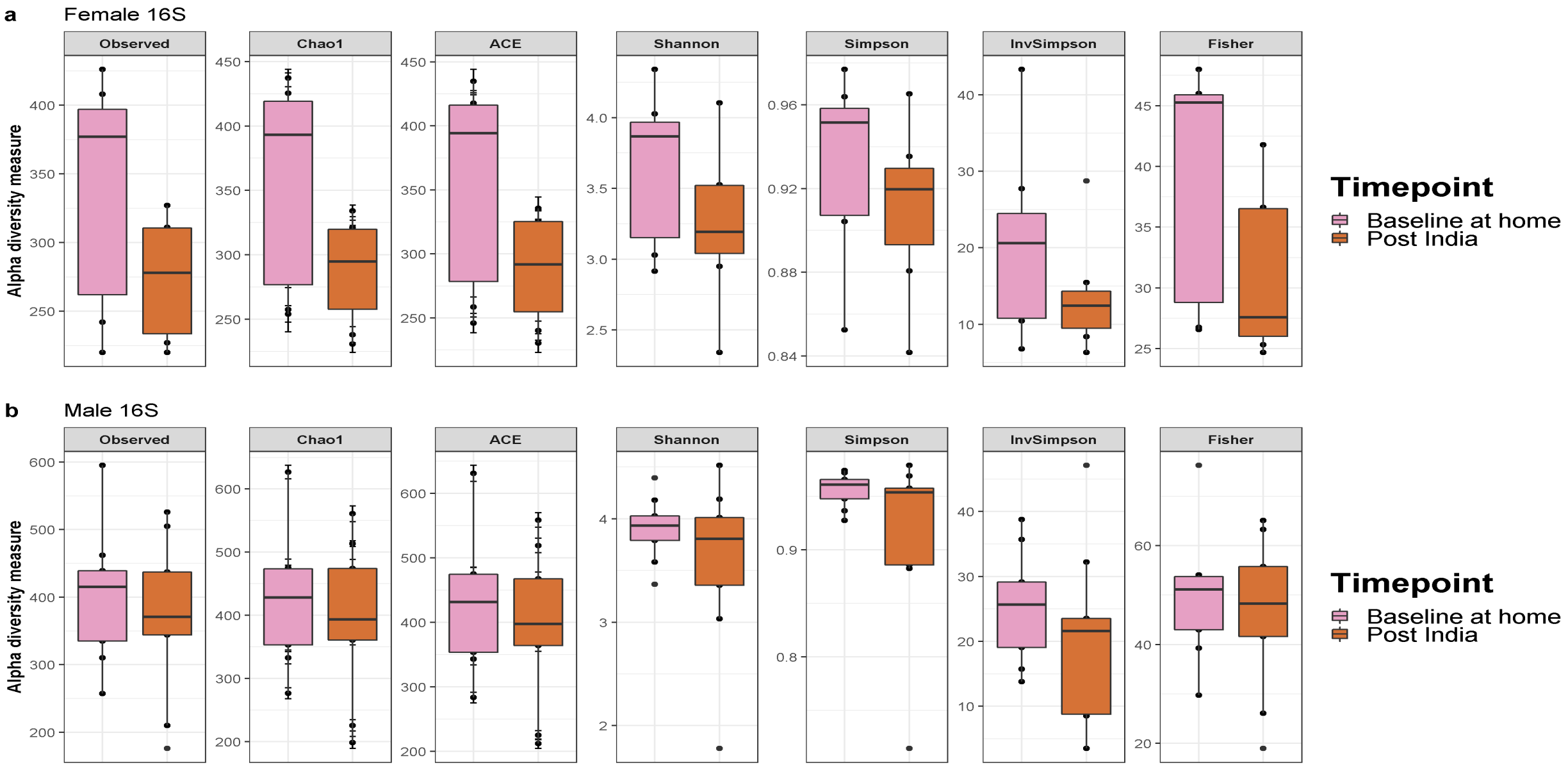




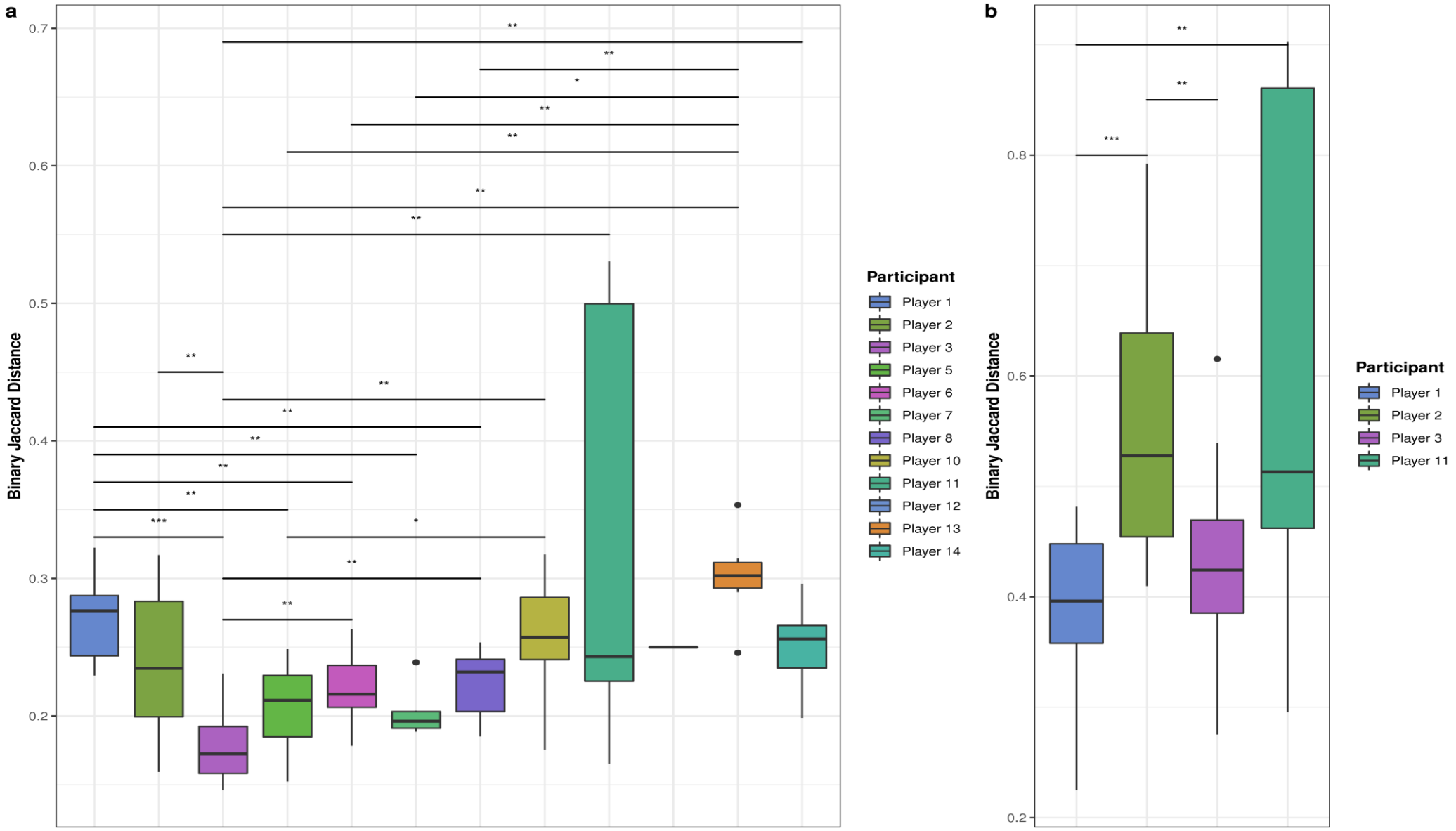


O'Donovan et al, Travel Medicine and Infectious Disease, 2019, Under Review

