



Reduction in systolic blood pressure following dietary fibre intervention is dependent on baseline gut microbiota composition

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Uncontrolled hypertension is a primary cause of non-communicable diseases and death globally⁽¹⁾. The gut microbiota plays a role in hypertension and dietary interventions high in fibre have been shown to lower blood pressure (BP)⁽²⁾. Not all participants respond to dietary fibre interventions, for reasons which are unclear. Here we aimed to identify responders of a high fibre intervention based on their baseline gut microbiome. Twenty treatment-naïve participants with hypertension received either placebo or 40g per day of prebiotic acetylated and butyrylated high amylose maize starch (HAMSAB) supplementation for 3 weeks in a phase II randomised cross-over double-blind placebo-controlled trial. Blood pressure was monitored at baseline and each endpoint by 24-hour ambulatory BP monitoring, with those experiencing a reduction between timepoints of ≥ 2 mmHg classified as responders. Baseline stool samples were collected and the V4-V5 region of the 16S gene sequenced. Taxonomy was assigned by reference to the SILVA database. The MaAsLin2 package was used for assessing the relationship between baseline gut microbiota and response to dietary intervention. Overall participants had significant reduction in 24-hour systolic BP (-6.1 mmHg, $p = 0.03$), with 14 individuals classified as responders and six individuals as non-responders. 13 genera were found to be differentially abundant between responders and non-responders. Genera significantly enriched in responders included *Dialister* ($\beta = 1.29$, $q = 1.921 \times 10^{-134}$), *Coprococcus* ($\beta = 1.26$, $q = 3.282 \times 10^{-121}$), *Bifidobacterium* ($\beta = 1.67$, $q = 1.11 \times 10^{-81}$), *Ruminococcus* ($\beta = 0.161$, $q = 1.11 \times 10^{-8}$) and *Roseburia* ($\beta = 0.82$, $q = 4.275 \times 10^{-2}$). Participants who experienced a decrease in systolic BP following a dietary fibre intervention had increased level of bacterial genera known to contain species that produce short-chain fatty acids (e.g. *Bifidobacterium*, *Roseburia* and *Ruminococcus*) at baseline. These data suggest that baseline microbiota composition contributes to the response to dietary fibre intervention trials in people with hypertension.

Keywords: hypertension; dietary fibre; microbiota

Ethics Declaration

Yes

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References

1. Murray CJL *et al.* (2020) *Lancet* **396**, 1223–1249.
2. Muralitharan RR *et al.* (2020) *Hypertension* **76**(6):1674–1687.