

Human stool metabolome differs upon 24-hour blood pressure levels and blood pressure dipping status: a prospective longitudinal study



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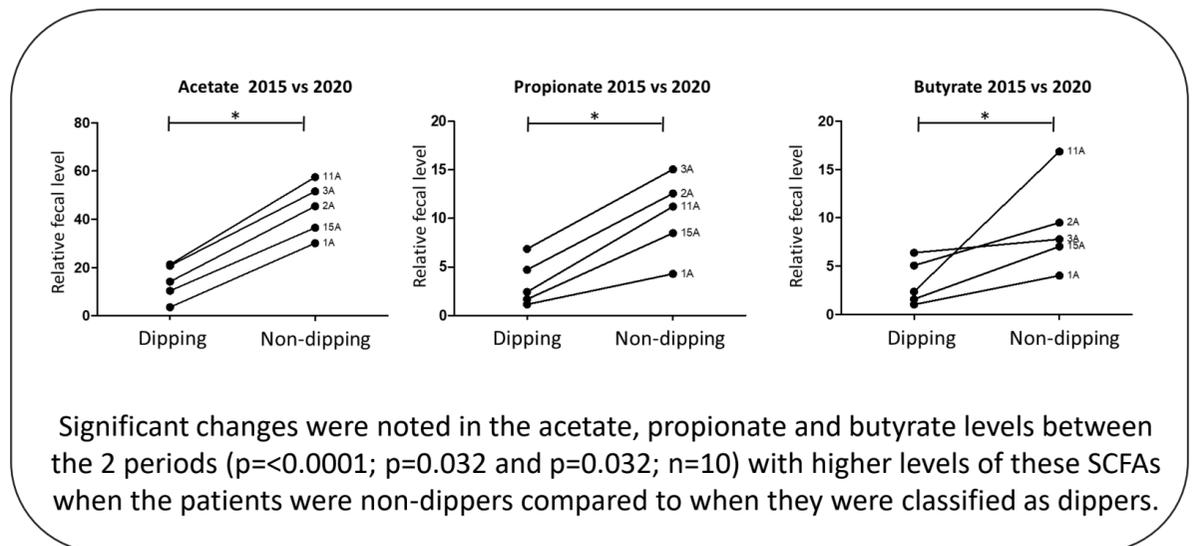
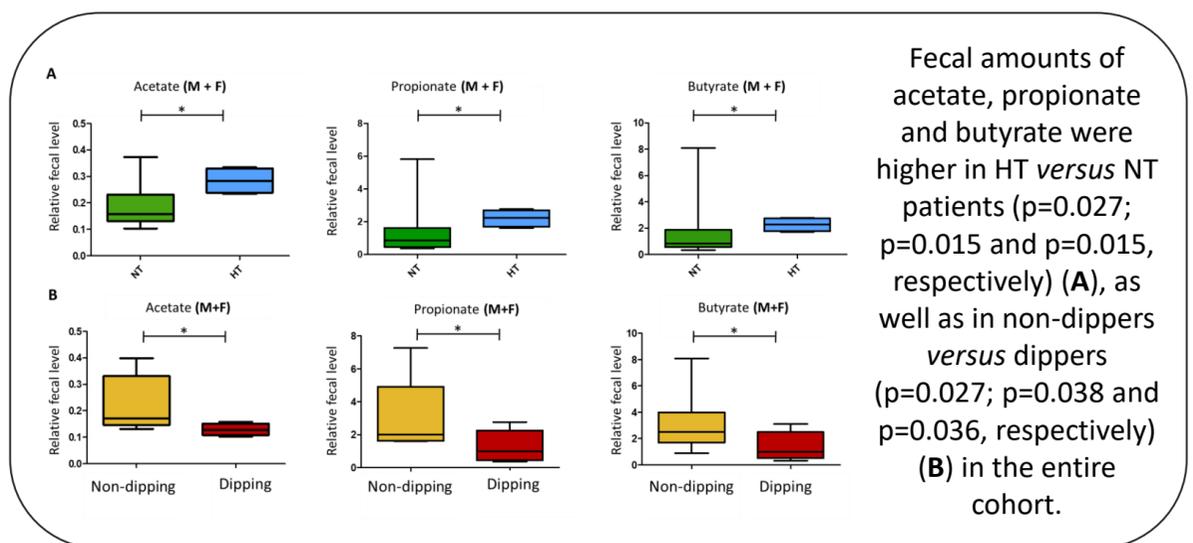
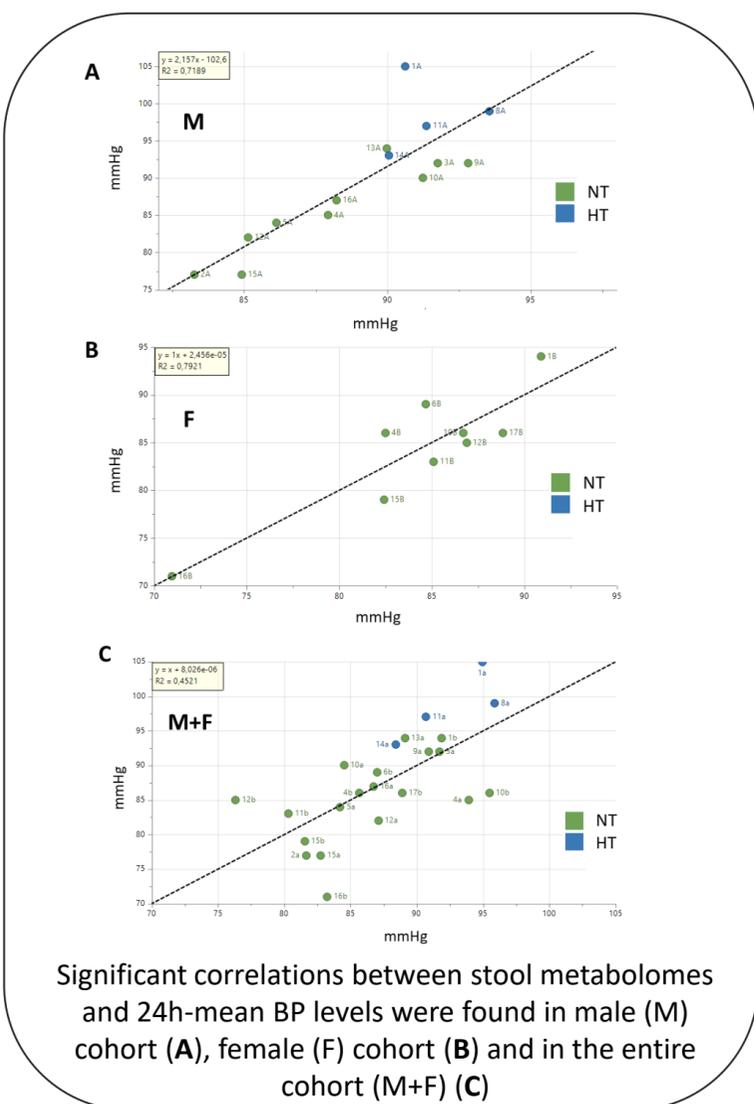
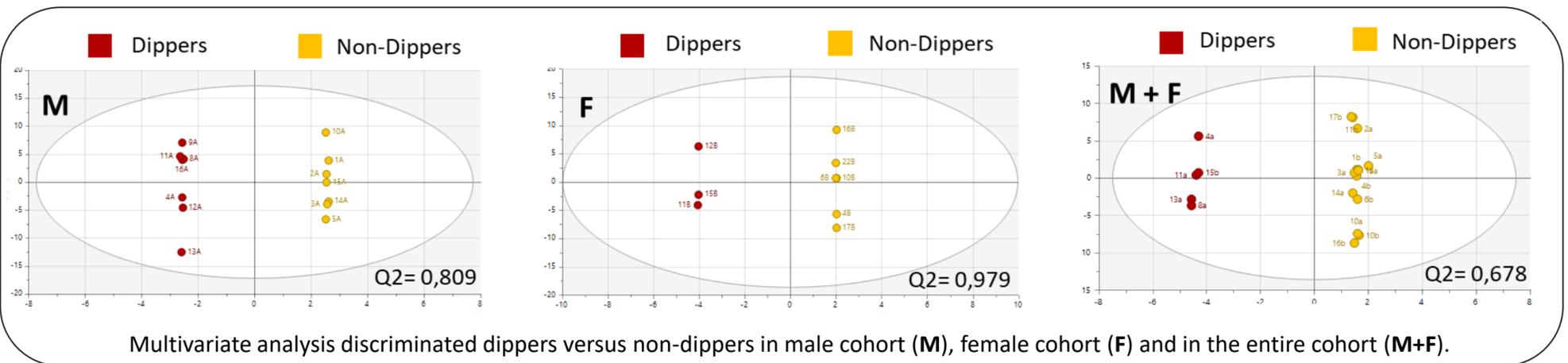
Introduction

