

Supplementary **Table 1.** Detailed study characteristics and outcomes of included studies investigating the effects of nutritional supplements, diet, and exercise on gut microbiota composition and athletic performance.

This table presents expanded data corresponding to the summary in Table 4 of the main manuscript.

Author, study design	N_Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
Probiotic and Postbiotic studies – single strain				
Gross et al. [22] RXT	N = 7 (3 male and 4 female), physically active Probiotic vs placebo <i>Veillonella atypica</i> FB0054, 14 d.	<i>α</i> -diversity, Shannon entropy ^{NS} between groups (p > 0.05) Baseline: 3.97 Pla: 3.96 Washout: 4.12 Int: 4.10 <i>β</i> -diversity, Bray curtis ^{NS} between grps No changes in specific taxa or functions after Pla, washout, or Int	Not reported	Treadmill TTE (s) at 100% $\dot{V}O_2$ peak Int: 346.1 ± 204.6 to 285.0 ± 204.3, PLA: 320.0 ± 317.6 to 306.7 ± 269.6 ^{NS} between groups Δ within group (mean difference ± SE) Int: 13.29 ± 100.13 s, 95% CI: - 79.32, 105.89, (p = 0.738) Pla: 61.14 ± 72.04 s, 95% CI: - 5.49, 127.77, (p = 0.066) Correlation Int: No correlation (r = 0.09) between Δ in <i>β</i> -diversity and Δ in TTE
Huang et al. [23] RCT	N = 20 male, triathletes Probiotic vs placebo <i>Lactiplantibacillus plantarum</i> PS128, 4 wk.	<i>α</i> -diversity, Shannon index Int: 4.4 Pla: 4.7 Int < Pla (p < 0.05) No baseline data reported. % Relative abundance (Phyla) Int: <i>Bacillota</i> 46.6%, <i>Bacteroidota</i> 47.0%, <i>Proteobacterota</i> 3.8%, <i>Actinomycetota</i> 2.1%, <i>Fusobacterota</i> 0.3% Pla: <i>Bacillota</i> 50.3%, <i>Bacteroidota</i> 41.6%, <i>Proteobacterota</i> 4.9%, <i>Actinomycetota</i> 1.0%, <i>Fusobacterota</i> 1.5% ^{NS} between groups. Relative abundance (Genus) <i>Anaerotruncus</i> (x10 ⁻⁴): Int 0, Pla 1.0 <i>Caproiciproducens</i> (x10 ⁻⁴): Int 0.1, Pla 1.0 <i>Coprobacillus</i> (x10 ⁻⁵): Int 0, Pla 3.3 <i>Desulfovibrio</i> (x10 ⁻⁵): Int 0, Pla 5.9 <i>Dielma</i> (x10 ⁻⁵): Int 0, Pla 2.6 <i>Family_XIII_UCG_001</i> (x10 ⁻⁵): Int 0.9, Pla 9.2	Acetic acid (mean, post only) Int: 4.7 ng/ml, Pla: 3.8 ng/ml Int > Pla (p < 0.05) Propionic acid (mean, post only) Int: 1.18 ng/ml, Pla: 0.5 ng/ml Int > Pla (p < 0.05) Butyric acid (mean, post only) Int: 0.5 ng/ml, Pla: 0.3 ng/ml Int > Pla (p < 0.05) Decanoic acid (mean, post only) Int: 0.005 ng/ml, Pla: 0.002 ng/ml ^{NS} Heptanoic acid (mean, post only) Int: 0.6 ug/ml, Pla: 0.4 ug/ml ^{NS} Hexanoic acid (mean, post only) Int: 1.7 ug/ml, Pla: 4.0 ug/ml ^{NS} Isobutyric acid (mean, post only)	Treadmill TTE (s) (mean, post only) Int: 1679 Pla: 1083 Int > Pla (p < 0.05) $\dot{V}O_{2max}$ (ml / kg / min) (mean, post only) Int: 59.2 Pla: 57.2 ^{NS} Correlation No correlation analysis between performance and microbiota reported.

