

Changes in dominant gut microbial species and metabolites in children with Crohn's disease during exclusive enteral nutrition

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The gut microbiota is implicated in the pathogenesis of Crohn's Disease (CD)⁽¹⁾. Exclusive enteral nutrition (EEN) is a successful treatment but its mode of action remains unknown⁽²⁾. We assessed changes in the fecal microbiota milieu during EEN.

Five faecal samples were collected from CD children; 4 during EEN (start, 15, 30, end EEN~60 days) and a fifth on free habitual diet. Two samples were collected from healthy controls. Faecal pH, bacterial metabolites (Figure) and quantitative changes (q-PCR) of total and 7 major bacterial groups implicated in CD were measured.

68 samples were from 15 CD children and 40 from 21 controls. Faecal pH and total sulphide increased and butyric acid decreased during EEN (Figure). *F. prausnitzii* spp. concentration significantly decreased after 30 d on EEN (Figure). In patients who responded to EEN, the magnitude of the observed changes was greater and the concentration of *Bacteroides/Prevotella* group also decreased. All these changes reverted to pre-treatment levels when the children returned to their free habitual diet.

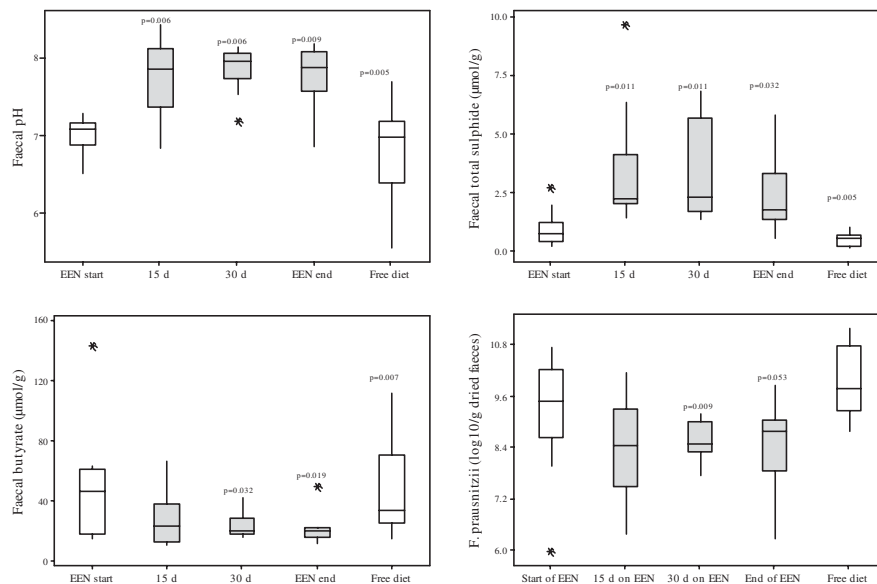


Fig. 1. Faecal pH, and concentrations (g/dry feces) of total sulphide, butyrate and *F. prausnitzii* spp. before, during and after EEN completion (free habitual diet)

EEN impacts on gut microbiota composition and changes faecal metabolic activity. It is difficult to infer a causative association between such changes and disease improvement but the results do challenge the current perception of a protective role for *F. prausnitzii* in CD.

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2. Gerasimidis K *et al.* (2011) *J Clin Gastroenterol* **45**, 234–9.