Research Letter

Epidemiological, clinical and genomic snapshot of the first 100 B.1.1.7 SARS-CoV-2 cases in Madrid

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A new SARS-CoV-2 variant, B.1.1.7, emerged in September in the UK, and is responsible for 76.6% of COVID-19 cases.1 This variant has also been reported in another 45 countries, 17 of them European.2,3 B.1.1.7 is considered to have higher transmissibility.4 It carries an unusually high number of specific mutations/deletions, 18, mostly non-synonymous and eight concentrate in the S gene,5 including several which might have relevant functional roles. The 69/70 deletion may be associated to immune response evasion6 and the N501Y substitution increases the affinity to the ACE2 receptor.7 These findings have raised the alarm of having to face a new variant with the potential to accelerate the spread of the pandemic. A recent report finds a realistic possibility that B.1.1.7 is associated with an increased risk of death.8

More data on the behaviour of the B.1.1.7 variant once imported are needed to further understand its potential risks at a wider context. The aim of this study was to analyse the first 106 incident COVID-19 cases in Madrid (650 000 inhabitants covered by our tertiary hospital) infected by the B.1.1.7 variant. We based our initial screening on the S gene signal dropout in the TaqPath assay (ThermoFisher, Waltham, USA) caused by the 69/70 deletion.9 This screening criterion, based on the S signal dropout, has been accepted as a suitable proxy to identify the B.1.1.7 variant, with 100% specificity over the past weeks in the UK.1

Our first B.1.1.7 case was diagnosed at week 52 (21 December 2020). The patient had a previous positive RT-PCR on December 15. In the month preceding this first B.1.1.7 case, the lineage B.1.177 represented 91% of the SARS-CoV-2 strains in our population and the remaining sequences were distributed among minority lineages (B.2, B.1.1.305, B.1.1.130, B.1.1.29, A.2, B.1.1.1 and B.1.88). Since December 15, and until February 1 (week 2, 2021), we diagnosed 106 COVID-19 cases candidates to be infected by B.1.1.7, and at the time of the writing of this manuscript; B.1.1.7 represents 62% of the total newly diagnosed COVID-19 cases (average value for week 10 [2021]).

Among the B.1.1.7 cases in our study, 51.9% were women and the average age of all study subjects was 40 years (range
A telephonic survey was performed to collect epidemiological and clinical information from 97 cases (approved by the ethical research committee of Gregorio Marañón Hospital; REF: MICRO.HGUGM.2020-042). Nine cases were asymptomatic, 79 had soft/moderate symptoms, and 14 were hospitalized (10 presented pneumonia, four were admitted to the intensive care unit and two deaths). Most cases (77.3%) had no comorbidities (Table 1). Regarding the potential links to the UK, six cases (6.19%) had recently arrived from the UK and all had been diagnosed at the end of December; 12 cases (12.37%) had had contact with people coming from the UK; the remaining 79 cases (81.44%) did not have any direct or indirect links with the UK, indicating a wide community transmission. Moreover, the first case in our study was among those without links to the UK; the partner of this patient, diagnosed the same day, worked in the district tribunal and was in high contact with the general public. This suggests that B.1.1.7 community transmission in Madrid may have started before December 15. The average number of additional cases (either preceding or subsequent) communicated by each B.1.1.7 carrier possibly linked to them was 3.07 [range 0–10].

Table 1. demographic and clinical features for the B.1.1.7 cases.

| Demographics          | Average | Range |
|-----------------------|---------|-------|
| Age                    | 39.63   | 1–92  |
| Total Percentage (%)   |         |       |
| Sex                    |         |       |
| Male                   | 51      | 48.11 |
| Female                 | 55      | 51.88 |
| COVID-19 symptoms      |         |       |
| Bilateral pneumonia    | 10      | 10.31 |
| Dyspnea                | 15      | 15.46 |
| Asthenia               | 28      | 28.87 |
| Fever                  | 23      | 23.71 |
| General unrest         | 18      | 18.55 |
| Diarrhoea              | 6       | 6.19  |
| Cephalgia              | 20      | 20.61 |
| Anosmia                | 16      | 16.50 |
| Cough                  | 18      | 18.55 |
| Rhinorrhea             | 10      | 10.31 |
| Myalgias               | 16      | 16.50 |
| Severity               |         |       |
| Asymptomatic           | 9       | 9.28  |
| Mild                   | 66      | 68.04 |
| Intermediate           | 13      | 13.40 |
| Severe                 | 9       | 9.28  |
| Health care requirement|         |       |
| Emergency              | 24      | 24.74 |
| Hospital admission     | 14      | 14.43 |
| ICU                    | 4       | 4.12  |
| Antecedents            |         |       |
| None of interest       | 75      | 77.32 |
| High blood pressure    | 6       | 6.18  |
| COPD                   | 1       | 1.03  |
| Asthma                 | 5       | 5.15  |
| Diabetes               | 2       | 2.06  |
| Ictus                  | 1       | 1.03  |
| Overweight/obesity     | 2       | 2.06  |
| Heart disease          | 2       | 2.06  |
| Autoimmune             | 1       | 1.03  |
| Oncological            | 2       | 2.06  |

We present valuable clinical and epidemiological data on the first 106 cases diagnosed with the new SARS-CoV-2 B.1.1.7 variant in Madrid that will help understand its dynamics once introduced into a new population. In our context, 16.3% of all newly diagnosed cases carry the B.1.1.7 variant 1 month after its first detection and most developed non-severe disease. The great
Figure 1. (a) Phylogenetic tree including the 88 sequences from specimens with the B.1.1.7 variant. Clustered cases are indicated with a colour code. Cases with epidemiological relationships are shown with a graphic link between them. The ring surrounding the tree indicates whether the cases had travelled from the UK, showed links to the UK or had no links to the UK. All Madrid sequences were uploaded to GISAID. Supplementary Methods. (b) Integration of the Madrid B.1.1.7 sequences from this study (circles sizes are proportional to the number of cases sharing each genotype) with a random subselection of 394 B.1.1.7 sequences among the 25624 sequences deposited from the UK in GISAID between 1 December 2020 and 28 January 2021.
majority of the cases infected with B.1.1.7, including the first identified case, had no direct or indirect links to the UK. Thus, even from the start, the increase of this variant in our context is mostly due to post-importation transmission events within the community rather than further imports. One of the transmission clusters identified by genomic viral analysis was very large and alerts on the need of more efficient control measures to minimize a rapid transmission of the B.1.1.7 variant.

Supplementary data
Supplementary data are available at JTM online.

Author’s contributions
Laboratory experimental tasks: P.C., M.H., V.M.D.C. Bioinformatic analysis: P.J.S.C., S.B.S., L.P.L., M.G.L. Sequencing: J.S.G. Microbiological data and databases: L.A. Clinical/epidemiological research: A.E. Data analysis: D.G.V., L.P.L. Analytical strategies, protocols, pipelines and funding: I.C., F.G.C. MS writing and revisions: D.G.V., L.P.L., P.M.

Conflict of interest
The authors declare no conflict of interest.

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