Medicine, Nursing and Health Sciences

# Does the gut microbiota bacterial abundance and composition influence the magnitude of intestinal integrity perturbations, systemic cytokinaemia, and gastrointestinal symptoms in response to exertional-heat stress?

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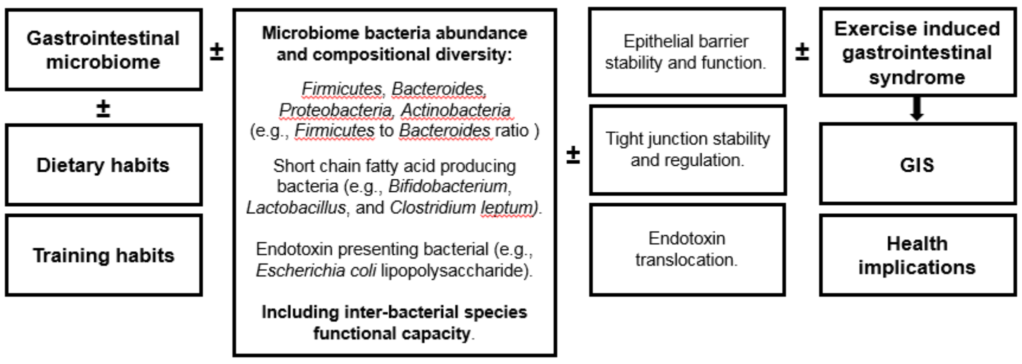
## INTRODUCTION

- Gastrointestinal integrity and functional perturbations, and subsequent systemic endotoxaemia and cytokinaemia are a common feature of exercise- '*exercise induced gastrointestinal syndrome*' (EIGS), especially when conducted in hot ambient conditions (e.g., $T_{amb}$ 35ºC).[1,2]

- Such perturbations can lead to gastrointestinal symptoms (GIS) and (or) health implication of sub-clinical or clinical nature, which have been linked to performance decrements.[3,4,5]

- Emerging evidence suggests the gastrointestinal commensal and pathogenic bacteria may potentially influence gastrointestinal perturbations in response to exertional-heat stress (**Figure 1**).[1]



**Gastrointestinal microbiome** ± **Microbiome bacteria abundance and compositional diversity:**

*Firmicutes*, *Bacteroides*, *Proteobacteria*, *Actinobacteria* (e.g., *Firmicutes* to *Bacteroides* ratio )

Short chain fatty acid producing bacteria (e.g., *Bifidobacterium*, *Lactobacillus*, and *Clostridium leptum*).

Endotoxin presenting bacterial (e.g., *Escherichia coli* lipopolysaccharide).

**Including inter-bacterial species functional capacity.**

±

**Dietary habits**

**Training habits**

± Epithelial barrier stability and function.

Tight junction stability and regulation.

Endotoxin translocation.

± **Exercise induced gastrointestinal syndrome**

**GIS**

**Health implications**

**Figure 1.** Gastrointestinal microbiota and exercise induced gastrointestinal syndrome: A speculative model.

**Aim:** To examine if the relative bacterial abundance and diversity of the intestinal microbiota influences the magnitude of markers characteristic of exercise-induced gastrointestinal syndrome (EIGS).

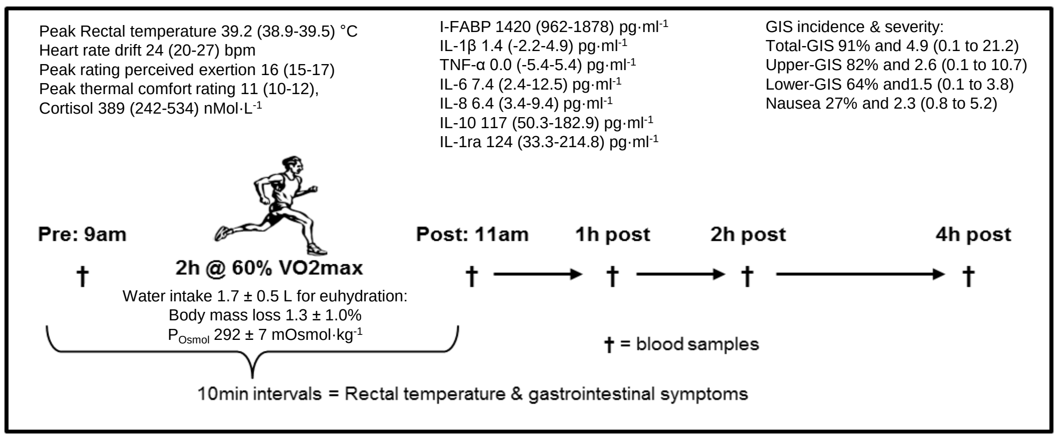
## METHODS

- After Human Research Ethics Committee approval, twenty-two endurance athletes [mean ± SD (male n= 13 and female n= 9): age 35 ± 8 years, nude body mass 64.9 ± 11.5 kg, height 1.73 ± 0.10 m, $VO_{2max}$ 58 ± 7 $ml \cdot kg^{-1} \cdot min^{-1}$] completed an exertional-heat stress trial (**Figure 2**).