Author, study design	N Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
		<i>Holdemania</i> (x10 ⁻⁵): Int 0.6, Pla 7.2 <i>Oxalobacter</i> (x10 ⁻⁵): Int 0, Pla 6.1 Int < Pla (p < 0.05) <i>Akkermansia</i> (x10 ⁻³): Int 5.0, Pla 1.3; <i>Bifidobacterium</i> (x10 ⁻²): Int 1.5, Pla 0.8; <i>Butyricimonas</i> (x10 ⁻³): Int 4.7, Pla 2.3; <i>Lactobacillus</i> (x10 ⁻³): Int 1.7, Pla 0.7; Int > Pla (p < 0.05)	Int: 0.050 ng/ml, Pla: 0.052 ng/ml ^{NS} <i>Isovaleric acid (mean, post only)</i> Int: 0.03 ng/ml, Pla: 0.04 ng/ml ^{NS} <i>Octanoic acid (mean, post only)</i> Int: 1.1 ug/ml, Pla: 0.7 ug/ml ^{NS} <i>Valeric acid (mean, post only)</i> Int: 0.07 ng/ml, Pla: 0.07 ng/ml ^{NS}	
Lee et al. [40] RCT	N = 53 (26 male and 27 female), physically active Probiotic vs heat-killed probiotic vs placebo TWK10: viable <i>Lactiplantibacillus plantarum</i> TWK10-hk: heat-killed <i>Lactiplantibacillus plantarum</i> , 6 wk.	<i>α</i> -diversity, Shannon index (median) ^{NS} within or between grps <i>β</i> -diversity, post intervention, between grp NMDS analysis with unweighted UniFrac: ^{NS} between TWK10 and TWK10-hk (p = 0.063) ^{NS} between TWK10 and Control (p-value not shown) TWK10-hk significant difference between Control (p = 0.036) <i>Unweighted UniFrac</i> : TWK10 significant difference between TWK10-hk (p < 0.0001) ^{NS} between TWK10 and Control (p = 0.072) ^{NS} between TWK10-hk and Control (p = 0.072) <i>β</i> -diversity, within grp TWK10-hk: significant difference (p < 0.0001, weighted UniFrac; p = 0.031, unweighted UniFrac). TWK10: ^{NS} (p = 0.172, weighted UniFrac; p-value not shown, unweighted UniFrac) Control: significant difference (p-value not shown, weighted UniFrac; p = 0.027, unweighted UniFrac) <i>Relative abundance (%) (Phylum)</i> <i>Bacillota</i> , <i>Bacteroidota</i> , <i>Actinomycetota</i> , <i>Proteobacterota</i> , <i>Verrucomicrobiota</i> : ^{NS} between grps <i>Family</i> <i>Akkermansiaceae</i> , <i>Enterobacteriaceae</i> , <i>Lactobacillaceae</i> , <i>Peptostreptococcaceae</i> , <i>Eggerthellaceae</i> , <i>Atopobiaceae</i> : ^{NS} between grps <i>Genus</i>	<i>All data reported in mM wet faeces</i> <i>Acetate</i> TWK10 Pre 5.30 ± 1.96 Post 8.56 ± 3.37 (p < 0.05) TWK10-hk Pre 6.48 ± 2.14 Post 10.63 ± 6.17 (p < 0.05) Control Pre 7.17 ± 2.53 Post 9.67 ± 5.25 ^{NS} ^{NS} between grps <i>Propionate</i> TWK10 Pre 2.00 ± 1.27 Post 2.51 ± 2.16 ^{NS} TWK10-hk: Pre 2.12 ± 0.88 Post 3.80 ± 3.81 (p = 0.0857) Control Pre 2.20 ± 0.44 Post 2.67 ± 1.11 ^{NS} ^{NS} between grps <i>Butyrate</i> TWK10: Pre 0.76 ± 0.56 Post 1.15 ± 0.64 (p = 0.0744) TWK10-hk: Pre 1.11 ± 0.71 Post 1.33 ± 0.77 ^{NS} Control Pre 0.96 ± 0.69 Post 1.45 ± 0.86 ^{NS} ^{NS} between grps	<i>Treadmill, TTE (min) at 85% $\dot{V}O_{2max}$</i> Post intervention: TWK10 17.55 ± 3.98 TWK10-hk 16.72 ± 5.91 Control 12.23 ± 2.08 TWK10 > Control (p < 0.001) TWK10-hk > Control (p < 0.001) Within grp: TWK10 ↑1.38-fold (p < 0.001) TWK10-hk ↑ 1.33-fold (p < 0.001) Control ^{NS} <u>Correlation</u> TWK10: TTE positively correlated with <i>Coriobacteriaceae</i> family (r = ~0.5) (p < 0.01). TWK10-hk: TTE positively correlated with <i>Veillonellaceae</i> family (r = 0.65) (p < 0.01) and negatively correlated with: <i>Eubacterium coprostanoligenes</i> , <i>Erysipelatoclostridiaceae</i> and <i>Lachnospiraceae</i> (correlation coefficient represented on heatmap, difficult to extract data) (p < 0.05).

Author, study design	N Intervention protocol	Microbiota measure/s#	SCFA measure/s#	Performance measure/s#
		<i>Faecalibacterium</i> , <i>Akkermansia</i> , <i>Roseburia</i> , <i>Escherichia-Shigella</i> , <i>Lachnospira</i> , <i>Lactococcus</i> , <i>Oscillibacter</i> : ^{NS} between grps (Phylum), within grp, compared to baseline <i>TWK10-hk</i> ↑ <i>Pseudomonadota</i> (p = 0.030) Family <i>TWK10</i> ↑ <i>Lactobacillaceae</i> (p = 0.039) <i>TWK10-hk</i> ↑ trend <i>Enterobacteriaceae</i> (p = 0.072), ↓ <i>Peptostreptococcaceae</i> (p = 0.030) Genus <i>TWK10</i> ↓ <i>Lachnospira</i> (p = 0.022) and ↓ trend <i>Faecalibacterium</i> (p = 0.077) <i>TWK10-hk</i> ↑ <i>Lactococcus</i> (p = 0.046) and <i>Escherichia-Shigella</i> (p = 0.038)		
Li et al. [28] RCT	N = 16 male, National top level cross-country skiers Probiotic vs control Yogurt with <i>Bifidobacterium animalis subsp. lactis</i> BL-99, 8 wk.	<i>α</i> -diversity, Shannon index Post Int: ^{NS} between grps (p = 0.28) <i>β</i> -diversity ^{NS} between grps (data not shown). Relative abundance, within grp, compared to baseline Control: ↑ two-fold <i>Bifidobacterium animalis</i> Int: ↑ forty-fold <i>Bifidobacterium animalis</i> No further data shown. Authors do not explicitly state whether there was a statistical significant difference between grps.	<i>Acetic acid</i> Int: ↑ 4.5 fold. Control: ↑ 3.4 fold ^{NS} Int > Control (p < 0.05) <i>Propanoic acid</i> Int: ↑ 2.0 fold. Control: ↑ 2.0 fold ^{NS} ^{NS} between grps <i>Butyric acid</i> Int: ↑ 4.0 fold. Control: ↑ 5.0 fold ^{NS} ^{NS} between grps <i>Valeric acid</i> Int: ↑ 2.0 fold. Control: ↑ 2.0 fold ^{NS} ^{NS} between grps <i>Correlation</i> Positive correlation (r > 0.5) between <i>Bifidobacterium animalis</i> and acetic acid, propanoic acid, butyric acid, valeric acid (p < 0.05)	<i>Treadmill</i> , $\dot{V}O_{2max}$ (ml / kg / min) Control: 55.9 ± 4.4 to 61.8 ± 3.2 (p < 0.01) Int: 55.8 ± 5.4 to 64.5 ± 2.6 (p < 0.01) <i>Post intervention:</i> Int > Control (p < 0.02) <i>60°/s Knee Joint Extensor Strength</i> (Nm/kg) Int: 5.0 ± 0.4 to 5.7 ± 0.4 (p < 0.01). Control 5.2 ± 0.6 to 5.1 ± 0.2 ^{NS} <i>60°/s Knee Joint Flexor Strength</i> Int: 2.0 ± 0.4 to 2.9 ± 0.6 (p < 0.05) Control: 2.3 ± 0.4 to 2.8 ± 0.5 ^{NS} <i>180 °/s Knee Joint Extensor Strength</i> Int: 4.0 ± 0.5 to 4.8 ± 0.6 (p < 0.05) Control: 3.9 ± 0.4 to 4.5 ± 0.5 (p < 0.05) <i>180 °/s Knee Joint Flexor Strength</i> Int: 2.2 ± 0.3 to 2.5 ± 0.6 ^{NS} Control: 2.1 ± 0.2 to 2.3 ± 0.5 ^{NS} <i>60°/s Knee Joint Extensor Strength, between grp, post intervention</i> Int: 5.7 ± 0.4 Control: 5.1 ± 0.2 (p < 0.05)
Lin et al. [25] RCT	N =21 (14 male and 7 female), well trained	Relative abundance (Phylum), post intervention Int: ↑ <i>Actinomycetota</i> and <i>Bacillota</i> vs Pla. Int: ↓ <i>Pseudomonadota</i> vs Pla.	Not measured	<i>12 min Cooper's Test</i> <i>3rd, 6th, 9th, 12th min: Total distance (m)</i>

