

Brief Report

Healthcare Workers Occupational Infection by Monkeypox Virus in Brazil

Richard Steiner Salvato^{1*}, Maria Leticia Rodrigues Ikeda^{2,3}, Regina Bones Barcellos¹, Fernanda Marques Godinho¹, Patrícia Sesterheim¹, Leticia Camiza Bulcão Bitencourt³, Tatiana Schäffer Gregianini⁴, Ana Beatriz Gorini da Veiga⁵, Fernando Rosado Spilki⁶ and Gabriel Luz Wallau⁷

¹ Centro de Desenvolvimento Científico e Tecnológico, Centro Estadual de Vigilância em Saúde, Secretaria Estadual da Saúde do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

² Secretaria Estadual da Saúde do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

³ Programa de Pós-Graduação em Saúde Coletiva, Universidade do Vale do Rio dos Sinos, São Leopoldo, Rio Grande do Sul, Brazil

⁴ Laboratório Central de Saúde Pública, Centro Estadual de Vigilância em Saúde, Secretaria Estadual da Saúde do Rio Grande do Sul, Porto Alegre, Rio Grande do Sul, Brazil

⁵ Universidade Federal de Ciências da Saúde de Porto Alegre, Porto Alegre, Rio Grande do Sul, Brazil

⁶ Laboratório de Microbiologia Molecular, Universidade Feevale, Novo Hamburgo, Rio Grande do Sul, Brazil

⁷ Departamento de Entomologia e Núcleo de Bioinformática, Instituto Aggeu Magalhães (IAM), FI-OCRUZ-PE, Recife, Brazil

*Corresponding author: richard-salvato@saude.rs.gov.br; Phone: +55 51 985767035

Abstract: We performed an epi and molecular characterization of two healthcare workers MPXV occupational infection. Five days after the sampling collection, nurses developed typical MPXV infection symptoms. Infection was confirmed by qPCR and whole genome sequencing. The most likely transmission route was through contact with fomites in the patient belonging/house.

Keywords: monkeypox; infection; healthcare

1. Introduction

The World Health Organization (WHO) confirmed a multi-country Monkeypox virus (MPXV) outbreak in May 2022. As of August 25th, 2022, 45,355 infections were described in 98 countries worldwide, 3,984 of which were detected in Brazil (1). The multi-country outbreak is driven by one of the two known MPXV genotypes, clade II lineage B.1 (<https://nextstrain.org/monkeypox/mpxv>); in Brazil, only lineages A.1, B.1, B.1.1 and B.1.7 have been detected so far (2). Typical symptoms of MPXV infection include fever, intense headache, lymphadenopathy, back pain, myalgia and intense asthenia. Skin eruptions usually begin within 1 to 3 days after the appearance of fever, evolving from macules to papules, vesicles, pustules and finally crusts, as for the end of the lesion (1,3). Although most of the human cases reported in the current outbreak are related to sexual contact with multiple partners, transmission may also occur through alternative routes such as direct contact with rash lesions, scabs, or body fluids from an infected person; touching objects, fabrics (clothing, bedding, or towels), or surfaces that have been used by an infectious patient; and also by contact with respiratory secretions (4,5). Transmission through fomites were reported (6) and, although this is not the major transmission route, it should be considered in MPXV transmission chains. Studies are currently ongoing to understand the epidemiology, sources of infection, and transmission routes of this outbreak. As reported by the WHO, until 22 August 2022, 256 cases have been identified among healthcare workers, but most were infected outside of the working place or are currently under investigation to determine infection source (7). Healthcare-associated infection has been confirmed in only three cases to this date (7). Here we describe a case of Monkeypox virus infection in two nurses after a home specimen collection from a patient in Brazil.

