Correspondence

No Evidence of Marseillevirus-like Virus Presence in Blood Donors and Recipients of Multiple Blood Transfusions

To the Editor—By using high-throughput sequencing (HTS), Popgeorgiev et al [1] reported the presence of giant blood Marseillevirus (GBM), a newly identified giant virus belonging to the proposed Marseilleviridae family [2–4] in a pool of samples collected from asymptomatic blood donors from southern France. The presence of GBM DNA was confirmed by a specific polymerase chain reaction (PCR) in 1 of 10 sera included in the pool submitted for HTS analysis and in 2 of 20 additional tested blood donations. Since these preliminary results suggested that GMB infection may be common in healthy blood donors, the same group investigated the prevalence of the virus in 174 blood donors and 22 patients from the French Mediterranean basin who had thalassemia and received multiple blood transfusions. GMB DNA was found in 4% of blood donations and in 9.1% of patients with thalassemia, and immunoglobulin G antibodies were detected in 12.6% of blood donors and 22.7% of patients with thalassemia, suggesting that this virus could be transmitted by transfusion [5].

To further study the risk of GMB exposure through transfusion, we investigated 339 subjects distributed in 3 groups. The first group included 50 patients who had undergone multiple transfusions (30 males and 20 females; median age, 33.5 years [range, 20–88 years]); had thalassemia major, sickle cell, or malignant diseases; had received >100 red blood cell units over their life; and were being prospectively followed at Tenon Hospital in Paris, France. For each patient, a sample collected at the end of the follow-up period (between 2008 and 2013) was analyzed. The second group included healthy blood donors, from whom 100 plasma specimens were collected in the Paris area in 2008 (information on sex and age were not available) and 50 plasma specimens were collected at the National Blood Center of Ouagadougou, Burkina Faso, in 2007 (29 males and 21 females; median age, 24 years [range, 18–56 years]). The third group included deferred blood donors from southern France who were tested positive for 1 viral marker: 39 were positive for human immunodeficiency virus (31 males and 8 females; median age, 35 years [range, 18–59 years]) and donated blood between 2000 and 2013, 50 were positive for hepatitis B virus (HBV; 41 males and 9 females; median age, 38 years [range, 18–66 years]) and donated blood between 2010 and 2013, and 50 were positive for hepatitis C virus (31 males and 19 females; median age, 45.5 years [range, 18–63 years]) and donated blood between 2010 and 2013.

GMB PCR was performed following the protocol developed by Popgeorgiev et al [5]. Water samples subjected to the same extraction process as clinical samples were added in each run as negative controls, and, because no human positive sample was available, Acanthamoeba polyphaga Marseillevirus DNA, obtained from an amoebal coculture (kindly provided by C. Desnues, Marseille, France), was used as positive control.

None of the 339 studied samples tested positive for Marseillevirus-like virus DNA. We excluded technical failures by excluding the presence of PCR inhibitors through the successful amplification of the HBV S gene in HBV-positive samples [6] and by improving PCR sensitivity by using several annealing temperatures (from 53°C to 60°C). The discrepancy between our results and those reported by Popgeorgiev et al could have been explained by prevalence variation according to region. However, none of the 139 samples (41%) that originated from the French Mediterranean basin, where GBM was originally discovered, were positive. Thus, our findings suggest that GBM might not be a novel agent infecting humans but, rather, may be a viral contaminant from laboratory environment or kit reagents, as previously reported for other viruses [7, 8]. Even though the contamination of a specific lot cannot be totally excluded, kit reagents could reasonably be assumed as not responsible for positive results, since we did not observe specific Marseillevirus amplification in negative extraction controls. Laboratory contamination should be carefully considered, especially when extensive investigations are conducted with viruses initially discovered in environmental samples. The human GBM infection could be supported by the presence of detectable virus-specific immunoglobulin G [5], but in the absence of a confirmatory assay, antibody cross-reactivity cannot be ruled out, as previously reported in several studies [7, 9]. Unfortunately, in the absence of validated immunoassays, the GBM seroprevalence could not be investigated in the present study.

In conclusion, our data show no evidence of Marseillevirus-like virus circulation in blood donors and recipients of multiple transfusions from France and Burkina Faso. Further investigations are required to confirm the reality of Marseillevirus infection in humans. More generally, this emphasizes the rigorous approach needed to establish the validity...
of new viral genomes discovered by high-throughput sequencing.

**Notes**

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