Author, study design	N_Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
	middle and long distance runners Probiotic vs placebo <i>Bifidobacterium longum subsp. longum</i> , 5 wk.	(p values not shown) <i>Genus:</i> Int: ↑ <i>Bifidobacterium</i> vs Pla (p = 0.0027). 9 fold ↑ in <i>Lactobacillus</i> count. <i>Species:</i> <i>Bifidobacterium longum subsp. longum</i> : Int: 0.95% ; ↑ 8.63-fold (p = 0.0178) Pla: 0.11% ^{NS} in amounts of common strains		^{NS} between grps at any time point (p > 0.05) <i>Δ in distance Pre to Post intervention</i> 6 th minute Int 72 ± 14 m Pla 4 ± 9m Int > Pla (p = 0.0014) 9 th minute: Int 116 ± 17 m Pla - 27 ± 21m Int > Pla (p = 0.0001) 12 th minute: Int 105 ± 16 m Pla - 56 ± 29m Int > Pla (p = 0.0001) <i>Post- vs Pre-test running distance, within grp</i> Int: ↑ at 3rd (p = 0.0051), ↑ at 6th (p = 0.0004), ↑ at 9th (p < 0.0001), and ↑ at 12th min (p < 0.0001) Pla: ↑ at 3rd min (p = 0.0051)
McDermott et al. [30] RCT	N = 28 (13 male and 15 female), runners Probiotic vs placebo <i>Lactobacillus helveticus</i> Lafti L10, 6 wk.	<i>Relative abundance, baseline</i> Int and Pla: No detectable levels of <i>Lactobacillus helveticus</i> Lafti L10. <i>Post intervention:</i> Int: <i>Lactobacillus helveticus</i> Lafti L10 recovered in 8/14, median strain recovery 10 ^{4.37} bacteria/mL (non-zero minimum: 10 ^{4.35} bacteria / mL; maximum: 10 ^{7.18} bacteria / mL) Pla: <i>Lactobacillus helveticus</i> Lafti L10 not detected No statistical testing of between grp changes	Not measured	<i>Treadmill, TTE (s)</i> Int: 1655 ± 230 to 1547 ± 215 (p = 0.23) Pla: 1344 ± 188 to 1565 ± 219 (p = 0.01) <i>Post intervention:</i> Int < Pla (p = 0.01)
West et al. [37] RCT	N = 88 (64 male and 35 female recruited), competitive cyclists Probiotic vs placebo <i>Limosilactobacillus fermentum</i> VRI-003 PCC, 11 wk.	<i>Microbiome Diversity16S rRNA</i> ^{NS} Δ's in bacterial diversity (data not shown) <i>All data reported as raw bacterial counts – no statistical testing of between grp changes.</i> <i>Total bacteria</i> Males: Int ↓ 0.5 × 10 ¹⁰ , Pla Pre: ↓ 0.5 × 10 ¹⁰ Females: Int ↑ 0.7 × 10 ¹⁰ , Pla ↓ 1.0 × 10 ¹⁰ <i>C. coccoides</i> Males: Int ↓ 2.3 × 10 ⁸ , Pla ↓ 3.4 × 10 ⁸ Females: Int ↔ 0, Pla ↓ 1.54 × 10 ⁹ <i>E. coli</i> Males: Int ↑ 6.4 × 10 ⁵ , Pla ↑ 6.8 × 10 ⁵ Females: Int ↑ 1.36 × 10 ⁷ , Pla ↑ 4.3 × 10 ⁴ <i>Bifibacteria</i> Males: Int ↓ 0.3 × 10 ⁷ , Pla ↓ 5.6 × 10 ⁶ Females: Int ↑ 0.7 × 10 ⁶ , Pla ↓ 6.1 × 10 ⁶ <i>Bacteroides</i> Males: Int ↑ 0.6 × 10 ⁶ , Pla ↑ 1.6 × 10 ⁶ Females: Int ↑ 1.3 × 10 ⁶ , Pla ↓ 4.4 × 10 ⁷	Not measured	<i>Incremental cycling ergometer test, $\dot{V}O_{2max}$</i> No substantial effect on training patterns or performance in post-testing $\dot{V}O_{2max}$ in Int vs Pla (data not shown).