2. The study

A man aged 40 years (Patient) presented with maculopapular lesions in the genital region, adenomegaly, myalgia, fever and chills on July 22, 2022. The patient had not traveled recently but reported intimate contact with multiple partners (four of those were identified and monitored for 14 days without symptoms). On July 29 the Healthcare Workers 1 and 2 (both females, nurses from municipal epidemiological surveillance service) carried out a home visit to specimen collection from the Patient. The healthcare workers wore personal protective equipment: safety glasses, disposable isolation gowns and N95 respirators. Lesion specimen collection was conducted using dry sterile swab procedure plastic gloves. After collection, the material was stored in a sample transport box and the worker sanitized hands with 70% ethanol. Gloves were used only during collection; in the remaining time at the patient's house and during sample box transport, the healthcare workers did not wear gloves, but the remaining personal protective equipment was used until the moment they returned to the workplace to store the collected material. Work materials such as clipboard, sample transport box and table were not sanitized. The healthcare workers did not have contact with other suspected/confirmed cases of monkeypox on the same day or in the following days. Subsequent real-time PCR assay performed on August 2nd confirmed that Patient was infected with MPXV of Clade II (cycle threshold value, Ct of 20).

On August 3rd, five days after specimen collection from Patient, the Healthcare Worker 1 presented a single lesion on the left ring finger with small macula with central umbilication (Figure 1A). No systemic symptoms or other lesions were observed until August 10th, when the patient presented increased hyperemia and appearance of a small papule laterally to the initial lesion. A real-time PCR test from a specimen collected from Healthcare Worker 1 on August 4th confirmed MPXV infection (Ct 22). On August 12th, Worker 1 presented lymphangitis in the left upper limb (Figure 1B) with worsening of hyperemia, and the finger lesion turned into a papule bleeding (Figure 1C). On August 13th she still had lymphangitis and a small papule appeared on her forearm. On August 15th, the fibrin in the lesion increased (Figure 1D) and on August 23rd fibrin reabsorption with crust formation occurred (Figure 1E).

Likewise, on August 3rd, the Healthcare Worker 2 also presented with a papule on the forearm, fever and adenomegaly (Figure 1F). On August 4th MPXV infection was confirmed by real-time PCR (Ct 36). The lesions spread to the face, progressively increasing until August 16th (Figure 1 G-H), but none of the lesions evolved to crust. Lesions began to decline on August 17th (Figure 1I) and on August 24th, Healthcare Worker 2 was released from isolation since all her lesions healed.



Figure 1. Skin lesions presented by the Healthcare Worker 1(A to E) and 2 (F to I) with confirmed monkeypox virus infection.

MPXV was detected in the clinical samples from the three individuals involved in this transmission chain by real-time PCR performed at the Centro Estadual de Vigilância em Saúde- CEVS (the State Center for Health Surveillance of Rio Grande do Sul State Department of Health), according to the protocol proposed by Li et al (2010) (8). Samples from Patient (Ct 20) and Healthcare Worker (Ct 22) were selected for whole genome sequencing due to higher viremia. Whole genome amplification was performed using the protocol established by Chen et al (2022) (9) and sequencing was performed on a Illumina Miseq sequencing platform (Illumina Inc, USA). The sequencing for the two samples was carried out in two distinct runs following the best practices avoiding cross-contamination. A negative control was included in all steps of each run, from the DNA extraction to sequencing. The pipeline implemented in ViralFlow (<https://github.com/dezordi/ViralFlow>) (10) was used to perform genome assembly, variant calling and consensus generation providing the MPXV reference genome MT903345.1. Analyses using the Nextclade tool (<https://clades.nextstrain.org>) showed that the sequenced genomes belong to MPXV Clade IIb sublineage B.1.1 and are 100% identical (Figure 2).

