**SUPPLEMENTARY RESULTS**

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| **Table S1**. Search strategy used for **Scielo**, and number of articles found. | | |
| **Search criterion 1** | **Search criterion 2** | **Items found**  **(Combining criteria**  **1 “AND” 2)** |
| Gut | Microbiota | 105 |
| **Total items found** | All the searches were combined using the operator “OR” so that duplicated articles were excluded from the final number of articles found. The final search term was: (gut AND microbiota). A refinement was made to exclude reviews: (REVIEW) | 105 |

The search recruited articles published until Julye 5th 2019; no lower date limit was set.

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| **Table S2**. Search strategy used for **Scopus,** and number of articles found. | | | | |
| **Search criterion 1** | **Search criterion 2** | **Search criterion 3** | **Search criterion 4** | **Items found**  **(Combining criteria**  **1 “AND” 2 “AND” 3 “AND” 4)** |
| Gut | Microbiota | Exercises OR Training | Human OR Humans | 131 |
| **Total items found** | All the searches were combined using the operator “OR” so that duplicated articles were excluded from the final number of articles found. The final search term was: (gut AND microbiota AND (exercises OR training ) AND human AND humans). A refinement was made to exclude reviews: (REVIEW) | | | 131 |

The search recruited articles published until July 5th 2019; no lower date limit was set.

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| **Table S3.** Search strategy used and number of articles found in **PubMed**. | | | | | | |
| **Search criterion 1** | **Search criterion 2** | **Search criterion 3** | **Search criterion 4** | **MeSH Entry Terms for**  **Criteria 4** | **Search criterion 5** | **Items found**  **(Combining criteria**  **1 “AND” 2 “AND” 3 “NOT” 4 “NOT” 5)** |
| “Gastrointestinal Microbiome” OR "Fecal Microbiota" OR "Cecal Microbiota" OR "Fecal Microbiota" | Exercises OR Training | Human | "Mice"[MeSH] | Mus  Mouse  Mus musculus  Mice, House  House Mice  Mouse, House  House Mouse  Mus domesticus  Mus musculus domesticus  domesticus, Mus musculus  Mice, Laboratory  Laboratory Mice  Mouse, Laboratory  Laboratory Mouse  Mouse, Swiss  Swiss Mouse  Swiss Mice  Mice, Swiss | Review | 232 |
| "Rats"[MeSH] | Rat  Rattus  Rattus norvegicus  Rats, Norway  Rats, Laboratory  Laboratory Rat  Laboratory Rats  Rat, Laboratory |
| "Animal Experimentation"[MeSH] | Experimentation, Animal  Animal Research  Research, Animal  Animal Experimental Use  Animal Experimental Uses  Experimental Use, Animal  Experimental Uses, Animal  Animal Experiments  Animal Experiment  Experiment, Animal  Experiments, Animal |
| "Models, Animal"[MeSH] | Animal Model  Animal Models  Model, Animal  Laboratory Animal Models  Animal Model, Laboratory  Animal Models, Laboratory  Laboratory Animal Model  Model, Laboratory Animal  Models, Laboratory Animal  Experimental Animal Models  Animal Model, Experimental  Animal Models, Experimental  Experimental Animal Model  Model, Experimental Animal  Models, Experimental Animal |
| "rats" OR "mouse" OR "mice" OR "rat” |  |
| **Total items found** | The final search term was: ((((((((((((((((((“Gastrointestinal Microbiome”) OR ((("Fecal Microbiota") OR "Cecal Microbiota") OR "Faecal Microbiota")))))) AND (((Exercises) OR Training))))) AND Human) NOT ((((((((((((((((((("Mice"[MeSH]) OR "Rats"[MeSH]) OR "Animal Experimentation"[MeSH]) OR "Models, Animal"[MeSH])) OR ("rats" OR "mouse"))) OR "mice")) OR "rat")))))))))))))))) NOT Review | | | | | 232 |

The search recruited articles published until July 5th 2019; no lower date limit was set. MeSH (Medical Subject Headings) is the National Library of Medicine controlled vocabulary thesaurus used for indexing articles for PubMed.

