Canadian Journal of Biotechnology

ISSN 2560-8304 Poster Presentation

Category: Bioinformatics

An integrated genomic analysis on miRNAs and SNPs associated with vitiligo to reveal potential drug candidates

Razia Rahman and Yasha Hasija

Department of Biotechnology, Delhi Technological University, Shahbad Daulatpur, Main Bawana Road, Delhi 110042, INDIA Presenting author: <u>razia.rahman91@gmail.com</u>

Abstract

Vitiligo is characterized by the occurrence of depigmented patches on the skin caused as a result of progressive loss of functional melanocytes. It is a polygenic disorder entailing both genetic and non-genetic factors intricately and as such is not yet clearly understood. Hence, a comprehensive understanding of the entire spectrum of disease susceptibility and pathogenesis remains a challenge. Emerging evidence over the decades underlines the cardinal role of miRNAs in disease development and having a significant role in melanocyte development and survival. Also, identifying the susceptible genes and their variants that influence disease onset is fundamental to unravel the rationale for disease susceptibility. We, therefore, applied a systems biology approach to identify potential miRNAs and their target genes to construct a miRNA-target gene network revealing essential miRNAs that might be significantly related to vitiligo. We further investigated the susceptible genetic variants associated with vitiligo and prioritized a few proteins in our protein-protein interaction network as significant hub proteins. Network-based polypharmacological studies of such hub proteins are helpful in analysing a large set of disease-associated proteins which might initiate better diagnosis with the feasibility of personalized treatment for vitiligo patients in the future. Our polypharmacogenomic systems analysis highlighted novel drug candidates and drug repositioning candidates for vitiligo. Furthermore, we investigated the pathogenic effect of the plausible single nucleotide polymorphisms (SNPs) using computational platforms and carried out preliminary protein modelling to implicate the role of SNPs in disease pathogenesis. Thus, our analysis unveiled significant findings which may provide an insight of the mechanisms of vitiligo development and progression, thereby, driving the way towards improved therapeutic and diagnostic interventions for vitiligo management.

Citation: Rahman, R. and Hasija, Y. An integrated genomic analysis on miRNAs and SNPs associated with vitiligo to reveal potential drug candidates [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 45. <u>https://doi.org/10.24870/cjb.2017-a32</u>

OPEN AC

© 2017 Rahman and Hasija; licensee Canadian Journal of Biotechnology. This is an open access article distributed as per the terms of Creative Commons Attribution-NonCommercial 4.0 International (https://creativecommons.org/licenses/by-nc/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.