Author, study design	N Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
		<i>Lactobacillus</i> Males: Int $\uparrow 5.8 \times 10^4$, Pla $\downarrow 2.8 \times 10^6$ Females: Int $\uparrow 7.0 \times 10^4$, Pla $\uparrow 6.9 \times 10^4$		
Wu et al. [38] RCT	N = 105 (75 male and 30 female), physically active Probiotic vs heat-treated probiotic vs placebo <i>Lactocaseibacillus paracasei</i> PS23 (L-PS23) HT-PS23, 6 wk.	<i>α-diversity, Shannon index and Chao1</i> Post Int: ^{NS} within or between grps <i>β-diversity, post intervention</i> L-PS23: significant difference vs Pla (p = 0.006) HT-PS23: ^{NS} vs Pla (p = 0.868) No baseline data reported. <i>Relative abundance (log10) (Genus), post intervention</i> <i>Lactocaseibacillus</i> : L-PS23 0.003 Pla 0.0002 (p < 0.05) <i>Streptococcus</i> : L-PS23 0.03 Pla 0.014 (p < 0.05) <i>Blautia</i> : L-PS23 0.1 Pla 0.070 (p < 0.05) <i>Lactobacillus</i> : L-PS23 0.0006 Pla 0.00008 (p < 0.05) L-PS23 > Pla (p < 0.05) <i>Prevotella</i> : L-PS23 0.03 Pla 0.093 (p < 0.05) L-PS23 < Pla (p < 0.05) <i>Lactocaseibacillus</i> : HK-PS23 0.0018 Pla 0.00026 <i>Collinsella</i> : HK-PS23 0.025 Pla 0.015 HT-PS23 > Pla (p < 0.05)	<i>SCFA (mg/g wet faeces)</i> <i>Acetic acid, propionic acid, butyric acid, isobutyric acid, valeric acid, or isovaleric acid</i> L-PS23 ^{NS} HT-PS23 ^{NS} Pla ^{NS} ^{NS} between grps	<i>Countermovement Jump (CMJ)[†]</i> <i>Post-EIMD compared to Pre-EIMD</i> All grps: At 3, 24 and 48 hrs, lower % changes in RFD and relative force peak (p < 0.05) L-PS23 and HT-PS23 less reduction in RFD vs Pla at 24 and 48 hrs (p < 0.0001) L-PS23 and HT-PS23 less reduction in relative force peak vs Pla at 3 and 24 hrs (p < 0.05) HT-PS23 less reduction in relative force peak vs Pla at 48 hrs (p = 0.0008) L-PS23 and HT-PS23 less reduction in CMJ vs Pla at 24 hrs (p < 0.05) HT-PS23 less reduction in CMJ vs Pla at 48 hrs (p = 0.0097) HT-PS23: ^{NS} from pre-EIMD in CMJ Time effect for RFD, relative peak force and CMJ (p < 0.0001) <i>Isotonic Muscle Strength: IMTP</i> <i>Post-EIMD compared to Pre-EIMD</i> All grps: At 3, 24 and 48 hrs, % changes in RFD and relative force peak were lower (p < 0.05) L-PS23 significantly less reduction in relative force peak vs Pla at 3 and 24 hrs (p < 0.05). HT-PS23 significantly less reduction in relative force peak vs Pla at 3, 24 and 48 hrs (p < 0.05) Time effect (p < 0.0001) <i>RFD</i> L-PS23 and HT-PS23: Less loss of peak RFD at 3, 24 and 48 hrs vs Pla (p < 0.05) Time effect (p < 0.0001) <i>Wingate Anaerobic Test (WAnT)</i> <i>Post-EIMD compared to pre-EIMD</i> All grps: At 3, 24 and 48 hrs, % changes in relative mean power and relative peak power were lower (p < 0.0001) L-PS23 and HT-PS23 less reduction of relative mean power vs Pla at 3, 24 and 48 hrs (p < 0.05) L-PS23 and HT-PS23 less reduction of relative peak power vs Pla at 24 and 48 hrs (p < 0.05) Time effect for relative mean power and relative peak power (p < 0.0001)

Author, study design	N Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
				<i>Fatigue Index:</i> <i>Post-EIMD compared to pre-EIMD</i> All grps: At 3, 24 and 48 hrs, % changes were greater (p < 0.0001) HT-PS23 lower increase at 24 hrs vs Pla (p < 0.05). L-PS23 and HT-PS23 smaller increases vs Pla at 48 hrs, (p < 0.05) Time effect (p < 0.0001) <i>Correlation</i> Data difficult to extract, represented in heat map: <i>Lactacaseibacillus</i> , <i>Streptococcus</i> , <i>Blautia</i> , <i>Lactobacillus</i> : positive correlation with improved performance in CMJ, IMTP, and WAnT, weak to moderate (r = 0.1 to 0.3). <i>Prevotella</i> : negative correlation with exercise performance including RFD % 24 hrs (r = --0.3), Wingate relative peak power (%) 48 hrs and Wingate Fatigue Index (%) 24 hrs (r = -- 0.2)
Probiotic studies – multi-strain				
Przewłócka et al. [35] Study 1 RCT	N = 23 male, well trained MMA athletes Probiotic vs control <i>Bifidobacterium lactis</i> W51, <i>Levilactobacillus brevis</i> W63, <i>Lactobacillus acidophilus</i> W22, <i>Bifidobacterium bifidum</i> W23, and <i>Lactococcus lactis</i> W58 + 5 mL Vit D3, 4 wk.	This was assessed in Przewłócka et al. [45].	This was assessed in Przewłócka et al. [45].	<i>Cycle ergometer, supramaximal sprints, triple WAnT</i> <i>W_{tot} (J/kg)</i> Int: 232 ± 14.06 to 240.72 ± 13.38 (p = 0.04) Control: 239.34 ± 19.46 to 238.37 ± 14.35 ^{NS} ^{NS} between grps <i>P_{max} (W/kg)</i> Int: 9.80 ± 0.83 to 10.00 ± 0.65 ^{NS} Control: 10.47 ± 0.95 to 10.39 ± 1.22 ^{NS} ^{NS} between grps <i>P_{max} (time (s))</i> Int: 6.67 ± 1.13 to 6.93 ± 1.88 ^{NS} Control: 6.93 ± 2.02 to 6.38 ± 1.56 ^{NS} ^{NS} between grps <i>MP (W/kg)</i> Int: 7.73 ± 0.47 to 8.02 ± 0.45 (p = 0.04) Control: 7.98 ± 0.65 to 7.95 ± 0.48 ^{NS} ^{NS} between grps <i>FI (w/kg/s)</i> Int: 0.17 ± 0.04 to 0.17 ± 0.04 ^{NS} Control: 0.20 ± 0.04 to 0.18 ± 0.06 ^{NS} ^{NS} between grps