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| **Table S4**. Search strategy used and number of articles found in **Web of Science**. | | | | |
| **Search criterion 1** | **Search criterion 2** | **Search criterion 3** | **Search criterion 4** | **Items found**  **(Combining criteria**  **1 “AND” 2 “AND” 3 “NOT” 4)** |
| ((Gut OR Intestinal OR Gastrointestinal OR Fecal OR Cecal OR Fecal) AND (Flora OR Microflora OR Microbiotas OR Microbiome OR Microbiomes)) | Exercises OR Training | Human | (Mice OR Rat\* OR (Experiment\* AND Animal\*) OR (Research\* AND Animal\*) OR mouse OR (model\* AND animal\*) | 151 |
| **Total items found** | All searches were combined using the operator “OR” so that duplicated articles were excluded from the final number of articles found. The final search term was: ((((((((((((((((((Gut) OR Intestinal) OR Gastrointestinal) OR Fecal) OR Cecal) OR Fecal)) AND (((((Flora) OR Microflora) OR Microbiotas) OR Microbiome) OR Microbiomes)))) AND (((Exercises) OR Training)) AND Human))) NOT (Mice OR Rat\* OR (Experiment\* AND Animal\*) OR (Research\* AND Animal\*) OR mouse OR (model\* AND animal\*))))))). Moreover, we refined excluding document types: (REVIEW) | | | 151 |

The search recruited articles published until July 5th 2019; no lower date limit was set.

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| **Table S5.** Observationalstudies that reported a relationship between exercise or physical activity and the gut microbiota of healthy adults. | | | | | | |
| **Study/Year** | **Subjects** | **Exercise Outcomes** | **Control of diet** | **Fecal sample collection** | **Gut microbiota analysis techniques** | **Main Findings** |
| Cross-sectional |  |  |  |  |  |  |
| McFadzean et al., 2014(44) | N=1493 | Participants self-reported physical activity levels:   * Never (N) =46 * Rarely (R)=45 * Occasionally (O)=301 * Regularly (r)=577 * Daily (D)=309 | Standardized diet: No  Adjusted for diet: No | 1 | qPCR: MyseqIllumina  Software: QIIME  Reference DB: Greengenes  Outcome: OTU | Statistical analysis: ANOVA, Bonferroni test  **↑** α-diversity in O, r and D groups (p<0.05) vs R  β-diversity: There were no distinctly different clusters according to physical activity.  Comparison between groups:   * Family:   + **↑** *Erysipelotrichaceae* (11.776% O) * Genus:   + **↑** *Lachnospira* (3.805% r)   + **↑** *Coprococccus* (1.665% r)   + **↑** *Oscillospira* (2.75% D) * Species:   + **↑** *F. prausnitzii* (17.94% D) |
| Estaki et al., 2016(35) | N=41(22 males/19 females) | Assessment of cardiorespiratory fitness (VO2max) by cycle test and metabolic cart.   * Incline: Continuous incremental ramp * Power: started at 50 W and increased by 30 W/min * End: participant reached self-declared exhaustion or when rpm fell below 50.   Participant’s group by VO2max:   * Low (33±4.8 VO2max): N=14 (25.5±3.3 years and 25.5±3.9kg/m2) * Moderate (41.9±4.3 VO2max): N=12 (24.3±3.7 years and 23.5±0.5kg/m2) * High (54.8±5.6 VO2max): N=13 (26.2±5.5 years and 22.8±5.5kg/m2) | Standardized diet: No  Adjusted for diet: No | 1 after test | qPCR: MySeq Illumina  Software: QIIME  Reference DB: Greengenes  Outcome: OTU | Statistical analysis: Spearman correlations  α-diversity positively correlated with VO2max (R2=0.204)  β-diversity: There were no distinctly different clusters according to cardiorespiratory fitness.  Correlation with VO2max:   * Order:   + **↑** *Clostridiales* * Families:   + **↑** *Lachnospiraceae*   + **↑** *Erysipelotrichaceae* * Genera:   + **↑** *Coprococcus*   + **↑** *Roseburia*   + **↑** *Adlercreutzia* * SCFAs:   + **↑** Butyrate   + **↓** Propionate   + **↓** Acetate |
| Yang et al., 2017(36) | N=71 Females, premenopausal | Assessment of cardiorespiratory fitness (VO2max) by cycle test:   * Power: Increased 25 W each 2 min. * End: participant reached self-declared exhaustion   Participant’s groups by VO2max:   * Low: N=24 (40.4 years and 31.7kg/m2) * Moderate: N=23 (39.7 years and 27.9kg/m2) * High: N=24 (30.6 years and 24.6kg/m2) | Standardized diet: No  Adjusted for diet: Yes (Fat %, energy from HC, protein, fat and alcohol by 3 days food records) | 1 | Flow cytometry-FISH | Statistical analysis: ANOVA, Sidak post-hoc test.  High vs Moderate and Low:   * Phylum:   + **↑** *Bacteroidetes* (High group) |
| Case and Control | |  |  |  |  |  |
