



ΕΛΛΗΝΙΚΗ ΔΗΜΟΚΡΑΤΙΑ

Εθνικόν και Καποδιστριακόν
Πανεπιστήμιον Αθηνών

— ΙΔΡΥΘΕΝ ΤΟ 1837 —



pMedGR

Εφαρμογές στην πανδημία SARS-CoV-2

Δ. Παρασκευής

Αναπληρωτής Καθηγητής Επιδημιολογίας και Προληπτικής Ιατρικής
Ιατρική Σχολή ΕΚΠΑ



Molecular Epidemiology of SARS-CoV-2 in Greece Reveals Low Rates of Onward Virus Transmission after Lifting of Travel Restrictions Based on Risk Assessment during Summer 2020

Evangelia Georgia Kostaki,^a Georgios A. Pavlopoulos,^{b,c} Kleio-Maria Verrou,^b Giannis Ampatzidis-Michailidis,^b Vaggelis Harokopos,^c Pantelis Hatzis,^{b,c} Panagiotis Moulos,^{b,c} Nikolaos Siafakas,^d Spyridon Pournaras,^d Christos Hadjichristodoulou,^e Fani Chatzopoulou,^f Dimitrios Chatzidimitriou,^{f,g} Periklis Panagopoulos,^h Panagiota Lourida,ⁱ Aikaterini Argyraki,^j Theodoros Lytras,^j Spyros Sapounas,^k Gerasimos Gerolymatos,^k Georgios Panagiotakopoulos,^k Panagiotis Prezerakos,^l Sotirios Tsiodras,^m Vana Sypsa,ⁿ Angelos Hatzakis,ⁿ Cleo Anastassopoulou,ⁿ Nikolaos Spanakis,ⁿ Athanasios Tsakris,ⁿ Meletios Athanasios Dimopoulos,^{b,o} Anastasia Kotanidou,^p Petros Sfikakis,^{b,q} Georgios Kollias,^{b,r,s} Gkikas Magiorkinis,^a and Dimitrios Paraskevis^a

^aDepartment of Hygiene, Epidemiology and Medical Statistics, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^bCenter of New Biotechnologies & Precision Medicine, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^cInstitute for Fundamental Biomedical Research, Biomedical Sciences Research Center "Alexander Fleming," Vari, Greece

^dLaboratory of Clinical Microbiology, ATTIKON University Hospital, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^eLaboratory of Hygiene and Epidemiology, Faculty of Medicine, Larisa, Greece

^fLabnet, Laboratories, Thessaloniki, Greece

^gDepartment of Microbiology, Medical School, Aristotle University of Thessaloniki, Thessaloniki, Greece

^h2nd Department of Internal Medicine, General Hospital of Alexandroupoli, Democritus University of Thrace, Alexandroupoli, Greece

ⁱInfectious Diseases Clinic A, Thoracic Diseases General Hospital Sotiria, Athens, Greece

^jSchool of Medicine, European University Cyprus, Nicosia, Cyprus

^kNational Public Health Organization, Athens, Greece

^lDepartment of Nursing, University of Peloponnese, Tripoli, Greece

^m4th Department of Internal Medicine, Attikon University Hospital, Medical School, National and Kapodistrian University of Athens, Athens, Greece

ⁿDepartment of Microbiology, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^oDepartment of Therapeutics, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^p1st Intensive Care Unit, General Hospital Evangelismos, National and Kapodistrian University of Athens, Athens, Greece

^q1st Department of Propaedeutic Internal Medicine, Medical School, National and Kapodistrian University of Athens, Athens, Greece

^rInstitute for Bioinnovation, Biomedical Sciences Research Center "Alexander Fleming," Vari, Greece

^sDepartment of Physiology, Medical School, National and Kapodistrian University of Athens, Athens, Greece

Gkikas Magiorkinis and Dimitrios Paraskevis made equal contributions to this work.

ABSTRACT The novel coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spread rapidly during the first months of 2020 and continues to expand in multiple areas across the globe. Molecular epidemiology has provided an added value to traditional public health tools by identifying SARS-CoV-2 clusters or providing evidence that clusters based on virus sequences and contact tracing are highly concordant. Our aim was to infer the levels of virus importation and to estimate the impact of public health measures related to travel restrictions to local transmission in Greece. Our phylogenetic and phylogeographic analyses included 389 full-genome SARS-CoV-2 sequences collected during the first 7 months of the pandemic in Greece and a random collection in five replicates of 3,000 sequences sampled globally, as well as the best hits to our data set identified by BLAST. Phylogenetic trees were reconstructed by the maximum likelihood method, and the putative source of SARS-CoV-2 infections was inferred by phylogeographic analysis. Phylogenetic analyses revealed the presence of 89 genetically distinct viruses

Citation Kostaki EG, Pavlopoulos GA, Verrou K-M, Ampatzidis-Michailidis G, Harokopos V, Hatzis P, Moulos P, Siafakas N, Pournaras S, Hadjichristodoulou C, Chatzopoulou F, Chatzidimitriou D, Panagopoulos P, Lourida P, Argyraki A, Lytras T, Sapounas S, Gerolymatos G, Panagiotakopoulos G, Prezerakos P, Tsiodras S, Sypsa V, Hatzakis A, Anastassopoulou C, Spanakis N, Tsakris A, Dimopoulos MA, Kotanidou A, Sfikakis P, Kollias G, Magiorkinis G, Paraskevis D. 2021. Molecular epidemiology of SARS-CoV-2 in Greece reveals low rates of onward virus transmission after lifting of travel restrictions based on risk assessment during summer 2020. *mSphere* 6:e00180-21. <https://doi.org/10.1128/mSphere.00180-21>.

