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Impact of concurrent training (HIIT + RT) on body composition and gut microbiota in postmenopausal women with overweight or obesity

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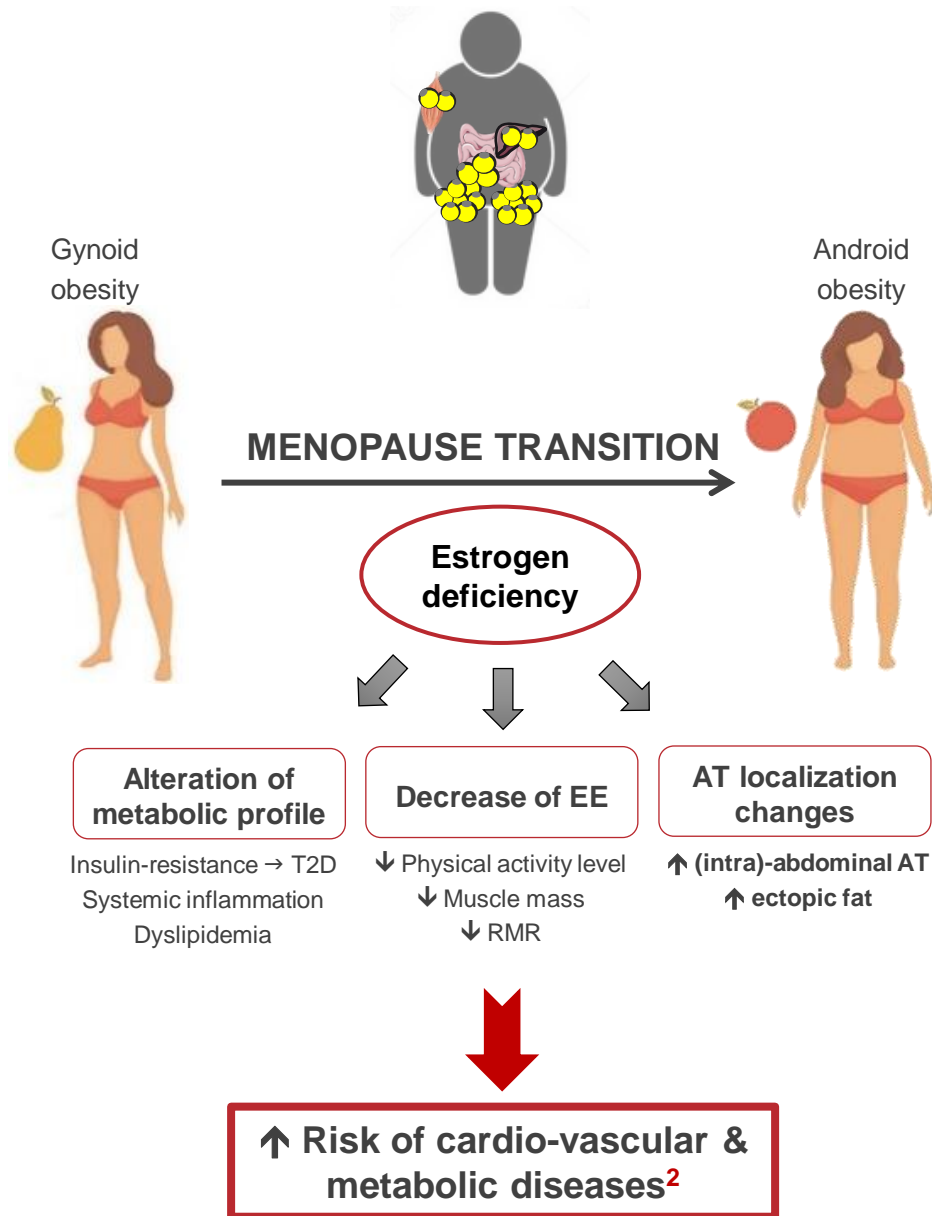
Impact of concurrent training (HIIT + RT) on body composition and gut microbiota in postmenopausal women with overweight or obesity



Effect of Concurrent Training on Body Composition and Gut Microbiota in Postmenopausal Women with Overweight or Obesity

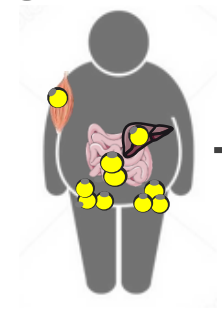
Marine Dupuit ¹, Mélanie Rance ², Claire Morel ², Patrice Bouillon ³, Audrey Boscaro ¹,
Vincent Martin, Emilie Vazeille ⁴, Nicolas Barnich, Benoit Chassaing ⁵, Nathalie Boisseau







