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Are cariogenic bacteria the major risk factor for dental caries in patients with ulcerative colitis?
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Background: Previous reports demonstrated a higher prevalence of dental caries in patients with ulcerative colitis (UC). The risk has been attributed to diet and changes in salivary environment. We aimed to characterise the prevalence of dental caries, salivary flow rates, salivary buffering capacity and cariogenic bacteria counts of Mutans streptococci (MS) and Lactobacillus spp. (LB) in UC patients and evaluate the association between these features, disease activity and duration, and drug therapy.

Methods: Cross-sectional study of UC patients followed in a tertiary inflammatory bowel disease clinic. All participants were submitted to a questionnaire, which included demographic data, oral hygiene practice and eating habits and a clinical observation with the assessment of the plaque index and decayed, missing and filled teeth (DMFT) index. Unstimulated and stimulated saliva were collected. Medical records, disease activity (Partial Mayo Score) and duration were also collected. Laboratory data included salivary flow rates, salivary buffering capacity (CRT® buffer) and cariogenic bacteria count (MS and LB) in saliva using the CRT® bacteria test (results: high or low counts).

Results: Thirty UC patients were recruited. The most common oral hygiene routines were teeth brushing once or more times a day (96.7%) and the use of fluoride toothpaste (73.3%). DMFT index (mean 16.17 ± 6.428) was not affected by the frequency of soft drinks, cakes, sweets and sugars between meals (p > 0.2). Patients with long-term disease showed a trend towards higher prevalence of dental caries (p = 0.06). Most patients presented normal salivary flow rates, both of unstimulated (73.3%) and stimulated saliva (60.0%), as well as high salivary buffering capacity (66.7%). No association was found among these features and age, gender, disease activity and duration or drug therapy. High MS and low LB count were observed in 73.3% and 60% of patients, respectively. Patients with active (100%) and longer duration of disease (88.9%) had higher MS count.

Conclusions: Higher prevalence of dental caries was observed in UC patients when compared with general Portuguese data, even though eating habits of UC patients were similar to the general Portuguese population. High MS count was the major risk factor for dental caries and it is probably part of the well-known UC dysbiosis.

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Colonic mucosa-associated microbiota analysis in newly diagnosed Lithuanian paediatric IBD cases
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Background: Dysbiotic changes in fecal microbiome composition in ulcerative colitis (UC) patients when compared with fecal microbiome of healthy individuals. It is not clear if these changes persist during remission periods. Some UC patients report a clinical relapse after a colonoscopy. We sought to evaluate the effect of polyethylene glycol (PEG) preparation on fecal microbiome of UC patients in clinical remission and healthy controls, through the application of 16S rRNA gene sequencing techniques.

Methods: All subjects received identical standard colonoscopy preparation with PEG. Samples were collected at different time points: −30, -1 day (before bowel preparation), the first formed stool sample after bowel preparation, +15, +30 and +60 days. We performed 16S rRNA gene sequencing techniques by amplification of the variable region V4. We used Chao1 to estimate microbiome diversity.

Results: Eleven UC patients in clinical remission and 12 Healthy controls (HC) were recruited. One hundred and thirty-seven samples were analysed. We obtained 3,892,300 high-quality sequences, with a mean base pair number of 314 and 338 Operational taxonomic Units (OTUs). At baseline, diversity in terms of Chao1 was significantly lower in UC patients compared with HC (Median: 132.3 vs. 188.2, p < 0.01). PEG induced a decline in Chao1 in both UC and HC subjects. The magnitude of this decrease was not different between the groups. The microbiome diversity returned to baseline levels at the +60 day time point. Neither Faecalibacterium prausnitzii (Fp) nor Escherichia coli counts were affected by PEG.

Conclusions: PEG induced a decline in Chao1 in both UC and HC subjects. The magnitude of this decrease was not different between the groups. The microbiome diversity returned to baseline levels at the +60 day time point. Neither Faecalibacterium prausnitzii (Fp) nor Escherichia coli counts were affected by PEG.

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Dysbiotic changes caused by polyethylene glycol in ulcerative colitis patients: "Lavage" or intrinsic effect?
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Background: Dysbiotic changes have been described in fecal microbiome composition in ulcerative colitis (UC) patients when compared with fecal microbiome of healthy individuals. It is not clear if these changes persist during remission periods. Some UC patients report a clinical relapse after a colonoscopy. We sought to evaluate the effect of polyethylene glycol (PEG) preparation on fecal microbiome of UC patients in clinical remission and healthy controls, through the application of 16S rRNA gene sequencing techniques.

Methods: All subjects received identical standard colonoscopy preparation with PEG. Only the UC patients underwent surveillance colonoscopy required by their treating physician. Stool samples were collected at different time points: −30, -1 day (before bowel preparation), the first formed stool sample after bowel preparation, +15, +30 and +60 days. We performed 16S rRNA gene sequencing techniques by amplification of the variable region V4. We used Chao1 to estimate microbiome diversity.

Results: Eleven UC patients in clinical remission and 12 Healthy controls (HC) were recruited. One hundred and thirty-seven samples were analysed. We obtained 3,892,300 high-quality sequences, with a mean base pair number of 314 and 338 Operational taxonomic Units (OTUs). At baseline, diversity in terms of Chao1 was significantly lower in UC patients compared with HC (Median: 132.3 vs. 188.2, p < 0.01). PEG induced a decline in Chao1 in both UC and HC subjects. The magnitude of this decrease was not different between the groups. The microbiome diversity returned to baseline levels at the +60 day time point. Neither Faecalibacterium prausnitzii (Fp) nor Escherichia coli counts were affected by PEG.

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