- Participants were provided with a standardised low FODMAP diet for 24 h prior to each trial.

- A mid-flow faecal sample (~30 g) was collected pre-exercise, and immediately stored at -80° C before analysis. Faecal microbiota taxonomy was determined by next generation sequencing on an Illumina MiSeq platform. Data were processed using the QIIME2 pipeline (v2019.1) establishing taxonomic classification with >95% confidence using SILVA. Bacterial phyla (n=11), family (n=42), and genus (n=159) ASVs were detected for relative abundance and α-diversity (Shannon index) determination.

- Whole blood samples were collected pre, post and during recovery. Plasma aliquots were used to determine intestinal fatty acid binding protein (I-FABP) and cortisol concentration by ELISA, and cytokine profile by multiplex.



Peak Rectal temperature 39.2 (38.9-39.5) °C
Heart rate drift 24 (20-27) bpm
Peak rating perceived exertion 16 (15-17)
Peak thermal comfort rating 11 (10-12),
Cortisol 389 (242-534) $nMol \cdot L^{-1}$

I-FABP 1420 (962-1878) $pg \cdot ml^{-1}$
IL-1β 1.4 (-2.2-4.9) $pg \cdot ml^{-1}$
TNF-α 0.0 (-5.4-5.4) $pg \cdot ml^{-1}$
IL-6 7.4 (2.4-12.5) $pg \cdot ml^{-1}$
IL-8 6.4 (3.4-9.4) $pg \cdot ml^{-1}$
IL-10 117 (50.3-182.9) $pg \cdot ml^{-1}$
IL-1ra 124 (33.3-214.8) $pg \cdot ml^{-1}$

GIS incidence & severity:
Total-GIS 91% and 4.9 (0.1 to 21.2)
Upper-GIS 82% and 2.6 (0.1 to 10.7)
Lower-GIS 64% and1.5 (0.1 to 3.8)
Nausea 27% and 2.3 (0.8 to 5.2)

**Pre: 9am** † **2h @ 60% VO2max** **Post: 11am** † → **1h post** † → **2h post** † → **4h post** †

Water intake 1.7 ± 0.5 L for euhydration:
Body mass loss 1.3 ± 1.0%
$P_{Osmol}$ 292 ± 7 $mOsmol \cdot kg^{-1}$

† = blood samples

10min intervals = Rectal temperature & gastrointestinal symptoms

**Figure 2. Schematic description of the experimental design**.
Data within presented as mean and 95% confidence interval.