FM loss



Diet

3



Physical activity



MICT

« Moderate Intensity Continuous Training »



HIIT

« High Intensity Interval Training »



+



RT

« Resistance Training »



Increase %MM ⁶

Time efficient strategy to reduce (intra-)abdominal FM ^{4,5,6}

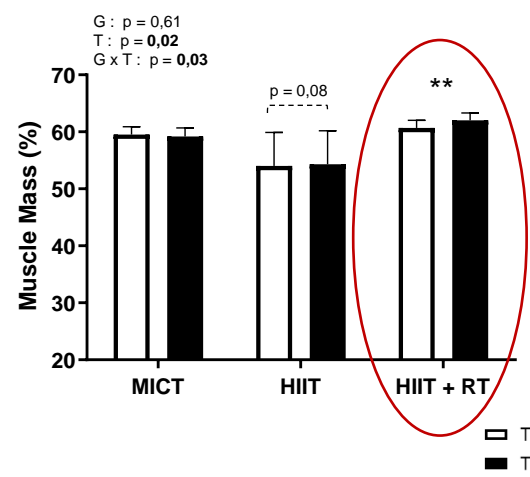
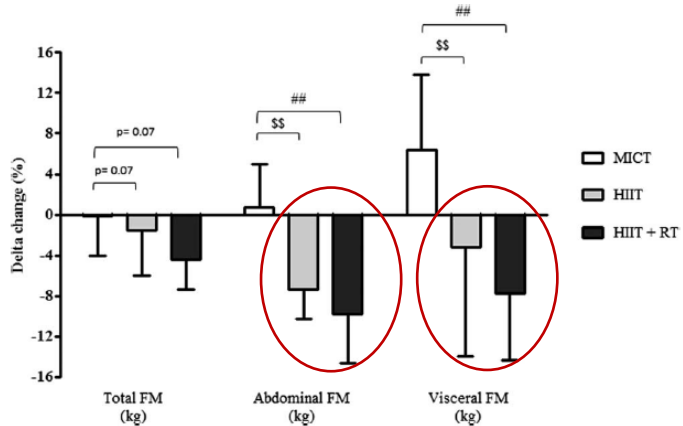
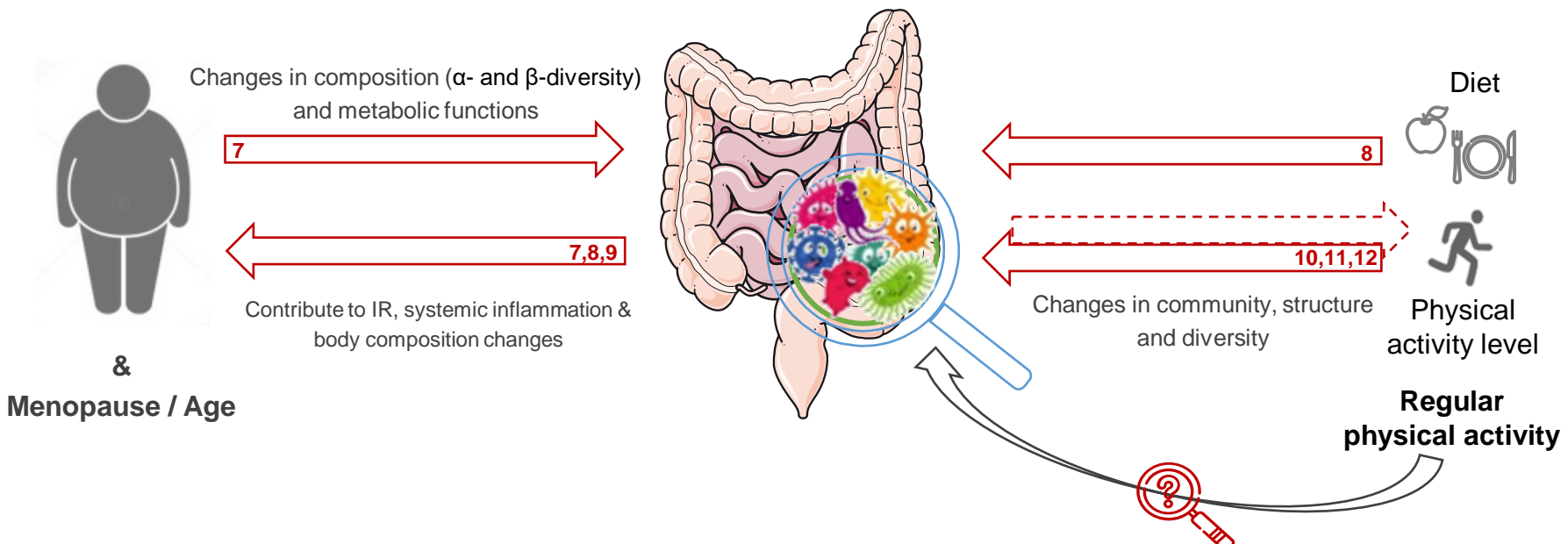
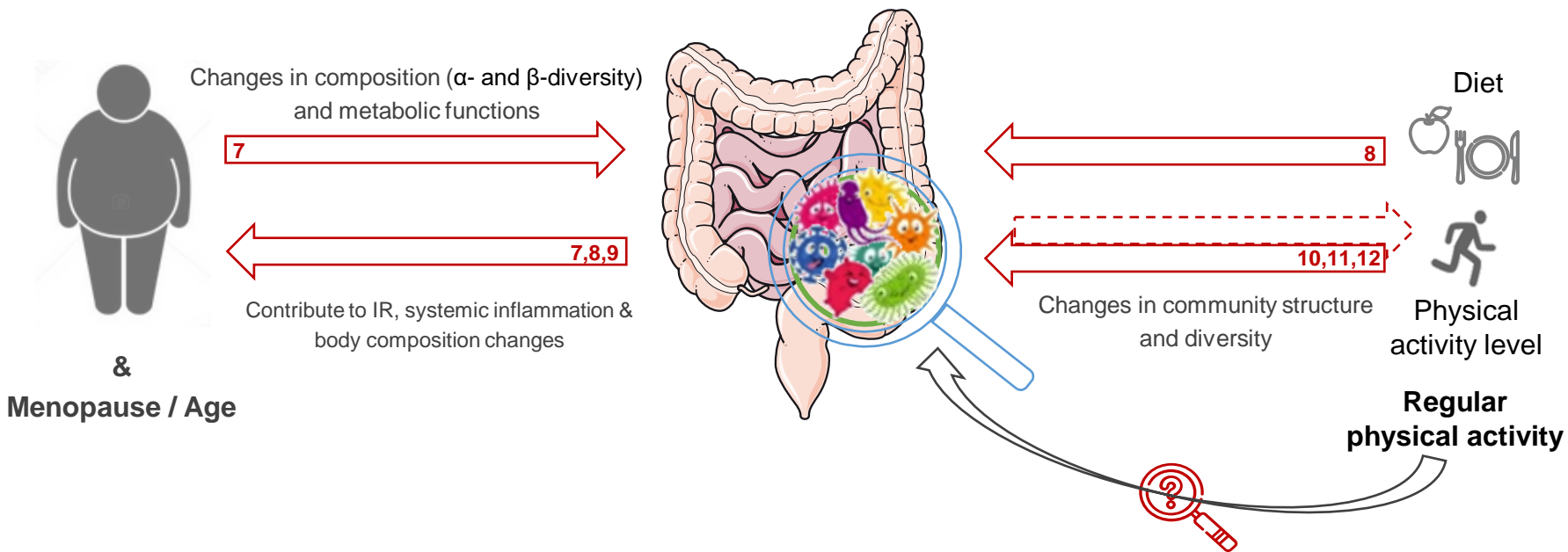


