Spatial Analysis of Epithelial-to-Mesenchymal Transition Dynamics and Fusobacterium nucleatum Associations in Colorectal Cancer (Year 3)

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Colorectal cancer (CRC) is a leading cause of cancer-related mortality in the United States, with metastasis responsible for the majority of CRC deaths. Emerging research suggests that microbial dysbiosis may influence tumor progression; however, the role of specific bacterial species in regulating metastatic pathways remains unclear. This study investigated the association between Fusobacterium nucleatum, an opportunistic member of the gut microbiome, and epithelial-to-mesenchymal transition (EMT), a critical process in cancer invasion and dissemination. Immunofluorescence assays were conducted on CRC and control tissue sections to evaluate expression of E-cadherin, Vimentin, and the presence of F. nucleatum. Cancerous tissues exhibited heterogeneous reduction of E-cadherin across five microscopic fields (composite scores 1–16; mean = 7.8), uniformly elevated Vimentin expression (composite score = 16), and consistent detection of F. nucleatum in all examined fields. In contrast, control tissues maintained maximal E-cadherin expression, minimal Vimentin staining, and showed no bacterial presence. These findings indicate EMT-like alterations occurring within F. nucleatum–positive tumor microenvironments. The observed co-occurrence of bacterial colonization and EMT marker dysregulation supports a potential role for F. nucleatum in promoting metastatic phenotypes in CRC. Future work will expand EMT marker analysis, investigate bacterial virulence factors such as FadA, and incorporate a LAMP assay to enable rapid, cost-effective detection of F. nucleatum in patient-derived samples. This approach aims to clarify microbe-driven mechanisms of cancer progression and advance microbiome-based strategies for early CRC detection and risk stratification.

Awards Won: