The Gut Microbiome Influences Progression of Ovarian Cancer in Mice via Modulation of the Immune System

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Ovarian cancer is the fifth leading cause of cancer deaths among women and has the highest mortality rate among gynecologic cancers. The immune cell infiltration of ovarian tumor tissues varies among women and is correlated with clinical outcomes. The mechanisms and factors that are underlying these differences however is unclear. The immune system has been shown to be linked to the composition of the gut microbiome and here, in mouse models of ovarian cancer, we demonstrate the modulation that the gut microbiome has on the immune system and thus on ovarian cancer development. Healthy animals that are genetically identical but were bred in different environments have distinct microbiota; we show that they also have differences in baseline immune status that correlate with the microbiome. Following tumor challenge, the distinct mouse population present different tumor development trajectories and the differences observed in the composition of the immune system remained consistent. Upon antibiotic treatment and therefore, a dysbiosis of the microbiota, there was a respective modulation of the immune system, both at baseline and after tumor challenge. This modulation was reflected in a phenotype shift, which delayed tumor progression.