| Clarke et al., 2014(45) | N=86 males   * Athletes: N=40 (28.8±3.8 years and 29.1±3kg/m2) * High BMI controls: N=23 (30.8±5.6 years) * Low BMI controls: N=23 (28.1±5.1 years). | Assessment of physical activity by EPIC-Norfolk questionnaire. | Standardized diet: No  Adjusted for diet: No | 1 | qPCR: Roche  Software: BLAST and QIIME  Reference DB: SILVA 16S rRNA  Outcome: OTU | Statistical analysis: Kruskal-Wallis and Mann-Whitney tests  **↑** α-diversity in athlete group  Athletes vs high BMI controls:   * Phylum:   + **↑** *Firmicutes*   + **↓** *Bacteroidetes* * Family:   + **↑** *Ruminococcaceae*   + **↑** *S24-7*   + **↑** *Succinivibrionaceae*   + **↑** *Akkermansiaceae* * Genus:   + **↑** *RC9 gut group*   + **↑** *Succinivibrio*   + **↑** *Akkermansia*   Athletes vs low BMI controls:   * Family:   + **↑** *Prevotellaceae*   + **↑** *Erysipelotrichaceae*   + **↑** *S24-7*   + **↑** *Succinivibrionaceae*   + **↓** *Lactobacillaceae* * Genus:   + **↑** *Prevotella*   + **↑** *Succinivibrio*   + **↓** *Lactobacillus*   + **↓** *Bacteroides* |
| Bressa et al., 2017(46) | N=40 Females, premenopausal.   * Active (A): N=19 (30.7±5.9 years and 24.4±4.5kg/m2) * Sedentary (S): N=21 (32.2±8.7 years and 22.9±3.0kg/m2) | 7 days of measurement of physical activity by accelerometer. | Standardized diet: No  Adjusted for diet: Yes (total energy, protein, carbohydrates, lipids, fiber, ethanol, vegetables, cereals, dairy products, fruits, processed meat, beer and coffee, by food frequency questionnaire) | 1 | qPCR: MySeq Illumina  Software: QIIME  Reference DB: Greengenes  Outcome: OTU | Statistical analysis: Bivariate correlation, Spearman correlation coefficients.  = α-diversity (A = S)  β-diversity: Distinctly different clusters seen according to physical activity.    Active vs Sedentary:   * Families:   + **↓** *Barnesiellaceae* (0.37±0.35% A; 0.86±0.65% S)   + **↓** *Odoribacteriaceae* (0.44±0.26%A; 0.66±0.40% S) * Genus:   + **↑** *Bifidobacterium*   + **↑** *Haemophilus*   + **↑** *Paraprevotella*   + **↑** *Coprococcus*   + **↑** *Ruminococcacear UC 1*   + **↓** *Desulfovibrionaceae UC*   + **↓** *Turicibacter*   + **↓** *Barnesiellaceae UC*   + **↓** *Odoribacter*   + **↓** *Ruminococcacear UC2*   + **↓** *Ruminococcus* * Species:   + **↑** *Faecalibacterium prausnitzii*   + **↑** *Roseburia hominis*   + **↑** *Akkermansia muciniphila* |
| Petersen et al., 2017(27) | N= 33 cyclists (22 males/11 females; 19-49 years)   * Professionals: N=22 * Amateurs: N=11 | Assessment of physical activity levels by questionnaires on the average number of hours of exercise per week (h/wk):   * 6-10h * 11-15h * 16-20h * >20h | Standardized diet: No  Adjusted for diet: Yes (questionnaire NR) | 1 | qPCR: MySeq Illumina  Software: R studio  References DB: RDP  Outcome: Abundance relative | Statistical analysis: Spearman rank and Fisher correlations  No significant differences between professionals and amateurs  According to exercise load:   * >20h/w:   + Genus: **↑** *Prevotella* (14.75%) * 16-20h/w:   + Genus: **↑** *Prevotella* (12.12%) * >11h/w:   + Genus: **↑** *Prevotella* (≥2.5%) * 6-10h/w:   + Genus: **↑** *Prevotella* (0.15%) |
| Barton et al., 2018(28) | N=86 males   * Athletes: N=40 (28.8±3.8 years) * Low BMI control: N=22 (28.1±5.1 years) * High BMI control: N=24 (30.8±5.6 years) | Assessment of physical activity levels by EPIC-Norfolk questionnaire. | Standardized diet: No  Adjusted for diet: No | 1 | qPCR: HiSeq Illumina  Software: HUMAnN2 V.0.5.0 pipeline.  References DB: Metacyc  Outcome: relative abundance | Statistical analysis: Kruskal-Wallis test  **↑** α-diversity in athlete group  Athletes vs control group:   * SCFAs   + **↑** Propionate   + **↑** Acetate   + **↑** Butyrate   + **↑** Valerate |
| Durk et al., 2018(33) | N=37   * Males: N=20 (25.9±2.7 years and 24.1±4.0 kg/m2 * Females: N=17 (25.4±1.8 years and 23.2±3.0 kg/m2) | Assessment of cardiorespiratory fitness (VO2max) by treadmill.   * Incline: increased by 2% every 2 minutes * Speed: constant * End: participant reached self-declared exhaustion. | Standardized diet: No  Adjusted for diet: No | 1 | qPCR: FAST SYBR Green  Software: Master Mix  Reference DB: NR  Outcome: NR | Statistical analysis:  VO2max positively correlated with the *Firmicutes/Bacteroidetes* ratio (r=0.48) |
| Mörkl et al., 2018(34) | N=88 females   * Athletes: N=20 (22.15±3.86 years) * Normal weight: N=26 (24.93±3.75 years) * Overweight: N=22 (25.32±3.98 years) * Obese: N=20 (26.9±6.09 years) | Assessment of physical activity levels by IPAQ score. | Standardized diet: No  Adjusted for diet: No | 1 | qPCR: Ion Torrent  Software: QIIME  Reference DB: NR  Outcome: OTU | Statistical analysis: ANOSIM y Adonis (QIIME test)  **↑** α-diversity in athlete group  β-diversity: Distinctly different clusters seen according to physical activity. |
