



Marseille, December 21<sup>st</sup>, 2020

**Dr D. Peter Drotman**  
**Editor-in-Chief**  
**Clinical Infectious Diseases**

Dear Dear Dr Peter Drotman,

Attached, please find a manuscript entitled “Genome sequence analysis enabled deciphering the atypical evolution of COVID-19 epidemics in Marseille, France” that we would like to submit to Clinical Infectious Diseases as an original research article. In this manuscript, we describe the COVID-19 epidemic that occurred in Marseille, France, and was caused by a 10 successive or concomitant SARS-CoV-2 variants that we characterized in patients’ specimens using genome sequencing. Genome sequence comparison enabled us to retrace the evolution of these variants, which were clearly distinct. As examples, the Marseille-1 variant appeared in sub-Saharan Africa, remained restricted to the Marseille area and disappeared in August when it was replaced by the Marseille-4 variant that was imported from Northern Europe by tourist and rapidly became majoritary. We believe that SARS-CoV-2 is able to genetically evolve rapidly and its variants to be spread internationally by travelers, including in areas beforehand exposed to other variants.

All authors have seen and approved the final version of the manuscript, contributed significantly to the work and do not have any conflict of interest in relation to this research.



The manuscript has neither been previously published nor is being considered for publication elsewhere.

I and Pr Didier Raoult will be the corresponding authors of the manuscript.

Yours, sincerely

**Pierre-Edouard FOURNIER**