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A cluster of measles linked to an imported case, Finland, 2017

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One imported and five secondary cases of measles were detected in Finland between June and August 2017. The measles sequences available for five laboratory-confirmed cases were identical and belonged to serotype D8. The large number of potentially exposed Finnish and foreign individuals called for close cooperation of national and international public health authorities and other stakeholders. Raising awareness among healthcare providers and ensuring universally high vaccination coverage is crucial to prevent future clusters and outbreaks.

A young Italian adult was diagnosed with measles in Finland in June 2017. During the stay in Finland and subsequent travel to Estonia, the case exposed altogether several hundred persons to measles. As of 11 August, five secondary cases of measles have been detected. As the investigation is still ongoing, we present here the preliminary findings and implemented control measures regarding this cluster of measles.

Case definition

In this investigation, a suspected case was any person who met clinical criteria (fever and maculopapular rash and cough/coryza/conjunctivitis). A probable case was any person who met clinical criteria and had an epidemiological link to a confirmed case. Confirmed cases were probable cases with laboratory evidence of infection with measles virus (detection of viral RNA with PCR and/or a positive IgM in serum).

Description of the cluster

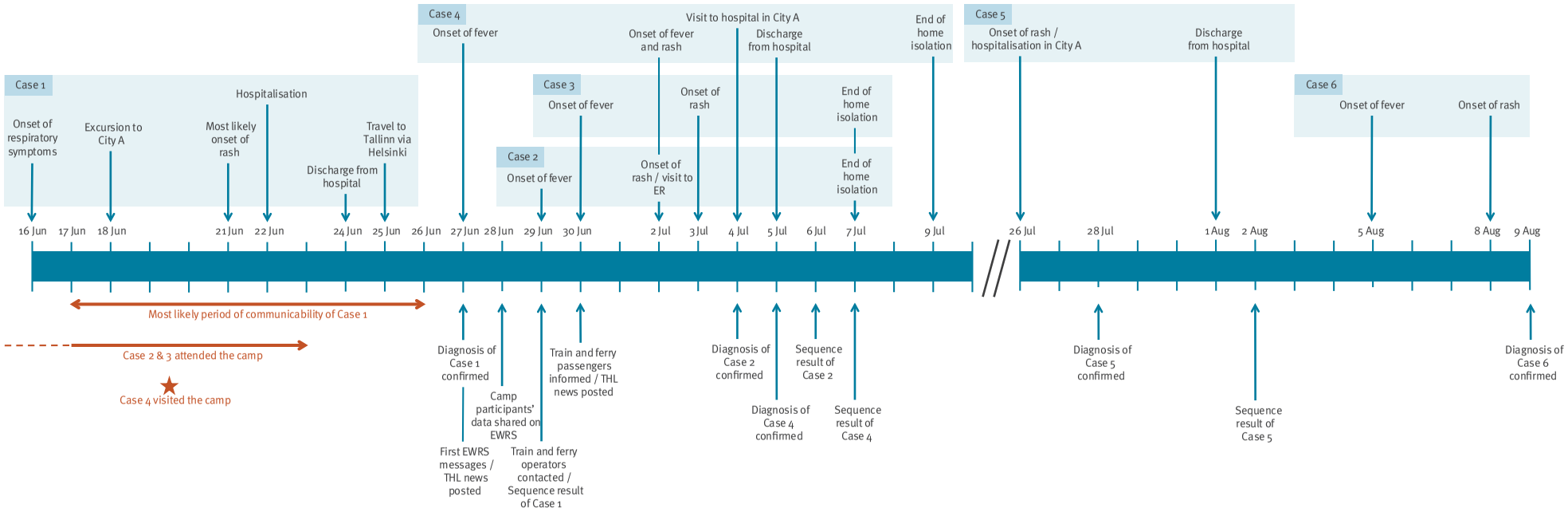
Index Case 1 was a young Italian adult who arrived in Finland on 11 June 2017 and attended an international camp in Finland from 12 to 25 June (Figure 1).

