

# Almonds and their impact on gastrointestinal physiology, luminal microbiology and gastrointestinal function: a randomised controlled trial

A.C. Creedon<sup>1</sup>, E. Dimidi<sup>1</sup>, E.S. Hung<sup>1</sup>, S.M. Scott<sup>2</sup>, C. Probert<sup>3</sup>, S.E. Berry<sup>1</sup> and K. Whelan<sup>1</sup>

<sup>1</sup>Department of Nutritional Sciences, King's College London, London, UK,

<sup>2</sup>Centre for Neuroscience, Surgery and Trauma, Queen Mary University of London, London, UK and

<sup>3</sup>Department of Molecular and Clinical Cancer medicine, University of Liverpool, Liverpool, UK

The gut microbiota and their metabolites are increasingly recognised for their roles in gut health. Almonds are nuts that are rich in fermentable nutrients and have physicochemical properties that result in poor nutrient bioaccessibility in the upper gastrointestinal tract<sup>(1)</sup>. Subsequently, intracellular nutrients reach the colon where they are available to the microbiota, and processing and mastication may influence this. A systematic review of randomised controlled trials investigating nut consumption and the gut microbiota revealed an effect of nuts on several bacterial genera, but not *Bifidobacteria*, while the quality of included trials was poor<sup>(2)</sup>. The aim of this study was to investigate the impact of almonds on faecal *Bifidobacteria* (primary outcome) and gut microbiology, physiology and symptoms.

Eighty-seven healthy adults with low fibre intake were randomised to receive whole almonds (56 g/d), ground almonds (56 g/d) or a control muffin (2/d) in place of their habitual snacks for 4 weeks. Faecal *Bifidobacteria*, gut microbiota composition and diversity (16S rRNA sequencing), short-chain fatty acids (SCFA; gas-chromatography), volatile organic compounds (gas-chromatography mass-spectrometry), gut transit time (wireless motility capsule), and stool output and symptoms (7-day diary) were measured at baseline and at end of study. Differences between groups were assessed by analysis of covariance (ANCOVA) or a non-parametric equivalent and corrected for multiple testing (Bonferroni (*p*) or Benjamini-Hochberg FDR (*q*)) where appropriate.

There were no differences in relative abundance of faecal *bifidobacteria* following 4-weeks consumption of whole almonds (8.7%, SD 7.7), ground almonds (7.8%, SD 6.9) or control (13.0%, SD 10.2; *q* = 0.613). There was no effect of almonds on gut microbiota at the phylum level or on diversity. At the genus level, almonds (whole and ground pooled) increased relative abundance of *Lachnospiraceae\_NK4A136\_group*, *Phascolarctobacterium* and decreased *Tyzerella* (all *p* < 0.05), however these were no longer significant following adjustment; and resulted in higher concentrations of butyrate (24.1 μmol/g, SD 15.0) in comparison to control (18.2, SD 9.1; *p* = 0.046). There was no effect of almonds on gut transit time, stool consistency or gut symptoms. There were no differences between the whole almond (low nutrient bioaccessibility) and ground almond (higher nutrient bioaccessibility) groups for any outcome.

Almond consumption does not exert a prebiotic effect on faecal *Bifidobacteria* in healthy adults, however, may influence gut microbiota at the genus level, and increase butyrate production.

## References

1. Ellis PR, Kendall CWC, Ren Y *et al.* (2004) *Am J Clin Nutr* **80**, 604–613.
2. Creedon AC, Hung ES, Berry SE *et al.* (2020) *Nutrients* **12**, 2347.