

# First whole genome sequences and phylogenetic analysis of SARS-CoV-2 virus isolates during COVID-19 outbreak in Tunisia, North Africa.

wasfi fares<sup>1</sup>, Anissa Chouikha<sup>1</sup>, Kais Ghedira<sup>1</sup>, Mariem Gdoura<sup>1</sup>, Dorra Rezig<sup>1</sup>, Sondes Haddad Boubaker<sup>1</sup>, Imene Ben Dhifallah<sup>2</sup>, Henda Touzi<sup>2</sup>, Walid Hammami<sup>2</sup>, ZIna Meddeb<sup>2</sup>, Amel Sedraoui<sup>1</sup>, Nahed Hogga<sup>1</sup>, Imen Abouda<sup>1</sup>, Aurelia Kwasiborski<sup>3</sup>, Veronique Hourdel<sup>3</sup>, Guillain Mikaty<sup>3</sup>, Valerie Caro<sup>3,4</sup>, Jean-Claude Manuguerra<sup>3</sup>, Nissaf Ben Alaya<sup>5</sup>, and Henda Triki<sup>1</sup>

<sup>1</sup>Institut Pasteur, University Tunis-El Manar, Tunis, Tunisia

<sup>2</sup>Institut Pasteur, University Tunis-El Manar, Tunis, Tunisia.

<sup>3</sup>Institut Pasteur, Paris, France

<sup>4</sup>Institut Pasteur

<sup>5</sup>Tunisian Ministry of Health

June 5, 2020

## Abstract

Full genomes sequences of six Tunisian SARS-CoV-2 strains were obtained from imported and locally transmission cases during the COVID-19 outbreak. Reported sequences were non-identical with 0.1% nucleotide divergence rate and clustered into 6 different clades with worldwide sequences. SNPs results favor the distribution of the reported Tunisian sequences into 3 major genotypes. These results indicate multiple introductions of the virus in Tunisia and add new genomic data on SARS-CoV-2 at the international level.

## Hosted file

Main\_text.doc available at <https://authorea.com/users/330423/articles/457189-first-whole-genome-sequences-and-phylogenetic-analysis-of-sars-cov-2-virus-isolates-during-covid-19-outbreak-in-tunisia-north-africa>

## Hosted file

Figure\_1.ppt available at <https://authorea.com/users/330423/articles/457189-first-whole-genome-sequences-and-phylogenetic-analysis-of-sars-cov-2-virus-isolates-during-covid-19-outbreak-in-tunisia-north-africa>