After developing fever and respiratory symptoms on 16 June and rash on 21 June, Case 1 was admitted to the hospital of City A and was isolated and monitored because enterovirus infection or measles was suspected. Serum and throat specimens were taken on 22 June. While the confirmatory laboratory results were still pending, the case was discharged and returned to the camp premises on 24 June. On 25 June, Case 1 travelled to Helsinki by train (without a designated seat, 3.5 hours) and to Tallinn by ferry (no cabin booked, 2.5 hours), staying one night before flying back to Italy. On 27 June, Case 1 was laboratory-confirmed for measles infection. The case self-reported to be vaccinated with two doses of measles-containing vaccine; however, the laboratory results contradicted this as the case tested negative for measles-specific IgG antibodies (Table).

Subsequently, five secondary cases of measles were identified (Figures 1 and 2). Four of them were laboratory-confirmed (Cases 2, 4, 5 and 6). Case 3 was classified as a probable case (no laboratory testing because of parental objection). Cases 2 and 3 were adolescent siblings living in City A. Both attended a summer camp organised at the same premises as the international camp. Both were placed in home isolation. Case 4 was a person working in a cafeteria in City B who had visited the camp premises on 19 June. Cases 2, 3 and 4 had lunch in the same canteen used by other camp attendees including Case 1. Epidemiological investigations for Case 5 are still ongoing but so far no link between other cases has been established. It is possible that there is an unknown case in the transmission chain. Case 6 was a close contact of Case 5, identified during contact tracing. The case had been vaccinated with two doses of the measles-mumps-rubella (MMR)

Figure 1

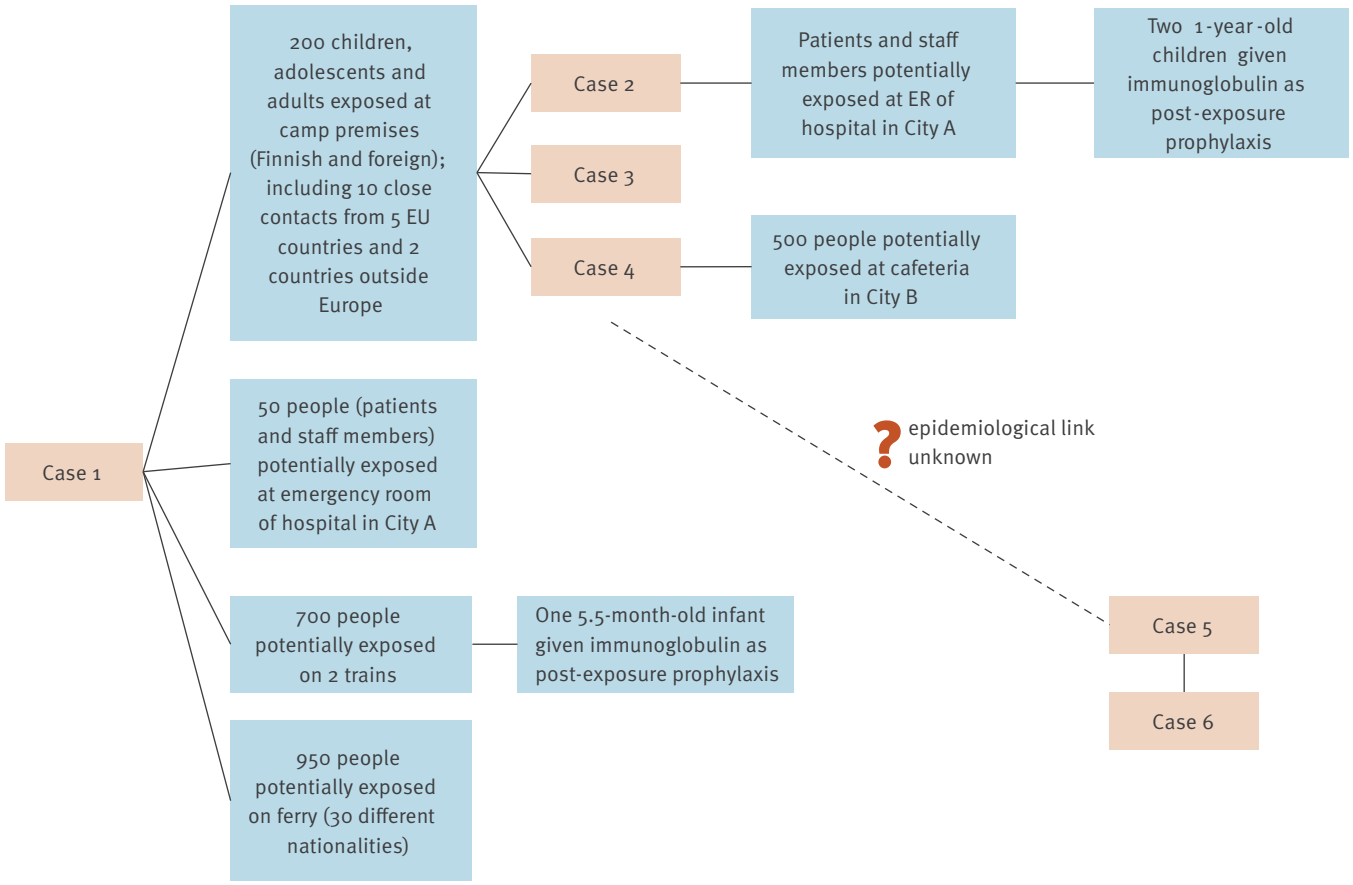
Timeline of the events, measles cases linked to importation, Finland, June–July 2017 (n = 6)



