Dysbiosis of Intestinal Butyrate-producing Bacteria in Saudi Pediatric Inflammatory Bowel Disease Patients

Try to follow this backbone:

Introduction

* Crohn disease (CD) (300 words)

What is it ? – relation to IBD – Historical background - type of IBD (mainly CD & UC) – Diffrance between CD & UC in signs and symptoms

* Epidemiology of CD
* Incidence & Prevalence: (300 words)

Worldwide > Middle East > Gulf Cooperation Council (GCC) Countries > Saudi Arabia

* Distribution by Age: (100 words)

Worldwide > Middle East > Gulf Cooperation Council (GCC) Countries > Saudi Arabia

* Distribution by Gender : (100 words)

Worldwide > Middle East > Gulf Cooperation Council (GCC) Countries > Saudi Arabia

* The etiology of CD (150 words)
* Risk Factors: ( try to relate this factors to the dysbiosis of gut Microbiota)
* The immune mechanisms involved in IBD
* Normal mucosal immunity (200 words)
* IBD immunopathology (200 words)
* Genetic (200 words)
* Gut Microbiota (200 words)
* Diet (200 words)
* Smoking (200 words)
* Infection (200 words)
* Immunization (200 words)
* Antibiotic consumption (200 words)
* Hygiene Hypostasis (200 words)
* Butyrate Producing Bacteria (BPB) (500 words)

What is Butyrate? – The important of butyrate for Gut – The 4 Pathways of Butyrate production in Bacteria.

* BPB in Healthy Humans: (700 words)

Mention the main BPB families and species in Westin, Middle east, GCC and Saudi Cohorts.

The difference between Adult and pediatric BPB

Give example the factors affecting the normal gut microbiota (geographic, economic, race, diet,)

* BPB in CD Pediatric (700 words)

Mention 10 studies showing the dysbiosis BPB in Westin, Middle east, GCC and Saudi Cohorts.

(Note: The 10 studies should be from Pediatric chron’s Cohort, using stool sample, using PCR or sequencing Technique)

Add a Table summaring the 10 studies (example below)

* Sample types used for studding intestinal microbiota (300 words)

Why the stool is the most use.

::::::: General instruction :::::::

* Use new references (2010 – 2020).
* Please consider the interconnection of ideas.
* Use my references below and add more.
* Use up to 60 references.
* See my attached file (proposal) to take overview.
* Contact me if you wont to edit something.

***Research and References:***

1. Arrieta, M.-C., et al., *The intestinal microbiome in early life: health and disease.* Frontiers in immunology, 2014. **5**: p. 427.

2. Louis, P., et al., *Diversity of human colonic butyrate‐producing bacteria revealed by analysis of the butyryl‐CoA: acetate CoA‐transferase gene.* Environmental microbiology, 2010. **12**(2): p. 304-314.

3. Santoru, M.L., et al., *Cross sectional evaluation of the gut-microbiome metabolome axis in an Italian cohort of IBD patients.* Scientific reports, 2017. **7**(1): p. 9523.

4. Tamboli, C., et al., *Dysbiosis in inflammatory bowel disease.* Gut, 2004. **53**(1): p. 1-4.

5. Buttó, L.F. and D. Haller, *Dysbiosis in intestinal inflammation: cause or consequence.* International Journal of Medical Microbiology, 2016. **306**(5): p. 302-309.

6. Neuman, M.G. and R.M. Nanau, *Inflammatory bowel disease: role of diet, microbiota, life style.* Translational Research, 2012. **160**(1): p. 29-44.

7. Weimers, P. and P. Munkholm, *The Natural History of IBD: Lessons Learned.* Current treatment options in gastroenterology, 2018: p. 1-11.

8. Sýkora, J., et al., *Current global trends in the incidence of pediatric-onset inflammatory bowel disease.* World journal of gastroenterology, 2018. **24**(25): p. 2741.

9. El Mouzan, M.I., et al., *Incidence of pediatric inflammatory bowel disease in Saudi Arabia: a multicenter national study.* Inflammatory bowel diseases, 2014. **20**(6): p. 1085-1090.

10. Bernstein, C.N. and F. Shanahan, *Disorders of a modern lifestyle: reconciling the epidemiology of inflammatory bowel diseases.* Gut, 2008. **57**(9): p. 1185-1191.

11. Lindberg, E., et al., *Smoking and inflammatory bowel disease. A case control study.* Gut, 1988. **29**(3): p. 352-357.

12. Chow, J. and S.K. Mazmanian, *A pathobiont of the microbiota balances host colonization and intestinal inflammation.* Cell host & microbe, 2010. **7**(4): p. 265-276.

13. Li, E., et al., *Inflammatory bowel diseases phenotype, C. difficile and NOD2 genotype are associated with shifts in human ileum associated microbial composition.* PloS one, 2012. **7**(6): p. e26284.

14. Allez, M. and L. Mayer, *Regulatory T cells: peace keepers in the gut.* Inflammatory bowel diseases, 2004. **10**(5): p. 666-676.