Author, study design	N Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
Przewłócka et al. [34] Study 2 RCT	N = 23 male, well trained MMA athletes Probiotic vs control <i>Bifidobacterium lactis</i> W51, <i>Levilactobacillus brevis</i> W63, <i>Lactobacillus acidophilus</i> W22, <i>Bifidobacterium bifidum</i> W23, and <i>Lactococcus lactis</i> W58 + 5 mL Vit D3, 4 wk.	<i>α</i> -Diversity, Inverted Simpson ^{NS} between grps (p = 0.086) β-diversity, Bray-Curtis, within grp Int: Significant Δ (p = 0.0005) Control: ^{NS} Δ (p = 0.145) Did not report difference between grps <i>Total abundance</i> Between grp <i>Class:</i> <i>Negativicutes</i> Int > Control (Est pairwise = 2.23, p = 0.032) <i>Firmicutes</i> Int < Control (Est pairwise = - 1.65, p = 0.009) <i>Family:</i> <i>Lachnospiraceae</i> Int < Control (Est pairwise = - 1.27, p < 0.001) <i>Peptostreptococcaceae</i> Int < Control (Est pairwise = - 2.69, p = 0.004) <i>Lactobacillaceae</i> Int < Control (Est pairwise = - 2.04, p = 0.018) <i>Genus:</i> <i>Faecalibacterium</i> Int > Control (Est pairwise = 1.21, p = 0.013) <i>Prevotella</i> Int > Control (Est pairwise = - 1.01, p = 0.002) <i>Collinsella</i> Int < Control (Est pairwise = - 0.93, p = 0.038) <i>Bacteroides</i> Int < Control (Est pairwise = - 0.041, missing p-value) <i>Species:</i> <i>Bacteroides fluxus</i> Int > Control (Est pairwise = 2.02, p = 0.002) <i>Roseburia inulinivorans</i> Int > Control (Est pairwise = 1.40, p = 0.005) <i>Within grp</i> <i>Class:</i> Int: ↑ <i>Negativicutes</i> (Est = 1.98, p = 0.006), ↓ <i>Firmicutes</i> (Est = - 1.68, p < 0.001). Control: ↓ <i>Firmicutes</i> (Est = - 0.75, p = 0.021). <i>Family:</i> Int: ↓ <i>Lachnospiraceae bacterium</i> (Est = -1.55, p < 0.001), ↓ <i>Peptostreptococcaceae bacterium</i> (Est = - 1.86, p = 0.005), <i>Genus:</i>	<i>SCFA (acetic acid, propionic acid, butyric acid, valeric acid) (%)</i> ^{NS} between grps <i>Post-intervention:</i> Propionate: Int ↓ ^{NS} Control ↓ (p = 0.004) Int < Control (p = 0.061)	<i>Graded cycle ergometry test</i> <i>$\dot{V}O_{2max}$ (ml/kg/min)</i> Int: 56.92 ± 0.83 to 56.37 ± 7.09 (p = 0.969) Control: 52.33 ± 5.06 to 52.48 ± 3.76 (p = 0.999) ^{NS} between grps <i>MAP (W)</i> Int: 317.50 ± 45.72 to 330.00 ± 42.16 (p = 0.096) Control 306.82 ± 33.70 to 311.36 ± 40.87 (p = 0.940) ^{NS} between grps <i>TTE (s)</i> Int: 496.30 ± 89.98 to 559.00 ± 68.99 (p = 0.023) Control: 489.91 ± 72.02 to 468.55 ± 102.03 (p = 0.685) Authors did not state whether there was a significant difference between grps at post-intervention.

