Western Surgical Association
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– Virtual Meeting –
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P 8. MICROBIAL DYSBIOSIS IS ASSOCIATED WITH ADENOMATOUS POLYPS

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Background: Microbial dysbiosis has been associated with colorectal cancer development. However, data is limited regarding the relationship of the microbiome and adenomatous polyps. Understanding the association between the microbiome and the host at this pre-neoplastic stage may point toward interactions which incite tumorigenesis.

Methods: We conducted a prospective single-center study including patients undergoing screening colonoscopy from October 2018-2019. Fecal samples were collected prior to initiation of the subject's bowel prep and saliva samples were obtained with an oral swab prior to the procedure. Patients were divided into cohorts based on the presence or absence of adenomatous polyps on screening colonoscopy. Microbial DNA was extracted from fecal and salivary samples, and amplicon libraries were generated using primers directed against the V4 region of the 16S rRNA gene and sequenced on an Illumina MiSeq instrument. The resulting 8.7 million reads (mean 38,677/sample) were quality filtered and processed using DADA2. Information regarding demographics, known risk factors for colorectal cancer and diet were obtained using a questionnaire and the electronic medical record. Results were analyzed using R statistical software.

Results: One-hundred ten patients underwent screening colonoscopy with mean age 60 years (range 41-78 years, SD 8). Polyps were identified in 44% of participants and were predominantly tubular adenomas (87%) and right-sided (58%). Patients with and without adenomas were similar in terms of age, sex, body mass index, race/ethnicity and family history of colorectal cancer. Consumption of alcohol, dietary practices, antibiotic use and probiotic use did not differ between those with or without adenomas. Smoking was associated with adenoma formation (26% for those without adenomas, 48% for those with adenomas, p-0.016), whereas regular activity was associated with the absence of adenomas (77% for those without adenomas, 58% for those with adenomas, p=0.032). We evaluated the microbial richness and diversity of fecal and salivary samples between the adenoma and non-adenoma groups. The Shannon entropy of the fecal microbiome was significantly lower in the adenoma group in comparison to the non-adenoma group (p=0.03). Conversely salivary samples did not reveal significant differences in Shannon entropy (p=0.51). There were taxonomic differences appreciated between adenoma formers and non-adenoma formers in both the fecal and salivary microbiomes. Fecal samples demonstrated significant ($p<0.05$) increases in Bifidobacterium, Blautia, Escherichia/Shigella, Coprococcus and a trend in Bacteroides (p=0.06) in those with adenomas. The salivary microbiome associated with adenomas demonstrated moderate but significant increases in Mycoplasma and Treoponema ($p<0.05$). Additionally, the diversity of the fecal and salivary microbiome diversity associates with polyp and host metadata, including number of polyps, polyp location, demographic characteristics, diet and exercise.

Conclusion: Patients with adenomas display a decrease in the overall richness and diversity of their microbial communities and also unique taxonomic differences in fecal and salivary samples in comparison to those without adenomas. Understanding these changes and the interactions with the host may offer novel prevention, screening and treatment strategies.