| ANOVA, analysis of variance; BMI, body mass index; DB, database; FISH, fluorescent in-situ hybridization; NR, not reported; OTU, operational taxonomic unit; qPCR, quantitative polymerase chain reaction; RDP, Ribosomal Database Project; RM, repetition maximum; SCFAs, short-chain fatty acids; UC, unclassified; VO2max, maximum volume of oxygen. Standardized diet: participants followed an established standard diet; Adjusted for diet: to statistically adjust the results based on nutritional questionnaires. | | | | | | |

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| **Table S6.** Summary of studies that reported very short-term exercise to have an effect on the gut microbiota of healthy adults. | | | | | | | |
| **Study/Year** | | **Subjects** | **Exercise Outcomes** | **Control Diet** | **Fecal sample collection** | **Gut microbiota analysis techniques** | **Main Findings** |
| Cohort | | |  |  |  |  |  |
| Lundgren-Kownacki et al., 2018(38) | N=12   * Males: N=6 (27.2±2.8 years and 24.0±2.0 kg/m2) * Females: N=6 (24.0±3.7 years and 23.8±1.1 kg/m2) | | 2 days of physical work: day 1 with water for rehydration and day 2 without rehydration (3h/d-34ºC, 60%RH).   * Activities involved: bricks, stepping, biking and arm crank at rotating intervals every 20 min | Standardized diet: Yes  (dinner the evening before each test day and standardized breakfast of an egg sandwich each test day.)  Adjusted for diet: No | 1 sample after each day | qPCR: NR  Software: GeneMapper and R  Outcome: 16S rRNA gene copies/g samples | Statistical analysis: Kruskal-Wallis test  α-diversity: there were no differences between days  Day 1 vs day 2:   * Family:   + = *Enterobacteriaceae* * Genus:   + = *Lactobacillus* |
| Zhao et al., 2018(39) | N=20 runners (16 males; 4 females) (31.3±6.1 years and 22.6±2.1kg/m2) | | * 1. km of half-marathon | Standardized diet: Yes  (same kind of food during the two sample time periods)    Adjusted for diet: No | 2 samples: before and after marathon | qPCR: HiSeq Illumina  Software: QIIME  Reference DB: RDP  Outcome: OTU | Statistical analysis: linear discriminant analysis, effect size analysis  = α-diversity between after and before the marathon  After vs before marathon:   * Phylum:   + **↑** *Actinobacteria* * Class:   + **↑** *Coriobacteria* * Order:   + **↑** *Coriobacteriales* * Family:   + **↑** *Coriobacteriaceae*   + **↑** *Succinivibrionaceae* * Genus:   + **↑** *Actinobacillus*   + ***↑*** *Pseudobutyrivibrio*   + ***↑*** *Collinsella*   + ***↑*** *Mitsuokella*   + ***↑*** *Ruminiclostridium* * Species:   + **↑** *Coprococcus\_2*   + **↑** *Ruminococcus bicirculans*   + ***↑*** *Collinsella aerofaciens* |
| Case and control | | |  |  |  |  |  |
| Shukla et al., 2015(37) | | N=10 (46.5±13 years, 24.6±3.3kg/m2 and 28.2±9.6 VO2max) | Assessment of cardiorespiratory fitness (VO2max) by cycle test:   * Speed: 60-70 rpm. Power increased 5 W each 20 s. * End: participant reached self-declared exhaustion * Min: 13.1±3.4 | Standardized diet: No  Adjusted for diet: No | 3 samples (baseline, and 48 and 72h post-exercise) | qPCR: Roche  Software: Explicet  Reference DB: RDP  Outcome: OTU. | Statistical analysis: ANOVA, Fisher test  72 h-post exercise vs baseline:   * Phylum   + **↑** *Bacteroidetes*   + **↑** Others (NR) |
| Scheiman et al., 2019(32) | | Cohort 1, N= 25:   * Marathoners: N=15 (11females; 27.1 years; 22.4 kg/m2) * Controls: N=11(6 females; 29.2 years, 22.9 kg/m2)   Cohort 2, N= 11 Ultramarathoners and Olympic rowers (6 females). | Cohort 1: 42.2 km Boston Marathon (Not for control participants)  Cohort 2: Not specify type of exercise | Standardized diet: No  Adjusting by diet: Yes (food frequency questionnaire) | Cohort 1: 5 samples collected in the previous 5 days of the marathon, and other 5 samples after the race. Total of 209 samples.  Cohort 2: 87 samples baseline and post-exercise | qPCR: MiSeq or HiSeq 2500 system  Software: Metagenomic Phylogenetic Analysis  Reference DB:  Outcome: Relative abundance | Statistical analysis: Wilcoxon rank-sum  test with continuity correction  After vs before exercise:  Cohort 1:   * Genus:   + **↑** *Veillonella* (marathoners)   + *=Veillonella* (controls)   Cohort 2:   * Genus:   + **↑** *Veillonella* (ultramarathoners and rowers) |
| ANOVA, analysis of variance; DB, database; NR, not reported; OTU, operational taxonomic unit; qPCR, quantitative polymerase chain reaction; RDP, Ribosomal Database Project; RH, relative humidity; VO2max: maximum volume of oxygen. Standardized diet: Participants followed an established standard diet; Adjusted for diet: to statistically adjust the results based on nutritional questionnaires. | | | | | | | |

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| **Table S7.** Summary of studies that reported medium/long-term exercise to influence the gut microbiota of healthy adults. | | | | | | | |
