Epidemiology of the 2022 Mpox Outbreak in the US
Veterans Health Administration

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\textbf{Background:} In May 2022, mpox cases were reported in non-endemic countries, including the United States. We examined mpox infections in the Veterans Health Administration (VHA).

\textbf{Methods:} Mpox diagnostic and whole genome sequencing (WGS) results, demographics, risk factors, hospitalizations, exposures, deaths, pharmacy, and immunization data were obtained from VHA data sources (5/23/22–5/31/23).

\textbf{Results:} Of 1,144 Veterans tested, 251 (21.9\%) were presumptive positive for Non Variola Orthopox (NVO) or NVO and Monkeypox virus (MPXV) confirmed positive. Incidence rate was 7.5 per 100,000 Veterans in care, with highest rate observed in Veterans aged 25-34 (13.83 cases per 100,000). Higher odds of NVO or NVO/MPXV positivity was associated with maleness, non-Hispanic Black race/ethnicity, syphilis or HIV positivity, or genital/rectal sample site, while older age and vaccination with JYNNEOS or vaccinia (smallpox) had lower odds. Among 209 with confirmatory testing, 90.4\% reported intimate contact and/or an epi link; 84.5\% were men who have sex with men (SM); 24.2\% received tecovirimat; and 8.1\% were hospitalized with 1 death.

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Eighty-six sequenced samples had evaluable WGS results. All were clade IIb, representing 10 different lineages from 20 states and the District of Columbia.

**Conclusion:** Mpox affected younger, MSM, non-Hispanic Black and HIV+/syphilis + males among US Veterans. Viral diversity was noted across geographic regions. At risk Veterans would benefit from vaccination and risk reduction strategies for mpox and other STIs.

**Key words:** monkeypox, Veterans, whole genome sequencing

**INTRODUCTION**

Mpox (Monkeypox) is a viral zoonotic disease caused by an orthopoxvirus in the *Poxviridae* family and endemic to western and central Africa. A global outbreak was first recognized in May 2022 with cases reported concurrently in endemic and non-endemic countries, including the United States. The World Health Organization (WHO) declared a Public Health Emergency of International Concern on July 23, 2022, followed by the US Department of Health and Human Services declaring a US Public Health Emergency on August 4, 2022.1,2

There are two recognized genetic clades of the virus, clade I originating in Central Africa and clade II associated with West Africa. Clade I is typically more transmissible and deadlier, while clade II tends to be more self-limited. Endemic spread is generally via animal-human transmission, while non-endemic spread is primarily via human-to-human contact.3,4 With human-to-human transmission, virus enters through broken skin, mucosal surfaces, or possibly via the respiratory tract.3 Monkeypox virus (MPXV) can also be transmitted via contaminated objects (such as clothing) or sharps injuries in healthcare settings or community settings (such as tattoo parlors). Mpox is most often characterized by a self-limited illness, however some cases may lead to severe illness and death. Patients typically present 1-21 days following exposure with symptoms that may include: rash, enlarged lymph nodes, fever, sore throat, headache, muscle aches, back pain, fatigue. Rash is typically seen on face, mouth, throat, hands, feet, groin, genital and/or anal region and may be painful and/or itchy, often evolving from macules and papules to vesicles and pustules that eventually crust over. Most infections are mild and resolve within 2-4 weeks after symptom onset, most often without requiring antiviral treatment.5 However, symptoms may persist longer or progress to disseminated infections in individuals with weakened immune systems, especially persons with advanced Human Immunodeficiency Virus (HIV) disease.6 Concomitant sexually transmitted infections, particularly gonorrhea, chlamydia and syphilis, have been reported in 17-31% of those tested.7-10