Editor Christina F. Spiropoulou, U.S. Centers for Disease Control and Prevention

Copyright © 2021 Kostaki et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

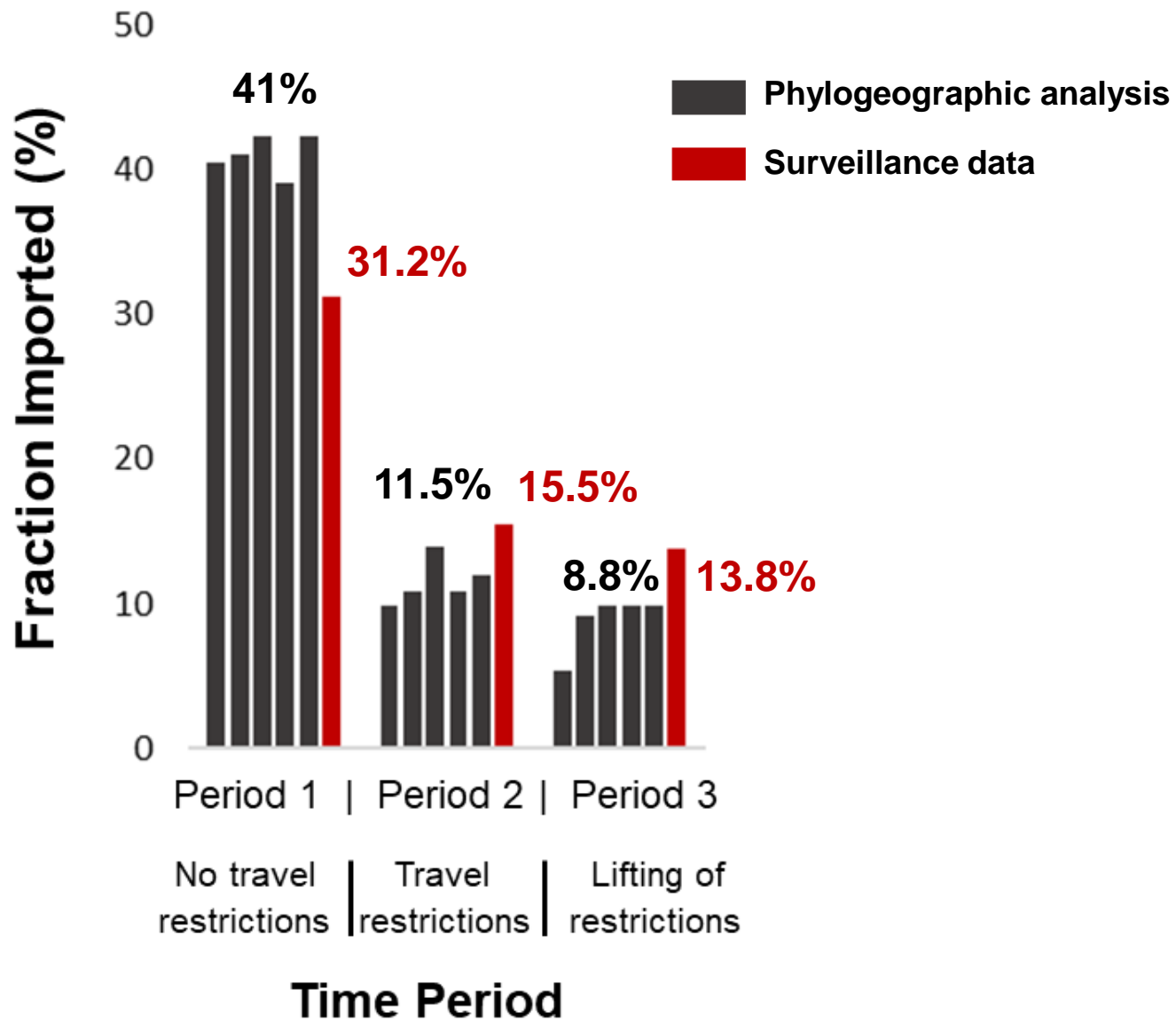
Address correspondence to Dimitrios Paraskevis, dparask@med.uoa.gr.