Dysbiosis of gut microbiota (GM) has been implicated in the pathophysiology of arterial hypertension (HT), via a putative role of food-derived short chain fatty acids (SCFAs) and other metabolites. Among the clinical manifestations of HT, the absence of a significant drop in blood pressure (BP) overnight (i.e. the non-dipping BP profile) has been associated with poor cardiovascular outcomes. The link between GM and non-dipping BP profile is unknown.

Methods

- **Patients.** After informed consent, 16 male patients and their female partners (n=10) were subjected to 24-hour ambulatory BP monitoring and categorized in 2 groups: HT (n=6 men and 1 women) and normotension (NT) (n=19). According to the conventional night/day BP ratio >0.9, 15 individuals (n=8 men and 7 women) were categorized as non-dippers (patients under anti-hypertensive treatment were excluded). Stools samples were collected.
- **Metabolomics.** This approach was conducted on stool samples using ¹H-NMR and 3 main SCFA (acetate, butyrate and propionate) were quantified.
- **Longitudinal study.** A 5-year comparative follow-up of BP profiles and stool metabolomes was done for male patients (2015 *versus* 2020).

Results



Conclusions

This 26-patient cohort highlights significant correlations between the stool metabolome and (i) BP levels and (ii) the non-dipping BP profile in both genders. SCFA levels were significantly different in patients changing of dipping status over the 5-year follow-up.