15. Fava, F. and S. Danese, *Intestinal microbiota in inflammatory bowel disease: friend of foe?* World journal of gastroenterology: WJG, 2011. **17**(5): p. 557.

16. Eckburg, P.B., et al., *Diversity of the human intestinal microbial flora.* science, 2005. **308**(5728): p. 1635-1638.

17. Goodman, A.L., et al., *Extensive personal human gut microbiota culture collections characterized and manipulated in gnotobiotic mice.* Proceedings of the National Academy of Sciences, 2011. **108**(15): p. 6252-6257.

18. Shade, A. and J. Handelsman, *Beyond the Venn diagram: the hunt for a core microbiomeemi\_2585.* 2011.

19. Lozupone, C.A., et al., *Diversity, stability and resilience of the human gut microbiota.* Nature, 2012. **489**(7415): p. 220.

20. Nicholson, J.K., et al., *Host-gut microbiota metabolic interactions.* Science, 2012: p. 1223813.

21. Hamer, H.M., et al., *The role of butyrate on colonic function.* Alimentary pharmacology & therapeutics, 2008. **27**(2): p. 104-119.

22. Vanhoutvin, S.A., et al., *Butyrate-induced transcriptional changes in human colonic mucosa.* PloS one, 2009. **4**(8): p. e6759.

23. Arpaia, N., et al., *Metabolites produced by commensal bacteria promote peripheral regulatory T-cell generation.* Nature, 2013. **504**(7480): p. 451.

24. Van den Abbeele, P., et al., *Butyrate-producing Clostridium cluster XIVa species specifically colonize mucins in an in vitro gut model.* The ISME journal, 2013. **7**(5): p. 949.

25. Louis, P., et al., *Restricted distribution of the butyrate kinase pathway among butyrate-producing bacteria from the human colon.* Journal of bacteriology, 2004. **186**(7): p. 2099-2106.

26. Schwiertz, A., et al., *Microbiota in pediatric inflammatory bowel disease.* The Journal of pediatrics, 2010. **157**(2): p. 240-244. e1.

27. Gevers, D., et al., *The treatment-naive microbiome in new-onset Crohn’s disease.* Cell host & microbe, 2014. **15**(3): p. 382-392.

28. Sokol, H., et al., *Low counts of Faecalibacterium prausnitzii in colitis microbiota.* Inflammatory bowel diseases, 2009. **15**(8): p. 1183-1189.

29. Chen, L., et al., *Characteristics of fecal and mucosa-associated microbiota in Chinese patients with inflammatory bowel disease.* Medicine, 2014. **93**(8).

30. De Filippo, C., et al., *Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa.* Proceedings of the National Academy of Sciences, 2010. **107**(33): p. 14691-14696.

31. Suzuki, T.A. and M. Worobey, *Geographical variation of human gut microbial composition.* Biology letters, 2014. **10**(2): p. 20131037.

32. Rehman, A., et al., *Geographical patterns of the standing and active human gut microbiome in health and IBD.* Gut, 2016. **65**(2): p. 238-248.

33. Angelakis, E., et al., *Gut microbiome and dietary patterns in different Saudi populations and monkeys.* Scientific reports, 2016. **6**: p. 32191.

34. Yasir, M., et al., *Comparison of the gut microbiota of people in France and Saudi Arabia.* Nutrition & diabetes, 2015. **5**(4): p. e153.

35. Hayashi, H., et al., *Diversity of the Clostridium coccoides group in human fecal microbiota as determined by 16S rRNA gene library.* FEMS microbiology letters, 2006. **257**(2): p. 202-207.

36. Zoetendal, E.G., E.E. Vaughan, and W.M. De Vos, *A microbial world within us.* Molecular microbiology, 2006. **59**(6): p. 1639-1650.

37. Větrovský, T. and P. Baldrian, *The variability of the 16S rRNA gene in bacterial genomes and its consequences for bacterial community analyses.* PloS one, 2013. **8**(2): p. e57923.

38. Louis, P. and H.J. Flint, *Development of a semiquantitative degenerate real-time PCR-based assay for estimation of numbers of butyryl-coenzyme A (CoA) CoA transferase genes in complex bacterial samples.* Applied and environmental microbiology, 2007. **73**(6): p. 2009-2012.

39. Vital, M., et al., *A gene-targeted approach to investigate the intestinal butyrate-producing bacterialcommunity.* Microbiome, 2013. **1**(1): p. 8.

40. Lewis, J.D., et al., *Inflammation, antibiotics, and diet as environmental stressors of the gut microbiome in pediatric Crohn’s disease.* Cell host & microbe, 2015. **18**(4): p. 489-500.

41. Sanders, M.E., et al., *An update on the use and investigation of probiotics in health and disease.* Gut, 2013. **62**(5): p. 787-796.

42. Fraher, M.H., P.W. O'toole, and E.M. Quigley, *Techniques used to characterize the gut microbiota: a guide for the clinician.* Nature reviews Gastroenterology & hepatology, 2012. **9**(6): p. 312.