FIGURE 2—Body composition changes (based on dual-energy x-ray absorptiometry imaging) between the baseline and the end of the 12-wk training program in the MICT (*n* = 8), HIIT (*n* = 10), and HIIT + RT (*n* = 9) groups. Data are presented as mean ± SD. delta change (%) = [(12 wk - baseline/baseline) × 100]. ##*P* ≤ 0.01: HIIT + RT vs MICT group. \$\$*P* ≤ 0.01: HIIT vs MICT group.



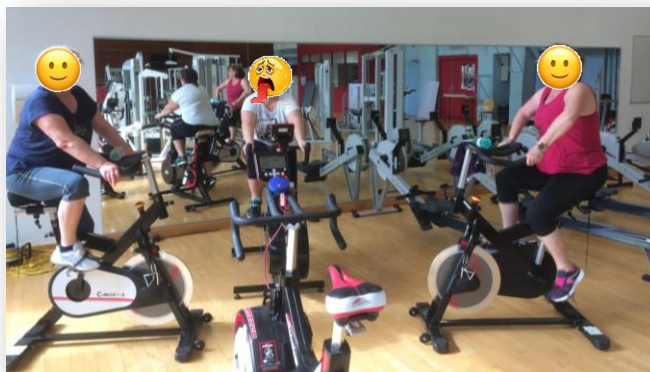
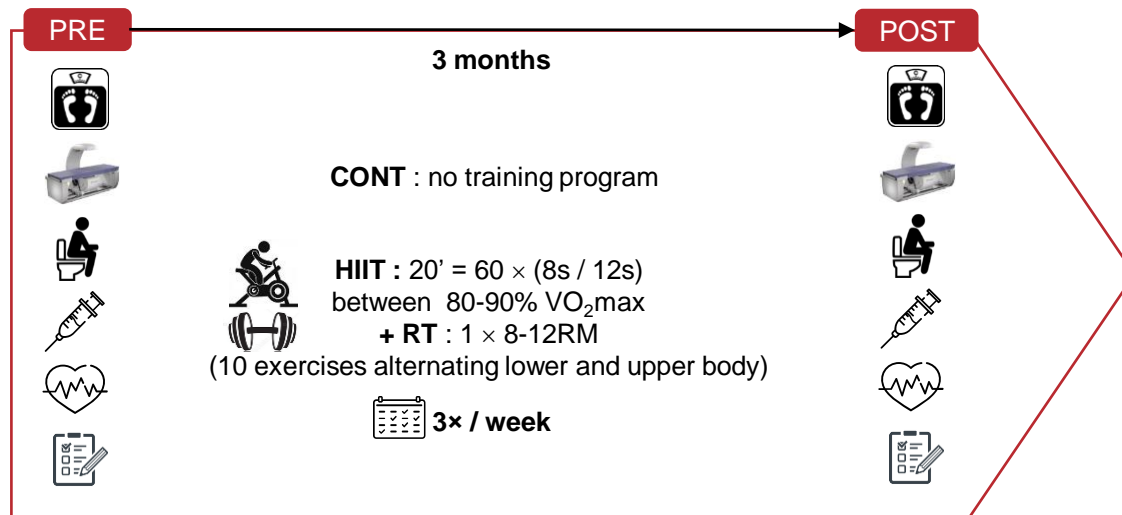


Evaluate the effect of a 12-wk HIIT + RT program on body composition and gut microbiota in nondieting postmenopausal women with overweight or obesity.

HIIT + RT (vs. CONT) : \downarrow total and (intra)-abdominal FM & \uparrow MM
 HIIT + RT (vs. CONT) : favorable alterations of gut microbiota composition









- Post-menopausal women
- + 50 years
- $25 \text{ kg.m}^{-2} < \text{BMI} < 40 \text{ kg.m}^{-2}$
- no hormonal treatment
- no antibiotic treatment





- 17 subjects
- 59.9 ± 5.0 years
- 31.3 ± 3.7 kg.m⁻²
- 36.3 ± 4.7 %MG

	CONT		HIIT + RT		ANOVA (p)		
	Pre	Post	Pre	Post	G	T	G × T
 VO₂max (mL.min⁻¹.kg⁻¹)	19.7 ± 3.6	20.5 ± 4.0	20.5 ± 5.7	23.2 ± 5.8**	0.46	0.001	0.037
PMA (Watts.kg⁻¹)	1.4 ± 0.3	1.4 ± 0.3	1.5 ± 0.5	1.8 ± 0.5***	0.29	≤ 10 ⁻³	≤ 10 ⁻³
 BMI (kg.m²)	31.5 ± 3.4	31.7 ± 3.3	30.3 ± 3.5	30.6 ± 3.5	0.30	0.048	0.80
 Body weight (kg)	80.3 ± 11.2	79.3 ± 10.7	77.8 ± 12.4	79.3 ± 12.5	0.78	0.047	0.87 
Fat mass (%)	33.0 ± 4.6	32.2 ± 4.0	35.2 ± 4.9	34.3 ± 4.0	0.29	0.045	0.64 
Muscle mass (%)	52.5 ± 4.7	53.2 ± 4.0	62.3 ± 4.8	63.2 ± 3.9	0.33	0.039	0.52 
Arm muscle mass (kg)	4.1 ± 0.3	4.0 ± 0.3	4.2 ± 0.6	4.4 ± 0.8*	0.34	0.59	0.05
R leg muscle mass (kg)	5.5 ± 0.6	5.5 ± 0.6	5.4 ± 0.6	5.6 ± 0.6*	0.94	0.011	0.043

➤ Overall, we observed a ↓ %FM and an ↑ %MM

→ Potentially due to relatively small number of participant and/or lifestyle changes in CONT group no detectable with questionnaires



- 17 subjects
- 59.9 ± 5.0 years
- 31.3 ± 3.7 kg.m⁻²
- 36.3 ± 4.7 %MG

VO₂max (mL.min⁻¹.kg⁻¹)PMA (Watts.kg⁻¹)BMI (kg.m²)

Body weight (kg)