## RESULTS

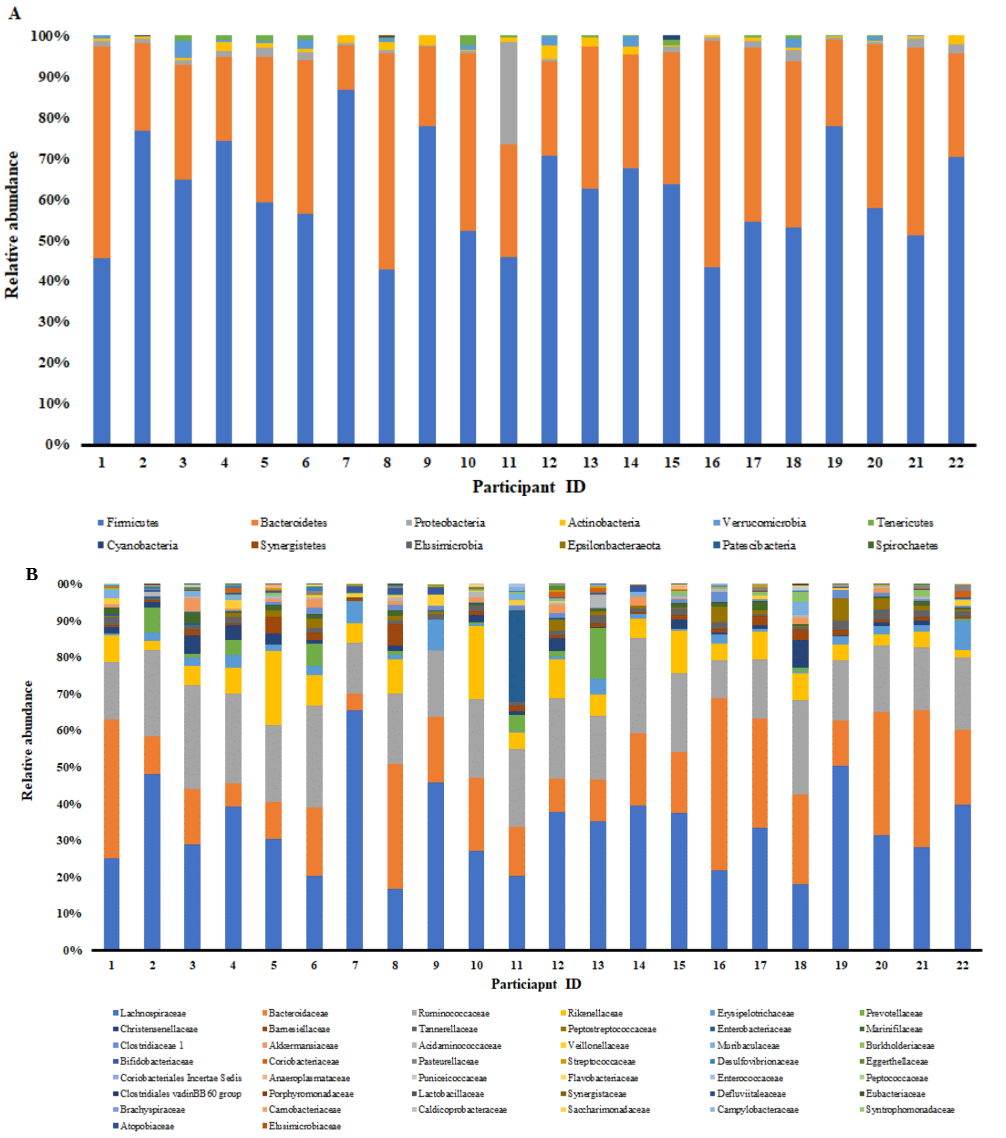


**Figure 3.** Relative abundance of intestinal bacterial phyla (A) and family (B) groups of endurance athletes before 2h running at 60% $VO_{2max}$ in $T_{amb}$ 35.2ºC and 25% RH. Individual participant composition (*n*= 22), in order of greatest to lower relative abundance: Shannon Equitability Index range 0.193 to 0.473 and 0.144 to 0.252, respectively.

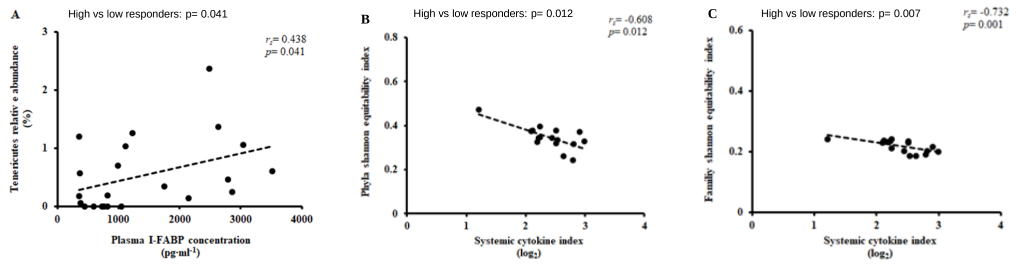


**Figure 4.** Correlations between intestinal injury with relative abundance of intestinal bacterial phyla *Tenericutes* (A), and systemic cytokine responses with phyla α-diversity (B) and family α-diversity (C) in endurance athletes before 2h running at 60% $VO_{2max}$ in $T_{amb}$ 35.2ºC and 25% RH. Individual participant composition (*n*= 22).

- Predominant inverse correlations between relative abundance of short chain fatty acid producing bacterial clusters and markers of thermoregulatory strain ($p \leq 0.05$).

- Predominant inverse correlations between relative abundance of short chain fatty acid producing bacterial clusters and GIS ($p \leq 0.05$). Supported by symptomatic and asymptomatic group comparisons ($p \leq 0.05$)

## CONCLUSION

- These landmark findings suggest that the intestinal microbiota composition may contribute to the magnitude of EIGS and thermal tolerance.

- A substantial amount of research is still needed to provide substantiation and justification for evidence-based intestinal microbiota altering nutritional interventions.

**References**

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