

Gastric Adenocarcinoma May Not Necessarily be Due to *Helicobacter pylori* or Microbial Infection

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Introduction

Gastric cancer is commonly thought to be caused by infection with *Helicobacter pylori*. This work sought to understand if other microbial species could be associated with a particular form of stomach cancer known as gastric adenocarcinoma. To this end, RNA-seq transcriptome of normal and diseased tissue with gastric adenocarcinoma from two patients were analysed by an in-house MATLAB RNA-seq processing software with a library of ribosomal proteins from different microbial species as reference genes. Results reveal no alignment of sequenced reads from normal and diseased tissue to any ribosomal protein genes from different microbial species. This suggests that gastric adenocarcinoma need not be associated with microbial infection. Overall, understanding the aetiological reason for a disease is the first step to finding ways to treat, and later, prevent similar occurrence of disease. Profiling of RNA-seq transcriptome of normal and diseased gastric tissue for microbial mRNA transcripts of ribosomal protein shows no alignment of sequenced reads, thereby, indicating that microbes need not be associated with gastric adenocarcinoma.

Description

Helicobacter pylori infection has been associated with onset of stomach cancers [1,2]. But, given the diversity of different types and severity of stomach and gastric cancer, could other microbial species be associated with the clinical manifestations of stomach cancers, or could they be the aetiological agents? This work sought to answer the above questions using public RNA-seq transcriptome of normal and diseased tissue of two patients with gastric adenocarcinoma. Sequenced reads from the transcriptome would be aligned with ribosomal protein genes of different microbial species to assess if microbes were present in either the normal or diseased tissue of the patient.

RNA-seq transcriptome of the two patients were downloaded from array express (Accession number: E-MTAB-8135). Both diseased tissue sample and normal tissue adjacent to the neoplasms were sampled. Reference genes for alignment of sequenced reads are ribosomal protein genes from different microbial species downloaded from a comprehensive library of ribosomal protein genes from different microbial species.

Transcriptome analysis was performed by an in-house MATLAB RNA-seq processing software, and a total of 100000 reads was processed for each transcriptome [3].

Results reveal no alignment of sequenced reads to any ribosomal protein genes from microbial species. This indicated strongly the absence of microbial species in the normal and disease gastric tissue of both patients. Hence, the results suggest that gastric adenocarcinoma need not be associated with microbial infection, which opens up the search for underlying disease-causing factors that, in mistuning the gastric tissue cells, result in a cancer pathology.

Conclusion

Overall, understanding the aetiological agent of a disease is the critical first step towards formulating a treatment plan. Gastric and stomach cancer has been commonly associated with *Helicobacter pylori* infection. However, analysis of public RNA-seq transcriptome of normal and diseased tissue of two patients with gastric adenocarcinoma reveals no alignment of sequenced reads with ribosomal protein genes of sampled microbial species. This suggests that gastric adenocarcinoma aetiology need not be associated with microbial infections, thereby, pointing to other factors that dysregulated the cell biological process of gastric cells as underlying mechanisms.

Conflicts of Interest

The author declares no conflicts of interest.

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References

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