Counotte et al. systemically reviewed all available evidence on the risk for sexual transmission of Zika virus (5). Data from case reports, case series, cohort studies, in vitro work, and animal studies indicate that the infectious period for sexual transmission of Zika virus is considerably shorter than the period during which viral RNA can be detected in semen. As a result, the World Health Organization now recommends male travelers with potential Zika virus exposure delay conception for ≥3 months rather than ≥6 months (6).

In our case, Zika virus RNA might have persisted in semen because of failed immune clearance secondary to the patient’s MRH or his immunosuppressive drug treatment. However, when advising returning male travelers in couples planning pregnancy, clinicians should be aware that Zika virus RNA shedding in semen might be intermittent and persist for longer in patients with immunosuppression.

Acknowledgments
We thank Tim Brooks, Steve Pullen, Azim Ansari, Megan MacDiarmid, and Paul Kleenerman for their valuable contributions.

About the Author
Dr. Petridou is an infectious diseases registrar working at the Rare and Imported Pathogens Laboratory at Porton Down, Salisbury, United Kingdom. Her research interest is in Zika virus infection and she previously worked as the Zika virus registrar at Porton Down.

References

Address for correspondence: Christina Petridou or Emma Aarons, Rare and Imported Pathogens Laboratory, Public Health England Porton, Salisbury, UK; email: christina.petridou@nhs.net or emma.aarons@phe.gov.uk

No Evidence for Role of Cutavirus in Malignant Melanoma

Ulrike Wieland, Steffi Silling, Martin Hufbauer, Cornelia Mauch, Paola Zigrino, Frank Oellig, Alexander Kreuter, Baki Akgül

Author affiliations: University of Cologne, Cologne, Germany (U. Wieland, S. Silling, M. Hufbauer, C. Mauch, P. Zigrino, B. Akgül); Institute of Pathology, Mülheim an der Ruhr, Germany (F. Oellig); Helios St. Elisabeth Hospital Oberhausen, University Witten/Herdecke, Witten, Germany (A. Kreuter)

DOI: https://doi.org/10.3201/eid2508.190096

Cutavirus was previously found in cutaneous melanoma. We detected cutavirus DNA in only 2/185 melanoma biopsies and in 0/52 melanoma metastases from patients in Germany. Viral DNA was localized in the upper epidermal layers. Swab specimens from healthy skin were cutavirus positive for 3.8% (9/237) of immunocompetent and 17.1% (35/205) of HIV-positive men.

Cutavirus, a novel human protoparvovirus with linear single-stranded DNA, has been detected in fecal samples from children with diarrhea and in cutaneous T-cell lymphomas (CTCL) (1,2). Recently, Mollerup et al. reported the identification of cutavirus in 1 of 10 cutaneous malignant melanomas using viral enrichment methods with high-throughput sequencing and real-time PCR (3). This discovery raised questions concerning tropism and pathogenicity of cutavirus in human skin. We performed a retrospective study to determine cutavirus DNA prevalence and viral load in a large collection of formalin-fixed paraffin-embedded tissue biopsy specimens of malignant melanomas and in forehead swabs of healthy skin of immunocompetent and HIV-positive persons in Germany.

We used 185 cutaneous malignant melanoma biopsy specimens from 179 patients and 52 melanoma metastases from 42 patients from Germany for analyses with cutavirus real-time PCR (Appendix, http://wwwnc.cdc.gov/EID/article/25/8/19-0096-App1.pdf). We detected cutavirus DNA only in 2 nodular malignant melanomas, located on the abdomen of a 64-year-old man (MM-A) and on the cheek of an 85-year-old woman (MM-B). Viral DNA loads in these biopsies were 0.3 (MM-A) and 2.8 (MM-B) cutavirus DNA copies per 10^6 globin gene copy. None of the 52 analyzed metastases carried cutavirus DNA (Table). The cutavirus PCR results of the 2 melanomas could be confirmed by sequencing and by in situ hybridization. In both melanomas, the cutavirus DNA–specific signals could be
detected only in the superficial layers and on the surface of the skin but not in the tumor cells (Appendix Figure).

