P – 325 Gut microbial community diversity is associated with systemic vascular endothelial growth factor A levels among colorectal cancer patients

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Introduction: Dysbiosis in the gut microbiota and activation of the angiogenic switch in the tumor microenvironment contribute to colorectal carcinogenesis.

Methods: Analyses of baseline fecal samples via 16S rRNA gene sequencing, and evaluation of angiogenic stimulators, vascular endothelial growth factor (VEGF) A and D, in patient sera among n=125 patients diagnosed with colorectal cancer in the ColoCare Study were used to explore the link between the gut microbiome and systemic biomarkers of angiogenesis.

Results: Baseline clinicopathologic and demographic characteristics were evaluated. Relative contributions of taxonomic groups identified through 16S sequencing were examined. Diverse microbial taxa, including previously cancer-associated microbes, were detected in fecal biospecimens. A significant association of gut microbial community diversity was observed by circulating VEGFA (Bray-Curtis metric: R² = 0.94; false discovery rate [FDR] q-value = 0.007; weighted Unifrac: R² = 0.95, FDR q-value = 0.026) but not by VEGFD (Bray-Curtis metric: R² = 0.81, FDR q-value = 0.77; weighted Unifrac: R² = 0.80, FDR q-value = 0.8) levels. Differences in systemic VEGFA or VEGFD levels were not directly correlated with individual taxa.

Conclusion: These findings suggest that microbial community-level function is important for driving the association between gut microbial community diversity and circulating VEGFA biomarker levels. Together, profiling of the microbial taxa and systemic angiogenesis biomarkers among colorectal cancer patients demonstrates that circulating levels of angiogenic stimulator VEGFA may reflect changes in the microbial ecosystem of the human gut that influence colorectal carcinogenesis.