| **Study/Year** | | **Participants** | **Exercise Outcomes** | **Control of diet** | **Fecal sample collection** | **Gut microbiota analysis techniques** | **Main Findings** |
| Cohort | | |  |  |  |  |  |
| Cronin et al., 2018(40) | | N=25 (11 males; 14 females) (35 years; 27.9 kg/m2) | 3 times per week over 8 weeks of concurrent training (endurance + resistance exercises):  Endurance exercise   * Intensity: moderate (Borg rate scale 5 to 7/10) * Min: 18 min until 32 min * Increasing 15% to 20%.   Resistance exercise:   * 7 machine-based resistance exercises. * Minimum: 3 sets of 8 repetitions in each machine. * Maximum: 3 sets of 12 repetitions in each machine. * Weight: 70% of the individual´s one-repetition maximum (1RM) value. | Standardized diet: No  Adjusted for diet: No | 2 samples (baseline, and after exercise period) | qPCR: HiSeq Illumina  Software: HUMAnN2  Reference DB: Metacyc database  Outcome: NR | Statistical analysis: ANOVA  = α-diversity between groups  β-diversity: Distinctly different clusters were seen after the intervention. |
| Munukka et al., 2018(29) | | N=17 women (36.8±3.9 years and 31.8±4.4 kg/m2) | 6 weeks of endurance training (cycling) 3d/wk 30-60min/d low-moderate intensity.   * Weeks 1– 2: 3 sets x40min steady-state cycling at low intensity * Weeks 3–4: 3x50min   + 3x10-min moderate intensity   + Rest, low intensity   Weeks 5–6: 60min   * + 4x10-min at moderate intensity   + Rest, low intensity | Standardized diet: No  Adjusted for diet: Yes (fat %, energy %, fiber %, sucrose % by 3 days food records). | 2 samples: baseline and post- exercise training | qPCR: MySeq Illumina  Software: QIIME  Reference DB: SILVA  Outcome: OTU | Statistical analysis: General linear model  α-diversity: there was no difference after exercise training  **↑** β-diversity after exercise at the genus level  After training vs baseline:   * Phylum   + **↓** *Proteobacteria*   + ***↑*** *Verrucomicrobia* * Family   + **↑** *Verrucomicrobiaceae* * Genus   + **↑** *Akkermansia* |
| Morita et al., 2019(30) | | N=29 women | Non-randomized intervention  endurance group   * N=17 (66-75 years; 18.9-23.1 kg/m2) * 7d/wk 60min/d 12 weeks brisk walking at an intensity of ≥ 3 metabolic equivalents (METs) as measured by accelerometer. * Increasing the intensity and duration as much as possible.   Resistance group:   * N=12 (66-77 years; 18.7-24.0 kg/m2) * 1 h/week for 12 weeks: strengthening the trunk muscle   Activities involved: arching–swaying, plank, pelvic rotation in the supine position, and bird-dog. | Standardized diet: No  Adjusted for diet: Yes (food frequency questionnaire) | 2 samples: basal and post exercise training | qPCR: Takara Thermal Cycler Dice TP650T  Software: GeneMapper  Reference DB: Human Fecal Microbiota T-RFLP profiling  Outcome: OTU | Statistical analysis: Wilcoxon Signed-rank test,  After interventions:  1.Endurance group:   * Genus:   + **↑** *Bacteroides*   + **↓** Others * Specie:   + **↓** *Clostridium subcluster XIVa*   2.Resistance group:   * Species:   + **↑** *Clostridium cluster IX* |
| Keohane et al., 2019(31) | | N=3 men (26.5±1.3 years; 24.4±1.4 kg/m2) | 3748.91 km east-west Transatlantic rowing race over 33 days and 22 hours; three participants. | Standardized diet: Yes  - 21 MJ per day during preparatory period  - 33.5 MJ per day during race  Adjusted for diet: No | 4 samples: baseline, mid-way point, before race finished and at 3 months post-race) | qPCR: Ilumina NextSeq  Software: HUMAnN2 V.0.99  Reference DB: -  Outcome: Abundance relative | Statistical analysis: -  **↑** α-diversity since mid-point until race end  Throughout the race for all participants:   * Genus:   + **↑** *Subdoligranulum* UC * Specie:   + **↑** *Dorea longicatena*   + **↑** *Roseburia hominis*   + **↓** *Bacteroides finegoldii* |
| Case and control | | |  |  |  |  |  |
| Allen et al., 2017(47) | N=32   * Normal weight: N=18 (9 males/ 9 females) (25.1±6.5 years). * Obese: N=14 (3 males/ 11 females) (31.2±8.5 years). | | 6 weeks of endurance training (cycling or treadmill [subjects chose]) 3d/wk 30-60 min/d moderate-vigorous intensity.   * Week 1: 30min at 60% HRR * Week 2: lasted 45 min =intensity * Week 3: 60 min at 60% HRR * Week 4-6: increased the intensity by 5% HRR each week * Week 6: 60 min at 75%HRR | Standardized diet: Yes  -7 food records  -Evaluators designed a 3-day food menu (with meal of 7 food records)  -Participants followed this 3-day food menu prior to each fecal collection.  Adjusted for diet: Yes | 3 samples. (Baseline, after 6 weeks of the intervention and after 6 weeks of washout). | qPCR: MySeq Illumina.  Software: QIIME  References DB: RDP  Outcome: OTU | Statistical analysis: PERMANOVA and ANOVA  α-diversity: no difference between groups after exercise or in the washout period  β-diversity: No distinct difference between groups after the intervention.  After training vs baseline:   * Order:   + **↑** *Clostridiales* * Genus:   + **↑** *Roseburia*   + ***↑*** *Lachnospira*   + **↑** *Faecalibacterium*   + **↑** *f\_Lachnospiraceae UC*   SCFAs in normal weight group:   * **↑**Acetate * **↑** Butyrate |
