

Association Between ACE 2 / TMPRSS 2 Gene Polymorphisms and Disease Severity During Covid-19 and Tuberculosis co-infection in Cameroon.

<u>Kameni Mary Ngongang^{1, 2}, Tchoupe Eric Berenger ^{2, 6}, Assam Jean Paul^{1,3}, Taya Jean Bosco^{1, 2}, Nzuno Marie Christine^{2, 5}, Severin</u>

Donald Kamdem^{2, 8} and Palmer Masumbe Netongo ^{2,4,6}

1. Department of Micriobiology, Faculty of Science, University of Yaounde I; 2. Molecular Diagnostic Research Laboratory, Biotechnology Center, University of Yaounde I; 3. Laboratory for Tuberculosis Research and Pharmacology, Biotechnology Centre, University of Yaounde I; 4.School of Science, Navajo Technical University, Crownpoint, USA ; 5. Department of Medical Laboratory Science, Faculty of Health Science, University of Buea, Cameroon ; 6. Department of Biochemistry, Faculty of Science, University of Yaounde I; 7. Faculty of Medicine and Biomedical Sciences, University of Yaoundé 1, Yaoundé, Cameroon; 8. School of Medecine University of UTAH, Salt Lake City, USA.

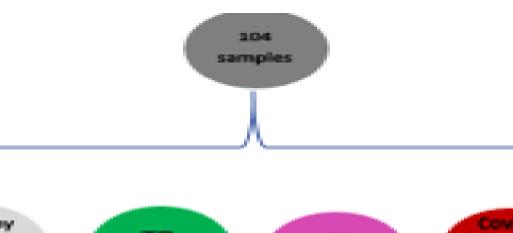
BACKGROUND

 Covid-19 and Tuberculosis (TB) share same pathogenesis and clinical presentation. Upon entry into the host, SARS-CoV 2 and *Mycobacterium* tuberculosis (MTB) induce pro-inflammatory cytokines which could lead to the cytokine storm.

METHODOLOGY

Study procedure : A cross sectional prospective study was carried at six hospital facilities in Yaoundé.

Study population :



- SARS-CoV2 depends on Angiotensin Converting Enzyme 2 (ACE 2) (receptor for entry into the host cell) and TMPRSS2 (for spike protein priming) to replicate. Interestingly, *MTB* infection increases the expression of ACE 2.
- A genetic change in ACE 2 and TMPRSS2 could influence susceptibility to these infections. We therefore hypothesized that genetic changes in ACE 2 and TMPRSS2 gene polymorphisms leads to increase disease severity in Covid-19 /TB co-infected patients.

OBJECTIVE

Determine the association between frequencies of ACE 2 /TMPRSS2 gene polymorphisms and disease severity during Covid-19 and TB co-infections in Yaounde, Cameroon.

