

## Brief Report

## Circulating SARS-CoV-2 variants in Italy, October 2020-March 2021

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**Abstract:** A growing number of emerging SARS-CoV-2 variants is being identified worldwide, potentially impacting the effectiveness of current vaccines. We report the data obtained in several Italian regions involved in the SARS-CoV-2 variant monitoring from the beginning of the epidemic and spanning the period from October 2020 to March 2021.

**Keywords:** SARS-CoV-2 virus, complete genome sequencing, COVID-19 RT-PCR testing, Spike protein, viral variants.

Starting from April 2020 when the Cluster 5 [1] variant was first described, multiple SARS-CoV-2 variants have emerged in different parts of the world. The B.1.1.7 lineage was first identified in the UK from a sample obtained in late September 2020 [2, 3], B.1.351 was identified in October 2020 in South Africa [4], and P.1 was identified in Brazil in December 2020 [5]. These variant strains show multiple changes (deletions and substitutions) in the spike protein (9 in B.1.1.7, 10 in B.1.351, and 12 in P.1) compared with the reference genome Wuhan-Hu-1 sequence (EPI\_ISL\_406800), some of which affect the receptor-binding domain (RBD) region. The major issue with these variants is their potential to outcompete and rapidly replace formerly prevalent lineages, first in the areas where they likely emerged and subsequently spread in many other countries [6-8]. In-

creased SARS-CoV-2 diversity raises the concern of escape from pre-existing immunity, elicited either by previous infection or by vaccination.

Here, we report data from several Italian centers located in Campania, Lazio, Lombardy, Liguria, Marche, Piedmont, Tuscany, Sicily and Umbria, involved in the SARS-CoV-2 variant monitoring from the beginning of the epidemic and spanning the period from October 2020 to March 2021.

Globally, we analysed data from 3,744 samples obtained by different techniques: RT-PCR variant screening assays (n=2,095), spike Sanger or next generation sequencing (n=649) and whole genome sequencing (WGS; n=1,000). Table 1 shows the data for each month.

Table 1. Data stratified according to months and methodologies.

Month	WGS* (n=1000)	Spike (n=649)	Real Time (n=2095)	Total (n=3744)
October 2020	137	20	1	158
November 2020	168	31	0	199
December 2020	139	34	0	173
January 2021	291	86	388	765
February 2021	193	214	827	1234
March 2021	72	264	879	1215

\*WGS. Whole genome sequencing.

The number of samples considered for variant monitoring increased from 4.2% (158/3744) in October to 32% (1198/3744) in March, due to the increasing interest in viral variants at global level. In the study period, the B.1.1.7 variant significantly increased, growing from 3.5% (6/173) in December, to 88.0% (1054/1198) in March ( $p<.001$ ). Particularly, from the second half of December this lineage was already present in Liguria (n=1 on the 18<sup>th</sup>), Campania (n=3, on the 28<sup>th</sup>) and Marche (n=2, on the 31<sup>st</sup>), with only one known case related to return from UK. The most important increase in its prevalence was observed from the second week of January (20/126, 16.0%) to the end of the same month (35/68, 51.5%) reaching 73.7% (171/232) at the end of February. In parallel, the prevalence of previously circulating variants significantly decreased from 99.4% (157/158) to 9.5% (114/3744). The P.1 lineage was first detected in the second half of January in Campania (n=1), Lombardy (n=1) and Umbria (n=2), subsequently setting at around 2% in February (33/1226) and March (24/1198). Only few B.1.351 and B.1.525 cases were identified, never reaching 1% of the total samples analysed, being firstly detected in Liguria at the end of January and in Campania in mid-February, respectively. The Scottish variant (B.1.258) was firstly observed in Campania, Marche and Piedmont in mid-October, 4 cases were reported in November in Campania (n=2) and Piedmont (n=2), thereafter it was only reported in Campania until February reaching a proportion of 18.5% (17/92) of total cases, including its descendant lineages (B.1.258.3, B.1.258.14). In mid-March, two cases of the New York lineage B.1.526 were identified in Marche. Figure 1 shows the main viral variants observed overtime. Concerning other variants, the main circulating lineage was B.1.177 that represented, together with its descendents (B.1.177.4, B.1.177.8, B.1.177.14, B.1.177.15, B.1.177.52, B.1.177.53, B.1.177.75), more than half of cases (50.4%, 54.3%, 66.1%, 71.4% and 59.8% from October to February). Despite limited data regarding lineage assignment in March (n=28), we observed a 27% prevalence of B.1 and B.1.177 lineages (Figure 1, Panel B). Clade assignment was available for a larger number of strains compared to lineage because these data was obtained also by spike sequencing highlighting the clear predominance of 20E(EU1) ranging from 43.2% (68/157) to 67.7% (189/279). Some noteworthy mutations were observed in different lineages: N439K in one lineage A and B.1, E484K in three B.1.177 and A222V+E484K+N501Y in clade 20E.