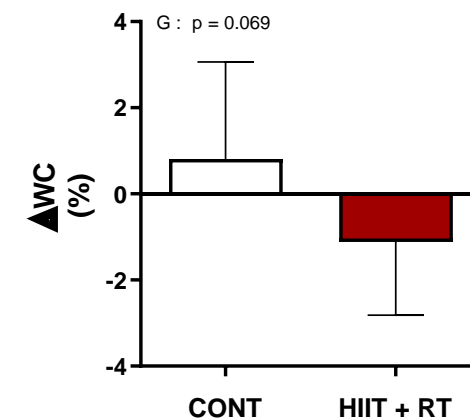
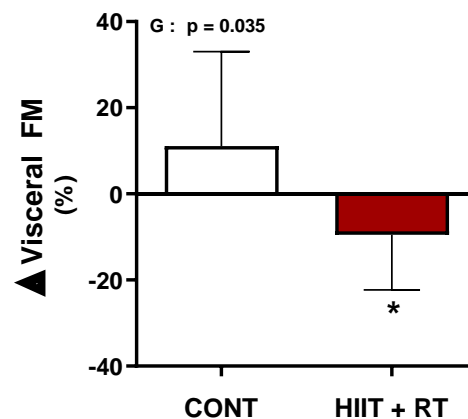
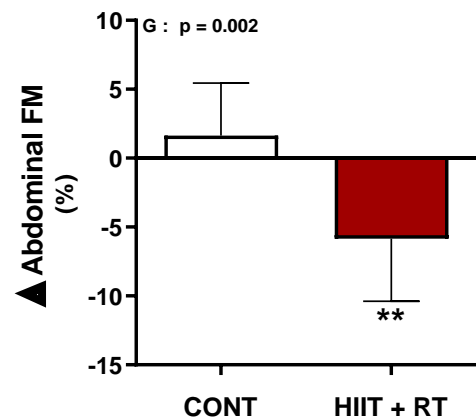
Fat mass (%)

Muscle mass (%)

Arm muscle mass (kg)

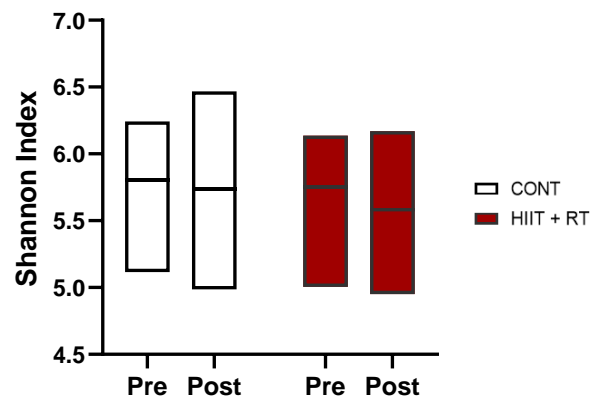
R leg muscle mass (kg)

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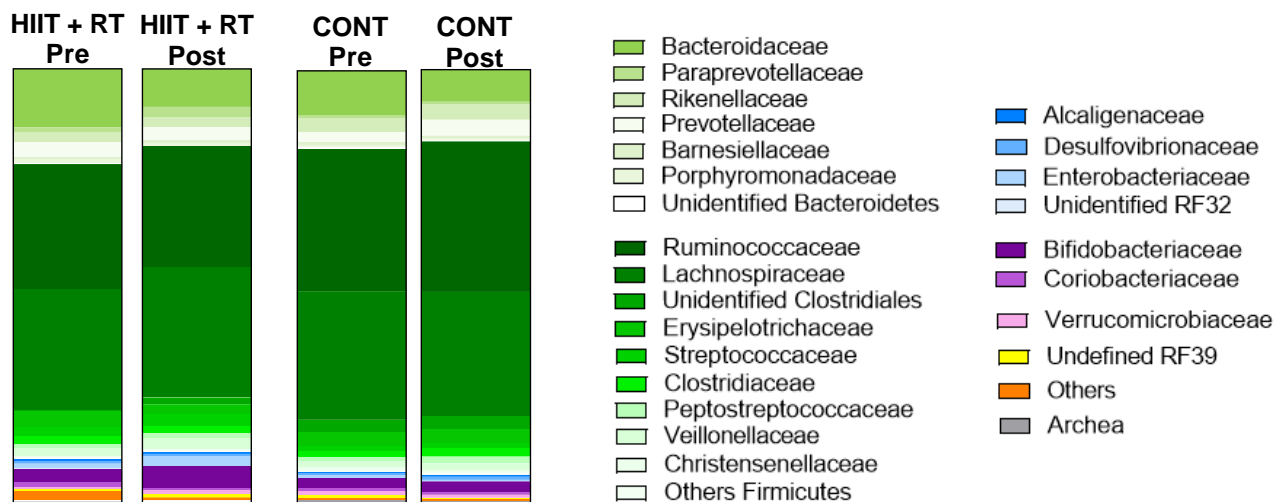


➤ Only HIIT + RT group ↑ physical fitness, ↓ abdominal, including visceral, FM and ↑ segmental MM.

