



Epidemiology of measles clusters/outbreaks during 2016-2017 in Oman

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ARTICLE INFO

Keywords:

Epidemiology
Measles
Outbreak
Clusters
Oman

ABSTRACT

Objectives: The epidemiology of measles in Oman has shown a decreasing trend since the introduction of vaccines with high coverage, even at the district level. Oman achieved elimination status in 2019. Currently, measles epidemiology is characterized by a small number of imported and importation-related cases with limited spread in the community. The main aim of the study is to describe the epidemiology of major measles outbreaks in Oman during 2016-2017.

Methods: This study involved a descriptive case-based record review of the national surveillance database for fever and rash illness.

Results: A total of 231 measles cases were reported during 2016-2017. Of the reported cases, 209 (90.5%) were laboratory-confirmed, 16 (6.9%) were clinically compatible, and six (2.6%) were epidemiologically linked cases. There were 10 clusters/outbreaks comprising 191 cases (185 laboratory-confirmed cases and six epidemiologically linked to a confirmed case) in various governorates of Oman during 2016-2017. The study population had a mean age of 11.4 years, ranging from 0.2 to 55 years across the outbreaks. The median age was 9 months. Approximately 50.7% of the cases involved infants aged ≤ 12 months, who were not yet eligible for measles vaccination. The second most affected age group were individuals aged 20-35 years. The largest and the longest cluster during 2016-2017 occurred in Dhofar and Sharqiyah, involving 90 cases attributed to genotype B3, which lasted for 32 weeks.

Conclusions: Multiple small outbreaks occurred simultaneously but were too brief to allow any particular genotype to establish itself as an endemic strain.

Introduction

Measles is a highly infectious disease caused by the measles virus, *Measles morbillivirus*. It is an RNA virus belonging to the *Paramyxoviridae* family. Initial symptoms typically include fever and maculopapular rash along with respiratory symptoms such as cough, rhinorrhea, and conjunctivitis. The measles virus spreads easily when an infected person breathes, coughs, or sneezes. It can cause severe disease with complications (pneumonia, encephalitis) and even death. Despite the availability of an effective and affordable vaccine, measles remains a major cause of death among young children globally. From 2000 to 2016, the annual global reported measles incidence decreased by 87%, from 145 to 19 cases per million persons, and annual estimated measles deaths decreased by 84%, from 550,100 to 89,780 per million persons; measles vaccination prevented an estimated 20.4 million deaths [1].

In 2012, the World Health Assembly endorsed the Global Vaccine Action Plan with the objective of eliminating measles in five World Health Organization (WHO) regions by 2020 [2].

The Region of the Americas, encompassing North and South America, has been certified by the WHO as having eliminated measles. Europe has also made significant strides toward this goal. However, considerable efforts are still required in the other four WHO regions to meet the target for measles elimination [3]. In 2013, six countries in the Eastern Mediterranean Region (EMR) reported a measles incidence of fewer than one case per million population, and three of these countries have not reported any endemic measles cases for the last 2-3 years. Oman was among these six countries and demonstrated a robust surveillance system, reporting an endemic measles incidence of fewer than five cases per million people [4].

Although measles elimination was declared in the United States in 2000, importations of measles cases from endemic areas of the world continue to occur, leading to secondary measles cases and outbreaks in the United States, primarily among unvaccinated persons [5]. In 2014, 23 measles outbreaks occurred, including one large outbreak of 383 cases, primarily among unvaccinated individuals, linked to the Philippines as imported/importation related [6].

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<https://doi.org/10.1016/j.ijregi.2024.100552>

Received 17 October 2024; Received in revised form 16 December 2024; Accepted 16 December 2024

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Measles was a common childhood infection in Oman before the introduction of the vaccine. The disease was endemic, with periodic outbreaks. The measles vaccine was introduced at 9 months in 1981 as part of the routine Expanded Programme on Immunization schedule. As a result, the cases continued to decline from approximately 40,000 during the early 1980s to 3675 in 1985. In March 1994, a second dose of the measles–rubella vaccine was introduced at 15 months of age. A catch-up campaign with this vaccine was also conducted for all individuals aged 15 months to 18 years, achieving a 94% coverage rate. As a result, the incidence of measles in Oman has declined markedly in recent years to fewer than one case per million people [7].

