In 1996–97, the last dengue virus serotype 2 (DENV-2) outbreak occurred in French Polynesia. In February 2019, DENV-2 infection was detected in a traveller from New Caledonia. In March, autochthonous DENV-2 infection was diagnosed in two residents. A DENV-2 outbreak was declared on 10 April with 106 cases as at 24 June. Most of the population is not immune to DENV-2; a large epidemic could occur with risk of imported cases in mainland France.

From March 2019 onwards, autochthonous dengue serotype 2 (DENV-2) infections have been detected in French Polynesia, an overseas collectivity of France in the South Pacific comprising ca 280,000 inhabitants and over 100 islands. On 10 April, French Polynesia public health authorities declared the beginning of the outbreak, 22 years after the last reported DENV-2 outbreak in 1996–97. Here, we describe the factors that could affect the magnitude of the outbreak and facilitate the spread of DENV-2 from French Polynesia to endemic and non-endemic areas, including European countries.

Detection of imported and autochthonous cases of DENV-2 infections in French Polynesia in 2019

On 10 February 2019, a DENV-2 infection was diagnosed on Tahiti island (Society archipelago, French Polynesia) in a traveller from New Caledonia (French territory in the south-west Pacific), where a DENV-2 outbreak was ongoing [1]. The traveller arrived 1 day before symptom onset. Two days after the case was confirmed, vector control measures (insecticide spraying and destruction of breeding sites) were implemented at all locations that were visited by the case in Tahiti. In addition, the French Polynesia public health authorities enhanced surveillance to quickly detect any subsequent DENV-2 cases. No additional case was detected until two inhabitants of the same neighbourhood in Papeete (Tahiti) tested positive for DENV-2 on 18 and 29 March, respectively; neither case had travelled abroad within 2 weeks.

On 10 April 2019, the public health authorities declared an outbreak as two separate clusters of DENV-2 cases, with no geographical or epidemiological link, had been confirmed on Tahiti island. As at 24 June, 102 DENV-2 cases were reported on Tahiti island; one case had just returned from Moorea island (Society archipelago) where the infection might have occurred; two other cases were imported from New Caledonia in February and April. DENV-2 infection was also detected in two residents from Nuku Hiva island (Marquesas archipelago) and two from Bora Bora island (Society archipelago) (Figure 1).

Between 10 February and 24 June 2019, fourplex real-time RT-PCR assay with serotype-specific primers and probes [2] was used to confirm DENV-2 infection in patients with symptoms suggestive of dengue (sudden high fever with headache, arthralgia and/or myalgia) in French Polynesia. Cases were defined as described in box.
patients tested positive for DENV-2 and 225 patients tested positive for DENV-1. Among the patients diagnosed with DENV-2 or DENV-1 infection, 69% and 42% were aged less than 20 years, 43% and 57% were males, and 8% and 6% were hospitalised, respectively; no severe symptoms were reported in any case. Demographic and clinical characteristics of the DENV-2 and DENV-1 cases are shown in Table 2.

**Phylogenetic analysis**

The complete envelope gene of DENV-2 strains isolated in 2019 from five inhabitants of Tahiti, including three locally acquired infections (GenBank accession numbers: MK905539, MK905540, and MK905541) and two imported cases from New Caledonia (MK905538 and MK905542) were sequenced as previously described [3].

Phylogenetic analysis showed that all DENV-2 strains collected in Tahiti belonged to the Cosmopolitan genotype and were more closely related to other strains isolated in French Polynesia in 2017 and 2018 (KY782125, KY782126, KY782127, MH807159 and MH807160), with percentages of homology ranging from 99.5% to 100% (Figure 2). The French Polynesia strains belonged to the same cluster as DENV-2 strains isolated in Tuvalu in 2014 (MG967223) and in Fiji during 2014–17 (KM279392, MG967229, and MG967231), with percentages of homology of more than 99.4%. Strains isolated in other Pacific islands such as the Solomon Islands were also closely related to the French Polynesia strains.
Islands in 2016 (KY495808) and the American Samoa in 2017 (MK244393) were more diverse with nt identity at 95.6% and 95.5%, respectively. The cluster including strains from French Polynesia, Tuvalu and Fiji and the cluster including strains from other Pacific islands were genetically closer to DENV-2 strains from Philippines (JN568265) and Australia (KY495814), respectively.

