Towards the human colorectal cancer microbiome

**Introduction**

Human colorectal cancer (CRC) is the 4th most commonly diagnosed cancer in the world. It is initiated by driver mutations in the stem cells at the base of the villus crypt. During the progression from adenoma to carcinoma, these cells become immortal and accumulate additional passenger mutations (Fearon 2011, Vogelstein & Kinzler 1993). The triggers for these mutations remain elusive.

In 2011, four large-scale data sets were published that describe the microbiota associated with CRC tumors.

**The CRC Microbiome**

Studies (1) through (4) show that certain bacterial taxa specifically inhabit the tumor niche, while others are enriched in the adjacent unaffected mucosa.

**Bacterial Drivers of CRC**

Bacterial drivers of CRC are gut bacteria with pro-carcinogenic features that may contribute to CRC development.

Driver bacteria may be outcompeted by passenger bacteria as the tumor progresses from an adenoma to a carcinoma.

**References**


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**Bacterial Passengers of CRC**

Bacterial passengers of CRC are relatively poor colonizers of a healthy intestinal tract, but gain a competitive advantage when the growing CRC tumor changes the local microenvironment (Tjalsma et al. 2012).

Passenger bacteria may either promote (opportunistic pathogens) or inhibit (preserve niche) tumor growth.

**Conclusions**

We propose that species found in the off-tumor samples are the typical colon microbiota for CRC patients. The identified species may act as driver bacteria for CRC. Screening for these species can identify patients with a high risk for developing CRC. They may be selectively targeted to prevent CRC.

Growth of the tumor alters the niche (loss of colonic barrier function, bleeding). This attracts passenger bacteria with a competitive advantage in the changed microenvironment.

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