Several strategies are now being adopted to increase immunization coverage, including a two-dose schedule, targeted immunization campaigns (mopping-up activities), supplementary immunization with vitamin A, national and regional mass immunizations, and the development of high-quality case-based measles surveillance supported by regional measles laboratories. Oman is one of the EMR countries to adopt these elimination strategies.

Oman entered the phase of elimination of measles from the year 1996. However, small outbreaks continued to occur in Oman periodically because of the accumulation of non-immune individuals exposed to imported cases. A total of 220 confirmed cases were reported in Oman from 2000 until 2015, comprising 12 clusters from the regions of Dhofar, North and South Batinah, Muscat, and Dakhiliyah. No clusters were reported in 2002–2004, 2006, 2008, or 2010–2012. The median duration of these clusters was 9 weeks. The lowest incidence was observed in 2003, with only one laboratory-confirmed case. These outbreaks mostly involved individuals exposed to imported measles cases, unvaccinated non-Omanis, those not due for vaccination, and those with unknown vaccination status. Thus, current measles epidemiology in Oman is determined by characteristics of the imported cases and their susceptible contacts.

Elimination does not equate to zero cases because imported cases may still occur when elimination has been achieved, with limited spread to susceptible persons. Over time, the accumulation of susceptible individuals due to a small proportion of vaccine failures could lead to outbreaks or epidemics [8].

Measles elimination is defined as the absence of endemic measles cases for a period of at least 12 months in the presence of adequate surveillance. Another indicator of measles elimination is a sustained measles incidence of fewer than one case per million people [9].

This study aimed to describe the epidemiological nature of a large measles outbreak from 2016 to 2017 in Oman. In addition, the study aims to verify laboratory evidence to determine the endemicity status of measles genotypes in Oman.

Methods

Oman has a population of nearly 4.5 million, residing in 11 governorates with 61 districts. Almost 45% of the Oman population are expatriates, mainly from East Asia. The key elements of measles surveillance include a sensitive and robust system, high reporting rates, and key performance indicators for surveillance. Case-based reporting of fever and non-vesicular maculopapular rash within 24 hours, including zero reporting, has been mandatory since 1991, and is conducted by the dedicated surveillance team at all levels of health care, including the private health institutions. Immunoglobulin M (IgM) testing for measles was initiated in 1996.

The case data are aggregated and analyzed at the national level. High-quality measles and rubella laboratory testing provides timely confirmation through polymerase chain reaction (PCR) and sequencing. The final case classification assignment is determined through consultation between the Department of Communicable Diseases, the Central Public Health Laboratory (CPHL), and the National Measles Committee.

This was a cross-sectional, record-based descriptive study of the outbreak-affected population across all age groups. The samples were

collected from all the reporting health institutions of suspected cases of measles in Oman and were tested at the virology section of the CPHL in Muscat, Oman, which is also a WHO reference laboratory.

The samples were tested for both measles and rubella and reported as IgM-positive or -negative. All IgM-positive cases were subjected to virus isolation by PCR. All measles and rubella IgM-negative samples were not processed further, and all PCR-positive cases were genotyped [7]. Diagnostic serology for measles IgM was conducted using a commercial indirect enzyme-linked immunoassay (ELISA) kit (Enzygnost, Siemens AG). Diagnostic real-time reverse transcriptase PCR and reverse transcriptase PCR kits supplied by the Centers for Disease Control and Prevention (CDC) were used for virus detection and genotyping, respectively. Genomic sequencing of the 450-nucleotide region of the nucleoprotein (N) gene of the measles virus was performed. All sequences were aligned according to viral genotype with the ClustalW algorithm integrated into the BioEdit software. The phylogenetic tree was constructed with the Mega 6 program, applying the Kimura two-parameter system and the neighbor-joining method with 1000 bootstrap replicates.

Epidemiologically, the measles cases were finally classified as discarded, laboratory-confirmed, clinically compatible, or epidemiologically linked cases as per the WHO and CDC guidelines [10]. Occurrence of two or more measles cases that are linked clinically (e.g., history of contact with a confirmed case), epidemiologically, and/or virologically is defined as an outbreak [11].

Statistical analysis

Collected data

The collected data variables, organized in Microsoft Excel, include age, gender, dates (onset, notification, sample collection, and result), place of reporting (governorate and district), nationality, vaccination status, source of infection, travel history, clinical features, laboratory details, case classification, and outcome.