The global outbreak beginning in 2022 was caused mostly by clade IIb virus and with somewhat atypical clinical presentation in that the lesions often started in the groin, anus, or mouth, appearing before or concurrently with other symptoms and not always associated with spread to other parts of the body. Transmission dynamics were also different compared to historical reports, with spread
most often via sexual contact and occasionally via close household contact or sharps injuries.\textsuperscript{11-14} Initial cases in the US were associated with international travel, but within a short time period, domestic transmission was reported in all 50 US states, District of Columbia (DC) and Puerto Rico. Most cases reported to CDC were among men who have sex with men (MSM), aged 21-55 years, and disproportionately affecting persons with HIV and those from racial and ethnic minority groups, including Black and Hispanic/Latino persons. Additionally, most fatal cases occurred in immunocompromised Black persons.\textsuperscript{13,15} In the first year of the outbreak, over 30,000 cases occurred, 1.2 million JYNNEOS (Bavarian Nordic, Hellerup, Denmark) third-generation smallpox vaccines were administered and over 6,900 individuals were treated with the antiviral medication: tecovirimat (TPOXX, SIGA Technologies, NYC, NY) in the United States via an expanded access, investigational new drug (IND) protocol.\textsuperscript{15}

US Veterans represent a potentially high-risk population for MPXV infections, including severe infections, given most enrollees in the Veterans Health Administration (VHA) are adult males, with higher rates of underlying comorbidities\textsuperscript{16,17} and because VHA is the largest single provider of HIV care in the US.\textsuperscript{18} As the largest integrated healthcare system in the US, VHA provides care to approximately 6.75 million patients annually across 1,321 care sites nationwide and to over 31,000 Veterans living with HIV.\textsuperscript{19,20}

The objectives of this study were to identify risk factors for non-variol orthopox/mopox virus (NVO/MPXV) test positivity by comparing characteristics of NVO/MPXV positive individuals with those who tested negative and to characterize the epidemiology of MPXV confirmed infections, including infection severity, hospitalization, and death as well as risk factors for infection exposure. In addition, we sought to evaluate VHA’s immunization efforts since the start of the outbreak and summarize genetic characterization of samples submitted for whole genome sequencing (WGS) to VHA’s Public Health Reference Laboratory (PHRL). Analyzing the impact of the mopox outbreak in VHA, particularly among racial and ethnic minority groups and individuals living with HIV, may help guide prevention, testing, treatment, and control strategies, including vaccination efforts for mopox.

METHODS

Data collection and epidemiologic analysis

VHA inpatient and outpatient medical encounters are maintained in a nationwide database of electronic health records (EHR), known as Veterans Information Systems and Technology Architecture (VistA). All data for this study were obtained from the Corporate Data Warehouse (a repository and health data warehouse comprised of VistA clinical data and other data systems) and VHA’s Praedico™ Public Health Surveillance System (Bitscopic, Los Angeles, CA), which compiles public health data from VistA across multiple EHR domains, including diagnostic
testing. The time frame for laboratory samples included in this study was May 23, 2022, through May 24, 2023.

For comparison of patients presumptive positive/confirmed positive for NVO/MPXV real-time polymerase chain reaction (qPCR) to those who were NVO qPCR negative, demographic variables extracted from the EHR included age, birth sex, race, ethnicity, facility state location, rurality of residence (based on Rural-Urban Commuting Area (RUCA) codes), sample site, JYNNEOS or vaccinia (smallpox) vaccination status, HIV or Sexually Transmitted Infection (STI) status, and most recent CD4 count and percent for those who were HIV positive prior to mpox diagnosis (obtained starting from 1/1/2021). HIV positive status was defined as presence of an International Classification of Diseases, Clinical Modification, 9th or 10th Revision (ICD 9 or ICD-10 diagnosis code for HIV (042, V08, 079.53; B20, B97.35, O98.7*, Z21) during any outpatient or inpatient encounter from January 1, 2000, through the study time frame. STI positive status was defined as presence of an ICD-10 diagnosis code for syphilis, gonorrhea, chlamydia, or anogenital herpes (A51*, A52*, A53*, A54*, A55*, A60*) during any outpatient or inpatient encounter from March 1, 2022, through the study time frame. Individuals were determined to have been vaccinated for smallpox/mpox if they fell into any of the following categories: 1) documented receipt of one or more JYNNEOS vaccine doses prior to NVO/MPXV test date, 2) documented receipt of vaccinia (smallpox) vaccine prior to NVO/MPXV test date, 3) birth date prior to 1972 and therefore assumed to have been vaccinated with vaccinia vaccine. Individuals who either had no documented receipt of vaccination or received vaccination after NVO/MPXV test date (and were not born before 1972) were considered unvaccinated. Incidence rates for NVO/MPXV positivity were calculated by age group per 100,000 Veterans in care, based on the VHA Support Service Center Capital Assets (VSSC) Unique Patients data cube.