| ANOVA, analysis of variance, DB, database; HRR, heart rate reserve; MJ, megajoules; METs, metabolic equivalent of task; NR, not reported; OTU, operational taxonomic unit; qPCR, quantitative polymerase chain reaction; RDP, Ribosomal Database Project; SCFAs, short-chain fatty acids; UC, unclassified. Standardized diet: Participants followed an established standard diet; Adjusted for diet: to statistically adjust the results based on nutritional questionnaires. | | | | | | | |

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| **Table S8.** Taxonomic ranks used in the studies included in the present review. The first column represents the different taxonomic classifications: phylum, class, order, family, genus and species; the second column represents the different microorganisms belong to those classifications. The numeration indicates the higher-level taxonomic rank to which a microorganism belongs. Each row shows the different articles examined, grouped by study type. | | | | | | | | | | | | | | | | | | | |
|  | | **Observational** | | | | | | | | | **Very short-term exercise Interventions** | | | | **Medium/long-term exercise Interventions** | | | | |
| **References** | | McFadzean et al., 2014 | Clarke et al., 2014 | Estaki et al., 2016 | Yang et al., 2017 | Bressa et al., 2017 | Petersen et al., 2017 | Barton et al., 2018 | Mörkl et al., 2018 | Durk et al., 2018 | Shukla et al., 2015 | Lundgren-Kownacki et al., 2018 | Zhao et al., 2018 | Scheiman et al., 2019 | Allen et al., 2017 | Cronin et al., 2018 | Munukka et al., 2018 | Morita et al., 2019 | Keohane et al., 2019 |
| **Alpha diversity** | | + | + | + | NR | 0 | NR | + | + | NR | NR | 0 | 0 | NR | 0 | 0 | 0 | NR | + |
| **Beta diversity** | | 0 | NR | 0 | NR | 0 | NR | NR | + | NR | NR | NR | NR | NR | 0 | + | + | NR | NR |
| **Phylum** | 1.*Firmicutes* | + | +/- | + | NR | +/- | NR | NR | NR | NR | NR | NR | + | + | + | NR | NR | +/- | + |
| 2.*Bacteroidetes* | NR | +/- | NR | + | +/- | + | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | + | +/- |
| 3.*Actinobacteria* | NR | NR | + | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 4.*Proteobacteria* | NR | + | NR | NR | +/- | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | - | NR | NR |
| 5.*Verrucomicrobia* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| **Class** | 1.1.*Clostridia* | + | + | + | NR | +/- | NR | NR | NR | NR | NR | NR | + | NR | + | NR | NR | +/- | + |
| 1.2.*Erysipelotrichia* | + | + | + | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.3.*Bacilli* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.4.*Negativicutes* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | + | NR | NR | NR | NR | NR |
| 2.1.*Bacteroidia* | NR | +/- | NR | NR | +/- | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | +/- |
| 3.1.*Actinobacteria* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 3.2.*Coriobacteriia* | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 4.1.*Deltaproteobacteria* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.*Gammaproteobacteria* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 5.1.*Verrucomicrobiae* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| **Order** | 1.1.1.*Clostridiales* | + | + | + | NR | +/- | NR | NR | NR | NR | NR | NR | + | NR | + | NR | NR | +/- | + |
| 1.2.1.*Erysipelotrichales* | + | + | + | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.3.1.*Lactobacillales* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.4.1.*Selenomonadales* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.4.2.*Veillonellales* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR |
| 2.1.1.*Bacteroidales* | NR | +/- | NR | NR | +/- | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | +/- |
| 3.1.1.*Bifidobacteriales* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 3.2.1.*Coriobacteriales* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 3.2.2.*Eggerthellales* | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.1.1.*Desulfovibrionales* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.1.*Aeromonadales* | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 4.2.2.*Pasteurellales* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 5.1.1.*Verrucomicrobiales* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| **Family** | 1.1.1.1.*Hungateiclostridiaceae* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.2.*Lachnospiraceae* | + | NR | + | NR | + | NR | NR | NR | NR | NR | NR | + | NR | + | NR | NR | - | + |
