UNITED EUROPEAN GASTROENTEROLOGY

ueg journal

October 2021
Volume 9, Issue 8

SSN 2050-6406 (Print)
ISSN 2050- 6414 (Online)
onlinelibrary.wiley.com/journal/20506414

09

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Abstract issue

29th United European Gastroenterology Week Virtual 2021

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Letter of Thanks for UEG Week 2021 Reviewers

United European Gastroenterology Journal
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Dear Colleagues,

On behalf of the UEG Scientific Committee, I would like to take this opportunity to thank you most sincerely for your contribution as an abstract reviewer for the original programme of UEG Week Virtual 2021.
The abstract reviewing process is a crucial aspect, ensuring the scientific quality and relevance of UEG Week. I know just how much time and effort reviewing abstracts takes, but without your expertise we would not have achieved the excellence in the abstract-based sessions, and UEG Week would not be the top international digestive diseases meeting that it has become today. It is encouraging to see the strength in this community, which has endured over the past two years, despite the circumstances!

Thank you!

We received a total of 1,966 abstracts for UEG Week 2021. In total, 1,482 abstracts were accepted, giving an acceptance rate of 75,4%. 210 abstracts will be delivered as oral presentations and 1,272 as posters. I am even more pleased to tell you that standards have again reached a very high level and we can expect most interesting research and great presentations. This high volume and high standard confirm that UEG Week is the most important forum at which to present your best research, independent of its format.

We have received 36 video cases and 229 clinical cases which were formally evaluated by the Scientific Committee for presentation. As in previous years, late breaking abstracts have been scored by the Scientific Committee.

The quality of reviewing this year was excellent, but if you have any further (positive or negative) comments, please do let us know! Finally, but most importantly, thanks to all investigators both within and outside Europe who have submitted their research to the meeting, and who are contributing to making UEG Week Virtual 2021 a great success!

Times change, world class science remains!

Herbert Tilg
Chair of the UEG Scientific Committee

Acknowledgements

(as of August 26, 2021; in alphabetical order)

United European Gastroenterology Journal
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EFFECTS OF LACTOFERRIN ON THE MICROBIOTA IN A MURINE MODEL OF ANTIBIOTICS-INDUCED DYSBIOSIS

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Introduction: The antibiotic administration can result in gut microbiota alterations that impact health, for instance the selection of opportunistic pathogens. In this context, the search for modulators of microbiota that prevent the side effects of antibiotics is an interesting field of research.

Bovine lactoferrin is a milk protein with numerous effects: anticancer, anti-inflammatory, antimicrobial and immune modulator activities [1] . However, its potential to counteract the side effects of antibiotics on the microbiota has not been fully studied.

Aims & Methods: The aim was to study the ability of native and saturated lactoferrin to reverse the effects of clindamycin on the intestinal microbiota in a murine model.

Male C57BL/6 mice of 8 weeks old were randomly divided into six groups (n=5 per group): vehicle, clindamycin (Clin), native bovine lactoferrin (nLf), nLf + clindamycin (nLf_Clin), iron-saturated bovine lactoferrin (sLf) and sLf + clindamycin (sLf_Clin). Vehicle received saline orally for 10 days. Clin was gavaged for 10 days with saline and on day 4 received a single IP injection of 200 µg of clindamycin. nLf and sLf were gavaged for 10 days with 35 mg of nLf or sLf respectively. The groups nLf_Clin and sLf_Clin were gavaged with nLf or sLf and on day 4 received an injection of clindamycin.

To corroborate the effects of the treatments, a second experiment was performed in the same way with male C57BL/6 mice of 12 weeks old (same breeder one year later). Faecal samples were obtained from the mice at the end of the treatments.

After extracting DNA from faecal samples (QIAamp Fast DNA Stoool Mini Kit, Qiagen), the V4 region of the bacterial 16S rRNA gene was amplified. Sequencing of the libraries was performed by Miseq platform (Illumina) and 2 x 250 bp paired-end reads were obtained.Sequence data were quality filtered, and differences in the composition and alpha and beta diversity were analysed using QIIME2 and R softwares.