→ Concordant with our previous study results ⁶



Mean gut microbiota composition per group, pre and post-intervention



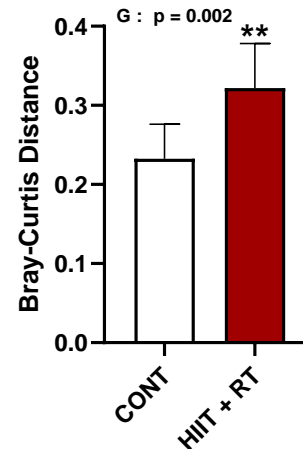
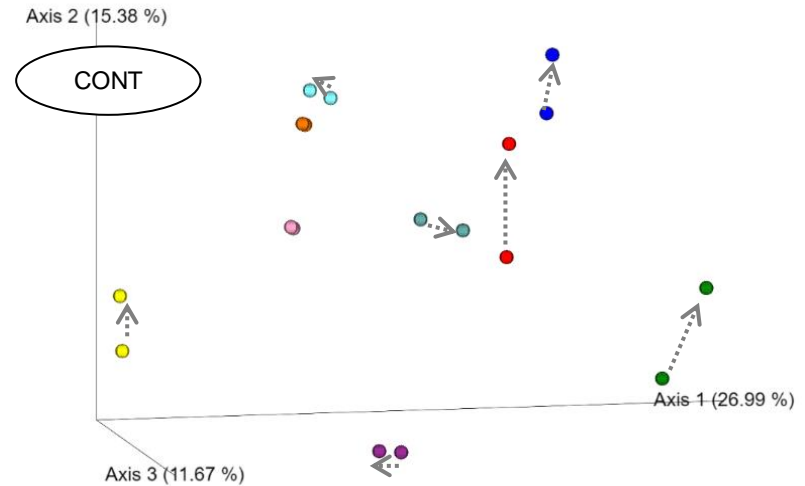
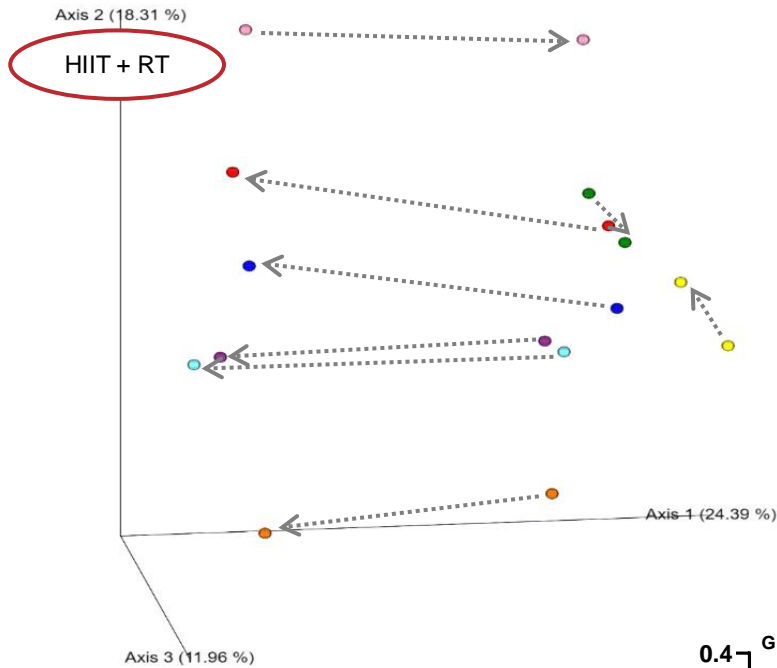
► **α -diversity** (Shannon's diversity index) : **no difference** between groups at **baseline** and **no change** at the study end.

