**Table 1.** Genotypic analysis between 3 groups (COVID, H1N1 and CONTROL) in the *IL17A* gene for addictive model.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene, reference SNP\* and variation** | **Groups** | **Homozygous 1/1** | **Heterozygous 1/2** | **Homozygous 2/2** | ***p*-value†** |
| ***IL17A***  **rs3819025**  **[G/A]** |  | **GG** | **AG** | **AA** |  |
| **COVID-19** | 3 (100) | 7 (43.7) | 9 (45.0) | 0.186a |
| **H1N1** | 0 (00.0) | 2 (12.6) | 8 (40.0) |
| **CONTROL** | 0 (00.0) | 7 (43.7) | 3 (15.0) | 0.170b |
|  |  |  |  |  |  |
| ***IL17A***  **rs2275913**  **[G/A]** |  | **GG** | **AG** | **AA** |  |
| **COVID-19** | 11 (55.0) | 9 (50.0) | 0 (00.0) | 0.355a |
| **H1N1** | 5 (25.0) | 4 (22.2) | 1 (100) |
| **CONTROL** | 4 (20.00) | 5 (27.8) | 0 (00.0) | 0.599b |

**Legend:** Genotype was expressed by number and percentage and a total percentage was show in column; **\***SNP identifier based on NCBI dbSNP; **†** Logistic regression for aCOVID-19 *vs* H1N1 and bCOVID-19 *vs* CONTROL.

**Table 2.** Genotypic frequency for tag SNPs in the *IL17A* gene in dominant and recessive models.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene, reference SNP\* and variation** | **Models** | **Model** | **COVID-19** | **H1N1** | ***p*-valuea** | **CONTROL** | ***p*-valueb** |
| ***IL17A***  **rs3819025 [G/A]** | **Dominant G** | **GG+AG** | 10 (52.7) | 2 (10.5) | 0.090**§** | 7 (36.8) | 0.449**§** |
|  | **AA** | 9 (45.0) | 8 (40.0) | 3 (15.0) |
|  |  |  |  |  |  |  |
| **Recessive G** | **AA+AG** | 16 (44.4) | 10 (27.8) | 0.532**§** | 10 (27.8) | 0.532**§** |
|  | **GG** | 3 (100.0) | 0 | 0 |
|  |  |  |  |  |  |  |  |
| ***IL17A***  **rs2275913 [G/A]** | **Dominant G** | **GG+AG** | 20 (52.6) | 9 (23.7) | 0.333**§** | 9 (23.7) | 0.719**§** |
|  | **AA** | 0 | 1 (100.0) | 0 |
|  |  |  |  |  |  |  |
| **Recessive G** | **AA+AG** | 9 (47.4) | 5 (26.3) | 0.796**†** | 5 (26.3) | 0.700**§** |
|  | **GG** | 11 (55.0) | 5 (25.0) | 4 (20.0) |

**Legend:** *IL17A* Genotypes were expressed by number and percentage and a total percentage was show in line; \*SNP identifier based on NCBI dbSNP; **†** Pearson’s chi-square or **§**Fisher’s exact for aCOVID-19 *vs* H1N1 and bCOVID-19 *vs* CONTROL.