The distributions of characteristics at the time of testing were compared between patients who tested positive for NVO/MPXV and those who tested NVO negative using Pearson’s Chi-square test for categorical variables and Mann-Whitney-Wilcoxon (MWW) test for continuous variables. We then performed binary logistic regression analysis using R version 4.3.0 (R Foundation for Statistical Computing, Vienna, Austria) to estimate the association of potentially relevant covariates with test positivity, adjusting for age, birth sex, race/ethnicity, rurality of residence, sample anatomic site, HIV, STI, and vaccination status, and expressed results as adjusted odds ratios (AORs) with 95% confidence intervals (CIs).

For the subset of patients with confirmatory MPXV testing, we additionally collected outpatient and inpatient encounters with monkeypox (B04)/orthopoxvirus (B08.09) diagnosis codes and performed chart reviews for exposure history, sexual contact among gay, bisexual and MSM, confirmation of HIV status, TPOXX receipt, and deaths.
Sample testing and whole genome sequencing

For patients who presented to VHA facilities, suspect lesions collected for testing were swabbed by clinical providers according to CDC instructions. Samples were submitted for NVO qPCR screen testing to state or local public health laboratories according to local criteria or VHA PHRL using the CDC NVO Screen Real-Time PCR Assay as described. Samples could also be sent to commercial laboratories that used their in-house NVO or NVO/MPXV qPCR assays. We performed manual chart review to determine whether specimens ordered by VHA providers but processed outside VHA had confirmatory testing for MPXV either via scanned laboratory reports or provider documentation of confirmatory testing. Samples sent to PHRL were shipped frozen in blue or dry ice as dry swabs. At PHRL, viral nucleic acid was extracted using the MagnaPure 96 (Roche Diagnostics, Indianapolis, IN) automated nucleic acid extraction platform and a QuantStudio Dx (ThermoFisher Scientific, Waltham, MA) was used for qPCR as described in the CDC NVO instructions for use. Samples positive with the CDC NVO qPCR assay were confirmed at PHRL using a laboratory developed test (LDT) MPXV confirmatory qPCR assay analyzing clade II-West African Strain (WAS) and Generic Strain (GEN) tumor necrosis factor receptor (TNFR) gene as previously described. Additional VHA patients who were cared for at non-VHA health care facilities were identified based on Monkeypox diagnosis codes and/or facility issue briefs submitted to VA Central Office and testing results were obtained via EHR review.

Samples confirmed at PHRL for MPXV that had cycle threshold (Ct) results ≤ 29, underwent MPXV whole genome sequencing (WGS) using previously extracted MPXV DNA used for the NVO screening assay and Nextera XT DNA Sample Preparation and Index Kits (Illumina, San Diego, CA) to generate libraries for WGS on an MiSeq (Illumina) according to manufacturer instructions. Generated FASTQ files were subjected to a previously published analytic pipeline, and generated FASTA files were further analyzed using NextClade to determine viral clade and lineage type. MPXV sequences were analyzed for single nucleotide polymorphisms (SNP) that defined the B.1 parent lineage and SNPs that defined B.1 sublineages that were distinct from the parent B.1 lineage. If the nucleotide substitution(s) were present, the lineage was reported. Phylogenetic analysis was performed using Nextclade. VA lineages were compared to type strains for clade IIb. VA lineage distribution and frequency was compared to other US lineages from sequences submitted to the Global Initiative on Sharing All Influenza Data (GISAID). Ct results were collected from samples tested at PHRL for orthopox DNA polymerase gene (E9L, VAC1) and human RNase P gene (RNP) using the NVO screening assay; and WAS and GEN TNFR genes from the MPXV confirmatory assay. Ct results from VAC1 were then compared to WAS and GEN among MPXV positive samples; and RNP Ct results were compared between positive and negative samples using Z-test.

