The present cross-sectional study comprised of consenting 580 subjects, of which 399 was confirmed type 2 diabetic subjects and 181 were controls. All the diabetic subjects were categorized into subjects with depression and subjects without depression. Disease association analysis revealed that sedentary life style was the strongest predictor which conferred approximately 4 fold higher risk of depression. Other independent predictors for depression were being a woman, duration of diabetes (DOD) >5 years, LDL>100mg/dl and TG>150mg/dl. Similarly independent predictors for diabetes were sedentary life style, LDL>100mg/dl and TG > 150mg/dl which almost doubled the risk of diabetes. The present study revealed 47.87 percent prevalence of depression in T2DM subjects of Punjab.

Risk association analysis for the SLC6A4 gene revealed that T allele of rs2020936 and rs3794808 added 1.52 and 1.74 times the risk of depression respectively whereas, T allele of rs2020936 and rs3794808 added risk of diabetes by 1.34 and 1.36 times respectively. For DRD4 gene, major alleles of rs3758653 and rs916455 and minor allele of rs747302 significantly influenced the risk of depression. Furthermore, major alleles of rs3758653 and rs1800955 contributed considerably to the risk of diabetes. Haplotype analysis exposed that TAT haplotype within SLC6A4 gene and TCTC haplotype within DRD4 gene increased the risk of depression by 2.19 and 4.15 times respectively in diabetes. The analysis also revealed that carriers of TCTT haplotype of DRD4 gene were at 3.10 times increased risk of diabetes than other subjects.

Gene-Gene (G x G) interaction analysis showed that SNPs with SLC6A4 and DRD4 gene communicated imparting depression and diabetes risk showing various forms of
interactive effects. Gene × Environmental (G × E) interaction analysis exhibited that both SLC6A4 and DRD4 genes interacted significantly with factors such as DOD > 5 years, BMI ≥ 30 kg/m², TG > 150 mg/dl, TC > 200 mg/dl, LDL > 100 mg/dl and HDL < 40 mg/dl for the risk of depression through marker, dominance and additive effects. It was revealed that two way epistatic effects existed between rs2020936 of SLC6A4 gene and rs747302 of DRD4 gene which worsened the risk of depression among diabetic subjects. The other epistatic effects observed were between SNPs rs3794808 and rs1800955 and between SNPs rs2020942 and rs747302. SNPs rs3794808 and rs3758653 as well as SNPs rs3758653 and rs916455 exhibited two way epistatic effects for the risk of diabetes in the population of Punjab.