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predominance, such differences between the efficacy and real-world effectiveness estimates highlight the importance of continued COVID-19 vaccine assessment and development as SARS-CoV-2 lineages continue to evolve. However, work showing increased protection of BNT162b2 against more severe outcomes, such as hospitalisation, in children and adolescents[6–9] remains an important reason to strongly encourage vaccine uptake in these populations.

Studies have shown that a BNT162b2 booster dose among adolescents increases protection against infection.[3,10] In May, 2022, the USA recommended a booster dose for 5–11-year-olds.[11] Whether a booster dose among children aged 5–11 years similarly increases protection against SARS-CoV-2 infection is not yet known, but we are hopeful that a booster will also benefit this younger population.

Growing literature paints a consistent picture that COVID-19 vaccination provides short-term protection for children and adolescents against SARS-CoV-2 infection during the omicron-predominant era, but the extent to which BNT162b2 vaccine protection persists beyond the 35 days after the second dose in children and 60 days after the booster dose in adolescents observed in Amir and colleagues' study is not clear. Monitoring the duration of COVID-19 vaccine protection will be a public health priority, especially as waning protection after two BNT162b2 doses has been observed in other paediatric studies.[3,6,8]

Consistent with findings from the USA[3,4] and England,[5] Amir and colleagues found substantially lower rates of confirmed SARS-CoV-2 infection among vaccinated children and among boosted adolescents compared with unvaccinated children and adolescents. We are encouraged by these results, which further emphasise the benefit of vaccinating children and adolescents with all recommended vaccine doses.

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# Monkeypox virus in human body sites and fluids: evidence for transmission

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With more than 50 000 cases worldwide in since May, 2022, and more than 95% of them in men who have sex with men, the monkeypox outbreak continues to represent a major medical and public health concern. Uncertainties persist regarding the transmission routes; together with epidemiological data, new insights are expected from the virological evaluation of the presence of monkeypox virus (MPXV) in different areas of the human body.

In this issue of *The Lancet Infectious Diseases*, Romain Palich and colleagues[1] report an extended evaluation of MPXV DNA in samples from skin, anus,

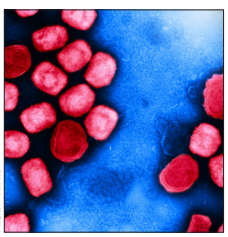
throat, blood, urine, and semen from 50 French monkeypox cases. MPXV detection was more frequent in skin (44 [88%] of 50), anus (30 [71%] of 42), and throat (36 [77%] of 47) samples than from blood (13 [29%] of 45), urine (nine [22%] of 41), or semen (13 [54%] of 24) samples. Similar studies have been reported in the past months, with largely overlapping findings showing widespread viral detection in different areas of the body (table). The highest viral DNA loads were consistently found in skin (Cycle threshold [Ct] 19·8) and anogenital swabs (Ct 20·9), suggesting intimate sexual contact as the main route of transmission. This finding is supported by the data on semen, which frequently has shown as DNA-positive in patients with MPXV.[1–3,6] Nevertheless, several questions regarding the contribution of the different bodily fluids to virus transmission need to be further addressed, also to better define the disease burden and the public health implications.

First, infectivity is a prerequisite for virus transmission. So far, virus isolation, whether in cell culture or animal models, is recognised as the only laboratory method to prove the presence of infectious viral particles in biological secretions. To date, evidence of replication-competent virus isolation has been reported only from skin (including anal swabs), oropharynx swabs, and semen samples.[7,8] However, this approach is laborious with biosafety and technical limitations. Viral load is commonly used as an estimate of the infectivity potential. MPXV DNA concentrations in clinical samples have recently shown to correlate with viral infectivity, with Ct values lower than 35 found more likely to be infectious by *in vitro* viral isolation.[7] On this assumption, the recent data showed that nasopharyngeal swabs, saliva, and feces mostly contain higher amounts of the virus, thus suggesting the potential for alternative routes of transmission. However, these studies have the intrinsic limitation of collecting samples from different districts at different times. Furthermore, contamination between contiguous matrices (eg, anorectal swabs contaminated by stool, or semen and urine contaminated by blood) might affect the detection. Therefore, further studies on different and larger cohorts, including multi-centre and multi-country cohorts, are required to characterise the factors influencing the MPXV compartmentalisation in the