Results: The taxonomic composition analysis revealed that most sequences were assigned to Firmicutes and Bacteroidota phyla. The Verrucomicrobiota, Proteobacteria and Actinobacteriota phyla were also present in all groups of treatment, although in lower proportions.

We analysed the bacterial communities of the groups in terms of alpha and beta-diversity. The number of different ASVs observed in most samples was in the range of 200-800. The Shannon index was in the range of 3.5-5, indicating the well-known high diversity of the gut bacterial community.

No differences were found in the Shannon index of the 8 weeks old groups of treatment ($p > 0,05$). However, in experiment with 12 weeks old mice, the Shannon indexes in nLf, nLf_Clin and sLf_Clin groups were statistically lower than vehicle ($p < 0,05$). Bray-Curtis beta diversity indices showed that the microbial community of vehicle was statistically different from the communities of Clin, nLf_Clin and sLf_Clin in both experiments. At family level, Bacteriodaceae, Prevotellaceae and Rikenellaceae decreased in Clin group. The treatment with nLf or sLf along with clindamycin could revert these effects, increasing the levels of bacteria in all these families.

Conclusion: Clindamycin induces alterations in the composition of the murine intestinal microbiota, reducing bacteria with anti-inflammatory properties such as Bacteriodaceae, Prevotellaceae or Rikenellaceae. Lactoferrin restores the normal levels of these anti-inflammatory bacteria and, therefore, could be a candidate for use as prebiotic in functional foods.

References: 1. Garcia-Montoya, I.A., et al., *Lactoferrin a multiple bioactive protein: An overview*. Biochimica Et Biophysica Acta-General Subjects, 2012. **1820**(3): p. 226-236.

Disclosure: Nothing to disclose.

P0202

LACTOSE MALABSORPTION BY THIRD-GENERATION HYDROGEN BREATH TEST: NEW DATA COLLECTION AND TIME IMPLEMENTATION

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Introduction: Hydrogen breath test (H_2BT) is nowadays the most widely used procedure in the diagnostic workup of lactose malabsorption and lactose intolerance.

Technique and interpretation of different hydrogen breath tests are outlined in this review.

This study aims to establish whether a simplified two-or-three sample test of a third generation of H_2BT may reduce time, costs, and staff resources without reducing sensitivity.

Aims & Methods: Data from 34 patients (22 men, 12 women) with a positive 4 h, nine-sample H_2BT were fully tested. Patients were stratified according to the degree of lactose malabsorption, the occurrence, and type of symptoms. Sensitivity in the H_2BT was tested taking into account two-sample tests (0 min and 120 min or 0 min and 210 min) or three-sample tests (0 min, 120 min and 180 min or 0 min, 120 min, and 210 min).

Results: Using a two-sample test (0 min and 120 min or 0 min and 210 min) the false-negative rate was 35.6% and 27.8%, respectively. With a three-sample test (0 min, 120 min and 180 min or 0 min, 120 min or 210 min), lactose malabsorption was diagnosed in 94.1% (32 of 34) patients and in 97.05% (33 of 34) patients, respectively. Of 20 patients with abdominal symptoms, 5 (26.6%) and 2 (12.2%) would have false-negative results with 0 min and 120 min or 0 min and 210 min two-sample tests, respectively. The three-sample tests, 0 min, 120 min and 180 min or 0 min, 120 min and 210 min, have a false-negative rate of 5.4% and 2.1%, respectively.

Conclusion: H_2BT is a inexpensive, useful, simple and safe diagnostic test in the evaluation of lactose malabsorption. The third generation quantitative detection of rare gases with the breath expiration with three-sample H_2BT is time-and cost-sparing without significant loss of sensitivity for the diagnosis, of lactose malabsorption and lactose intolerance.

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Disclosure: Nothing to disclose.