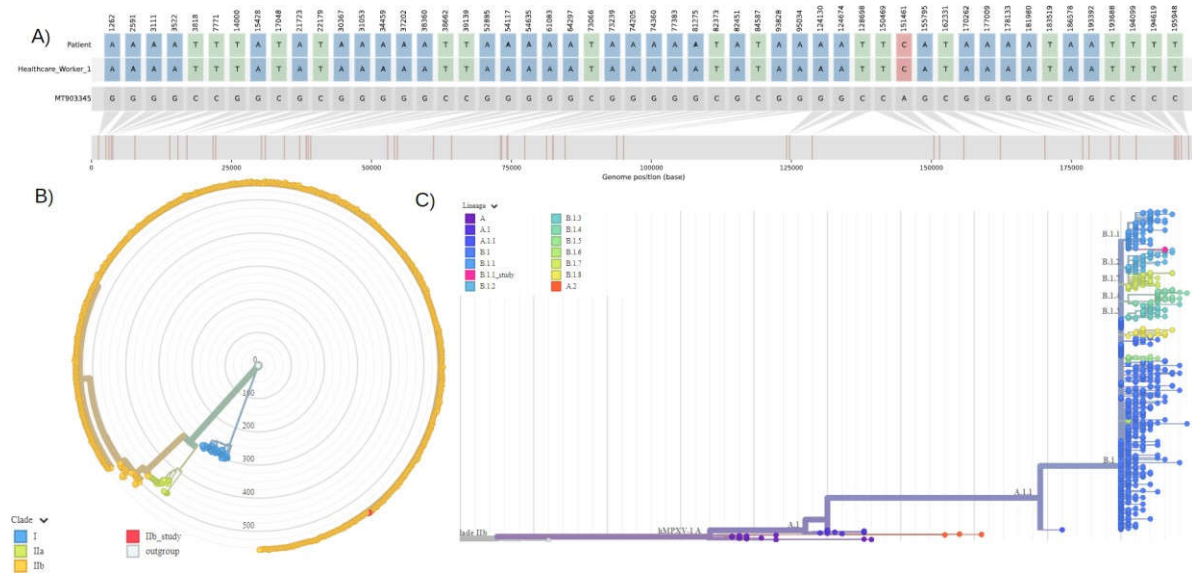


Figure 2. A) Representation of SNPs occurring in the MPXV genome sequences from Patient and Healthcare Worker 1. The summarized representation was made using the Snipit tool (<https://github.com/aineniamh/snipit>). B) Maximum likelihood phylogenetic tree showing the two sequenced genomes in this study along with 919 MPXV sequences from worldwide subsampled by Nextclade. C) Phylogenetic tree focusing on the MPXV Clade IIb.

3. Conclusion

The present report adds further evidence that the MPXV transmission and infection can happen in diverse situations driven by close physical contact with infectious patients and are not confined to certain population groups with particular sexual behavior. The interaction of patients with healthcare workers provides a window of opportunity for MPXV transmission (5). As such, it has been recognized as an important issue in the community transmission containment of MPXV outbreaks (5) along with patient diagnosis and quarantine. There are specific mandatory regulations regarding the use of personal protective equipment and the deployment of vaccination campaigns to protect healthcare workers (11). The present case report highlights the possibility of fomite transmission route of MPXV, suggesting that MPXV virus particles are infectious and resistant to environmental conditions (12). Therefore, extreme caution needs to be taken with general protection equipment and house objects used by suspected cases. Here we proposed specific measures to prevent and/or curtail monkeypox infection through fomites: I) isolate ill persons from uninfected persons; II) practice good hand hygiene and use appropriate personal protective equipment to protect household members if ill or caring for ill persons at home (e.g., a surgical mask, long sleeves and pants, and disposable gloves); III) use an Environmental Protection Agency-registered disinfectant with an emerging viral pathogens claim that is found on EPA's List Q for disinfection of surfaces and IV) vaccination campaigns of high risk groups including healthcare workers.

To the best of our knowledge, this is the first well characterized event of healthcare workers confirmed infection during the 2022 outbreak of international concern.

Funding: This work was supported by Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAPERGS/MS/CNPq 08/2020-PPSUS, Grant process 21/2551-0000059-7) and by Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq, Brazil, Grantprocess 402586/2021-2). G.L.W. is supported by the Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) through their productivity research fellowships (303902/2019-1). ABGV holds a Research Fellowship (PQ2) from Conselho Nacional de Desenvolvimento Científico e Tecnológico (Grant process 306369/2019-2).

Ethics declarations: The authors declare no competing interests. Both healthcare workers signed a consent form for the use of their clinical data, and for the publication of anonymised photographs.

Data Availability Statement: Consensus sequences were deposited in the GISAID under epi accession numbers EPI_ISL_14465517 and EPI_ISL_14676265.