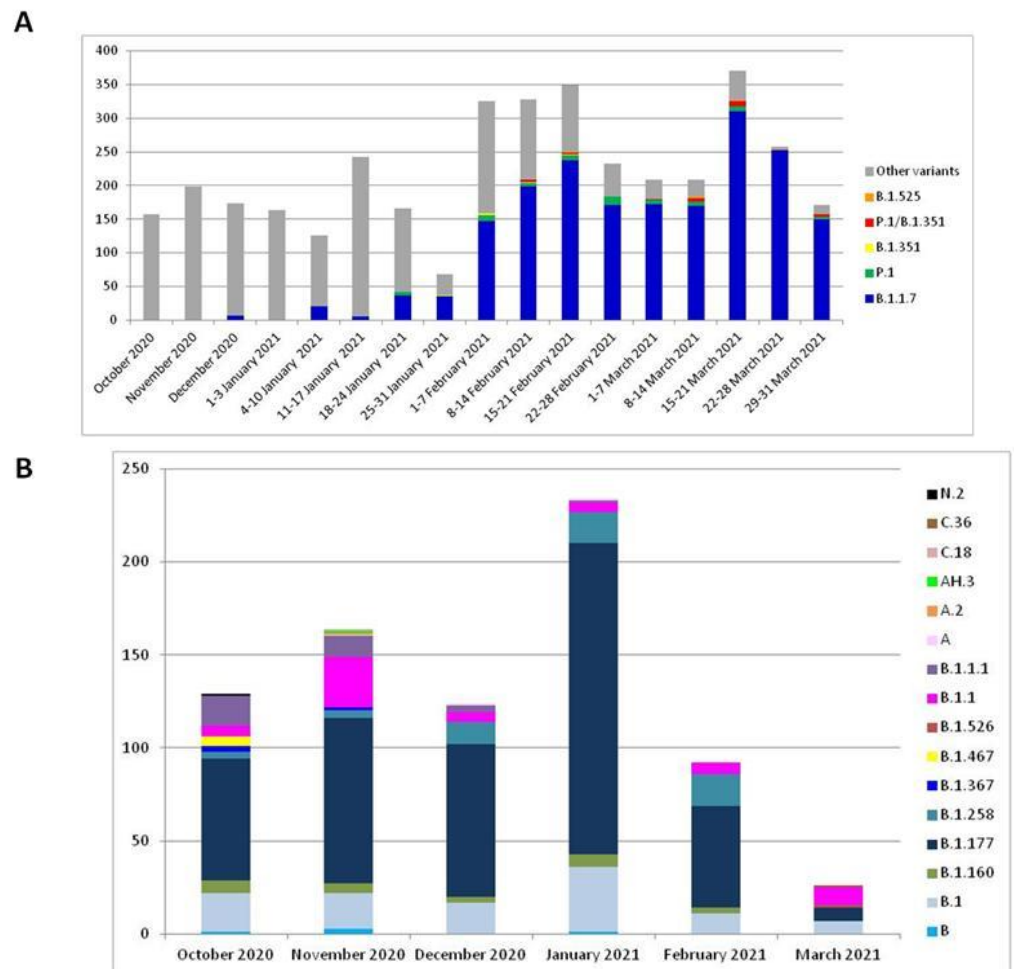


Figure 1. SARS-CoV-2 viral variants observed overtime in Italy. Panel A highlights the variants of concern; panel B shows all other circulating lineages.

This study provides insights into the rapid change in the prevalence of SARS-CoV-2 variants over six months in Italy. Interestingly, we observed the first entry of B.1.1.7 in Lombardy in October, earlier than reported by other Italian studies [9,10] but in line with the identification of first retrospective data in UK on 20 September [11]. This data was obtained from RT-PCR and unfortunately could not be confirmed with WGS because of high cycle threshold of such sample. In addition to known variants of concern, we documented other minor variants that could be early warnings of upcoming changes. Continuous monitoring of all variants is mandatory to comprehensively investigate and keep track of virus evolution, particularly along with expanding vaccination still based on original strains that have been largely substituted by novel variants.

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