Decrease in microbial diversity post India

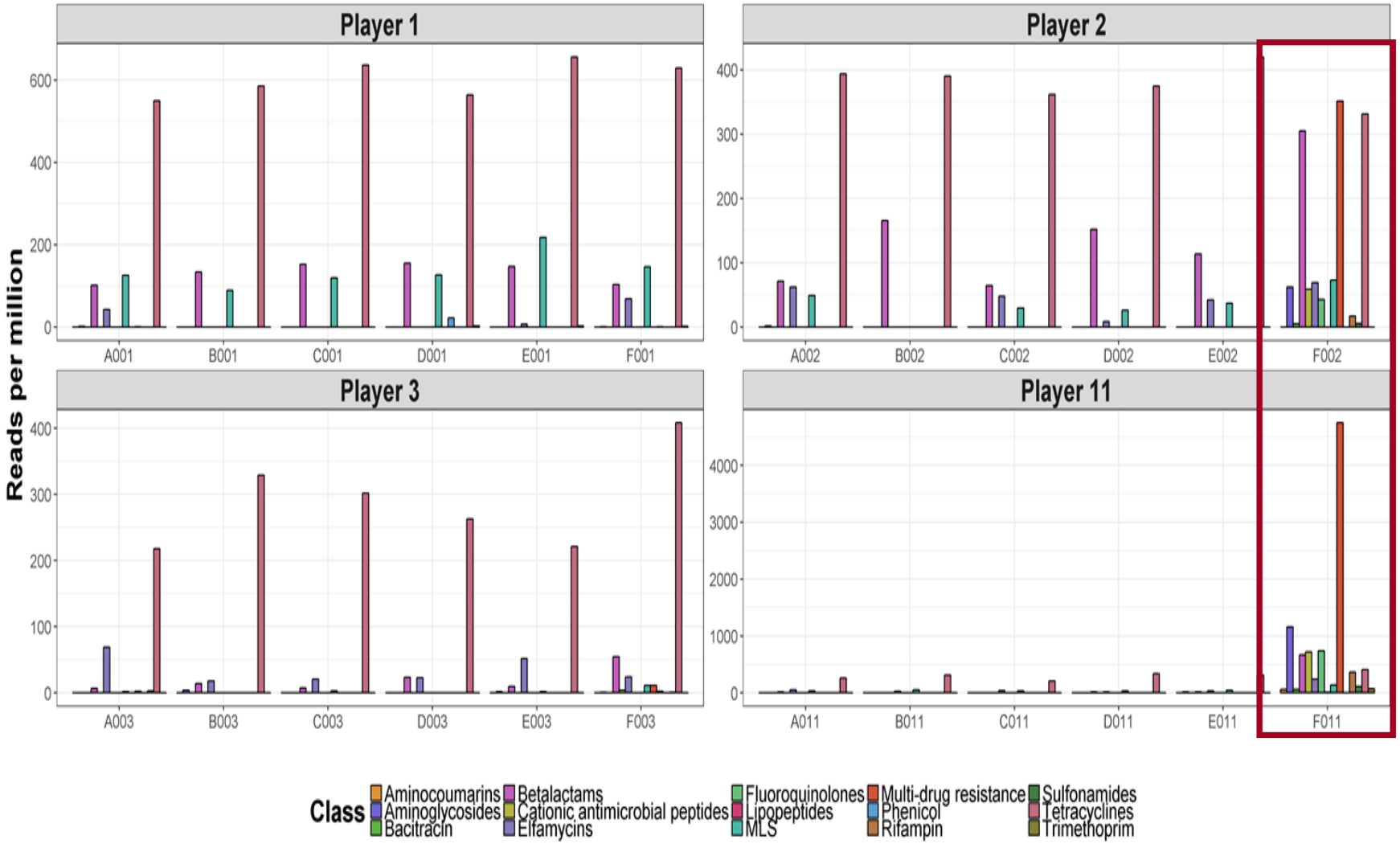


Microbial stability



Functional Analysis

Antibiotic resistance gene profiles