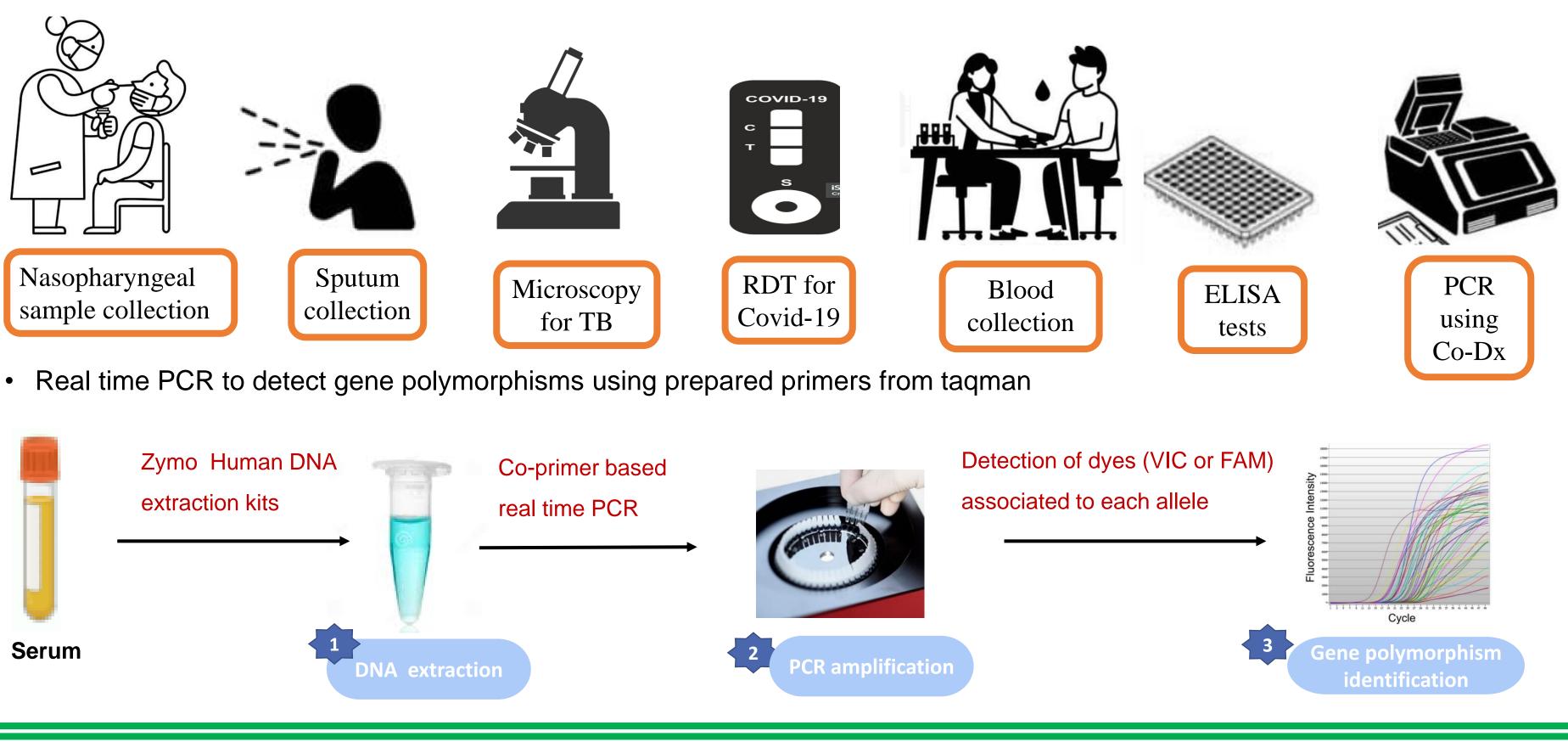
List of abbreviations

Angiotensine Converting Enzymes (ACE 2), Transmembrane Serine Protease 2 (TMPRSS2), Single Nucleotide Polymorphism (SNP), Alanine amino transferase (ALT), Aspartate amino transferase (AST), Creatinine (CREA), Interleukine (IL), Severe acute respiratory syndrome (SARS-CoV2).



Laboratory procedures :

