**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]  | MusMouseMus musculusMice, HouseHouse MiceMouse, HouseHouse MouseMus domesticusMus musculus domesticusdomesticus, Mus musculusMice, LaboratoryLaboratory MiceMouse, LaboratoryLaboratory MouseMouse, SwissSwiss MouseSwiss MiceMice, Swiss | Review | 232 |
| "Rats"[MeSH]  | RatRattusRattus norvegicusRats, NorwayRats, LaboratoryLaboratory RatLaboratory RatsRat, Laboratory |
|  "Animal Experimentation"[MeSH]  | Experimentation, AnimalAnimal ResearchResearch, AnimalAnimal Experimental UseAnimal Experimental UsesExperimental Use, AnimalExperimental Uses, AnimalAnimal ExperimentsAnimal ExperimentExperiment, AnimalExperiments, Animal |
| "Models, Animal"[MeSH]  | Animal ModelAnimal ModelsModel, AnimalLaboratory Animal ModelsAnimal Model, LaboratoryAnimal Models, LaboratoryLaboratory Animal ModelModel, Laboratory AnimalModels, Laboratory AnimalExperimental Animal ModelsAnimal Model, ExperimentalAnimal Models, ExperimentalExperimental Animal ModelModel, Experimental AnimalModels, 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: QIIMEReference DB: GreengenesOutcome: 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: RocheSoftware: BLAST and QIIMEReference 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: NoAdjusted 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 IlluminaSoftware: 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 IlluminaSoftware: R studioReferences DB: RDPOutcome: Abundance relative | Statistical analysis: Spearman rank and Fisher correlationsNo 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 groupAthletes 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 GreenSoftware: Master MixReference DB: NROutcome: 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: NoAdjusted for diet: No | 1 | qPCR: Ion TorrentSoftware: QIIMEReference DB: NROutcome: OTU | Statistical analysis: ANOSIM y Adonis (QIIME test)**↑** α-diversity in athlete groupβ-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: NRSoftware: GeneMapper and R Outcome: 16S rRNA gene copies/g samples  | Statistical analysis: Kruskal-Wallis testα-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: QIIMEReference DB: RDPOutcome: OTU | Statistical analysis: linear discriminant analysis, effect size analysis= α-diversity between after and before the marathonAfter 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: RDPOutcome: 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 systemSoftware: Metagenomic Phylogenetic Analysis Reference DB: Outcome: Relative abundance | Statistical analysis: Wilcoxon rank-sumtest 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: HUMAnN2Reference DB: Metacyc databaseOutcome: NR | Statistical analysis: ANOVA= α-diversity between groupsβ-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: SILVAOutcome: OTU | Statistical analysis: General linear modelα-diversity: there was no difference after exercise training **↑** β-diversity after exercise at the genus levelAfter training vs baseline: * Phylum
	+ **↓** *Proteobacteria*
	+ ***↑*** *Verrucomicrobia*
* Family
	+ **↑** *Verrucomicrobiaceae*
* Genus
	+ **↑** *Akkermansia*
 |
| Morita et al., 2019(30) | N=29 women  | Non-randomized interventionendurance 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 TP650TSoftware: GeneMapper Reference DB: Human Fecal Microbiota T-RFLP profilingOutcome: 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 NextSeqSoftware: HUMAnN2 V.0.99Reference DB: -Outcome: Abundance relative | Statistical analysis: -**↑** α-diversity since mid-point until race endThroughout 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: RDPOutcome: OTU | Statistical analysis: PERMANOVA and ANOVAα-diversity: no difference between groups after exercise or in the washout periodβ-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 analyzedby “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.  |