Analysis

The participants were stratified by sociodemographic factors (age, gender, nationality, and governorate). Descriptive analyses of frequencies and proportions for categorical data were calculated and presented in tables and graphs.

Results

A total of 29 outbreaks, including 237 cases, were reported from 2013 to 2022. The largest outbreak occurred in 2016–2017, after which a national measles, mumps, and rubella Supplementary Immunization Activity (SIA) was conducted, leading to a reduction in outbreaks, as shown in Figure 1.

During 2016–2017, 231 measles cases were reported. Among these, 209 (90.5%) cases were confirmed through laboratory tests, 16 (6.9%) were clinically compatible, and six (2.6%) cases were epidemiologically linked. Out of the 231 cases, 191 were related to outbreaks, while the remaining 40 cases were sporadic, unrelated to the outbreaks, and featured distinct genotypes and sequence IDs. There were 10 clusters or outbreaks, which accounted for 191 (82.7%) cases, including 185 laboratory-confirmed cases and six epidemiologically linked cases across various governorates of Oman during the period. Three outbreaks with 60 cases were observed in 2016, five outbreaks with 37 cases in 2017, and two outbreaks spanned both years, totaling 94 cases. The largest outbreak occurred in Dhofar and Sharqiyah with 90 cases, followed by an outbreak in South Sharqiyah with 36 cases, as shown in Table 1 and Figure 2. Additionally, there were 40 isolated sporadic cases, constituting 17.3% of the cases, which had distinct genotypes different from those observed in the outbreak cases.

The most common genotypes isolated were B3, D4, and D8. Although these genotypes were isolated multiple times, their sequence IDs were distinct; hence, they were classified as separate outbreaks (Figure 2).

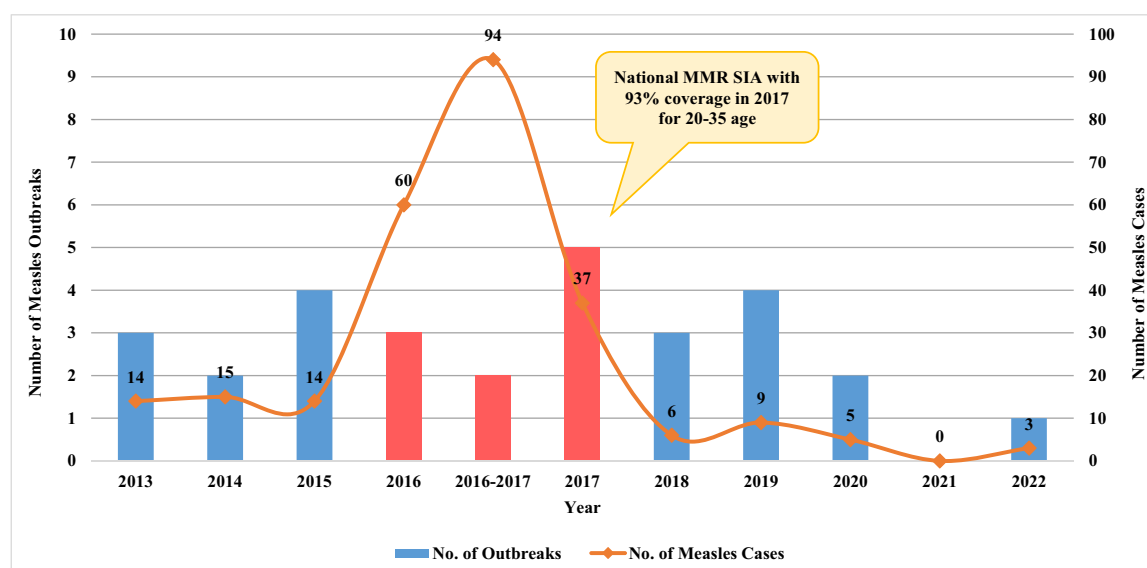


Figure 1. Number of measles outbreaks and cases from 2013 to 2022. MMR, measles, mumps, rubella; SIA, Supplementary Immunization Activity.

Table 1

Classification of clusters/outbreaks in various governorates of Oman during 2016-2017.