→ Concordant with previous studies ^{13,14,15}

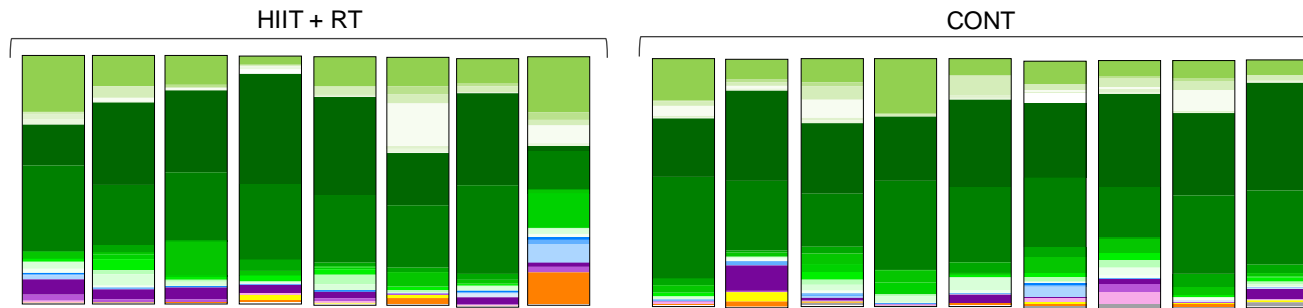
► **Taxonomy analysis** : **no significant group difference** at phylum and here family levels after the 12-wk program.

→ Small number of participant AND high inter-individual variability

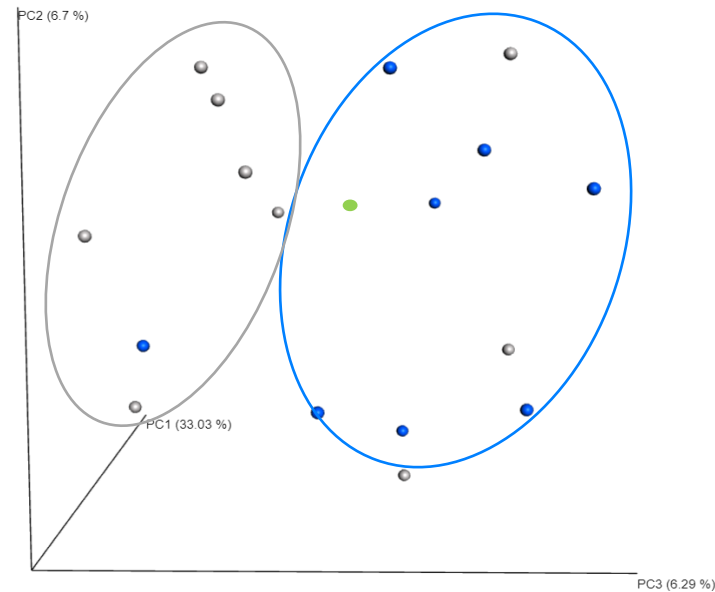
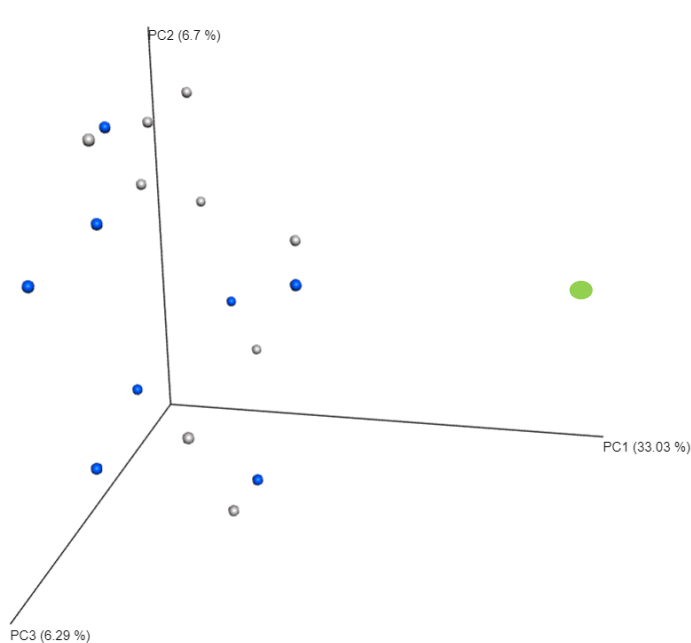
→ Different collection and analysis techniques + confounding effect of factors (age, diet, metabolic profile, training modalities...)



