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Interactions between the breast microbiota and host gene expression in breast cancer development

One in eight women will be diagnosed with breast cancer in their lifetime, and despite the prevalence of this disease, much is unknown about the factors involved in its initiation. Because the gut microbiota has been implicated in the development of many diseases through regulation of the host immune function, we hypothesized that the breast tissue microbiota regulates host gene expression to influence breast cancer development. We utilized paired microbial composition data obtained through 16S rRNA gene sequencing and human gene expression data obtained from total RNA sequencing from healthy ($n = 6$) and precancerous ($n = 6$) breast tissue. Correlation analyses based on Spearman's coefficients were performed to correlate differentially expressed host genes with bacterial taxa and putative bacterial functions for the healthy and precancerous groups. In the healthy group, there were 0 significant gene-bacterium and 41 significant gene-function correlations. In the precancerous group, there were 2 significant gene-bacterium and 13 significant gene-function correlations. The increased number of correlations between gene expression and bacterial function suggests increased crosstalk between the host and microbiota in healthy tissue. These findings demonstrate a variety of interactions between microbes and host cells with tumor development, and further studying these interactions may help us better diagnose and treat breast cancer.