ER: emergency room; EWRS: Early Warning and Response System; THL: National Institute for Health and Welfare.

Figure 2

Epidemiological links between confirmed measles cases and potentially exposed groups, Finland, June–July 2017 (n = 6)



ER: emergency room; EU: European Union.

vaccine in childhood; all other secondary cases were unvaccinated (Table).

Laboratory findings

Healthcare providers were asked to send all clinical samples from suspected measles cases to the measles reference laboratory of the Finnish National Institute for Health and Welfare (THL). Measles sequences available for five cases were identical and genotyped as D8 (Table). Based on the Measles Nucleotide Surveillance database, this strain was identical to strains isolated in Italy during 2017 and to a strain identified in a British traveller, and it shared very high nucleotide similarity (›99.78%) with more than 600 sequences detected on five continents between 2015 and 2017, indicating recent global spread of nearly identical measles viruses [1,2].

Six suspected cases were discarded after laboratory analysis. In addition, three potentially exposed, asymptomatic people tested negative for measles.

Control measures

Following the laboratory confirmation of Case 1 on 27 June, local, regional and national public health authorities promptly undertook contact tracing for the index and all subsequently identified cases. The contacts of suspected cases were mapped already while waiting for confirmation. Potentially exposed people were contacted after each case had been confirmed. THL communicated all available details of potentially exposed individuals of foreign nationality to the respective countries of origin. Countries in the European Union/European Economic Area (EU/EEA) were contacted through the Early Warning and Response System (EWRS), and non-EU/EEA countries through the World Health Organization (WHO) International Health Regulations (IHR) National Focal Points.

Hundreds of people were estimated to be potentially exposed to the confirmed cases (Figure 2). However, the degree and likelihood of exposure differed. Potentially exposed people were instructed to check their measles immunity status and to get vaccinated if necessary. They were also informed about the actions required if they experienced symptoms compatible with measles. Whenever possible, local health authorities contacted potentially exposed individuals personally. Other means of communicating this information included the publication of bulletins, both locally and by THL.

Table

Summary of the laboratory findings measles cases linked to importation, Finland, June–July 2017 (n = 6)

	Vaccination status	Serology		qPCR	Genotype
		IgG	IgM		
Case 1	Unvaccinated				
Serum		Negative	Positive	ND	ND
Throat swab		ND	ND	Positive (Ct 25.76)	D8
Case 2	Unvaccinated				
Serum		Negative	Negative	ND	ND
Throat swab		ND	ND	Positive (Ct 23.61)	D8
Case 4	Unvaccinated				
Serum		Positive	Positive	ND	ND
Throat swab		ND	ND	Positive (Ct 23.77)	D8
Case 5	Unvaccinated				
Serum		Low positive	Positive	ND	ND
Throat swab		ND	ND	Positive (Ct 28.94)	D8
Case 6	2x MMR				
Serum		Positive	Negative	ND	ND
Throat swab		ND	ND	Positive (Ct 26.79)	D8

Ct: cycle threshold; ND: not done; MMR: measles-mumps-rubella vaccine; qPCR: real-time PCR; THL: National Institute for Health and Welfare.
Detection of measles-specific IgG and IgM antibodies was performed in serum samples (Euroimmun AG, Germany). Viral RNA was detected by real-time PCR directed against measles nucleoprotein gene. Infections with rubella virus and parvovirus B19 were ruled out. The sequences obtained for Cases 1, 2, 4, 5 and 6 are available via the MeaNS database (sequence ID: 114109, 114110, 114456, 116427 and 113656) and GenBank (accession numbers: MF409015, MF443206, and MF448447; accession numbers for Cases 5 and 6 not yet available).