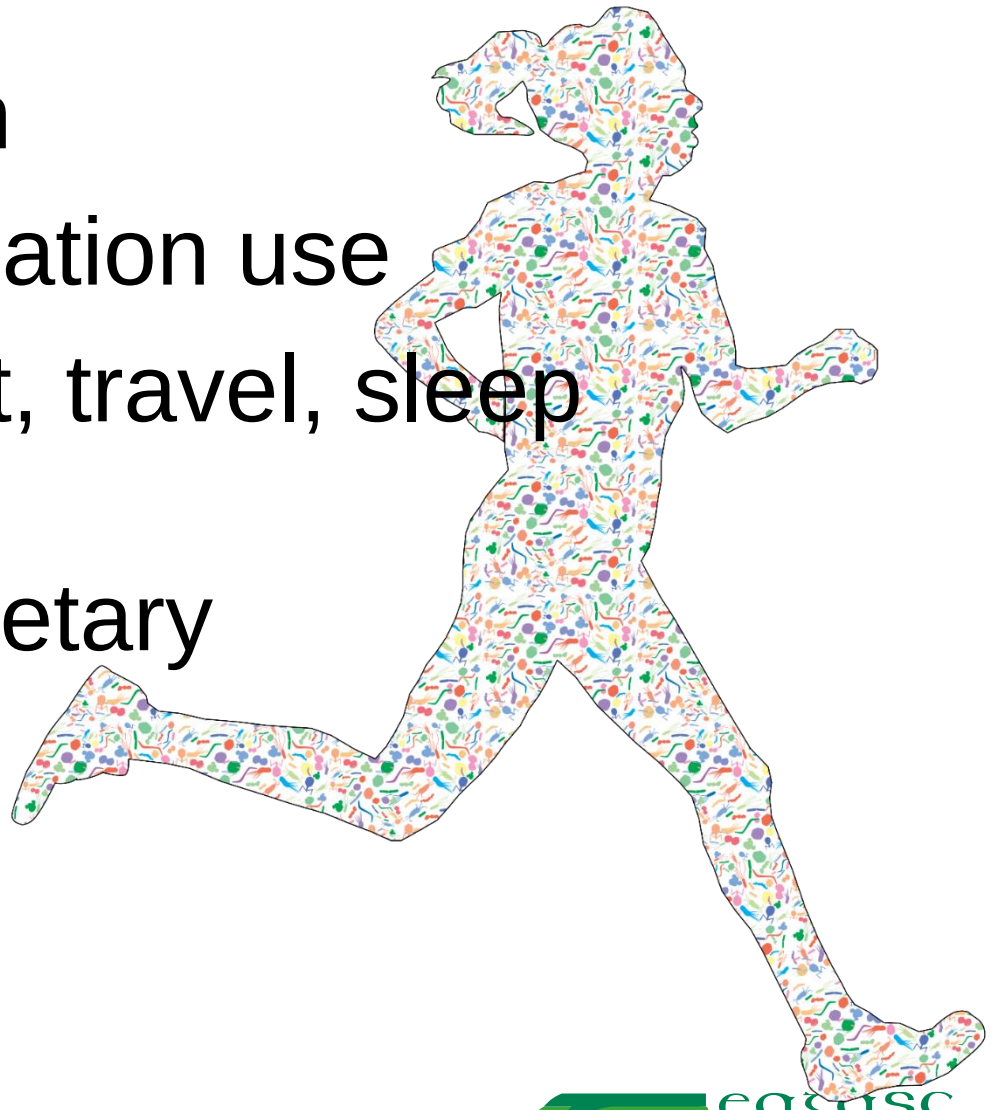


Conclusions

- Travel and associated dietary alterations impacts the gut microbiome.
- Microbiome is stable in those who didn’t report GI distress.
- In athletes who reported GI distress there was an increase in Antibiotic resistance and virulence genes.
- Scope to test the use of prophylactic probiotic.

