The Association of Polymorphisms rs2055314, rs2272522 and rs331894 in Close Homologue of L1 gene (CHL1) with Schizophrenia in the State of Qatar

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Background: Previous reports demonstrated polymorphisms in the CHL1 gene located on chromosome 3p26 (close homologue of L1) are associated with schizophrenia among different ethnic populations. The aim of this study is to investigate the associations of the haplotypes of the theses genetic marker (SNPs) of CHL1 gene locus: rs2055314 (C/T), rs2272522 (C/T) and rs331894 (A/G) with schizophrenia patients in Qatar populations.

Methods: A case control study association was carried out on 48 Qatari schizophrenic patients [from Psychiatry Hospital, Hamad Medical Corporation, Qatar] and 47 unrelated, healthy, control Qatari subjects. Schizophrenia was diagnosed according to the Diagnostic and Statistical Manual of Mental Disorders—Fourth Edition (DSM-IV) criteria for schizophrenia by two independent psychiatrists. Genotyping of SNP rs2055314 (C/T) rs2272522 (C/T) and rs331894 (A/G) was carried out by the 5' nuclease assay using TaqMan MGB probe by means of an ABI 7500 [Applied Biosystems].

Results: All SNPs are within the Hardy-Weinberg Equilibrium (HWE). The frequency distribution of the genotype rs2055314 (C/T) revealed that (35.30%), (31.25%), had CC and (35.30%), (29.41%), had TT among control and schizophrenic patients, respectively with P value= 0.034. The minor allele frequency (T) was 0.361 for all subjects, with odds ratio =0.84 and 95% CI was (0.37-1.91) with P value= 0.67 between cases and controls. Using the genetic recessive model, odds ratio was 4.00 and 95% CI was (0.96-16.69) with P value= 0.05 between cases and controls. The frequency distribution of the genotype rs331894 (G/A) revealed that (12.77%), (6.25%), had GG and (40.42%), (50.00%) had GA, and (47.65%), (43.75%) had AA among control and schizophrenic patients, respectively with P value= 0.005 between cases and controls. Using the genetic recessive model, odds ratio was 0.28 and 95% CI was (0.12-0.65) with P value= 0.002 between cases and controls. Using the genetic recessive model, odds ratio was 22.00 and 95% CI was (2.40-221.49) with P value= 0.0005 between cases and controls.

Conclusion: Our findings therefore strengthen the association between the CHL1 gene markers; rs2055314 and rs331894 with schizophrenia and also support the view that cell adhesion molecules could be involved in the etiology of this disease among Qatari patients.

The Association of Transcription Factor 7-like 2 [TCF7L2] Gene with Gestational Diabetes Mellitus in State of Qatar

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Background: Genetic and environmental factors are highly related with gestational diabetes mellitus (GDM) and type 2 diabetes (T2D). Our objective was to explore whether some genetic variants such as rs12255372, rs7903146 of TCF7L2 gene are significantly associated with the risk of gestational diabetes mellitus among Arabian population.

Methods: A case control study was designed for such genetic association study. A total of 159 unrelated pregnant women (114 Arab; 40 gestational diabetes mellitus cases and 74 controls and 45 non-Arab; 11 gestational diabetes mellitus and 34 controls) were recruited from antenatal care unit of HMC. Blood sample were drawn for DNA extraction, then genotyped for TCF7L2 gene variants (rs12255372, and rs7903146) using TaqMan real time PCR assay. Plasma was used for biochemical analysis including glucose, insulin and adiponectin.

Results: The CC, CT and TT genotype frequencies of the TCF7L2 rs7903146 variants was not significantly different between the control and gestational diabetes mellitus cases (39.4%, 50,0%, 10.6% vs. 40.6%, 43.8%, and 15.6%, p=0.444) among Arab populations, respectively. Only, the T allele of rs12255372 variant was significantly associated with risk of gestational diabetes mellitus with odds ratio of 2.370, (95% of CI 1.010-5.563) with the p value of 0.047 among Arab subjects using the genetic dominant model after adjustment of BMI and age. The other polymorphism rs7903146 was not significantly associated with GDM among Arab and non-Arab subjects. No significant difference was observed for glucose, insulin and adiponectin hormone after 50g glucose load by genotyping of both variants.

Conclusion: The TCF7L2 rs12255372 variant is associated with an increased risk of gestational diabetes mellitus in Arab women. Further studies are needed with larger sample sizes.