In addition, all passengers on the involved trains and ferry for whom contact information (email address) was available were contacted through the respective operators in several languages. Healthcare providers were informed about the measles cases and given instructions on the actions required (prompt sampling, specimen shipment and isolation) if measles was suspected. The media also followed the event actively.

Discussion

Measles outbreaks continue to occur in several EU/EEA countries, affecting especially countries where the vaccination coverage with two doses of the MMR vaccine is below the 95–99% threshold [3-6]. This cluster highlights the risk of importation of the measles virus by travellers originating from countries with intense transmission of the virus (a widespread outbreak is ongoing in Italy [3]), to countries without autochthonous transmission where the disease may spread among unprotected citizens.

In Finland, two doses of the MMR vaccine have been administered at 14–18 months and six years of age since the introduction of the vaccine in 1982 [7]. The national coverage has remained above 95% from the mid-1990s [8,9]. Since 1996, autochthonous measles transmission has stopped, and all transmission chains have been traced back to index cases who contracted the disease abroad [10]. However, in 2017, the coverage for birth cohort 2014 with at least one dose of MMR vaccine remains under 95% in one third of all Finnish health centre areas [11].

Cases 2, 3 and 4 were individuals belonging to the same immigrant community residing in Finland. The vaccination status of immigrant groups other than asylum seekers and refugees is currently not systematically screened, increasing the risk for the spread of measles and other vaccine-preventable diseases. Currently, some municipalities organise an introductory/screening visit to their healthcare centre when an immigrant receives rights to use the municipal healthcare services, but many do not make use of this opportunity. While children are followed up at well baby centres and schools, and some of the adults in occupational healthcare, there are other groups of immigrants who may live in Finland for years without any contact to healthcare services. The screening visits offered to immigrants should be promoted and used to check and update vaccination status.

In the absence of autochthonous transmission, recognition and control of measles may pose a challenge to healthcare professionals and public health authorities. Even in a highly immunised population, pockets of susceptible individuals may exist. The possibility of measles must be considered when encountering patients with compatible symptoms, especially travellers from a country or region known to have measles outbreaks. As Case 1 claimed to have been twice vaccinated, measles was not considered as the most likely cause

of symptoms, and the case was discharged while the laboratory results were pending. However, the index case increased the awareness of physicians, and the subsequent cases were recognised promptly. Thanks to increased awareness, three asymptomatic, potentially exposed people were also tested for measles.

During this event, diagnostic tests for Cases 1 and 2 were delayed because of several reasons (public holidays, misunderstandings about specimen shipment). With highly contagious diseases such as measles, early detection and laboratory diagnostics as well as isolation of patients during the infectious period are essential to prevent further disease transmission. National guidelines for investigation and control of measles in Finland exist, and awareness of the guidelines among the healthcare professionals needs strengthening. This relatively rare event in Finland underlined the importance of having reference laboratory functions and epidemiological expertise integrated at the public health institute, facilitating efficient response to similar public health threats. Maintaining the integration was one priority recommendation in the recent Joint External Evaluation of Finland's IHR core capacities [12].

This cluster also emphasised the importance of national and international cooperation of public health authorities, transportation operators and the media. Contact tracing in mass gatherings and public transportation may prove challenging, especially when individuals representing various nationalities have been present. When reaching out to individuals personally is not feasible, the role of timely and accurate media coverage as well as the assistance of transportation operators and their information channels become significant. In this instance, the train operator sent a message to all the 398 customers with registered email address travelling on the same train as Case 1, and 274 of them opened it. A somewhat lower opening rate (58%) was observed among ferry passengers (data only available for Finnish passengers).

