

Genomic epidemiology of the main SARS-CoV-2 variants circulating in Italy in 2020 and 2022 period

Annalisa Bergna¹, A. Lai¹, Carla Della Ventura¹, Bianca Bruzzone², Alessandro Weisz³, Morena d'Avenia⁴, Sophie Testa⁵, Carlo Torti⁶, Caterina Sagnelli⁷, Angela Menchise⁸, Gaetano Brindicci⁹, Daniela Francisci¹⁰, Ilaria Vicenti¹¹, Nicola Clementi¹², Annapaola Callegaro¹³, Emmanuele Venanzi Rullo¹⁴, Sara Caucci¹⁵, Vanessa De Pace², Andrea Orsi², Stefano Brusa¹⁶, Francesca Greco¹⁷, Vittoria Letizia¹⁸, Emilia Vaccaro¹⁹, Gianluigi Franci³, Francesca Rizzo³, Fabio Sagradi⁵, Leonardo Lanfranchi⁵, Nicola Coppola⁷, Annalisa saracino⁹, Michela Sampaolo²⁰, Silvia Ronchiadin²¹, Massimo Galli¹, Agostino Riva¹, and Gianguglielmo Zehender¹

¹University of Milan

²IRCCS AOU San Martino-IST

³Universita degli Studi di Salerno Dipartimento di Medicina Chirurgia e Odontoiatria Scuola Medica Salernitana

⁴ASL Bari

⁵Azienda Socio Sanitaria Territoriale di Cremona

⁶Universita degli Studi Magna Graecia di Catanzaro Dipartimento di Scienze Mediche e Chirurgiche

⁷University of Campania "Luigi Vanvitelli

⁸AOR San Carlo Potenza

⁹University of Bari

¹⁰Santa Maria della Misericordia" Hospital

¹¹Universita degli Studi di Siena Dipartimento di Biotecnologie Mediche

¹²Università "Vita-Salute" San Raffaele

¹³Department of Infectious Diseases

¹⁴University of Messina

¹⁵Universita Politecnica delle Marche Dipartimento di Scienze Biomediche e Sanita Pubblica

¹⁶Universita degli Studi di Napoli Federico II Dipartimento di Scienze Mediche Traslazionali

