**Mutations in ace2 gene Modulate Cytokine Levels and Alter Immune Responses in Mycobacterium tuberculosis and SARS-CoV-2 co-infection: A Cameroonian cohort.**

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**Supplementary Document.**

**Supplementary Table 1:** Genotype frequencies distribution of single nucleotide polymorphisms of *ace2* and *tmprss2* genes. Chi-square test was used to determine statistically significant differences in genotype frequencies among the groups (Control, COV, TB, and TBCOV). A *p-value* of less than 0.05 was considered significant.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Groups** | **Genotypes** | **P-value** |
| **Homozygous GG n (%)** | **Heterozygous AG n (%)** | **Homozygous AA n (%)** |
| ***ace2*** | **rs4646142** | Control (n= 24) | 2 (8.4) | 22 (91.6) | 0 (0) | <0.05 |
| COV (n = 31) | 6 (19.4) | 25 (80.6) | 0 (0) |
| TB (n = 43) | 0 (0) | 43 (100) | 0 (0) |
| TBCOV (n = 21) | 3 (14.3) | 17 (80.9) | 1 (4.8) |
| **rs2074192** | Control (n= 24) | 4 (16.7) | 20 (83.3) | 0 (0) | <0.05 |
| COV (n = 31) | 7 (22.5) | 24 (77.4) | 0 (0) |
| TB (n = 43) | 0 (0) | 9 (20.9) | 32 (74.4) |
| TBCOV (n = 21) | 2 (9.5) | 3 (14.3) | 17 (80.9) |
| **rs147311723** | Control (n= 24) | 0 (0) | 24 (100) | 0 (0) | <0.05 |
| COV (n = 31) | 8 (25.8) | 18 (58.1) | 5 (16.1) |
| TB (n = 43) | 3 (6.8) | 29 (67.4) | 11 (25.6) |
| TBCOV (n = 21) | 1 (4.8) | 20 (95.2) | 0 (0) |
| **rs35803318** | Control (n= 24) | 1 (4.2) | 23 (95.8) | 0 (0) | ns |
| COV (n = 31) | 6 (19.4) | 25 (80.6) | 0 (0) |
| TB (n = 43) | 1 (2.3) | 42 (97.7) | 0 (0) |
| TBCOV (n = 21) | 0 (0) | 21 (100) | 0 (0) |
| **rs4646140** | Control (n= 24) | 8 (33.3) | 12 (50) | 4 (16.6) | <0.05 |
| COV (n = 31) | 19 (61.3) | 10 (32.3) | 2 (6.5) |
| TB (n = 43) | 22 (51.2) | 21 (48.8) | 0 (0) |
| TBCOV (n = 21) | 13 (61.9) | 5 (23.8) | 3 (14.2) |
| **rs4646116** | Control (n= 24) | 0 (0) | 23 (95.8) | 1 (4.2) | <0.05 |
| COV (n = 31) | 1 (3.2) | 30 (96.8) | 0 (0) |
| TB (n = 43) | 0 (0) | 43 (100) | 0 (0) |
| TBCOV (n = 21) | 2 (9.5) | 18 (85.7) | 1 (4.8) |
|  |  | Homozygous CC | Heterozygous CG | Homozygous GG |  |
| **rs4240157** | Control (n= 24) | 3 (12.5) | 21 (87.5) | 0 (0) | ns |
| COV (n = 31) | 3 (9.7) | 28 (90.3) | 0 (0) |
| TB (n = 43) | 13 (30.2) | 30 (69.8) | 0 (0) |
| TBCOV (n = 21) | 2 (9.5) | 19 (90.5) | 0 (0) |
| **rs6632677** | Control (n= 24) | 0 (0) | 20 (83.3) | 4 (16.7) | <0.05 |
| COV (n = 31) | 1 (3.2) | 29 (93.5) | 1 (3.2) |
| TB (n = 43) | 0 (0) | 40 (93.0) | 3 (6.9) |
| TBCOV (n = 21) | 1 (4.8) | 14 (66.7) | 6 (28.6) |
|  |  | Homozygous CC | Heterozygous CA | Homozygous GG |  |
| **rs2285666** | Control (n= 24) | 0 (0) | 24 (100) | 0 (0) | 0.004 |
| COV (n = 31) | 0 (0) | 31 (100) | 0 (0) |
| TB (n = 43) | 0 (0) | 43 (100) | 0 (0) |
| TBCOV (n = 21) | 3 (14.3) | 17 (80.9) | 1 (4.8) |
|  |  | Homozygous AA | Heterozygous AG | Homozygous GG |  |
| **rs4646179** | Control (n= 24) | 0 (0) | 24 (100) | 0 (0) | ns |
| COV (n = 31) | 1 (3.2) | 30 (96.8) | 0 (0) |
| TB (n = 43) | 2 (4.7) | 40 (93) | 1 () |
| TBCOV (n = 21) | 2 (9.5) | 19 (90.5) | 0 (0) |
| ***tmprss2*** |  |  | Homozygous CC | Heterozygous CA | Homozygous AA |  |
| **rs75603675** | Control (n= 24) | 0 (0) | 24 (100) | 0 (0) | ns |
| COV (n= 31) | 1 (3.3) | 29 (93.5) | 1 (3.3) |
| TB (n = 43) | 0 (0) | 43 (100) | 0 (0) |
| TBCOV (n= 21) | 1 (4.76) | 18 (85.7) | 2 (9.5) |
|  |  | Homozygous CC | Heterozygous CA | Homozygous AA |  |
| **rs61735791** | Control (n= 24) | 0 (0) | 24 (100) | 0 (0) | ns |
| COV (n= 31) | 3 (9.8) | 28 (90.3) | 0 (0) |
| TB (n = 43) | 0 (0) | 43 (100) | 0 (0) |
| TBCOV (n= 21) | 0 (0) | 21 (100) | 0 (0) |
|  |  | Homozygous CC | Heterozygous CT | Homozygous TT |  |
| **rs12329760** | Control (n= 24) | 2 (8.3) | 22 (91.7) | 0 (0) | ns |
| COV (n= 31) | 2 (6.5) | 29 (93.5) | 0 (0) |
| TB (n= 43) | 5 (11.6) | 38 (88.4) | 0 (0) |
| TBCOV (n=21) | 2 (9.5) | 19 (90.5) | 0 (0) |

Abbreviations: TB: Tuberculosis positive; COV: COVID-19 positive and TBCOV: Tuberculosis and COVID-19 association.

\*\*\*End of Supplementary Document\*\*\*