The data utilized in this study were obtained for the purpose of public health operations in VHA. No additional analyses outside of public health operational activities were performed. Therefore, this study was deemed to meet the requirements of public health surveillance as defined in 45 CFR.
This project was approved by the Stanford University Institutional Review Board (Protocol ID 47191, “Public Health Surveillance in the Department of Veterans Affairs”) and written informed consent was waived.

RESULTS

We identified 1,144 unique patients tested for NVO (and if presumptive positive using MPXV confirmatory testing) from 48 states/territories/District of Columbia, with 1,055 (92.2%) male and median age of 46 years (IQR 25). Two hundred fifty-one (21.9%) were presumptive positive/positive, 802 (70.1%) negative and 91 (8%) equivocal or inconclusive by the NVO screening assay and not further tested, with positive tests peaking in August 2022 (Supplemental Figure 1). Age group 25 to 34 years had the highest incidence rate (13.83 cases per 100,000 unique patients in VHA care) (Supplemental Table 1).

Median age of those testing positive for NVO/MPXV was 41 years (IQR 16), and 51 years (IQR 27) for those testing NVO negative (p <0.001) (Table 1). Risk factors associated with higher odds of NVO/MPXV test positivity (compared to those testing negative) included male birth sex (AOR=6.77; 95% CI 2.03-42.06), non-Hispanic Black race/ethnicity (AOR=1.98; 95% CI 1.12-3.63), genital or rectal sample site (AOR=1.80; 95% CI 1.26-2.58), HIV positive status (AOR=2.43; 95% CI 1.68-3.52), and syphilis positive status (AOR=1.83; 95% CI 1.25-2.69). Residence in urban areas and gonorrhea and chlamydia STI diagnosis were not significantly associated when adjusted for age, birth sex, race/ethnicity, sample site, vaccination status, and other diagnoses in the logistic regression model. Among individuals with positive HIV status, median CD4 count did not differ between those testing positive for NVO/MPXV (586.5 cells/µL; IQR 371.5) compared to those testing negative (590 cells/µL; IQR 364) (p=0.905). Vaccination with JYNNEOS or vaccinia (smallpox) vaccine had lower odds of NVO/MPXV test positivity (AOR=0.33; 95% CI 0.22-0.48). Breakdown of vaccination status by NVO negative or NVO/MPXV presumptive/confirmed positive test result is detailed in Supplemental Table 2. Overall, from July 2022 through May 2023, over 8,000 JYNNEOS vaccination doses were administered in VHA to over 4,400 unique Veterans.

Among 209 with positive confirmatory MPXV testing (from PHRL and other testing laboratories) from 29 states plus the District of Columbia, 207 (99.0%) were birth sex male (includes two transgender females), primarily in 25-44 age group (131, 62.7%). The majority were non-Hispanic Black race/ethnicity (108, 51.7%) and 24 (11.5%) were Hispanic/Latino ethnicity. CA (45), TX (26) and DC (22) had the highest number of confirmed positives. VHA outpatient Monkeypox ICD-10 coded encounter(s) were present in 141 (67.5%) and 189 (90.4%) reported intimate contact exposure and/or epidemiological link. Additionally, 175 (84.5%) were MSM and 113 (54.1%) were HIV positive. Besides HIV, 109 (52.2%) had one or more ICD-10-coded sexually transmitted infection(s) (STIs), including syphilis (40.7%), herpesvirus (10.1%), gonococcal (12.0%) and chlamydial (9.1%) infections.
Treatment of confirmed MPXV positive individuals with TPOXX in VHA was identified in 51 (24.4%) and 17 (8.1%) were hospitalized with an assigned B04/B08.09 diagnosis code. Among those hospitalized, only 2 had history of vaccination (in 2005 and 2007, respectively), 13 received TPOXX. There was 1 death in a patient with end-stage HIV/AIDS with multiple co-morbidities and opportunistic infections, including mpox.