Cluster	Year	Governorate	Laboratory-confirmed measles (Genotype-Distinct ID)	Epidemiologically linked	Total cases	Outbreak duration (weeks)
1	2016	Dhofar 1	16 (D8-4279) + 1 (IgM + Epilinked)	3	20	28
2		North-South Sharqiyah, Dhofar	33 (D4-4577) + 3 (IgM + Epilinked)		36	17
3		Dhofar 2	4 (B3-4766 ^a)		4	2
4	2016-2017	Dhofar, South Sharqiyah, Buraimi, Muscat	76 (B3-4298) + 11 (IgM + Epilinked)	3	90	32
5		Dhofar 3	4 (B3-4770 ^a)		4	5
6	2017	Muscat, Dhofar, North Sharqiyah	13 (D8-4861 ^a)		13	11
7		Buraimi, Dhofar	2 (B3-4194 ^a)		2	10
8		Dakhiliyah, Muscat	7 (B3-2585 ^a) + 8 (IgM + Epilinked)		15	4
9		Muscat, Al Khoud	5 (B3-5014 ^a)		5	6
10		Muscat, Quriyat	1 (D8-2279) + 1 (IgM + Epi)		2	2
Total			185	6	191	

Ig, immunoglobulin.

^a Phylogenetically distinct genotype sequence ID.

Only 1% of patients had a travel history outside Oman and were classified as imported cases (one from India, one from Pakistan). Among the remaining 99% of cases, the imported index case was not identified. These cases were classified as importation-related on the basis of the isolated genotype.

The study population (191 cases), spanning 10 outbreaks from 2016 to 2017, had a mean age of 11.4 years. The median age was 9 months, with an interquartile range of 26.2 (Q1 = 0.8, Q3 = 27.0, minimum = 0.2, maximum = 55, range = 54.9). Approximately 50.7% of the cases involved infants aged <12 months, who were not yet eligible for measles vaccination. The second most affected age group were individuals aged 20-35 years, accounting for 23% of the cases (Figure 3). Approximately 4% of patients received one dose of the vaccine (partially vaccinated), and another 4% received two doses (fully vaccinated). Immunization status was unknown for 36% of the patients, most of whom were adults.

The distribution of male and female patients was 53.9% and 46.1%, respectively. Most were Omani nationals (181, 94.8%). The non-Omani cases included one each from Bangladesh and Tunisia, two each from

Egypt and Pakistan, and three from India. All of the patients had mild to moderate illness with no complications, sequelae, or death.

The duration of outbreak clusters is presented in Table 1. The largest and most extended cluster during 2016-2017 occurred in Dhofar and Sharqiyah, involving 90 cases (87 laboratory-confirmed and three epidemiologically linked cases). This cluster, attributed to genotype B3 (4298), lasted for 32 weeks.

The epidemic curve (Figure 4) illustrates that several small outbreaks occurred simultaneously but were of brief duration, preventing any single genotype from becoming established as an endemic strain over a 1-year period. This indicates that while multiple measles genotypes were present, none persisted long enough to dominate or maintain a continuous presence in the population.

Discussion

Since 1993, Oman experienced its largest and most prolonged measles outbreak in 2016-2017 [6]. The outbreak was due to multiple measles importations into a low-immunity group, comprising adults

Governorate/ Province	2016 - 3 Outbreaks (60 cases)												2017 - 5 Outbreaks (37 cases)											
	2016-2017 - 2 outbreaks (94 cases)																							
	Month												Month											
	1	2	3	4	5	6	7	8	9	10	11	12	1	2	3	4	5	6	7	8	9	10	11	12
Dhofar	2		4	4	7	2	1	1	9	10	13	11	25	4	8	2								
Buraimi											1	1												
S. Sharqiyah									2	1			1											
Muscat															1		4	1				1	1	
S. Sharqiyah							1	5	8	12	8													
N. Sharqiyah							1																	
Dakhiliyah																2	10							
Muscat																3								
Dhofar										1														
Dhofar										1	3	1	3				3							
Muscat																1	3	4	1					
N. Sharqiyah																	1							
Buraimi																		1						
Dhofar																1								

MV Genotype, Distinct Seq. ID, Name Strain, Epi - Information	D8 - 4279 - Index case not imported	D8 - 4861 - Index case not imported
	B3 - 4298, MVs/Kabul.AFG/20.2014/3 - Index case not im ported	
	D4 - 4577 - Index case not Imported	B3 - 4194, MVs/Islamabad.PAK/1.13/ - Imported from Pakistan
	B3 - 4766 - Index case not imported	B3 - 5014 - Index case not imported
	B3 - 4770 - Index case not imported	
Note: Other than outbreak cases are sporadic imported cases with different distinct sequence ID		B3 - 2585, MVs/Kansas.USA/1.12/ - Index case not imported
		D8 - 2279, MVs/Victoria.AUS/6.11/ - Imported from India

Figure 2. Distribution of measles outbreak cases genotype according to governorate during 2016-2017 (N = 191).
MV, measles virus.