- **β -diversity** : pre- and post-intervention **microbiota composition changed** in most patients from **HIIT+RT group** whereas it remains **stable in CONT group** which was confirmed by the **higher Bray-Curtis distance**



High inter-individual variability at baseline → normalization

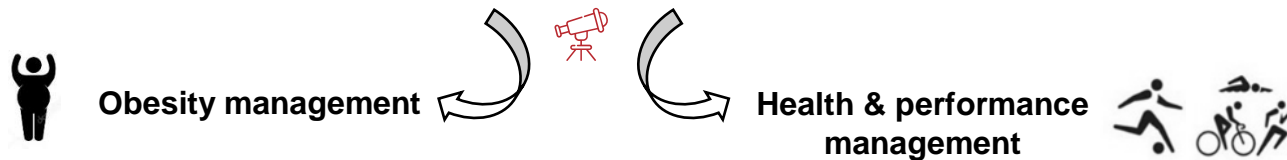


- Normalized baseline value
- CONT
- HIIT + RT

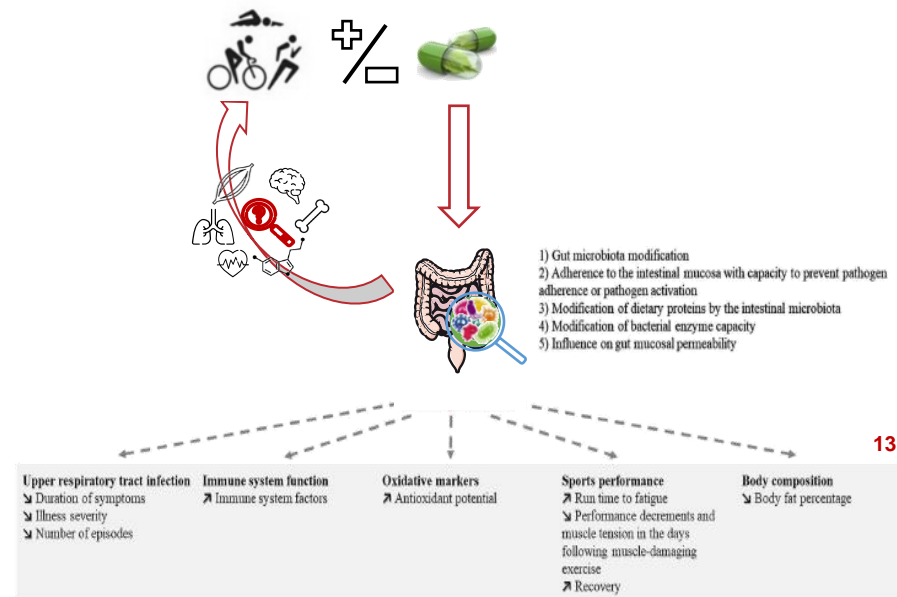
- Overall fecal microbiota composition was changed in both groups at the end of the study.
- Based on axes 2 and 3, the PCoA plots highlighted a **clear intervention based clustering**

Take home message

- HIIT + RT could be proposed in nondieting postmenopausal women with overweight / obesity to reduce total and (intra-)abdominal fat mass and to increase muscle mass.
- HIIT + RT may specifically modulate fecal microbiota composition.



Modulate / Optimize gut microbiota composition and functions through physical activity and/or diet ?

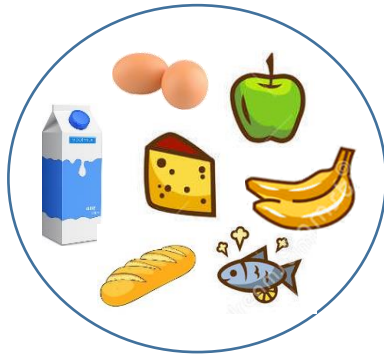


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Thanks for your attention

Alpha et Beta-diversity

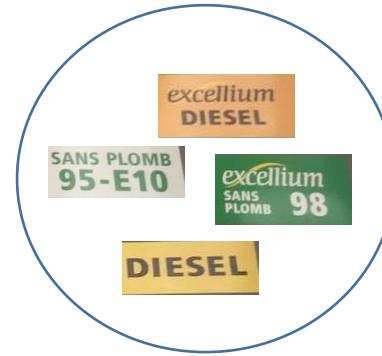
Microbiote A



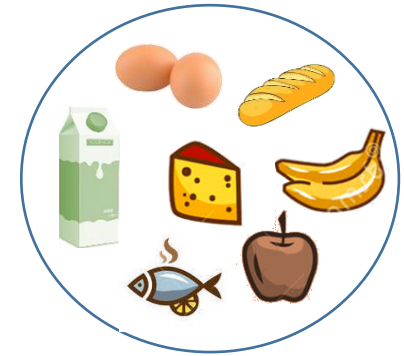
Microbiote B



Microbiote C



Microbiote D



Bacteria = available products

Alpha-diversity

= richness which can be determined on one sample



Gut microbiota A, B et D have **a large** α -diversity, whereas the gut microbiota C has **a poor** α -diversity

Beta-diversity

= richness and diversity compared between community



β -diversity of A and D gut microbiota are **very close**, whereas B and C are **distant**.