To analyze the prevalence of cutavirus on healthy nonlesional skin, we used 442 forehead swab specimens from 237 immunocompetent men and 205 HIV-positive men that were available from a previous study (4) (Appendix). We found cutavirus DNA significantly more frequently on the skin of HIV-positive men than on the skin of healthy controls (17.1% vs. 3.8%; p<0.001 by 2-sided χ² test; Table). Among HIV-positive men, we found a trend for a higher cutavirus prevalence in patients with AIDS compared with those without AIDS (14/59 [23.7%; 95% CI 14.7–36.0] vs. 19/140 [13.6%; 95% CI 8.9–20.2]; p = 0.078 by 2-sided χ² test). The range of viral DNA loads found in the 44 cutavirus-positive skin swabs was 0.004–268.75 (median 0.41; interquartile range [IQR] 0.0–3.57); there was no significant difference between HIV-negative and HIV-positive men (p = 0.389 by Mann-Whitney-U test; Table).

Mollerup et al. found cutavirus DNA in 1 of 10 melanomas from Denmark and suggested investigating the role of cutavirus in cutaneous cancer (3). We detected cutavirus DNA in only 2 of 185 melanoma biopsy specimens and in none of 52 metastases. In situ hybridization localized the viral DNA on the surface of the 2 cutavirus-positive melanomas and not within the malignant cells. Our data therefore argue against an oncogenic role of cutavirus in malignant melanoma.

Väisänen et al. found cutavirus DNA in 2.9% of 136 skin biopsy specimens from 123 organ transplant recipients and in none of 159 skin biopsy specimens of 98 healthy adults (5). In accordance with Väisänen et al., we also found cutavirus more frequently in immunosuppressed patients than in healthy (immunocompetent) adults. Their finding related to healthy adults is in contrast to our results; however, we analyzed not skin biopsy specimens but widespread skin swab specimens covering ≈10 cm² of forehead skin (4). Our cutavirus DNA prevalence data on normal skin of immunocompetent adults (3.8%) are in line with cutavirus IgG seroprevalence rates reported for adults in Finland, Iran, and Kenya (4.2%–5.6%). Lower cutavirus IgG seroprevalence rates have been found in the United States (0%) and Iraq (1%) (6).

A pathogenic role of cutavirus has been investigated in further malignancies. Concerning CTCL, conflicting results have been reported. Phan et al. have found cutavirus DNA in 23.5% (4/17) (1) and Väisänen et al. in 16% (4/25) of CTCL of the mycosis fungoides type (5). Our group recently analyzed 189 biopsies of various cutaneous B- and T-cell lymphoma types and detected cutavirus DNA only in 5.8% of 104 mycosis fungoides biopsy specimens (7). In contrast, Bergallo et al. could not detect cutavirus in 55 CTCL samples (8). The in situ hybridization results of a cutavirus-positive mycosis fungoides sample analyzed by Phan et al. pointed to a localization of the viral DNA in the superficial parts of the lesion (1), similar to the results we show. Therefore, it remains unclear whether cutavirus plays a role in the development of CTCL. Recently, Dickin-son et al. could not detect cutavirus in oropharyngeal and oral cavity squamous cell carcinomas (9).

In summary, our data on cutavirus DNA prevalence and localization argue against an oncogenic role of cutavirus in malignant melanoma. However, oncoletic properties of this virus or viral hit-and-run oncogenesis cannot be excluded (10). Cutavirus seems to be more frequent on healthy skin of immunosuppressed patients than on the skin of immunocompetent persons and could be part of the human skin virome. It is possible that cutavirus is an apathogenic virus shed from human skin.

**Acknowledgments**

We thank Monika Junk for excellent technical assistance. The study was supported by intramural funds of the Faculty of Medicine of the University of Cologne (Koeln Fortune no. 2680-9067-01 and 2680-9159-01) and by the Deutsche Forschungsgemeinschaft (DFG, German Research Foundation, project no. 73111208–SFB 829 [Z4 project to C.M.]).

