Single-cell analysis reveals dysregulation of the immune system linked to poor prognosis in *Fusobacterium nucleatum*-infected colorectal cancer

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Fusobacterium nucleatum (Fn) is commonly detected in colorectal cancer (CRC) and worsens patient survival. *Fn* appears to play a role in colorectal cancer carcinogenesis through suppression of the antitumor immune response. Aiming to uncover the underlying mechanisms, we collected 42 samples of surgically removed colon tissues from patients newly diagnosed with colon cancer. To analyze the bacterial community composition within these tissues, we utilized amplicon sequencing, targeting the V4 variable region of the 16S rRNA. We performed single-cell RNA sequencing (scRNA-seq) analysis of tumor-infiltrating immune cells from *Fn*-infected [Fn (+)] and *Fn*-uninfected [Fn (−)] patients. By utilizing gene expression signature derived from scRNA-seq data and bulk transcriptome profiles of the TCGA cohort, we identified immune cell types associated with *Fn* infection in CRC. Using RNA velocity and cell-cell interaction analysis of single-cell transcriptome data, we unraveled immune cell subtypes modulated by *Fn* infection. Furthermore, trajectory-based differential expression analysis and single-cell gene network analysis shed light on how the intratumor immune system is disturbed by *Fn* infection. A novel gene signature had a poor prognostic impact in patients with *Fn*-infected tumors, compared with *Fn*-uninfected patients in the TCGA cohort. Overall, this study identified a novel potential *Fn*-related immune evasion mechanism, beyond suppression of T cell-mediated immune response. Novel gene signatures with a poor prognostic impact can be used for patient stratification and developing targeted strategies in patients with *Fn* infection.