| 1.1.1.3.*Ruminococcaceae* | + | + | NR | NR | +/- | NR | NR | NR | NR | NR | NR | + | NR | + | NR | NR | NR | + |
| 1.1.1.4.Family UC | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.2.1.1.*Erysipelotrichaceae* | + | + | + | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.3.1.1.*Lactobacillaceae* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.4.1.1.*Selenomonadaceae* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.4.2.1.*Veillonellaceae* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR |
| 2.1.1.1.S24-7 | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.2.*Rikenellaceae* | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.3.*Prevotellaceae* | NR | + | NR | NR | + | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 2.1.1.4.*Barnesiellaceae* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.5.*Odoribacteraceae* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.6.*Bacteroidaceae* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | - | + |
| 3.1.1.1.*Bifidobacteriaceae* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 3.2.1.1.*Coriobacteriaceae* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 3.2.2.1.*Eggerthellaceae* | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.1.1.1.*Desulfovibrionaceae* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.1.1.*Succinivibrionaceae* | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 4.2.2.1.*Pasteurellaceae* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 5.1.1.1.*Akkermansiaceae* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| 5.1.1.2.*Verrucomicrobiaceae* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| **Genus** | 1.1.1.1.1.*Ruminiclostridium* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.2.1.*Coprococcus* | + | NR | + | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.2.2.*Roseburia* | NR | NR | + | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | + |
| 1.1.1.2.3.*Lachnospira* | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR |
| 1.1.1.2.4.*Pseudobutyrivibrio* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.2.5.*Lachnospiraceae* UC | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR |
| 1.1.1.2.6.*Clostridium cluster XIVa* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.1.1.2.7.*Dorea* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.1.1.3.1.*Faecalibacterium* | + | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR |
| 1.1.1.3.2.*Oscillospira* | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.1.1.3.3.*Ruminococcaceae* UC1 | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.1.1.3.4.*Ruminococcaceae* UC2 | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.1.1.3.5.*Ruminococcus* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.3.6.*Subdoligranulum* UC | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.1.1.4.1.*Clostridium cluster IX* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.2.1.1.1.*Turicibacter* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.3.1.1.1.*Lactobacillus* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.4.1.1.1.*Mitsuokella* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.4.2.1.1.*Veillonella* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR |
| 2.1.1.1.1.*Rikenellaceae* RC9 gut group | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.3.1.*Prevotella* | NR | + | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 2.1.1.3.2.*Paraprevotella* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.4.1.*Barnesiellaceae* UC | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.5.1.*Odoribacter* | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.1.1.6.1.*Bacteroides* | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | - |
| 3.1.1.1.1.*Bifidobacterium* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 3.2.1.1.1.*Collinsella* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 3.2.2.1.1.*Adlercreutzia* | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.1.1.1.1.*Desulfovibrionaceae* UC | NR | NR | NR | NR | - | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.1.1.1.*Succinivibrio* | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.2.1.1.*Haemophilus* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 4.2.2.1.2.*Actinobacillus* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 5.1.1.1.1.*Akkermansia* | NR | + | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR |
| **Species** | 1.1.1.2.1.1.*Coprococcus\_2* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 1.1.1.2.2.1.*Roseburia hominis* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.1.1.2.7.1.*Dorea longicatena* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + |
| 1.1.1.3.1.1.*Faecalibacterium prausnitzii* | + | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 1.1.1.3.5.1.*Ruminococcus bicirculans* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | + |
| 2.1.1.3.1.1.*Prevotella copri* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | - |
| 2.1.1.6.1.1.*Bacteroides finegoldii* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 3.2.1.1.1.1.*Collinsella aerofaciens* | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR |
| 5.1.1.1.1.1.*Akkermansia muciniphila* | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| **SCFAs** | 1.Propionate | NR | NR | - | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| 2.Acetate | NR | NR | - | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR |
| 3.Butyrate | NR | NR | + | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR |
| 4.Valerate | NR | NR | NR | NR | NR | NR | + | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR | NR |
| Green cells (+) indicate a positive relationship with, or an effect of exercise or physical activity on, alpha and beta diversities, different microorganism or SCFAs. Red cells (-) indicate a negative relationship with, or null effect of exercise or physical activity on, alpha and beta diversities, different microorganism or SCFAs. Yellow cells (+/-) indicate positive and negative results detected between exercise or physical activity and different microorganism. Symbol (0) indicated no relationship seen between exercise/physical activity and alpha and beta diversities. “NR” indicates that the above types of relationship were not reported. SCFAs: Short-chain fatty acids. | | | | | | | | | | | | | | | | | | | |

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| **Table S9.**Methodological quality of clinical trials using PEDro Scale | | | | | | | | | | | | |
| **Study/Year** | **\*1** | **2** | **3** | **4** | **5** | **6** | **7** | **8** | **9** | **10** | **11** | **Score** |
| Observational studies | | | | | | | | | | | | |
| *Cross-sectional* | | | | | | | | | | | | |
| McFadzean et al., 2014 (44) | N | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Estaki et al., 2016 (35) | Y | N | N | Y | Y | N | N | Y | Y | Y | Y | 6 |
| Yang et al., 2017 (36) | Y | N | N | Y | Y | N | N | Y | Y | Y | Y | 6 |
| *Case and control* | | | | | | | | | | | | |
| Clarke et al., 2014 (45) | Y | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Bressa et al., 2017 (46) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Petersen et al., 2017 (27) | Y | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Barton et al., 2018 (28) | Y | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Durk et al., 2018 (33) | Y | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Mörkl et al., 2018 (34) | Y | N | N | N | N | N | N | Y | Y | Y | Y | 4 |
| Short-term exercise studies | | | | | | | | | | | | |
| *Cohort* | | | | | | | | | | | | |
| Lundgren-Kownacki et al., 2018 (38) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Zhao et al., 2018 (39) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| *Case and control* | | | | | | | | | | | | |
| Shukla et al., 2015 (37) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Scheiman et al., 2019 (32) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Medium/long-term exercise studies | | | | | | | | | | | | |
| *Cohort* | | | | | | | | | | | | |
| Cronin et al., 2018 (40) | Y | Y | Y | Y | N | N | N | N | Y | Y | Y | 6 |
| Munukka et al., 2018 (29) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Morita et al., 2019 (30) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| Keohane et al., 2019 (31) | Y | N | N | Y | N | N | N | N | Y | Y | Y | 4 |
| *Case and control* | | | | | | | | | | | | |
| Allen et al., 2017 (47) | Y | N | N | Y | N | N | N | Y | Y | Y | Y | 5 |
| 1: Eligibility criteria specified; 2: Individuals randomly allocated; 3: Allocation concealed; 4: Groups similar at baseline regarding most important prognostic indicators; 5:  “Blinded” participants; 6: “Blinded” therapist; 7: “Blinded” assessors; 8: Measures of at least one key outcome obtained from more than 85% of participants; 9: Data analyzed  by “intention to treat”; 10: Statistical comparisons between groups; 11: Point measures and measures of variation.  \* Item number 1 not used to calculate PEDro score because it influenced external validity but not internal or statistical validity of trial.  Y, criteria satisfied; N, criteria not satisfied. | | | | | | | | | | | | |