Sharma et al. (2017) Can J Biotech, Volume 1, Special Issue, Page 79
https://doi.org/10.24870/cjb.2017-a66

Canadian Journal of Biotechnology

ISSN 2560-8304

Poster Presentation OPEN ACCESS

Category: Clinical Genomics

MACF1 gene variant rs2296172 is associated with type 2 diabetes susceptibility in the Bania population group of Punjab - India

Varun Sharma[1], Itty Sethi[1], Indu Sharma[1], Gurvinder Singh[1,3], Ankit Mahajan[2], Arshia Angural[1], A.J.S. Bhanwer[3], Manoj K. Dhar[2], K.K. Pandita[4], Vinod Singh[1], Ekta Rai[1] and Swarkar Sharma[1]

[1]Human Genetics Research Group, Department of Biotechnology, Shri Mata Vaishno Devi University, Katra 182320, INDIA

[2]Department of Biotechnology, University of Jammu, 180006, INDIA

[3]Guru Nank Dev University, Amritsar, INDIA

[4]H.no:62, Lane 11, Swarn Vihar, Muthi, Jammu, J&K, INDIA

Abstract

Microtubule Actin Cross linking Factor 1 (*MACF1*) gene variant rs2296172 has been associated with Type 2 Diabetes (T2D). However, this variant has never been evaluated as such in Indian populations. We replicated this variant in pooled population of Northwest India and specifically in an endogamous caste group, Bania of Punjab, India. We genotyped variant rs2296172 by Taqman allele discrimination assay in 651 T2D patients and in 568 healthy controls from Northwest India. The association of the SNP with T2D was evaluated by case - control association study design. The SNP rs2296172 of *MACF1* was found to be significantly associated with T2D with p value = 0.009 in Northwest Indian population but allelic distribution was observed to be deviated from Hardy-Weinberg equilibrium (HWE). Assuming population stratification the most plausible cause, we further evaluated the samples belonging to Bania caste group from Punjab, India. We observed significant association of this SNP with T2D with OR = 1.71 (1.03-2.83) at 95%CI, (p =0.03) and sample set following HWE. *MACF1* variant rs2296172 was found to be associated with T2D in endogamous ethnic population group (Bania) of Punjab, India. Deviation from Hardy-Weinberg equilibrium in the pooled population group from Northwest India, underlines that Indian population sub structure exists and may have implications in association studies. Thus, ideal case - control association study design in Indian populations is to evaluate endogamous population groups rather than the conventional practice of pooling samples based on geography or linguistic affinities only.

Citation: Sharma, V., Sethi, I., Sharma, I., Singh, G., Mahajan., A., Angural, A., Bhanwer, A.J.S., Dhar, M.K., Pandita, K.K., Singh, V., Rai, E. and Sharma, S. MACF1 gene variant rs2296172 is associated with type 2 diabetes susceptibility in the Bania population group of Punjab - India [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 79. https://doi.org/10.24870/cjb.2017-a66