Received 25 February 2021

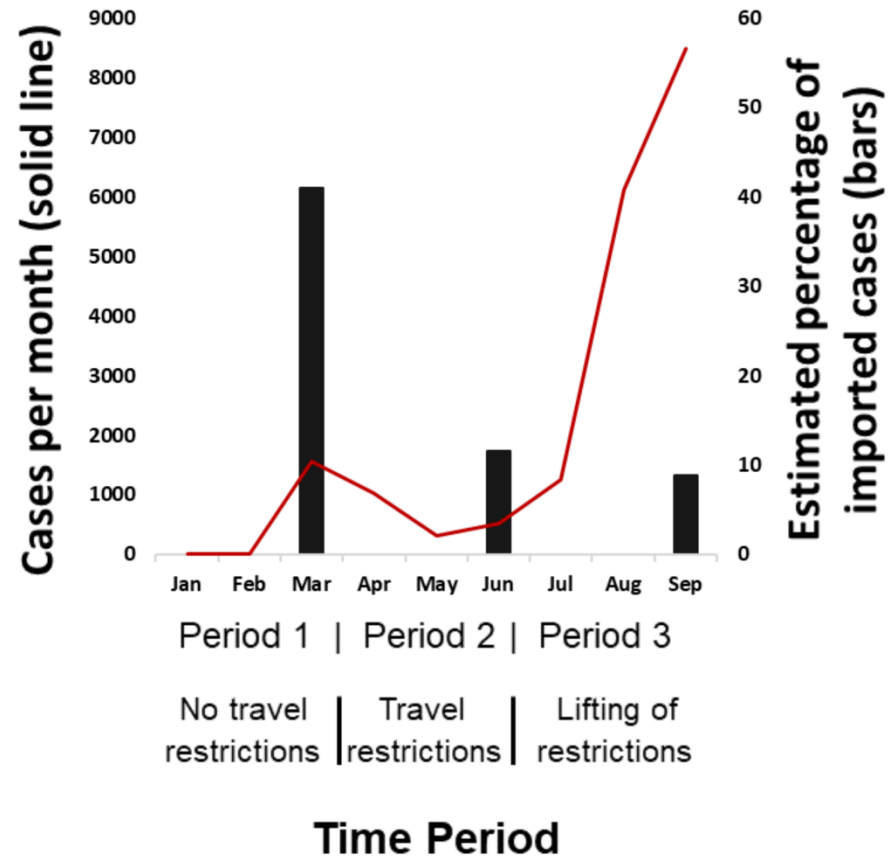
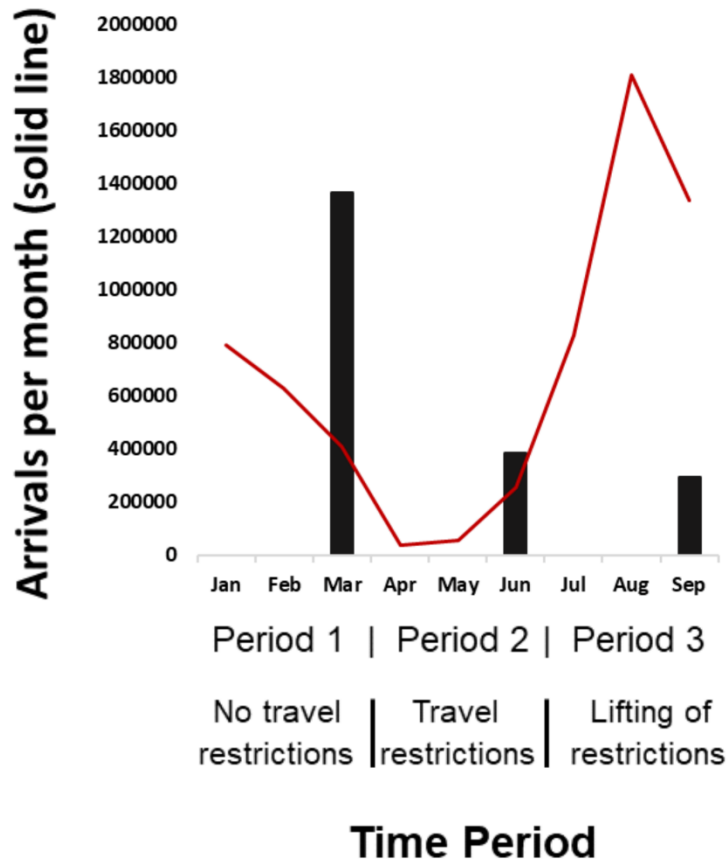
Accepted 6 June 2021

Published 30 June 2021

Εισαγόμενες λοιμώξεις



Εισαγόμενες λοιμώξεις αριθμός αφίξεων και κρούσματα SARS-CoV-2 στην Ελλάδα



Χρονολογημένη τοπολογία αλληλουχιών
πρώτης περιόδου δειγματοληψίας

 Greece
 Globally sampled references
Time Period 1
(No travel restrictions)

Χρόνος προέλευσης:

15 Φεβρουαρίου 2020

[95% HPD:

2 Φεβρουαρίου 2020

- 26 Φεβρουαρίου 2020]

