عنوان مقاله:

Investigation of the effect of pd۱.۱, pd۱.۵, and pd۱.۹ mutations on pd۱ gene function with a system biology approach

محل انتشار:

مجله نوآوری علوم پزشکی و داروسازی آسیای مرکزی, دوره 1, شماره 1 (سال: 1400)

تعداد صفحات اصل مقاله: 7

نویسندگان:

.Mohammad Reza Roshandel - *Urology Department of Icahn School of Medicine, Mount Sinai Hospitals, NY, USA*

.Hawri Mustafa Bakr - *Department of Basic Science, College of Medicine, Hawler Medical University, Erbil, Iraq*

.Ramin Lak - *Pars Advanced and Minimally Invasive Medical Manners Research Center, Pars Hospital, Iran*

Ruqaya Muhammed Ghareeb Taher Al Barzinji - *Department of Basic Science, College of Medicine, Hawler Medical University, Erbil, Iraq.*

.Khonaw Kader Salh - *Department of Basic Science, College of Medicine, Hawler Medical University, Erbil, Iraq*

.Kharman Saeed Ibrahim - *Department of Basic Science, College of Medicine, Hawler Medical University, Erbil, Iraq*

.Feyan Mirdan Abdullah - *Department of Basic Science, College of Medicine, Hawler Medical University, Erbil, Iraq*

خلاصه مقاله:

Programmed cell death ۱ (pd۱) is an immune-inhibitory receptor that is expressed in activated T cells. This gene may play a role in inhibition of actual anti- microbial and anti-tumor immunity. In human, this gene is located on the long arm of chromosome ۲. This gene has many variations that three of which are more common. This study was aimed to investigate the influence of pd۱.۱, pd۱.۵, and pd۱.۹ variations on function of pd۱gene based on a bioinformatics approach. In this study, the EPD and PROMO webserver was used to evaluate the pd۱.۱ variation as a promoter mutation. It has been detected in the promoter region by EPD, while the transcription factor arrangement was evaluated by the PROMO server. But, some bioinformatics tools such as ProtScale – ExPASy and Ramachandran plot assay web servers were used to evaluate the effects of codding polymorphisms. Obtained data from EPD showed that the promoter of pd۱ contains ۶۰ nucleotides. Evaluation of upstream of pd۱ revealed that the number of transcription factors could alter the pd۱.۱ variation. With regard to the pd۱.۵ polymorphisms, the result showed that it is considered as a synonymous variation, but the pd۱.۹ was known as a nonsynonymous mutation. Thus, the pd۱.۹ could alter the hydrophobicity and Ramachandran plots of PD۱. The pd۱.۵ mutation may impact the expression of the pd۱gene because it changes the transcription factor arrangement on the upstream of pd۱. Also, the pd۱.۹ substitution could alter the hydrophobicity and Ramachandran plots of protein.

کلمات کلیدی:

PD۱ protein, genetic mutations, Bioinformatics, promoter region, Gene function