Why study microbiome for performance

- Non-invasive measure of health
- changes following illness/medication use
- Pre-empt impacts of stress, diet, travel, sleep patterns injury etc.
- Supports the effectiveness of dietary interventions
- Monitor GI distress



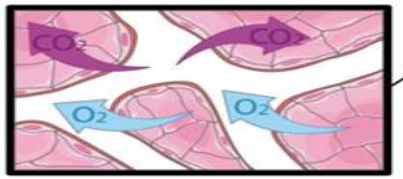
Fitness and gut health

Influencing factors

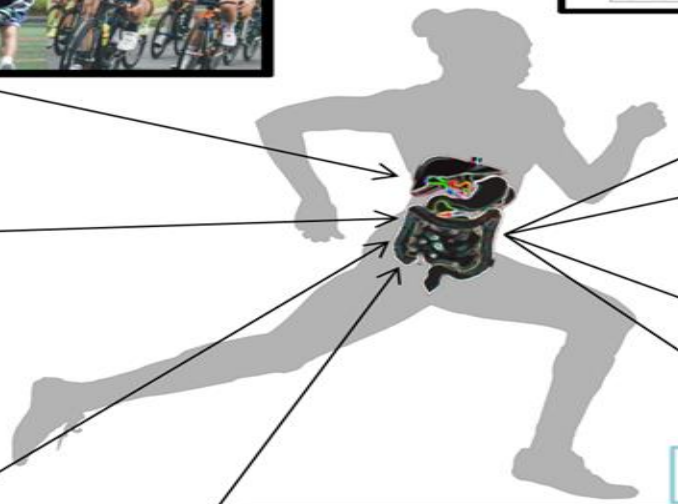
Type of sport

Travel

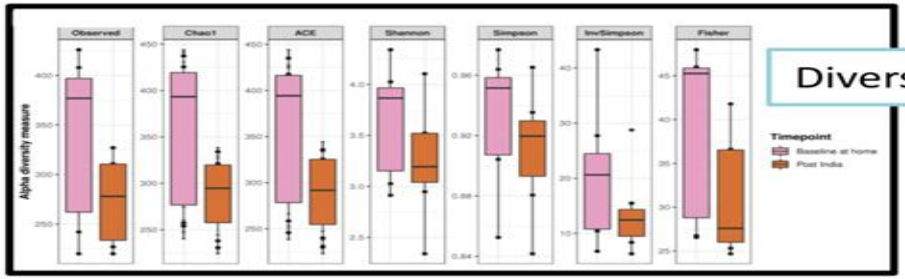
VO_2 max



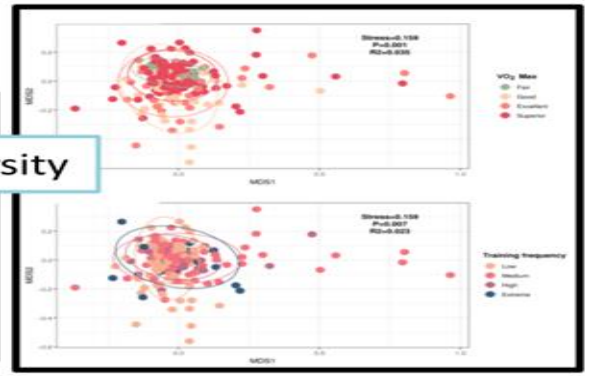
Training frequency



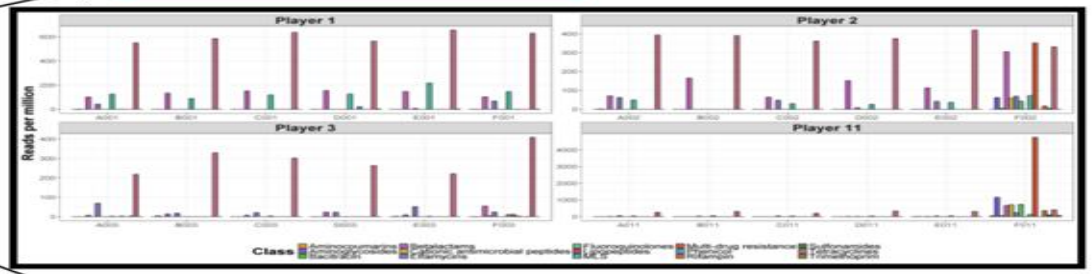
Gut microbiome aspects impacted



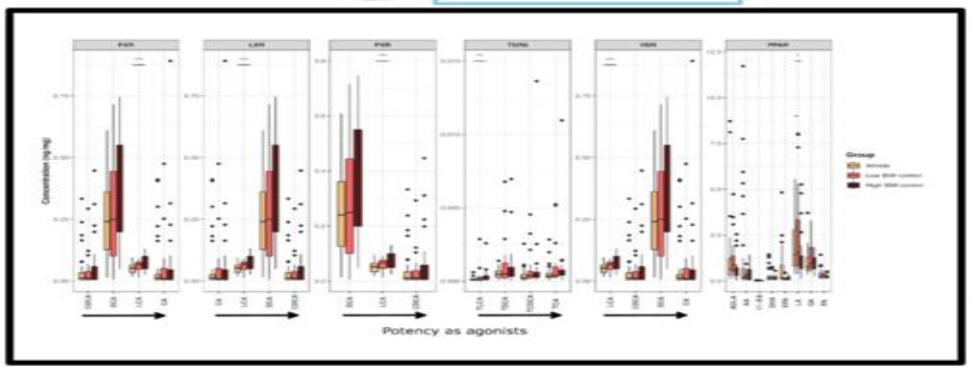
Diversity



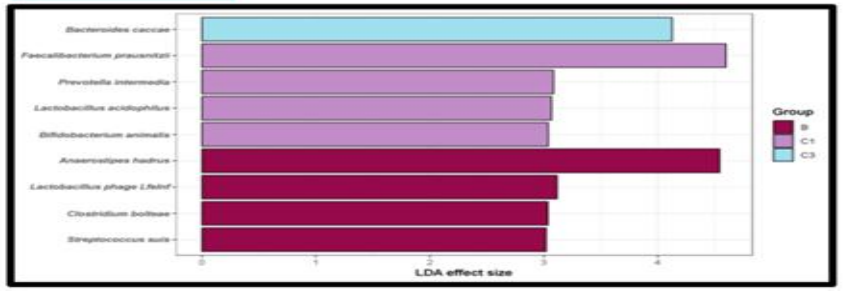
Antibiotic resistance



Metabolites



Species



Acknowledgements

- Prof. Paul Cotter
- Prof. Fergus Shanahan
- Dr. Fiona Crispie
- Dr. Peter Skuse
- Dr. Sharon Madigan
- Prof. Mick Molloy
- Eanna Falvey
- Dr. Eileen Murphy
- Trevor Woods
- Helena Nugent
- Dr. Siobhan Clarke
- Dr. Ciara O'Donovan
- Dr. Wiley Barton
- Dr Owen Cronin

All athletes both elite and non

IronMan study

- Dr. Jamie Pugh
- Dr . Greg Grosicki
- Dr. Susan Joyce
- Prof Graeme Close
- Karina Quitler
- Dr. Laura Wosniska

Metabolomics (Imperial College London)

Prof. Elaine Holmes

Dr. Nicholas Penney

Dr. Isabel Garcia-Perez

"Between gut instincts, gut feelings and gut reactions my abs get a great workout."