Acknowledgments: We thank Chantal Vogels, Nicholas Chen and Nathan Grubaugh for sharing an aliquot of primers and the protocol of MPXV amplicon-based sequencing. We thank the two nurses who accepted to be included in this report providing detailed clinical information and their images from lesions evolution. The acquisition of Illumina Miseq was funded by the Brazilian Ministry of Health and the Monkeypox diagnosis in Rio Grande do Sul is funded by the State Department of Health. We thank everyone from Rio Grande do Sul State Department of Health working on the Monkeypox outbreak response.

References

1. WHO Health Emergency Dashboard [Internet]. [cited 2022 Aug 26]. Available from: <https://extranet.who.int/public-emergency/#>
2. Khare S, Gurry C, Freitas L, Schultz MB, Bach G, Diallo A, et al. GISAID's Role in Pandemic Response. CCDCW [Internet]. 2021 Dec 3 [cited 2022 Aug 27];3(49):1049–51. Available from: <https://weekly.chinacdc.cn/en/article/doi/10.46234/ccdcw2021.255?viewType=HTML>
3. Monkeypox [Internet]. [cited 2022 Aug 26]. Available from: <https://www.who.int/news-room/fact-sheets/detail/monkeypox>
4. McCollum AM, Damon IK. Human Monkeypox. Clin Infect Dis [Internet]. 2013 Oct 24 [cited 2022 Aug 26];58(2):260–7. Available from: <https://academic.oup.com/cid/article-pdf/58/2/260/961034/cit703.pdf>
5. Vaughan A, Aarons E, Astbury J, Brooks T, Chand M, Flegg P, et al. Human-to-Human Transmission of Monkeypox Virus, United Kingdom, October 2018 - Volume 26, Number 4—April 2020 - Emerging Infectious Diseases journal - CDC. [cited 2022 Aug 26]; Available from: <https://wwwnc.cdc.gov/eid/article/26/4/pdfs/19-1164.pdf>
6. Mauldin MR, McCollum AM, Nakazawa YJ, Mandra A, Whitehouse ER, Davidson W, et al. Exportation of Monkeypox Virus From the African Continent. J Infect Dis [Internet]. 2022 Apr 19;225(8):1367–76. Available from: <http://dx.doi.org/10.1093/infdis/jiaa559>
7. Multi-country outbreak of monkeypox, External situation report #4 - 24 August 2022 [Internet]. [cited 2022 Aug 26]. Available from: <https://www.who.int/publications/m/item/multi-country-outbreak-of-monkeypox--external-situation-report-4-24-august-2022>
8. Li Y, Zhao H, Wilkins K, Hughes C, Damon IK. Real-time PCR assays for the specific detection of monkeypox virus West African and Congo Basin strain DNA. J Virol Methods [Internet]. 2010 Oct;169(1):223–7. Available from: <http://dx.doi.org/10.1016/j.jviromet.2010.07.012>
9. Chen NFG, Gagne L, Doucette M, Smole S, Buzby E, Hall J, et al. Monkeypox virus multiplexed PCR amplicon sequencing (PrimalSeq) V.2 [Internet]. protocols.io. 2022 [cited 2022 Aug 26]. Available from: <https://www.protocols.io/view/monkeypox-virus-multiplexed-pcr-amplicon-sequencing-cd8ds9s6>
10. Dezordi FZ, Neto AM da S, Campos T de L, Jeronimo PMC, Aksenov CF, Almeida SP, et al. ViralFlow: A Versatile Automated Workflow for SARS-CoV-2 Genome Assembly, Lineage Assignment, Mutations and Intrahost Variant Detection. Viruses [Internet]. 2022 Jan 23 [cited 2022 Aug 26];14(2):217. Available from: <https://www.mdpi.com/1999-4915/14/2/217>
11. CDC. Monkeypox in the U.S [Internet]. Centers for Disease Control and Prevention. 2022 [cited 2022 Aug 27]. Available from: <https://www.cdc.gov/poxvirus/monkeypox/clinicians/infection-control-healthcare.html>
12. Factors affecting the likelihood of monkeypox's emergence and spread in the post-smallpox era. Curr Opin Virol [Internet]. 2012 Jun 1 [cited 2022 Aug 26];2(3):335–43. Available from: <http://dx.doi.org/10.1016/j.coviro.2012.02.004>