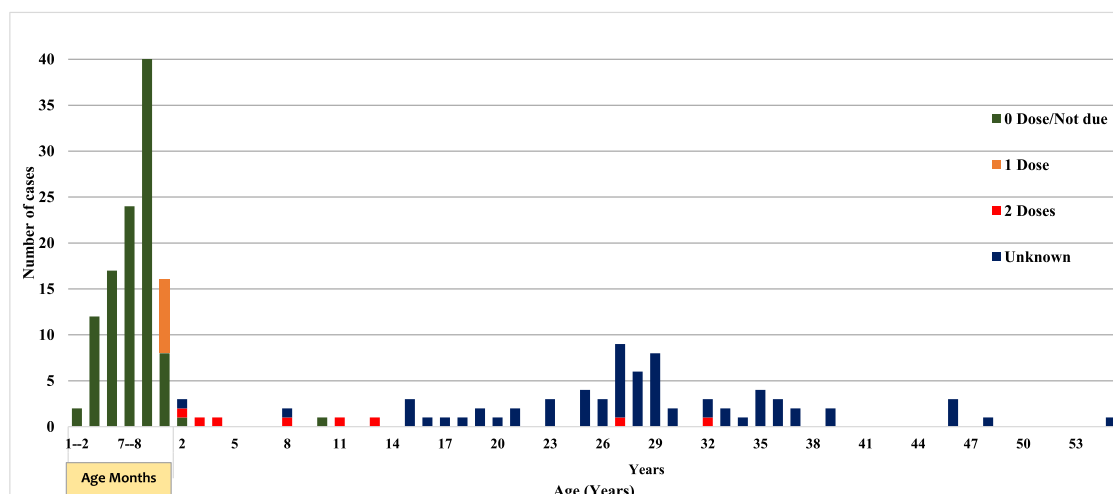


Figure 3. Measles outbreak cases according to age and vaccination status, 2016-2017 (N = 191).

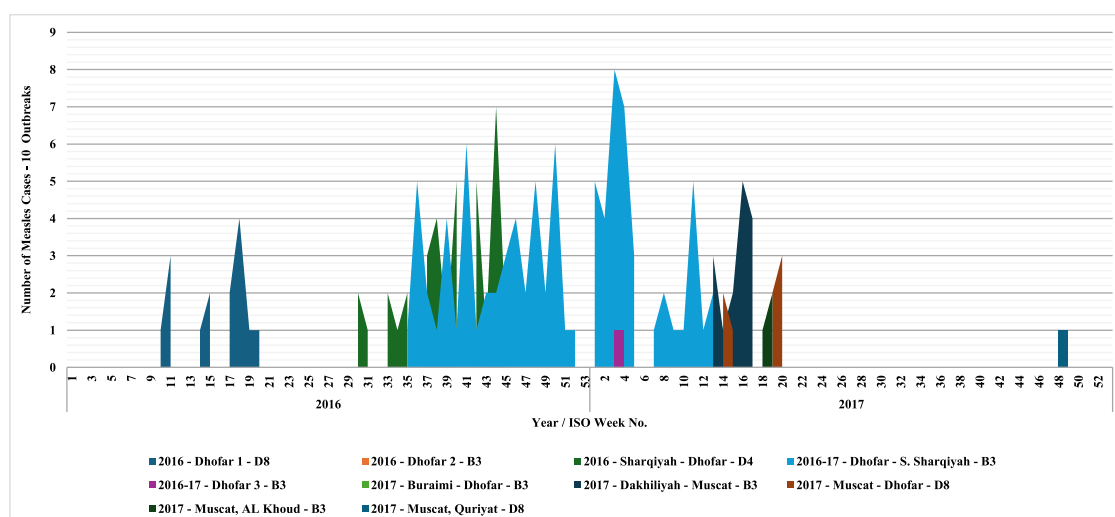


Figure 4. Measles epidemic curve of 10 clusters in Oman according to ISO week number, 2016-2017. ISO, International Organization for Standardization.