Author, study design	N Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
		Int: ↑ <i>Bacteroides</i> (Est = 0.259, p < 0.001), ↑ <i>Faecalibacterium</i> (Est = 1.03, p = 0.002), ↑ <i>Prevotella</i> (Est = 3.62, p < 0.001), ↓ <i>Collinsella</i> (Est = - 1.28, p = 0.003) <i>Species:</i> Int: ↑ <i>Bacteroides fluxus</i> (Est = 2.11, p < 0.001), ↑ <i>Roseburia inulinivorans</i> (Est = 0.74, p = 0.030)		
Wang et al. [36] RCT	N = 19 (15 male and 4 female), active amateur marathon runners Probiotic vs placebo <i>Lactobacillus acidophilus</i> and <i>Bifidobacterium longum</i> , 5 wk.	Heatmap illustrating relative abundance of top 12 bacterial Phyla, difficult to extract data therefore qualitative analysis provided. <i>Relative abundance (Phylum)</i> Int: More abundant <i>Bacteroidota</i> , <i>Bacillota</i> , <i>Pseudomonadota</i> , and <i>Actinomycetota</i> vs Pla. (p-values not shown). <i>Genus:</i> <i>Lacticaseibacillus</i> : Int > Pla (p = 0.001). <i>Olsenella</i> , <i>Weissella</i> , and <i>Anaerostipes</i> : Int > Pla (p < 0.05). <i>Cloacibacillus</i> and <i>Alphaproteobacteria unclassified</i> : Int < Pla (p < 0.01). Pre to post intervention: Int: ↑ in <i>Bifidobacterium longum</i> ^{NS}	Not measured	<i>Cooper's Test</i> <i>Total distance (km)</i> Int: 2.88 ± 0.57 to 3.01 ± 0.60 (p < 0.05) Pla: 2.68 ± 0.41 to 2.71 ± 0.44 (p > 0.05) ^{NS} between grps (p = 0.323)
Önes et al. [32] RCT	N = 21 female, professional soccer players Probiotic vs control Kefir, 28 d.	<i>α-Diversity, Shannon index</i> ^{NS} between grps. <i>Chao1 richness index</i> Int: ^{NS} between pre- and post-intervention (p > 0.05). <i>β-diversity</i> Significant difference between Int and Control (Bray–Curtis, p = 0.018; Jaccard, p = 0.016). Int: ^{NS} between pre- and post-intervention <i>Relative abundance (%)</i> <i>Phylum:</i> Dominant Phyla: <i>Bacillota</i> and <i>Bacteroidota</i> in all conditions. Int: ↓ <i>Pseudomonadota</i> Pre 2.6% Post 2.4% Int: ↑ <i>Verrucomicrobiota</i> Pre 1.9% Post, 3.3% Int: ↑ <i>Euryarchaeota</i> Pre 1.4% Post, 3.0% (no p-values reported)	Not measured	<i>VO_{2max} and finishing speeds, 30-15 Intermittent Fitness Test (IFT)</i> Pre- and post-intervention values not explicitly reported. No numerical comparison of changes in <i>VO_{2max}</i> or finishing speed between groups provided. Int: Athletes categorised into high performance grp exhibited a higher abundance of <i>Faecalibacterium prausnitzii</i> (27.19%) and <i>P. copri</i> (17.48%) (p-value not reported). Int: Athletes categorised into low-performance grp had a higher relative abundance of <i>Dorea formicigenerans</i> (28.43%) and <i>Oxalobacter formigenes</i> (25.89%) (p-value not reported). Other correlations reported between athletic performance and microbiota ^{NS}

Author, study design	N_Intervention protocol	Microbiota measure/s#	SCFA measure/s#	Performance measure/s#
		<i>Genus:</i> Dominant Genus included <i>Prevotella</i>, <i>Bacteroides</i>, and <i>Faecalibacterium</i> in all groups. Int: ↓ <i>Bacteroides</i> Pre 15.7% Post, 13.5% Int: ↓ <i>Faecalibacterium</i> Pre 14.8% Post 13.6% Int: ↑ <i>Akkermansia</i> Pre 2.4% Post 4.1% Int: ↑ <i>Bifidobacterium</i> Pre 2.4% Post 4.1% (no p-values reported) <i>Species:</i> Int: ↑ <i>A. muciniphila</i> Pre 4.1% Post 8.5% Int: ↑ <i>Roseburia faecis</i> Pre 6.4% Post 7.5% (no p-values reported)		
<i>Nutrient</i>				
Morita et al. [39] RCT	N = 31 male, physically active	<i>α-Diversity</i> ^{NS} difference between grps. <i>β-diversity</i> ^{NS} differences between grps. <i>Relative abundance</i> <i>After 4 and 8 wks, between grps:</i> FL and αCD groups: ^{NS} ↑ <i>B. uniformis</i> vs Pla. <i>At 4 and 8 wks compared to baseline, within grps:</i> FL: ↑ <i>B. uniformis</i> at 4 and 8 wks (p = 0.038 and 0.011) αCD: ↑ <i>B. uniformis</i> at 8 wks (p = 0.036) Pla: ^{NS} ↑ <i>B. uniformis</i> at 4 and 8 wks <i>Δ B. uniformis abundance, between 0 and 8 wks, median interquartile range:</i> αCD: 3.99×10^{10} (9.73×10^9 to 9.48×10^{10}) copies/g FL: 1.46×10^{10} (1.15×10^9 to 4.84×10^{10}) copies/g Pla: 3.74×10^8 (-2.56×10^{10} to 3.76×10^{10}) copies/g ^{NS} between grps	Not measured	<i>10 km TT exercise bike</i> ^{NS} in FL or Pla at any time points. <i>After 4 and 8 wks, within grp</i> αCD: shorter completion times at 4 wks (p = 0.004) and 8 wks (p = 0.014) compared to baseline <i>At 8 wks, between grp</i> Completion times: αCD < Pla (p = 0.010)
Onishi et al. [33] RCT	N = 81 male, physically active	<i>Relative abundance, B. uniformis, cells/g</i> Post intervention: ^{NS} between grps <i>Baseline vs 4 and 8 wks, within grps:</i> Int: 0 wks 4.04×10^{10} (8.09×10^9–9.50×10^{10}), 4 wks 9.33×10^{10} (3.40×10^{10}–2.04×10^{11}) (p < 0.001), 8 wks: 8.03×10^{10} (2.18×10^{10}–2.10×10^{11}) (p < 0.001).	Not measured	<i>10 km TT (s) exercise bike</i> <i>Completion times compared to baseline</i> αCD: 0 wks: $1,139.5 \pm 130.3$, 4 wks: $1,088.0 \pm 124.8$, 8 wks: $1,073.2 \pm 116.7$ (p < 0.001 and p < 0.001) Pla: 0 wks: $1,158.2 \pm 145.3$, 4 wks: $1,122.3 \pm 123.5$, 8 wks: $1,126.4 \pm 133.6$ (p = 0.009 and p = 0.026)