Among samples from 824 patients tested at PHRL (thereby providing Ct values for anatomic collection site comparisons and sequencing that were otherwise not accessible or available from other testing sites) using the NVO screening assay, 178 (21.6%) were NVO presumptive positive. Of these, 173 were confirmed MPXV positive, 4 were MPXV negative and one was not tested for MPXV. Of the 4 patient samples that were NVO presumptive positive and MPXV negative, the confirmatory MPXV GEN and WAS qPCR Cts were negative. When Ct for samples using the NVO screening assay was compared to the Ct using the MPXV confirmatory assays, there was no significant difference comparing VAC1 (mean 24.4, range 11.9 - 37) to GEN (mean 24.0, range 13.5-39.7, p = 0.37) or WAS (mean 25.0, range 15.2 - 40, p = 0.31), respectively. There was a small but significant difference in RNP Ct comparing NVO presumptive positive (mean 26.9, range 19.5 – 39.7) and negative (mean 29.8, range 0 – 39.31) samples (p < 0.01).

No significant difference was noted comparing the NVO Cts of genital or rectal samples (mean 24.4, range 14.7 – 37.0) to those of non-genital/rectal samples (mean 24.8, range 15.3 – 38.33), p = 0.71. No significant difference was also noted comparing the Cts of MPXV GEN and WAS between the anatomic groups described.

Of 173 MPXV confirmed samples, 118 (68%) samples based on Ct threshold < 29 were sequenced. We observed that 19 of 27 (70%) and 5 of 91 (5%) with whole genome coverage of < 70% or > 70%, respectively, did not have all the required SNPs for lineage designation. Therefore, using a conservative approach, we considered that 86 of 91 patient samples with >70% whole genome coverage had evaluable WGS results based on specific SNPs that defined lineages. All MPXV variants were clade IIb, representing 10 different lineages from 20 states and the District of Columbia (Table 2 and Supplemental Figure 2). The B.1.2 variant was most common (33) detected in 13 states, followed by B.1 (28) in 14 states. In our cohort, all B.1 sublineages were contemporaneously represented with B.1.

**DISCUSSION**

Among a national cohort of VHA patients who were tested for NVO/MPXV during the 2022-2023 US outbreak, risk factors having the highest odds for NVO/MPXV positivity included male birth sex, HIV positivity, non-Hispanic Black race/ethnicity, syphilis diagnosis and genital/rectal specimen collection. JYNNEOS/vaccinia vaccination and older age were protective factors. CDC reports that the highest risk race/ethnicity groups in the US were non-Hispanic Black and Hispanic persons, while our study found only non-Hispanic Blacks at significant risk. Like other studies,
we found that NVO/MPXV positivity was associated with HIV and syphilis positivity. As a large national healthcare system, VHA surveillance capability was enhanced by the availability of data on patients who presented with mpox signs/symptoms but tested negative, which is an advantage compared to other prior evaluations and reporting systems.

Our finding of sample sites taken from genital or rectal lesions being associated with NVO/MPXV positivity was not surprising as Ct values from these sites have been shown to be lower than from other body sites, indicating that proper sampling from high-yield body sites may decrease false negative or equivocal/inconclusive results. However, our results are different from controlled studies documenting the appearance, duration and swabbing of rash/lesions and corresponding Cts. These controlled studies demonstrated lower Cts from skin followed by rectal swab sites, with Ct levels related to lesion duration. Ultimately, the Ct values collected at the ideal time and anatomic sites could be used to determine the MPXV infectivity. A study from Israel described a correlation between Cq (quantification cycle like Ct) values and in-vitro infectivity of African green monkey kidney cell line (BSC-1). Samples with Cq > 35 resulted in either no or minimal infection.

Although JYNNEOS vaccination occurred significantly less among those with an mpox diagnosis in a recent study, documentation of JYNNEOS vaccination in our study was very low in both NVO/MPXV positive and negative patients. Prior vaccination with vaccinia (smallpox) vaccine is thought to provide little protection against mpox if given greater than 3 years before exposure. Our data poses an interesting question regarding the possibility that in our large cohort of individuals vaccinated with vaccinia, (during their military service and/or due to being born prior to 1972), protection against mpox may possibly have been conferred by vaccinia vaccination rather than JYNNEOS (Supplemental Table 3). This phenomenon was reported in a recent systematic review and an additional recent study confirmed the existence of long-term cross-neutralizing antibodies elicited by prior vaccinia vaccination and seen in higher levels among individuals born before 1980.

