

The Philippine First Pox Case: A Multidisciplinary Approach to Investigation and Analysis

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DESCRIPTION

The first confirmed case of monkey pox infection in a Filipino with a clinical presentation distinct from the classic cases previously reported in endemic countries of Central and West Africa prior to the 2022 outbreak, in light of the World Health Organization's declaration of the multi-country monkey pox outbreak as a Public Health Emergency of International Concern (PHEIC) [1]. We discuss the dermatopathological and gross manifestations of monkey pox infection on dark skin in Southeast Asia. We also go over the unique use of shotgun metagenomics sequencing to characterize the infecting virus and the comprehensive procedure of monkey pox quantitative real-time Polymerase Chain Reaction (qPCR) testing for diagnostic confirmation [2]. This was an example of a 31-year-old male Filipino who has visited many European nations. Five well-defined, umbilicated pustules with erythematous borders appeared on his upper lip, left gluteal region, bilateral knees, and left ankle. These lesions were non-tender. The results of the skin punch biopsy pointed to a possible viral infection [3]. An infection with monkey pox from Clade II (formerly the West African clade) was verified by (qPCR) Polymerase Chain Reaction detection and amplification of the G2R_G, G2R_WA, and C3L gene targets. The current multi-country epidemic of monkey pox has been linked to a genome sequence that belongs to the B.1.3 lineage of Clade Ibis, as shown by shotgun metagenomics sequencing [4]. Although metagenomics sequencing and varicella PCR of the skin lesion did not reveal the presence of the varicella virus, the serologic varicella IgM test was positive. The individual was released and kept in seclusion at home until all of the scabs had come off [5,6]. Patients with risk factors, such as potential close physical contact with infected persons in places where monkey pox cases have been documented, should be suspicious for monkey pox if they develop pustules. The patient's skin lesions showed dermatopathological characteristics that were non-specific for monkey pox infection but consistent with a viral infection [7]. To verify monkey pox infection from Clade II, the qPCR methodology has to be established and optimized. The etiologic agent of the first laboratory-confirmed case of monkey pox in the Philippines, which

belongs to Clade Ibis and is mostly to blame for the global epidemic of monkey pox in 2022, was effectively characterized by metagenomics sequencing. Prompt case identification and development of a diagnostic capacity for verification and testing are crucial parts of the nation's defense against monkey pox [8]. Given that more confirmed instances of monkey pox have been found in non-endemic nations, patients who go to locations where the disease is actively spreading and have risk factors such as potential close physical contact with infected persons should be suspicious for monkey pox infection if they develop pustules [9]. The skin lesions in this verified instance included dermatopathological results that were compatible with a viral infection. In this instance, confirmation of a West African clade monkey pox infection required the development and refinement of a qPCR methodology [10]. The novel application of shotgun metagenomics sequencing to characterize the etiologic agent is demonstrated in this case study. According to the findings of the sequence study, the first occurrence of monkey pox in the Philippines is associated with the Monkey Pox Virus hMPXV Clade Ibis, a subclade of the B.1.3 lineage connected to the recent monkey pox outbreak in several European nations, and more particularly, to the previous West African clade (formerly known as Clade II) [11]. The varicella serologic IgM results are more likely to be false positives due to the negative varicella PCR of the skin lesions, which is corroborated by the lack of varicella DNA on the sequencing.

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