¹⁷UOC Microbiology and Virology

¹⁸AORN Sant'Anna and San Sebastiano di Caserta

¹⁹AOU 'S Giovanni di Dio e Ruggi d'Aragona' Università di Salerno

²⁰IRCCS Ospedale San Raffaele

²¹Intesa Sanpaolo Innovation Center

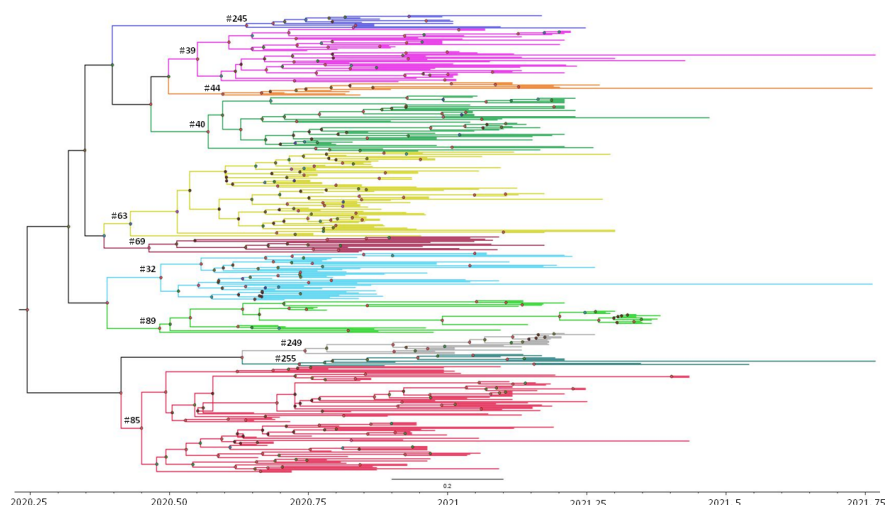
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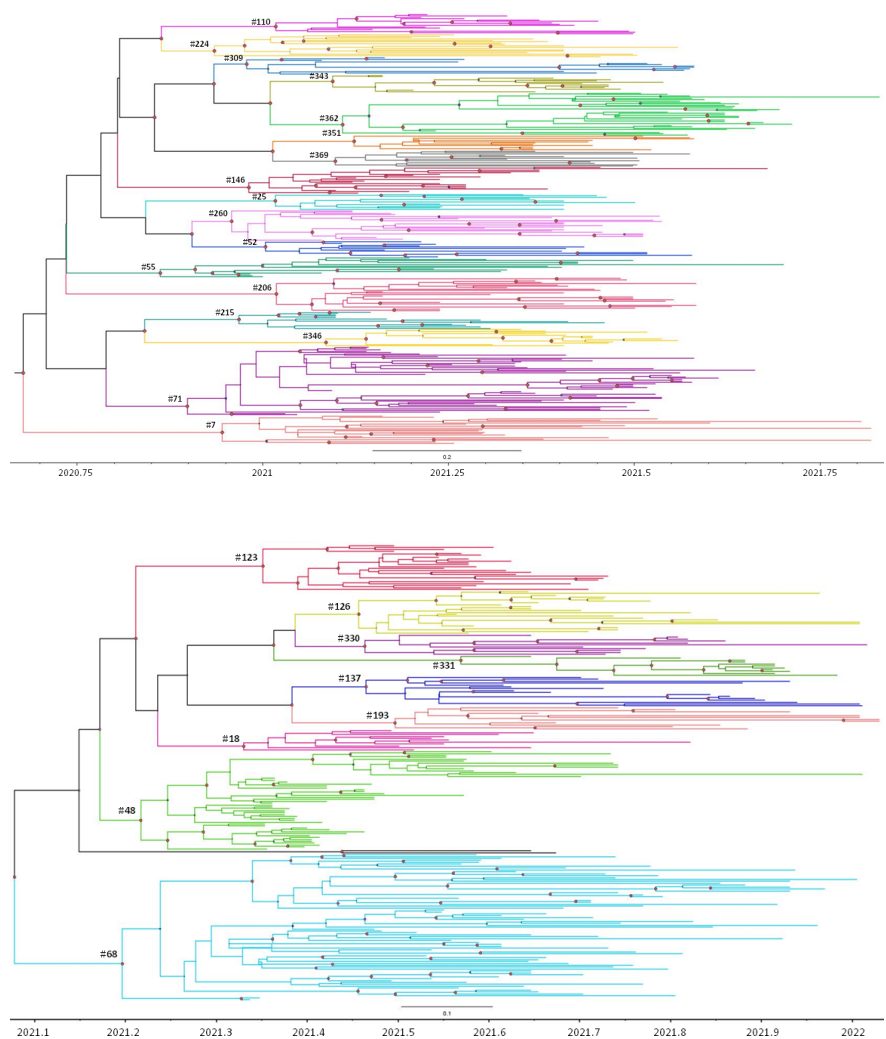
Abstract