Among our confirmed MPXV cases, we found a high percentage with intimate contact exposure histories, MSM, HIV, and STIs documented in medical records. These findings align with previous studies that have reported high proportion of MPXV infected individuals among adult MSM, those living with HIV, and from specific racial and ethnic minority groups. Other studies have also documented high rates of concomitant STIs in patients with mpox. High rates of HIV, MSM and STIs among mpox cases suggests the importance of testing for HIV and STIs, as well as discussing vaccination, HIV PrEP and STI prevention strategies, where applicable, for patients who present with possible mpox.

Although VHA had relatively few mpox cases, testing in VHA peaked in August 2022 with the highest incidence rate observed among Veterans aged 25-34 (13.83 per 100,000 Veterans in care). While the VHA peak was consistent with that reported by CDC, the incidence rate for Veterans aged 18-64 (7.5 per 100,000 Veterans in care) was lower than published US population rate of
13.5 per 100,000 for persons aged 15-64.\textsuperscript{15,37} TPOXX administration was documented in 24.4% of VHA confirmed mpox cases compared with 22.8% administration rate for the US overall through May 11, 2023.\textsuperscript{15} Our hospitalization rate of 8.1% was similar albeit slightly higher than a recent metanalysis of global mpox reports which found a hospitalization rate of approximately 7.3% and a reported hospitalization rate of 7.5% among unvaccinated individuals from 29 US jurisdictions.\textsuperscript{38,39}

Our study has several limitations. Our sample of NVO/MPXV positives was small and our Veteran population is older and predominantly male which may not represent the general population. Race/ethnicity data was missing in ~8% of our patients, which could have impacted our results. Some NVO presumptive positive individuals were not confirmed using a specific MPXV qPCR assay (or documentation of confirmatory testing was unavailable in the EHR). Some patients with mild, self-limited illness may not have presented for care or may have presented with epidemiological history but before development of rash, so they were not tested. Poor sampling/swabbing technique may have led to equivocal or inconclusive test results, which was seen in 8% of VHA samples. Documentation of sample anatomic site was not available in 38% of samples (Supplemental Table 3). Early in the epidemic, some facilities were not aware that testing could be performed within VHA, and patients were referred to health departments or non-VHA facilities for testing. Our data sources do not contain clinical records for patients who received care in non-VHA health care settings unless these services were ordered and paid for by VHA. For these reasons, our data likely under captures mpox in VHA. Similarly, some VHA patients were referred to their local health department or other facilities to obtain TPOXX and JYNNEOS vaccine until VHA facilities were able to obtain it locally. Therefore, MPXV testing, JYNNEOS vaccination, and ICD-coded Monkeypox encounters occurring under these circumstances outside VHA were not represented in our study.

Only samples received by PHRL had WGS performed. Over 40% of the samples had high Cts and were not sequenced, limiting our analysis of variants. However, 97.5% of non-sequenced samples came from the same 21 states and District of Columbia and generally had the same proportions of patients by state as those that were sequenced (Supplemental Table 4). In addition, we did not include samples that were sequenced and had low coverage (< 70%); or in a few with > 90% coverage, even though a designation was made by Nextclade, because we were not confident that a variant designation was accurate if lineage-specific SNPs were missing. In terms of the challenges concerning MPXV WGS using a metagenomic approach where despite lower Ct and high genome-wide coverage affected our ability to designate some sublineages,\textsuperscript{40} an amplicon based MPXV WGS approach for improved results is now available.\textsuperscript{41} Nevertheless we confirmed seeing many of the sublineages found in the US and represented in GISAID (Supplemental Table 5) and add to literature demonstrating contemporaneously geographic diversity of variants in the US among Veterans.

