Original Article

Physiogenomics in Etiopathogenesis of Cholangiocarcinoma

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Abstract

Objective: Cholangiocarcinoma is a serious malignancy that is very common in the tropical countries. It is a kind of deadly primary hepatobiliary tumor. There is a wide spectrum of tumors with varying differentiation and malignancy grades. Although it has been known for a long time inmmedicine, there is no clear cut that this deadly cancer is genetic disorder or not. A systemic approach on the pathophysiology and genomics can provide useful information and help better understand the pathogenesis of cholangiocarcinoma. **Methods:** In this work, a standard bioinformatics physiological genomics analysis of cholangiocarcinoma was performed. **Result:** According to this work, there is no identified physiogenomics relationship for the cholangiocarcinoma. **Conclusion:** This might imply that the cholangiocarcinoma is directly due to environmental insult. It implies that there should be no specific gene that might contribute to the increased risk in the etiopathogenesis of cholangiocarcinoma.

Keywords: *Physiogenomics, pathogenesis, cholangiocarcinoma*

Introduction

At present, genomics approach is widely used in medical research.[1] Of several applied genomics techniques, physiological genomics is a very useful application that can be helpful for interpreting the function to genes within the human genome. In other words, how the genome linking to physiology can be identified.[1] The physiogenomics can be helpful for assessment on the pathophysiology of many complex diseases. Cholangiocarcinoma is a kind of serious gastrointestinal malignancies. It is a type of primary hepatobiliary tumor that has various forms of tumor differentiations and malignancy grades.[2,3] Although this cancer has been determined and mentioned in clinical gastroenterology for a long time, there is no clear cut on the etiophatlogy.[1,2] Whether this cancer is a genetic disorder or not is still a big question.[2,3] A systemic approach on the pathophysiology and genomics might provide useful data that can help better understand on the etiopathogenesis of cholangiocarcinoma. In this work, physiological genomics analysis for cholangiocarcinoma was performed using standard bioinformatics technique.

Materials and Methods

This work is a bioinformatics simulation study. The physiogenomics analysis was performed using standard consomics technique.[4,5] The standard bioinformatics tool, namely, PhysGen was used for all simulations in this bioinformatics study. In brief, this tool is used for the testing function of relevant genes and its physiology presentation based on the strategy, namely, targeting induced local lesions in genomes that have an ability to detect allelic series of possible point mutations in focused genes.[6,7] For simulating, the human genome was used as template and the primary input ontology term is "cholangiocarcinoma." Analysis on focused gene was done in range v 2.02 with length 1 Mbp. The protocol used in this study is the same as used in previously publications by the authors' laboratory.[8-12]

Results

According to this work, there is no identified physiogenomics relationship.

Discussion

Cholangiocarcinoma is an important malignancy in the gastrointestinal tract. Etiopathogenesis of cholangiocarcinoma is complex, and there is still no clear

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information on the pathophysiology of this malignancy. Its etiology is believed to be multifactorial and might be due to both genetic and environmental factors.[2,3] At present, it is widely accepted that cholangiocarcinoma cell growth is a regulated by some genetic processes.[13] A loss or inactivation of some specific genes tumor suppressors is believed to be the root cause and such loss might give rise to tumurogenesis.[13] Alison noted that chronic inflammatory insult to the biliary tract epithelium is the beginning point of abnormality of cholangiocytes that might further develop into a more abnormal growth and cholangiocarcinoma.[14] In addition, the sustained epithelial proliferation of inflammatory cells adjuncted by growth factors and DNA-damaging agents (such as reactive oxygen and nitrogen species) will result in irreversible permanent genetic destructed cells.[13-15] However, there is no verification that those mentioned genetic processes are directly related to the final occurrence of malignancy or not.

Here, the authors used a physiogenomics bioinformatics approach to assess the physiogenome in cholangiocarcinoma. According to this work, the simulation shows that no gene has a significant genetic relationship to the ethiopathogenesis of cholangiocarcinoma. This might imply that the cholangiocarcinoma is directly due to external environmental underlying factors without any specific genetic effect. No gene is identified as a contributor to the high risk in the etiopathogenesis of cholangiocarcinoma. Indeed, the recent reports already showed the importance of epigenetic factor in tumorogenesis of cholangiocrcinoma. The epigenetic alterations in promoter region hypermethylation and histone deacetylation are the presently mentioned pathomechanism for tumorogenesis process of cholangiocarcinogenesis.[16] As reported by Sandhu *et al*., epigenetic DNA hypermethylation was reported as an important step in pathogenesis cholangiocarcinoma.[16] Recently, Cheng *et al*. also mentioned for the epigenetic effect of Dicer, a member of the Ribonuclease III family of endoribonucleases, on the tumorogenesis process of cholangiocarcinoma.[17]

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Conflicts of interest

There are no conflicts of interest.

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