aged 20-35 years who likely received only one vaccine dose during childhood. Additionally, children aged <12 months, too young to be vaccinated, were exposed to imported or importation-related cases in Oman. Similar measles outbreaks have been reported among persons with low vaccination coverage or immunity in the United States and Europe [12,13]. In our study, 4.2% (8/191) of the individuals affected by the measles outbreaks had received two doses of vaccination. A minor portion of these data is already reflected in the recently published article from Oman [14]. Waning immunity may also be a minor contributing factor in Oman, similar to findings of various studies abroad [15,16].

Thus, measles epidemiology during the elimination phase in Oman is determined by the characteristics of the imported cases and their susceptible contacts. Interrupting measles transmission is challenging because of the complexity of the outbreak, including numerous chains of transmission driven by importation and accumulation of susceptible individuals. However, no complications or deaths were reported during this outbreak.

Many countries lost their elimination status in 2019. The Americas, which were declared free of measles in 2016, had recently reestablished endemic virus transmission in Venezuela and Brazil, leading to a loss of regional elimination status. The United States has similarly experienced several outbreaks following measles importations. However, the United States has maintained its elimination status despite several outbreaks, a situation similar to that in Oman [17].

The B3 genotype is more common in Africa and Yemen and D4 and D8 in the Indian subcontinent [18]. Oman shares a border with Yemen, and most of the expatriate population in Oman is from the Indian subcontinent. Hence, the most common genotypes isolated in our study were B3, D8, and D4. During the elimination phase, molecular characterization and sequencing of the measles virus is essential because the same genotype may differ in structure and origin. Hence, detailed genotype analysis will help in classification of measles disease outbreaks. A portion of the data from these years is already reflected in the recently published measles and rubella elimination article from Oman [14]. In our study, outbreaks involving similar genotypes were sequentially distinct and of different epidemiological origins and hence considered separate outbreaks, similar to findings from studies in South Korea [19].

A coordinated approach is crucial to ending measles outbreaks, as evidenced by Oman's successful elimination efforts after the 2016-2017 outbreak through key actions [14,17,20]:

(i) Sustained high routine vaccination coverage: Maintain 95% coverage with two doses of the measles vaccine through routine immuniza-

tion programs. (ii) Identifying and addressing immunity gaps: Conduct serosurveys to identify immunity gaps and address them through SIAs and targeted catch-up campaigns. Organize vaccination drives in expatriate communities, workplaces, and schools to address immunity gaps. (iii) Strengthening surveillance systems: Train health workers and engage communities for prompt measles case reporting. Strengthen laboratory capacity to confirm outbreaks and monitor virus strains. (iv) Rapid response to outbreaks: Deploy rapid response teams for outbreak investigations, targeted vaccinations, and public health measures such as quarantine and isolation to limit spread. (v) Public awareness and advocacy: Disseminate accurate information on vaccine safety and effectiveness, combat misinformation, and engage trusted community and religious leaders to build confidence and advocate for vaccination.

Conclusion

Our study reports that multiple measles outbreaks occurred simultaneously during 2016-2017. However, these outbreaks did not last long enough to sustain any particular genotype to establish itself as an endemic strain. It is important to implement immediate control measures for reported imported measles cases and to conduct population immunity studies to identify immunity gaps, followed by SIAs.

Declarations of competing interest

The authors have no competing interests to declare.

Funding

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Ethics committee approval and written informed consent

The Sultanate of Oman Ministry of Health approved the publication of the data. This study is a retrospective, record-based analysis of routine surveillance data.

Author contributions

Prakash KP was involved in writing the manuscript, preparation of figures and tables and data analysis. Noura Al-Farsi was involved in-charge of fever and rash surveillance program and data collection.

Samira Al-Mahruqi and Aisha Al-Busaidy are responsible for laboratory aspects of the study. Bader Al-Rawahi, Seif Al-Abri, Amal Al-Maani are disease surveillance and control program in-charge oversaw the activities and review manuscript.

Data availability statement

The data are available upon request from the Sultanate of Oman Ministry of Health. Additionally, laboratory data are routinely shared with the World Health Organization.

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