**Table 1) Characteristics of patients and controls included in the study .**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Consanguinity**  | **Patients NO (%)** | **Control No. (%)** | **Chi-square\*/t test\*\*** | **P Value** |
|  |
| **Yes** | **6 (19,4%)** | **6 (15,4%)** | **0.192\*** | **0.661(NS)** |
| **No** | **25 (80,6%)** | **33 (84,6%)** |
|  |
| ***Family history of autism***  |
| **Yes** | **3(9,7%)** | **0 (0%)** | **3.943\*** | **0.047 (S)** |
| **No** | **28 (90,3%)** | **39 (100%)** |
|  |
| ***Family history of epilepsy***  |
| **Yes** | **5(16,1%)** | **0 (0%)** | **6.774\*** | **0.009 (S)** |
| **No** | **26 (83,9%)** | **39 (100%)** |
|  |
| ***History of prematurity:*** |
| **Yes** | **3 (9,7%)** | **0 (0%)** | **3.943\*** | **0.047 (S)** |
| **No** | **28 (90,3%)** | **39(100%)** |
|  |
| ***Feeding*** |
| **Breast** | **20 (64,5%)** | **31 (79.5%)** | **1.958\*** | **0.162(NS)** |
| **Artificial** | **11 (35,5%)** | **8 (20,5%)** |
| **Mean gestational age (weeks)** | **39 ± 1.25** | **39.1 ± 0.5** | **0.408\*\*** | **0.676(NS)** |
| **Mean birth weight (kg)** | **2.67 ± 0.389** | **3.03 ± 0.309** | **4.205\*\*** | **0.0001(HS)** |
| **Mean age for sitting (month)** | **8.5 ± 1.1** | **6.65 ± 0.87** | **7.653\*\*** | **<0.0001(HS)** |
| **Mean age at weaning (year)** | **1.59 ± 0.3** | **1.61 ± 0.31** | **0.273\*\*** | **0.786(NS)** |
| **Mean age at 1st spoken word (year)** | **2.6 ± 0.69** | **1.13 ± 0.18** | **11.553\*\*** | **<0.0001(HS)** |
| **Mean level of IQ score** | **66.13±8.20** | **96 ± 8.8** | **14.654\*\*** | **<0.0001(HS)** |

 **(Table 2)** A1298C genotype polymorphism and segregation of alleles among patients and control

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Group**  | **patients** | **control** | **Chi square** | **P value** |
| **AA genotype** | **7****(22.6%)** | **31****(79.5%)** | **24.700** | **<0.001** |
| **AC genotype** | **13****(41.9%)** | **7****(18%)** |
| **CC genotype** | **11****(35.5%)** | **1****(2.5%)** |
| **Total** | **31****(100%)** | **39****(100%)** |
| **A-allele (N, %)** | **27(43.55%)** | **69(88.46%)** | **32.332** | **<0.001** |
| **C-allele (N, %)** | **35(56.45%)** | **9(11.54%)** |
| **Total** | **62 (100%)** | **78(100%)** |

**(Table 3) Percentage of C667 genotypes and alleles among patients and control**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Group** | **Case** | **Control** | **Chi square** | **P value** |
| **C667 (Normal )** | **12****(38.6%)** | **35****(89.8%)** | **20.984** | **<0.001** |
| **C667T (Hetero)** | **15****(48.4%)** | **4****(10.2%)** |
| **667T (Mutant)** | **4****(13%)** | **0****(0%)** |  |
| **Total** | **31****(100%)** | **39****(100%)** |
| **C allele****No. (%)** | **39(62.90%)** | **74(94.87%)** |  |  |
| **T Allele****No. (%)** | **23(37.09%)** | **4(5.13%)** | **22.679** | **<0.001** |
| **Total** | **62(100%)** | **78(100%)** |

**(Table 4)** Correlation between psychological assessment and **A1298C** genotype in patients.

| **AC** | **CARS** | **IQ** | **DSM** |
| --- | --- | --- | --- |
| **AA(Normal)** | **35.857±5.429** | **69.571±7.35** | **6.714±0.488** |
| **AC (Hetero)** | **37.538±5.710** | **66.538±7.47** | **7.385±1.325** |
| **CC (Mutant)** | **38.091±4.721** | **63.455±9.29** | **7.091±0.944** |
| **ANOVA** | **0.391** | **1.236** | **0.680** |
| **P value** | **0.680** | **0.306** | **0.409** |

 **(Table 5)** Correlation between psychological assessment and **C667**genotype

| **C667** | **CARS** | **IQ** | **DSM** |
| --- | --- | --- | --- |
| **C667 (normal)** | **38.750±4.654** | **66.417±7.810** | **7.333±1.073** |
| **C667T (hetero)** | **36.200±5.570** | **66.000±7.606** | **7.000±1.134** |
| **667T (mutant)** | **37.500±5.686** | **65.750±13.376** | **7.000±0.817** |
| **ANOVA** | **0.790** | **0.013** | **0.350** |
| **P value** | **0.464** | **0.987** | **0.708** |