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		Pla: 0 wks 4.73×10^{10} ($1.12 \times 10^{10} - 1.71 \times 10^{11}$), 8 wks 1.41×10^{11} ($1.78 \times 10^{10} - 2.53 \times 10^{11}$) (p = 0.002)		Completion times, post intervention αCD $1,073.2 \pm 116.7$ Pla $1,126.4 \pm 133.6$ (p = 0.016) $\dot{V}O_{2max}$ and PWC 75% HR_{max} ^{NS} within or between grps.
Diet				
Furber et al. [27] RCT	N = 16 male, highly trained endurance runners Diet vs diet vs diet Habitual diet vs HPD vs HCD, 22 d.	<i>HPD effects:</i> <i>Reduced Viral Diversity</i> HPD: ↓ Fisher-alpha diversity of inducible viruses (IV) (p = 0.04), did not return to pre-intervention levels. <i>Altered Viral Composition:</i> HPD: significant Δ's occurred in both free viral particle (FVP) (R² = 0.15; p = 0.023) and inducible virus (IV) (R² = 0.16; p = 0.016) communities. <i>Sk1virus Expansion</i> HPD: Δ in viral diversity and composition largely due to ↑ Sk1virus. <i>Leuconostoc bacteria correlation</i> HPD: Strong positive correlation between Sk1 virus and <i>Leuconostoc</i> bacteria. <i>Decreased abundance of Bifidobacterium spp.</i> <i>HCD effects:</i> <i>Bacterial community changes</i> HCD: greater impact on bacterial community composition compared to viral compartment. ^{NS} overall community shifts. <i>Specific bacterial abundances</i> HCD: strongly associated with ↑ <i>Leuconostoc</i>, <i>Lactococcus</i>, and <i>Collinsella</i> (R² > 0.6). <i>Streptococcus</i> substantially ↓ (R² > 0.6). HCD: Associated with expansion of <i>Ruminococcus</i> and <i>Collinsella</i> bacterial spp. <i>Viral Community Changes</i> HCD: ↑ Cc31virus, which was negatively correlated with <i>Streptococcus</i> and IV Cafeteria virus.	Not measured	<i>Treadmill, 10 km TTE (s)</i> HPD: Pre 128.3 ± 29.3, post-intervention 98.4 ± 31.8, ↓ 23.3% (p < 0.001) Returned to habitual diet: 125.3 ± 32.39 HCD: Pre 182.2 ± 44.4, post-intervention 194 ± 45.5, ↑ 6.5% (p = 0.05) Returned to habitual diet: 184 ± 38.9 <i>Association between microbiota and performance</i> HPD: Greater Δ in overall FVP community composition in participants whose performance at TTE was reduced. HCD: Participants whose TTE improved showed greater microbial stability, with lower within-subject community dissimilarity, and maintenance of a subject-specific gut microbiota. HCD: Non-improving subjects were less distinguishable from one another.
Mancin et al. [29] RCT	N = 16 male, semi-professional soccer players	<i>α-Diversity, OTU and Shannon's ENS</i> ^{NS} effects of time, group, or time × group interaction: OTUs number and Shannon's ENS	Not measured	<i>Maximal strength, isometric, quadriceps</i> ^{NS} within or between grps

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	Diet vs diet KEMEPHY ketogenic Mediterranean diet (KDP) vs Western diet, 30 d.	<i>Relative abundance (%) (median)</i> <i>Phylum:</i> KDP: ↓ <i>Actinobacterota</i> Pre 4.3% Post 1.7% WD: ↑ <i>Actinobacterota</i> Pre 1.7% Post 2.3% KDP < WD (p = 0.021) <i>Post intervention:</i> KDP: <i>Clostridia</i> UCG-014, <i>Butyricimonas</i>, <i>Odoribacter</i>, and <i>Ruminococcus</i> more abundant vs WD. WD: <i>Bifidobacterium</i>, <i>Butyricoccus</i>, and <i>Acidaminococcus</i> more abundant vs KDP. Numerical data not shown. <i>Correlation</i> CHO intake negatively correlated with Δ $\dot{V}O_2$ of <i>Odoribacter</i> genus (r = - 0.59) Fat intake negatively associated with <i>Fusicatenibacter</i> genus (r = - 0.53)		<i>Yo-yo Intermittent Test (m)</i> KDP 880.4 ± 244 to 1123 ± 266 (p < 0.001) WD 683 ± 388 to 911 ± 378 (p < 0.001) ^{NS} between grps. <i>CMJ (cm)</i> KPD 40.4 ± 6.5 to 43.6 ± 6 (p < 0.001) WD 37.3 ± 2.9 to 38.6 ± 4.1 (p < 0.001) ^{NS} between grps.
Murtaza et al. [31] RCT	N = 29 male, highly competitive race walkers Diet vs diet vs diet HCHO vs PCHO vs LCHO, 3 wk.	<i>Genus-level taxonomic profiles</i> 7/29 <i>Prevotella</i>-predominant cluster 20/29 <i>Bacteroides</i>-dominant cluster Remaining two points from same athlete (participated in both training periods) <i>Bacillota</i>-dominant cluster Above clusters sustained throughout training and diet- intervention. HCHO and PCHO: minor, subtle changes in microbial community composition. <i>α-Diversity</i> ^{NS} between baseline and post dietary interventions. <i>Relative abundance</i> HCHO and PCHO: ^{NS} change in any specific taxa. LCHF: Significant differences in stool microbiota profiles pre- and post-intervention (RDA p = 0.020) and (Anosim p = 0.029). LCHF: ↓ <i>Faecalibacterium</i> spp. (p = 0.0003), ↑ <i>Dorea</i> <i>spp.</i> (p = 0.007) and ↑ <i>Bacteroides</i> (p = 0.002).	Not reported.	<i>Post intervention, $\dot{V}O_2$ peak during race walking increased in all grps[#]: (p < 0.001, 90% CI: 2.55, 5.20%)</i> <i>O₂ uptake (expressed as a percentage of new $\dot{V}O_2$ peak) at a speed approximating 20km race pace (90% CI)[#]</i> HCHO: -7.047, -2.55 PCHO: -5.18, -0.86 LCHF: maintained at pre-intervention levels <i>Mean race 10km walk time (90% CI)[#]</i> HCHO: 6.6% (4.1, 9.1%) PCHO: 5.3% (3.4, 7.2%) LCHF: -1.6% (- 8.5, 5.3%). <i>Correlation</i> ^{NS} correlations between <i>Bacteroides</i>, <i>Faecalibacterium</i> and <i>Dorea</i> and any performance measures at baseline. Significant negative correlations after consumption of LCHF between <i>Bacteroides</i> and fat oxidation (r = - 0.72, p = 0.02) Significant negative correlations after consumption of LCHF diet between <i>Dorea</i> spp. and exercise economy (r = -0.65, p = 0.04).

