In conclusion, we have shown that the PVL-encoding phage has entered distinct staphylococcal lineages, although its prevalence differs per clonal group. PVL is associated with skin and soft tissue infections but not with bacteremia, which suggests that PVL is not likely to be involved in the pathogenesis of bacteremia. Infections caused by PVL-positive Staphylococcus aureus strains have been documented since the 1930s. Expansion and increased incidence of such infections, however, are more recent, and further epidemiologic studies for tracking this phenomenon are still warranted.

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Small Anellovirus in Hepatitis C Patients and Healthy Controls

To the Editor: Torquetenovirus (TTV) and torquetenominivirus (TTMV) are characterized by a small, negative-sense, circular, single-stranded DNA genome and by an extraordinary ability to produce chronic plasma viremia. Indeed, >80% of humans harbor variably high viral loads of TTV, TTMV, or both, in plasma, regardless of geographic provenance, age, sex, and health conditions (1). Currently, TTV and TTMV are classified as distinct species in the floating (although closely linked to the family Circoviridae) genus Anellovirus, but their extreme genetic heterogeneity and some distinctive features in genomic organization have led some to suggest that they should be classified as an independent family (2,3). Most recently, after examining serum specimens from patients with symptoms of an acute viral infection by using DNase sequence-independent single-primer amplification, Jones et al. (4) identified, among other viruses, 2 novel TTV- and TTMV-like agents. Because of their even smaller genomes (~2.4 and 2.6 kb vs. 3.6–3.8 kb for TTV and 2.8–2.9 kb for TTMV), these agents were named small anelloviruses (SAVs).

Because tissue culture and serologic methods are not yet available, diagnosis of anellovirus infection relies exclusively on viral DNA detection. We tested 55 Italian hepatitis C patients (mean age 56 ± 14 years, male/female ratio 30/25, 53 TTV positive) and, for comparison, 35 healthy donors (mean age 36 ± 12 years, male/female ratio 17/18, 33 TTV positive) for SAV in plasma by using the polymerase chain reaction (PCR) primers described by Jones et al. (4), followed by direct ampiclon
sequencing. To increase assay sensitivity, a heminested PCR format was adopted that used a sense primer designed in a segment of the untranslated region that is highly conserved among all anelloviruses (5'-TCAAGGGGCA ATTCCGGGCT-3'). We found 5 positive results among the hepatitis C patients (9.1%, all of whom were TTV positive) and 3 positive results among healthy controls (8.6%); and all were confirmed by sequence data.

The amino acid sequences inferred from the coding segment of the amplicon of SAV in this study and the corresponding sequences of the 10 SAV in GenBank at the time of this writing were then aligned with representative TTV and TTMV sequences (online Appendix Figure 1, available from http://www.cdc.gov/ncidod/EID/vol12no07/06-0234-G1.htm). This method allowed us to identify the motif WX'H5H2CX8C2H, which is highly characteristic of the open reading frame 2 (ORF2) of anelloviruses (5), in all SAVs. SAV sequences, as well as a large number of TTVs and all TTMVs, were then used to construct a phylogenetic tree and to calculate the extent of genetic divergence within SAV, TTV, and TTMV. Although a precise phylogenetic description will require the analysis of full-length ORF2, the SAV sequences clustered quite separately from those of TTV and TTMV, and the extent of divergence observed among SAV was huge and in the same range as among TTV or TTMV. Furthermore, SAVs obtained from hepatitis C patients and healthy participants were intermingled (online Appendix Figure 2, available from http://www.cdc.gov/ncidod/EID/vol12no07/06-0234-G2.htm).

While this study was under way, Biagini et al. reported a 12% prevalence of SAV viremia in French blood donors (6). Our results confirm the high prevalence of SAV viremia in healthy persons and extend the finding to hepatitis C patients. Our data, combined with those of Biagini et al., indicate that, since SAV clusters separately from previously identified anelloviruses, it should be considered a distinct species (or possibly genus). This would increase the already high genetic diversity of anelloviruses, further arguing for the appropriateness of creating a separate viral family.

Because the clinical and viral parameters of hepatitis C in SAV-positive patients were not significantly different from those in the SAV-negative patients (data not shown), our results suggest that, similar to TTV (7), SAV has little or no effect on the course of hepatitis C. Although anelloviruses have not yet been definitively linked to any specific disease, evidence is growing that they might be involved in acute respiratory diseases in children (8,9). Furthermore, florid TTV replication in the respiratory tract correlated with severity of lung impairment in children with asthma (10). A precise appreciation of the wide range of viruses classified within the anelloviruses is a prerequisite to understanding such disease associations and the disease-inducing potential of these viruses in general.

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