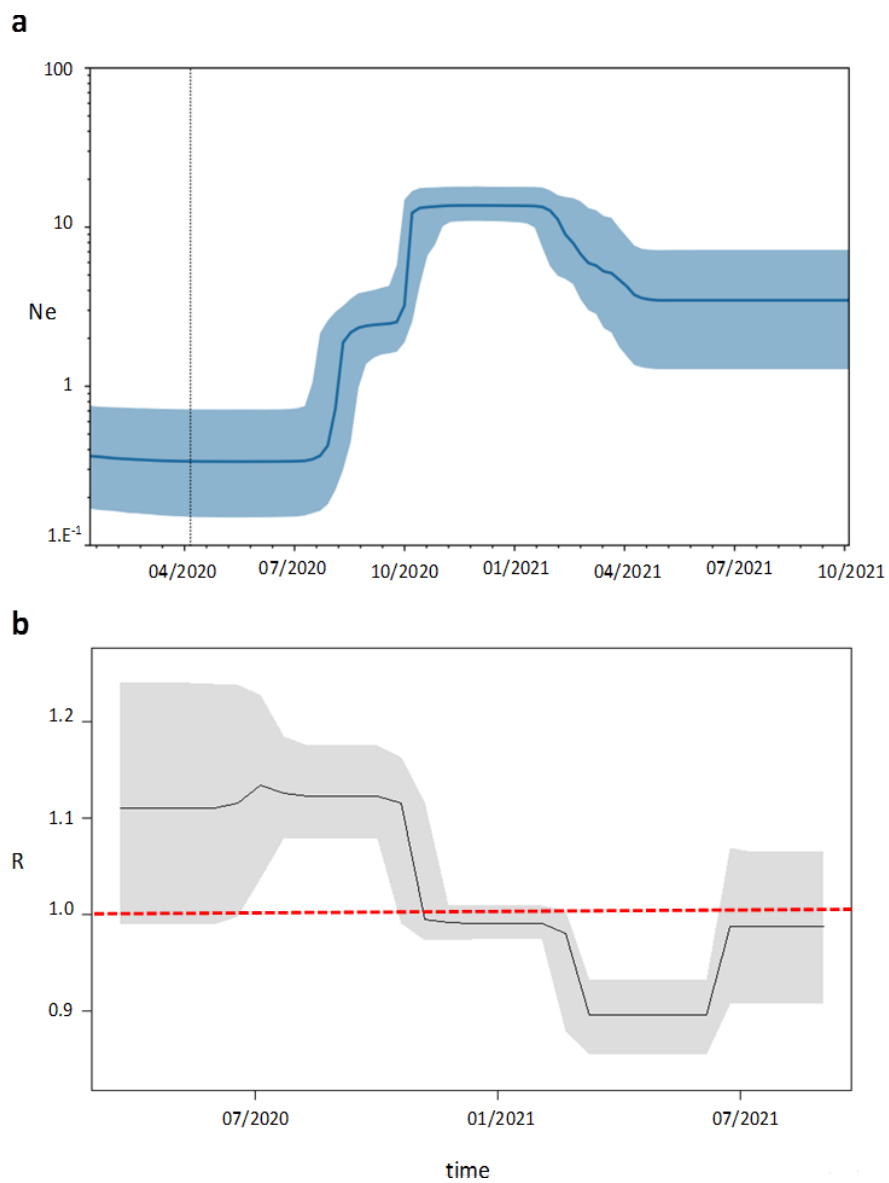
Since the beginning of the pandemic, SARS-CoV-2 has shown a great genomic variability, resulting in the continuous emergence of new variants that has made their global monitoring and study a priority. This work aimed to study the genomic heterogeneity, the temporal origin, the rate of viral evolution and the population dynamics of the main circulating variants (20E.EU1, Alpha and Delta) in Italy, in August 2020-January 2022 period. For phylogenetic analyses, two datasets were evaluated for each variant, the former comprising international genomes and the latter focusing on clusters containing at least 70% of Italian sequences. The international dataset showed 26 (23% Italians, 23% singleton, 54% mixed), 40 (60% mixed, 37.5% Italians, 1 singleton) and 42 (85.7% mixed, 9.5% singleton, 4.8% Italians) clusters with at least one Italian sequence, in 20E.EU1 clade, Alpha and Delta variants, respectively. International clusters presented tMRCAs between 13/06/2020-27/07/2021. R_e values showed the highest level between May-June until autumn 2020 in 20E.EU1 clade. The Alpha variant showed an increase in the R_e in December 2020, when the highest mean value was estimated. Delta variant presented two peaks: the first between March-May, and the second between June-July 2021. The present work highlighted a different evolutionary dynamic of studied lineages with a high concordance between epidemiological parameters estimation and phylodynamic trends suggesting that the mechanism of replacement of the SARS-CoV-2 variants must be related to a complex of factors involving the transmissibility, as well as the implementation of control measures, and the level of cross-immunization within the population.