Author, study design	N_ Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
<i>Exercise</i>				
Zhong et al. [26] RCT	N = 14 female, physically active Exercise vs control 4 x wk, 60 min, including warm-up (10 min), aerobic exercise (20 min), resistance exercise (25 min), and cool down (5 min), 8 wk.	<i>α-Diversity</i> ^{NS} between grps <i>Within grp</i> Int: ↑ Sobs (p = 0.008), ↑ Chao index (p = 0.017), and ↑ Ace index (p = 0.002) Int: ^{NS} Shannon (p = 0.177) and Simpson (p = 0.401) <i>Relative abundance, post intervention, between grps:</i> <i>Class:</i> <i>Betaproteobacteria:</i> Int 0.45 ± 0.44 Control 1.63 ± 1.48 (p = 0.008) <i>Bacilli:</i> Int 0.20 ± 0.22 Control: 0.130 ± 0.08 (p = 0.027) <i>Order:</i> <i>Burkholderiales:</i> Int 0.45 ± 0.44 1.63 ± 1.48 (p = 0.008) <i>Lactobacillales:</i> Int 0.197 ± 0.220 Control 0.130 ± 0.083 (p = 0.027) <i>Family:</i> <i>Sutterellaceae:</i> Int 0.44 ± 0.45 Control 1.63 ± 1.48 (p = 0.008) <i>Bacteroidaceae:</i> Int 19.11 ± 20.23 Control 51.80 ± 12.54 (p = 0.009) <i>Genus:</i> <i>Holdemania:</i> Int 0.006 ± 0.006 Control 0.016 ± 0.019 (p = 0.030) <i>Anaerostipes:</i> Int 0.121 ± 0.124 Control 0.440 ± 0.289 (p = 0.008) <i>Bacteroides:</i> Int 19.11 ± 20.23 Control 51.80 ± 12.54 (p = 0.009) <i>Within grp:</i> <i>Order</i> Int: ↑ <i>Coriobacteriales</i> Pre: 0.56 ± 1.11 Post: 2.75 ± 6.28 (p = 0.012) <i>Family:</i> Int: ↑ <i>Coriobacteriaceae</i> Pre 0.56 ± 1.11 Post 2.75 ± 6.58 (p = 0.012) <i>Genus:</i>	<i>Not reported.</i>	<i>2-min step-test (counts)</i> Int 97.50 ± 18.81 to 102.63 ± 14.32 ^{NS} Control 85.85 ± 18.07 to 85.83 ± 18.07 ^{NS} between grps <i>Grip strength (kg)</i> Int 21.28 ± 5.90 to 21.40 ± 6.01 ^{NS} Control 22.28 ± 4.97 to 20.47 ± 4.36 ^{NS} between grps <i>Grip strength / weight</i> Int 0.399 ± 0.077 to 0.403 ± 0.080 ^{NS} Control 0.423 ± 0.099 to 0.382 ± 0.078 ^{NS} between grps <i>30-s chair stand test (counts)</i> Int 19.50 ± 1.77 to 18.25 ± 1.98 ^{NS} Control 17.17 ± 2.71 to 16.17 ± 2.32 ^{NS} between grps <i>Timed up and go test (s)</i> Int 5.93 ± 0.40 to 5.79 ± 0.94 ^{NS} Control 6.61 ± 1.06 to 6.59 ± 0.79 ^{NS} between grps <i>Chair sit-and-reach (cm)</i> Int 10.00 ± 6.55 to 19.06 ± 9.49 (p = 0.002) Control 8.58 ± 5.50 to 9.50 ± 7.74 ^{NS} Int > Control (p = 0.0004) <i>Single leg standing with eyes closed (s)</i> Int 7.67 ± 4.22 to 11.86 ± 7.77 (p = 0.046) Control 6.88 ± 1.96 to 5.16 ± 1.87 ^{NS} Int > Control (p = 0.013) <i>Correlation</i> Chair sit-and-reach: negatively associated with <i>Betaproteobacteria</i> (r = − 0.704, p = 0.005).

Author, study design	N_Intervention protocol	Microbiota measure/s [#]	SCFA measure/s [#]	Performance measure/s [#]
		Int: ↑ <i>Asaccharobacter</i> Pre 0.015 ± 0.028 Post 0.034 ± 0.050 (p = 0.028) Int: ↑ <i>Collinsella</i> Pre 0.52 ± 1.06 Post 2.64 ± 6.09 (p = 0.028) Int: ↑ <i>Fusicatenibacter</i> Pre 0.208 ± 0.186 Post 0.983 ± 0.887 (p = 0.049) Int: Significant main effect of time for <i>Asaccharobacter</i> (F = 4.875, p = 0.047).		Single-leg standing with eyes closed: negatively associated with <i>Holdemania</i> (r = − 0.553, p = 0.040). Grip strength: negatively associated with <i>Betaproteobacteria</i> (r = − 0.551, p = 0.041).

CHO: carbohydrate, EIMD: exercise-induced muscle damage, HPD: high protein diet, HCD: high carbohydrate diet, HCHO: high carbohydrate, IMTP: isometric mid-thigh pull, Int: Intervention, LCHO: low carbohydrate, LCHF: low carbohydrate, MMA: mixed martial arts, ^{NS} Not significant, PCHO: periodised carbohydrate, high fat, Pla: Placebo, Pre: Prebiotic intervention, RCT: Randomised control trial, RFD: rate of force development, RXT: Randomised crossover trial, WAnT: Wingate anaerobic test based, wk: weeks, [†]: Performance data from Lee et al. [24], [#]: Performance data from Burke et al. [75].

[#] Measures: Δ in mean/median from pre- to post-intervention period unless otherwise indicated.