■ РЕФЕРАТИ СТАТЕЙ, ОПУБЛІКОВАНИХ В «CYTOLOGY AND GENETICS», № 2, 2020 р.

ASSOCIATION OF *SLC30A8*, *CDKAL1*, *TCF7L2* AND *HHEX* GENE POLYMORPHISMS WITH TYPE 2 DIABETES IN THE POPULATION OF NORTH EAST INDIA

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India currently has the second largest number of individuals suffering from diabetes across the world. Hence, it is pertinent to explore the genetic variations in Indian populations to comprehend the extent of genetic heterogeneity. We studied the association of gene variations of four candidate genes [SLC30A8 (rs11558471), CDKAL1 (rs94655871), TCF7L2 (rs12255372) and HHEX (rs1111875)] with Type 2 Diabetes (T2D) in the North East Indian population on whom there is very little data available. DNA was extracted from 155 diabetic patients and 100 non-diabetic controls. Genotyping was performed by Polymerase chain reaction-Restriction fragment length polymorphism (PCR-RFLP). Logistic regression analysis was performed to detect the association between genetic variants and type 2 diabetes. The CT genotype of rs9465871 (CDKAL1 gene) showed significant protection against diabetes [OR = 0.39 (0.17–0.91), p = 0.029] as compared to the CC genotype even after adjusting for age, sex and BMI. When analysed under a recessive model, the GG genotype of rs1111875 (HHEX gene) also showed significant protection against diabetes [OR = 0.38 (0.18–0.82), p = = 0.014] as compared to the AA+AG genotypes. Both these findings did not remain significant after Bonferroni threshold of p = 0.0041 was applied. There is considerable variation in the pattern of association of these genes with T2D amongst the North East Indian population, when compared to the other ethnically and geographically diverse Indian populations.

Key words: hyperglycaemia; genetics; diabetes; north east India.

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АСОЦІАЦІЯ ГЕННОГО ПОЛІМОРФІЗМУ *SLC30A8*, *CDKAL1*, *TCF7L2* ТА *HHEX* З РОЗВИТКОМ ЦУКРОВОГО ДІАБЕТУ 2 ТИПУ У НАСЕЛЕННЯ ПІВНІЧНО-СХІДНОЇ ІНДІЇ

Нараз Індія займає друге місце у світі за кількістю осіб, що хворіють на діабет. Отже, важливо дослідити генетичні варіації серед населення Індії, аби зрозуміти обсяги генетичної гетерогенності. Ми вивчали асоціацію генетичних варіацій чотирьох генів-кандидатів [*SLC30A8* (rs11558471), *CDKAL1* (rs94655871), *TCF7L2* (rs12255372) та *HHEX* (rs1111875)] з розвитком цукрового діабету 2 типу (T2D) у населення північно-східної Індії, дані щодо яких обмежені. ДНК отримали від 155 осіб, що хворіють на діабет, та 100 осіб контрольної групи без діабету. Генотипування виконували за допомогою полімеразно-ланцюгової реакції-поліморфізму довжин рестрикційних фрагментів (PCR-RFLP). Логістичний регресивний аналіз було застосовано з метою виявлення асоціації між генетичними варіантами та цукровим діабетом. Генотип CT rs9465871 (*CDKAL1* ген) продемонстрував значний захист від розвитку цукрового діабету [OR = 0,39 (0,17–0,91), p = 0,029] порівняно з генотипом CC навіть після коригування в розрізі віку, статі та ІМТ. Під час аналізу на рецесивній моделі генотип GG rs1111875 (HHEX ген) також продемонстрував значний захист від розвитку цукрового діабету [OR = 0,38 (0,18–0,82), p = 0,014] порівняно з генотипами AA+AG. Обидва ці результати втратили свою значимість після застосування порогу Бонферонні в p = 0,0041. Існує значна варіативність у схемі асоціації цих генів з розвитком цукрового діабету серед населення північно-східної Індії порівняно з іншими етнічно та географічно різноманітними групами населення Індії.

Ключові слова: гіперглікемія; генетика; цукровий діабет; північно-східна Індія.

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Received August 09, 2018
Received October 05, 2019
Accepted March 18, 2020