Discussion

In French Polynesia, the first outbreak of known DENV serotype occurred in 1944 [4]. Each of the four serotypes of DENV has caused several monotypic epidemics until 2013 [5] when an outbreak involving two different serotypes (DENV-1 and DENV-3) was reported [6], concomitantly to the transmission of Zika virus during 2013–14 [7] and then chikungunya virus during 2014–15 [8]. While DENV-3 stopped being detected in December 2014 [5], DENV-1 transmission was still reported as at 24 June 2019 [9]. During the period of monotypic endemic transmission of DENV-1, DENV-2 infection was detected in February 2017 in Tahiti from three travellers from Vanuatu participating in a soccer contest [3] and then in June 2018 in two residents of Raiatea island (Society archipelago) that had not recently travelled abroad [9]. Before the detection of those cases, the last DENV-2 epidemic had occurred in 1996–97 and autochthonous DENV-2 infection was reported for the last time in December 2000 [5].

The last DENV-2 outbreak in French Polynesia was reported more than 20 years ago. It has been shown that this time period was necessary for this serotype to re-emerge, as a sufficient proportion of the non-immune hosts has increased [3, 6]. Serosurveys conducted in 2014 and 2018 in schoolchildren from Tahiti aged between 6 and 16 years found that none of them were immune against DENV-2, as they were all born after the last outbreak [12, 13]. Serosurveys conducted in the general population from the five archipelagos in

<table>
<thead>
<tr>
<th>Characteristics</th>
<th>DENV-2</th>
<th>DENV-1</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n = 106</td>
<td>%</td>
</tr>
<tr>
<td>Age group (years)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt; 20</td>
<td>73</td>
<td>69</td>
</tr>
<tr>
<td>≥ 20</td>
<td>33</td>
<td>31</td>
</tr>
<tr>
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<td></td>
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</tr>
<tr>
<td>Male</td>
<td>46</td>
<td>43</td>
</tr>
<tr>
<td>Female</td>
<td>60</td>
<td>57</td>
</tr>
<tr>
<td>Outcome</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Hospitalisation</td>
<td>8</td>
<td>8</td>
</tr>
<tr>
<td>Severe casesa</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

DENV-1: dengue virus serotype 1; DENV-2: dengue virus serotype 2.

a Severe cases are defined as patients with at least one of the following symptoms: severe plasma leakage, severe haemorrhage and/or severe organ impairment.

| Table |
|-----------------|--------|--------|
| Demographical and clinical characteristics of the DENV-2 (n=106) and DENV-1 (n=225) cases reported, French Polynesia, 10 February–24 June 2019 |

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levels of population immunity against DENV-2 (51% and 18%, respectively) were lower than for the other serotypes (respectively 88% and 80% for DENV-1, 67% and 55% for DENV-3, and 61% and 42% for DENV-4) [12]. Altogether, those findings support the existence of a high risk for a large DENV-2 outbreak to occur in French Polynesia.

Despite multiple importations and autochthonous transmission of DENV-2 detected in French Polynesia during 2017–18, no infection was reported until 2019. Concomitant circulation of DENV-1 could have played a negative role in the transmission dynamics of DENV-2, as there may be competition between different serotypes for transmission by the mosquito host [14]. Another possible explanation for the absence of
transmission of DENV-2 was a drier and colder season between April and October, which might have had a negative impact on mosquito density and vectorial capacity for transmission of the virus [15].

Despite the implementation of vector control, surveillance and prevention measures by the French Polynesia public health authorities, viral transmission could not be stopped and cases were reported on other islands shortly after the detection of the first imported and autochthonous DENV-2 infection in Tahiti. Given the frequency of air and sea links between Tahiti and the other islands, it is possible that DENV-2 could rapidly spread across French Polynesia. In addition, due to the frequent air travel exchanges between French Polynesia and non-endemic continental countries e.g. mainland France, DENV-2 could be introduced into these countries and cause outbreaks during the summer, which is the most favourable season for mosquito-borne transmission in temperate countries. For example, a DENV-1 outbreak following an imported case from French Polynesia was reported in South of France August–September 2015 [16]. Consequently, countries where competent vectors are prevalent need to be alerted to the risk of importation of DENV-2 from French Polynesia.

Conflict of interest
None declared.

Authors’ contributions
Maite Aubry and Van-Mai Cao-Lormeau wrote the manuscript. Elsa Dumas-Chastang was responsible for laboratory testing of blood samples from dengue suspected patients at the Institut Louis Malarède. Tuteraríi Paoaafaité performed viral genome sequencing, and Anita Teissier conducted phylogenetic analyses. Mapotoeke Mihiau and Marine Giard conducted the investigations of DENV-2 cases. All co-authors critically reviewed the manuscript.

References

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