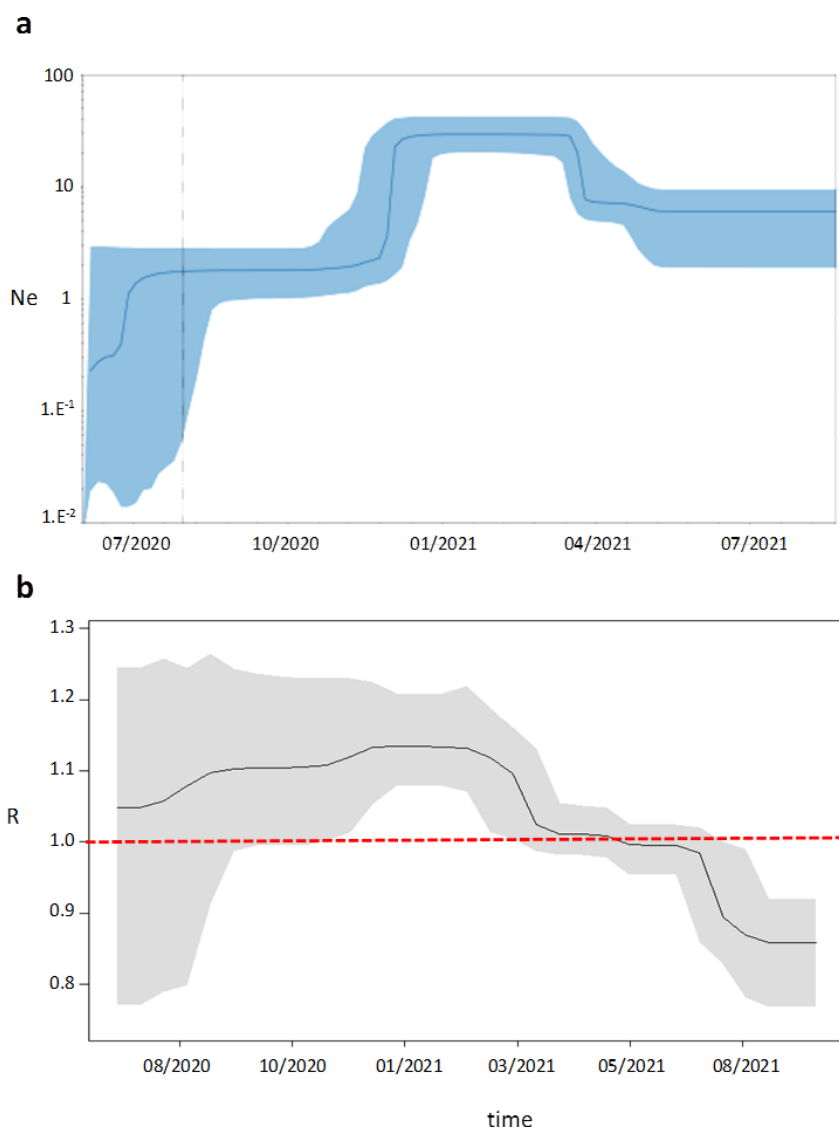
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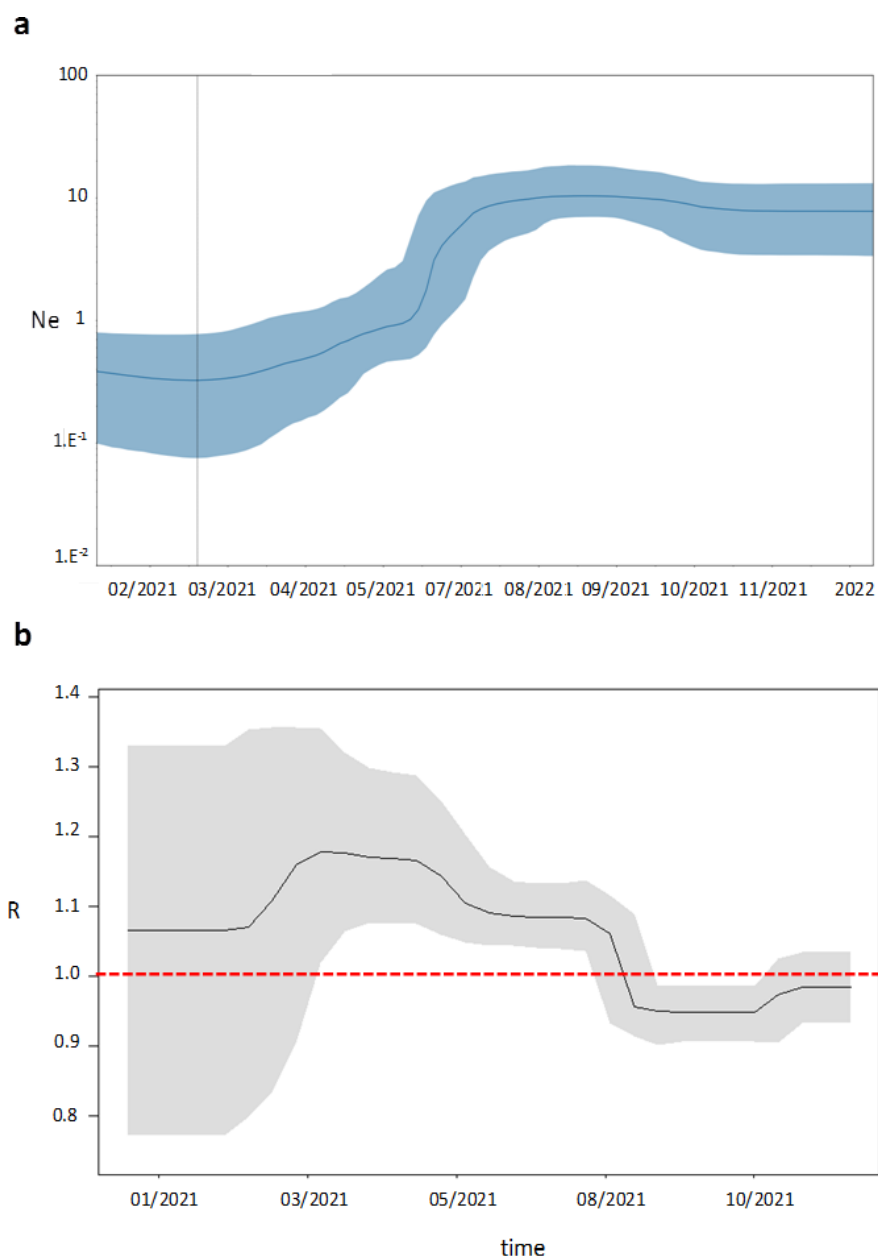
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