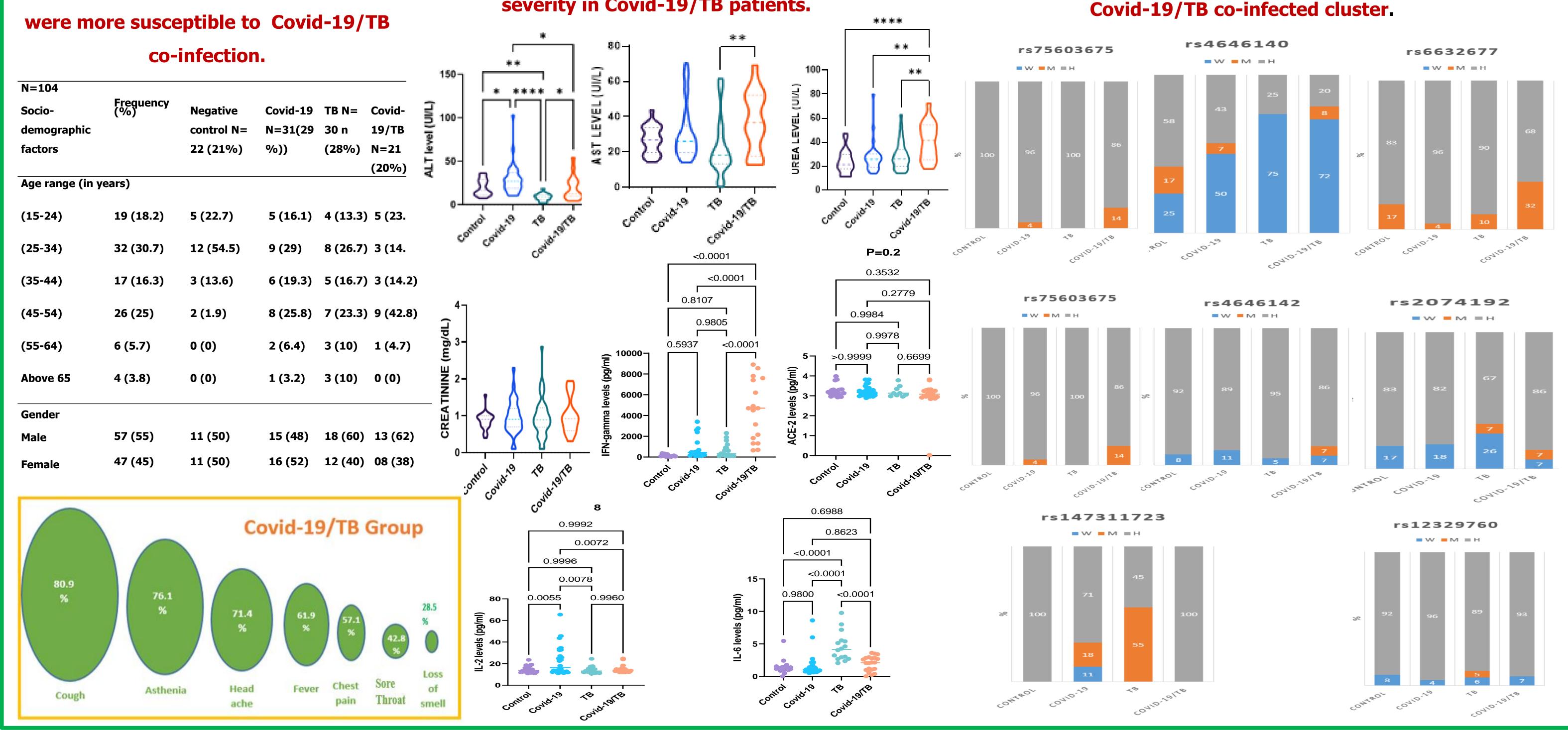
Real-time PCR using SARAGENE kits detecting IS 6110 and MPB 64 genes from MTB complexe and Logix smart ABC kits detecting Influenza A/B, SARS-CoV2.



RESULTS

1: Age range (45-54 years) and males

2 : Increased expression of some markers of disease 3: Higher frequency of genetic variations in ACE 2/TMPRSS2 among



severity in Covid-19/TB patients.

CONCLUSION

Alteration of kidney and liver functions as well as increased inflammatory response in Covid-19/TB subjects in this study show the synergetic effects of these two diseases. Despite the higher frequency of ACE 2 and TMPRSS2 gene polymorphisms among co-infected patients, some variations of these polymorphisms were observed across our study population indicating the need for further genotypic characterization of ACE 2 and TMPRSS2 variants among the Cameroonian population.

ACKNOWLEDGEMENTS

This work was funded by European and Developing Countries Clinical Trials Partnership (EDCTP) via the Clinical Characterisation of Covid 19 Protocol (CCP) project. We thank the Molecular Diagnostics Reaserch Laboratory (MDRL) where the study was carried out and the International Pandemic Science Conference (IPSC) secretariat for supporting our participation in this congress.