In conclusion, this report highlights the epidemiology of mpox among VHA enrollees during the 2022-2023 national outbreak. Demographic features of patients testing positive for NVO/MPXV
were consistent with previous reports, including among HIV positive, MSM and non-Hispanic Black individuals. Timing and incidence rates of mpox among Veterans followed similar trends compared with reported national cases, particularly among younger age groups. As a national healthcare system report, this study provides a supplemental source of data on mpox, including observed MPXV lineages and viral diversity; and among patients who tested negative. Providers should continue to encourage vaccination among patients at highest risk for infection with mpox and test for mpox in patients with compatible exposure histories and documented risk factors, even in the absence of travel history to an endemic region. Additional, targeted public health messages, education and prevention strategies are needed to ensure at-risk patients are receiving timely testing, treatment, and follow-up.

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**Conflicts of Interest:** All authors declare no conflict of interest.

The contents and opinions of this manuscript are those of the authors and do not necessarily represent those of the United States Government or the Department of Veterans Affairs.

**Data Availability Statement:** The data that support the findings of this study are available from the corresponding author upon reasonable request.

**Author Contributions:** Conceptualization, CLO, GO, MH; Methodology, CLO, CT, CE, GO, MH; validation, CLO, GO, PS, MH; formal analysis, CLO, GO, CT, TE, CE, MH; resources, MH; data curation, CLO, GO, CE, CT, TE; writing-original draft preparation, MH, CLO; writing-review and editing, PS, GO, CT, CE, TE, MH; supervision, MH, CLO; project administration MH, CLO. All authors have read and agreed to the final version of the manuscript.

**Footnote Page**

(1) No authors have a commercial or other association that might pose a conflict of interest.

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(3) Some of the information contained in the manuscript was presented as a poster presentation at IDWeek 2023, October 11-15, 2023, in Boston, MA. Abstract: 899.
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TABLES AND FIGURES (SEE SEPARATE FILE ATTACHMENTS)

Table 1. Characteristics of Patients Testing Positive or Negative for Non-Variola Orthopox or Mopox Virus (NVO/MPXV), and Risk Factors Associated with Test Positivity, Veterans Health Administration, May 2022 – May 2023.

<table>
<thead>
<tr>
<th>Variable</th>
<th>NVO/MPXV Positive</th>
<th>NVO/MPXV Negative</th>
<th>P value b</th>
<th>Adjusted Odds Ratio (95% Confidence Interval) c</th>
<th>P value c</th>
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<tbody>
<tr>
<td>Total</td>
<td>251 (23.8)</td>
<td>802 (76.2)</td>
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<tr>
<td>Median Age at Diagnosis</td>
<td>41 (IQR 16)</td>
<td>51 (IQR 27)</td>
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<td>0.98 (0.96-0.99)</td>
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<td>Birth Sex</td>
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<td>Male</td>
<td>249 (99.2)</td>
<td>726 (90.5)</td>
<td>&lt;0.001</td>
<td>6.77 (2.03-42.06)</td>
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<td>Hispanic/Latino</td>
<td>27 (10.8)</td>
<td>67 (8.4)</td>
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<td>Non-Hispanic Black</td>
<td>139 (55.4)</td>
<td>302 (37.7)</td>
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<td>1.98 (1.12-3.63)</td>
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<td>Non-Hispanic White</td>
<td>65 (25.9)</td>
<td>336 (41.9)</td>
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<td>1.24 (0.68-2.32)</td>
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<td>Rurality of Residence e</td>
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<tr>
<td>Urban residence</td>
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Table 2. Mpox Virus Variant Type and Number among Veteran Patients by Testing Facility State, Veterans Health Administration, May 2022-May 2023.

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South Carolina 2 0 0 2 0 0 0 0 0 0 0 0
Texas 12 6 0 6 0 0 0 0 0 0 0 0
Virginia 4 1 0 1 2 0 0 0 0 0 0 0
Washington D.C. 9 2 0 4 2 1 0 0 0 0 0 0
TOTALS 86 28 3 33 9 6 2 2 1 1 1 1

Yellow highlight indicates sample number of lineage or sublineage present for US state or District of Columbia.

References


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