| | Participants | HIV-positive | Skin* | | Anogenital | | Nasopharynx | | Plasma | | Urine | | Semen | | Saliva | | Fecal matter | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct | MPXV DNA prevalence | Median Ct |
| France (Palich et al, 2022)[1] | 50 | 22/50 (44%) | 44/50 (88%) | 20 | 30/42 (71%) | 21 | 36/47 (77%) | 27 | 13/45 (29%) | 33 | 9/41 (22%) | 31 | 13/24 (54%) | 28 | NA | NA | NA | NA |
| Spain (Peiró-Mestres et al, 2022)[2] | 12 | 4/12 (33%) | 12/12 (100%) | 20 | 11/12 (92%) | 23 | 10/12 (83%) | 31 | NA | NA | 9/12 (75%) | 35 | 7/9 (78%) | 32 | 12/12 (100%) | 29 | 8/12 (67%) | 24 |
| 16 countries (Thornhill et al, 2022)†[3] | 528 | 218/528 (41%) | 512/528‡ | .. | .. | .. | 138/528 (26%) | NA | 35/528 (7%) | NA | 14/528 (3%) | NA | 29/32 (91%) | NA | NA | NA | NA | NA |
| France (Mailhe et al, 2022)[4] | 264 | 73/256 (29%) | 252/258 (98%) | 23 | NA | NA | 150/197 (76%) | 32 | 8/26 (31%) | 36 | NA | NA | NA | NA | NA | NA | NA | NA |
| Spain (Tarín-Vicente et al, 2022)[5] | 181 | 72/181 (40%) | 178/180 (99%) | 23 | 43/55 (78%) | 27 | 82/117 (70%) | 32 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA |
| Italy (Raccagni et al, 2022)[6] | 36 | 15/36 (42%) | 36/36§ (100%) | .. | .. | .. | .. | .. | 24/36 (67%) | 34 | 8/36 (22%) | NA | 22/36 (61%) | 34 | NA | NA | NA | NA |

Data are n/N (%) unless otherwise specified. Ct=cycle threshold. MPXV=monkeypox virus. NA=not available. *Includes perianal skin. †Argentina, Australia, Belgium, Canada, Denmark, France, Germany, Israel, Italy, Mexico, Portugal, Spain, Switzerland, The Netherlands, UK, and USA. ‡Refers to skin or anogenital samples combined. §Refers to either skin, anogenital, or oropharyngeal samples combined.

***Table:*** **Large case series reporting prevalence of MPXV DNA and median Ct of positive samples at PCR in at least two different bodily fluids**



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different anatomical sites (ie, exposure and clinical presentation).

Second, clinicians remain unaware of whether the virus can persist within immune-privileged sites, and for how long. Palich and colleagues showed that viral clearance appeared to be relatively rapid, as most tested samples resulted MPXV-negative or weakly positive (below Ct 35) within 14 days after symptom onset. However, data are still scarce and to date MPXV detection and viral shedding kinetics, also in the prodromal stages, are largely unknown. For example, we know that related poxviruses have both primary and secondary viremias, but so far, MPXV viremia has only been assessed in late disease stages. Although poxvirus transmission with transfusion has been documented only once with smallpox,[9] these investigations are urgent, with potential implications for public health outside the current transmission chains (ie, in blood and tissue donations).

Finally, to better understand the biology, evolution, and spread of the virus causing the current outbreak, research efforts should be made regarding MPXV genome mapping and phylogenetic characterisation. Viral sequencing has refined phylogeny, with eight B.1 MPXV sub-lineages reported to date. A high number of mutations have been found in the viruses of the current outbreak,[10] but whether these variations influenced MPXV transmissibility and virulence remains to be elucidated. Such notable diversification probably arises from long-term asymptomatic circulation leading to host adaptation, but previous smallpox vaccine-elicited immunity and different routes of transmission could also account for some of the phenotypic variations observed.

In conclusion, more extensive investigations are needed to obtain a coherent understanding of transmission factors that have permitted the extraordinary penetration of active MPXV infection into human communities worldwide. Notably, infection of animal hosts, including pets of confirmed cases or rodents infected by human stools in wastewaters, could further drive endemicity outside Africa. If this transmission continues, monkeypox cases are likely to increase in numbers outside of the community of men who have sex with men.

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# The role of chemoprophylaxis in eliminating forest malaria and preventing simian malaria in humans

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The regional elimination and eventual eradication of human malaria will require addressing the most difficult, persistent, and stubborn pockets of transmission.[1] In recent years, southeast Asia has made tremendous progress towards regional elimination, revealing forest malaria to be one such challenge. Most foci of transmission remaining in the region are among migrant populations that spend time in the forest and are located far from access to care.[2] Although most research on forest malaria has focused on the