---

Table. Cutavirus DNA detection and DNA load in cutaneous malignant melanomas, melanoma metastases, and forehead swabs of healthy nonlesional skin from persons in Germany*

<table>
<thead>
<tr>
<th>Sample type</th>
<th>No. samples analyzed</th>
<th>No. cutavirus DNA–positive samples† (%; 95% CI)</th>
<th>Median cutavirus DNA load (IQR)‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>Malignant melanoma tumor biopsies§</td>
<td>185</td>
<td>2 (1.1; 0.3–3.9)</td>
<td>0.30; 2.82#</td>
</tr>
<tr>
<td>Malignant melanoma metastases§**</td>
<td>52</td>
<td>0 (0; 0–6.9)</td>
<td>NA</td>
</tr>
<tr>
<td>Skin swabs of HIV-positive men§</td>
<td>205</td>
<td>35 (17.1; 12.5–22.8)</td>
<td>0.33 (0.66–3.81)</td>
</tr>
<tr>
<td>Skin swabs of healthy male controls§</td>
<td>237</td>
<td>9 (3.8; 2.0–7.1)</td>
<td>2.31 (0.19–11.72)</td>
</tr>
</tbody>
</table>

*Bold type indicates statistical significance. IQR, interquartile range; NA, not applicable.
†All samples were analyzed with CUTA-UPL5 real-time PCR as described in the Appendix (https://wwwnc.cdc.gov/EID/article/25/8/19-0096-App1.pdf).
‡Cutavirus DNA load was determined in all cutavirus DNA–positive samples and was defined as cutavirus DNA copies per β-globin gene copy.
§Details of the biopsies and skin swab specimens are provided in the Appendix.
**For 6 of the melanoma metastases, the primary tumor was also analyzed and was cutavirus DNA negative. The 2 patients with cutavirus DNA–positive melanomas (MM-A and MM-B) did not have metastatic disease.
Intrafamily Transmission of Monkeypox Virus, Central African Republic, 2018

Camille Besombes, Ella Gonofio, Xavier Konamna, Benjamin Selekon, Rebecca Grant, Antoine Gessain, Nicolas Berthet, Jean-Claude Manuguerra, Arnaud Fontanet, Emmanuel Nakouné

About the Author
Dr. Wieland is a professor of virology at the Institute of Virology of the University of Cologne, Germany. Her research interests include diagnosis and epidemiology of viral diseases.

References


Address for correspondence: Ulrike Wieland, University of Cologne Institute of Virology, Fuerst-Pueckler-Str. 56, 50935 Cologne, Germany; email: ulrike.wieland@uni-koeln.de

Intracyter episcopatus System 2019

Monkeypox, a zoonotic disease caused by an Orthopoxvirus, has clinical signs and symptoms in humans similar to smallpox and a case-fatality rate of 10% (1). The specific reservoir species for monkeypox virus remains, to a large extent, unidentified (2). Spillover events of monkeypox have been reported in remote forest areas of Central and West Africa. After zoonotic infection, the virus can be transmitted from person to person (1).

To date, human monkeypox outbreaks in the Central African Republic (CAR) have been small: ≤10 cases, restricted to a family or village. Primary infection in these outbreaks occurred from contact with wild fauna, with secondary transmission among close contacts in the community (3,4) and limited nosocomial transmission (5). Since 2000, the Virology Laboratory of the Institut Pasteur de Bangui (IP Bangui), a regional reference center for monkeypox, has reported 20 monkeypox outbreaks across several regions of CAR, totaling ≈100 cases, particularly in the region of Lobaye (3,4). In 2018 alone, IP Bangui investigated 6 different outbreaks in CAR, indicating a possible increase in frequency of outbreaks (6,7).

On September 27, 2018, a healthcare worker from Zomea Kaka health center in Lobaye reported to IP Bangui about 3 cases of suspected monkeypox in an Aka Pygmy family. A 25-year-old female sought care at the health center, 10 km from her village, for maculopapular rash and lesions. She was afebrile. Her signs and symptoms indicated