Conclusion

In Finland, a country with nationally high MMR vaccination coverage, extensive outbreaks of measles are unlikely to occur. However, transmission chains among unimmunised individuals linked to an imported case are possible. A prompt response and the cooperation of health authorities, the media and possible other stakeholders are crucial to interrupt transmission chains as soon as possible. Ensuring universally high vaccination coverage is essential to prevent clusters and outbreaks in the future.

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Conflict of interest

None declared.

Authors' contributions

All authors contributed to the investigation and were involved in the discussion of the control measures. ES contributed to the data collection, prepared Figure 2 and wrote the manuscript. VZ prepared Figure 1 and wrote the manuscript. ES and VZ equally contributed to the manuscript. SV was the infectious disease specialist on duty during the event and provided the clinical details of the cases. SM contributed to the data collection. UE reviewed the manuscript. JvB wrote the manuscript. AH and MK provided laboratory input. CSK reviewed the manuscript. TP led the response and reviewed the manuscript. JS led the response, coordinated data collection and reviewed the manuscript. All authors read and approved the final manuscript.

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Geneva: WHO; March 2017. Licence: CC BY-NC-SA 3.0 IGO. Available from: https://extranet.who.int/spp/sites/default/files/jeeta/WHO-WHE-CPI-2017.24-Report-eng.pdf

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Ongoing large measles outbreak with nosocomial transmission in Milan, northern Italy, March–August 2017

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A large measles outbreak has been ongoing in Milan and surrounding areas. From 1 March to 30 June 2017, 203 measles cases were laboratory-confirmed (108 sporadic cases and 95 related to 47 clusters). Phylogenetic analysis revealed the co-circulation of two different genotypes, D8 and B3. Both genotypes caused nosocomial clusters in two hospitals. The rapid analysis of epidemiological and phylogenetic data allowed effective surveillance and tracking of transmission pathways.

A large measles outbreak has been ongoing in Milan and surrounding areas, a densely populated area with nearly 4 million inhabitants. Rapid and active surveillance was set up by the Subnational Reference Laboratories (SRL) Milan, established as part of the measles and rubella surveillance network MoRoNet [1] in March 2017, with 303 investigated cases at the time of submission of this report. We present a detailed analysis of the period 1 March to 30 June 2017, with the aim to conduct a complete and rapid characterisation of wild-type measles virus (MV) strains circulating.

Confirmation and investigation of cases and clusters in Milan

From 1 March to 30 June 2017, 233 suspected cases of measles were investigated: there were 203 (87%) laboratory-confirmed cases (median age: 30 years; range: 2 months–77 years) and 30 (13%) were discarded. Overall 60% (n = 121) of the confirmed cases were individuals aged 15–39 years and 6% (n = 12) were ≤ 1 year of age; 88% (n = 179) were not vaccinated and 12% (n = 24) were vaccinated (six with two doses of measles-mumps-rubella (MMR) vaccine, 10 with one dose, and eight did not know the number of doses). According to the epidemiological regional database, 108 of 203 were sporadic cases and 95 were related to 47 clusters. Cases were classified as sporadic when an epidemiological link to other cases could not be established.

Molecular surveillance for cases and clusters

The genotype of MV strains was successfully identified in 187 of 203 (92%) of the confirmed cases by sequencing the highly variable region of nucleoprotein (N) gene (N-450) [2]. Phylogenetic analysis revealed that the MV strains belonged to genotypes D8 and B3.

The most common genotype detected was genotype D8 (86%; 160/187 cases) which was related to 77 cases in 42 clusters and 83 sporadic cases. All of the D8 cases and clusters were autochthonous or from unknown source.

In March 2017, the B3 genotype was detected in five imported cases: two sporadic cases and three cases which subsequently caused three import-related clusters. From April to end of June 2017, a further 14 autochthonous sporadic cases and one cluster were reported. The geographical and temporal distribution, respectively, of sporadic cases and clusters related to D8 and B3 genotypes are shown in Figure 1 and Figure 2.

Measles virus genotype D8

Phylogenetic analysis showed that all the D8 sequences (n = 160) fell into the Osaka lineage (MVi/Osaka. JPN/29.15; similarity range: 99–100%). From March to May, D8 MV strains mainly caused clusters in work and family settings, which occurred principally in the north-eastern area of Milan. During the week starting

Figure 1

Geographical distribution of measles cases and clusters, with genotypes, Milan, 1 March–30 June 2017 (n = 187 cases)

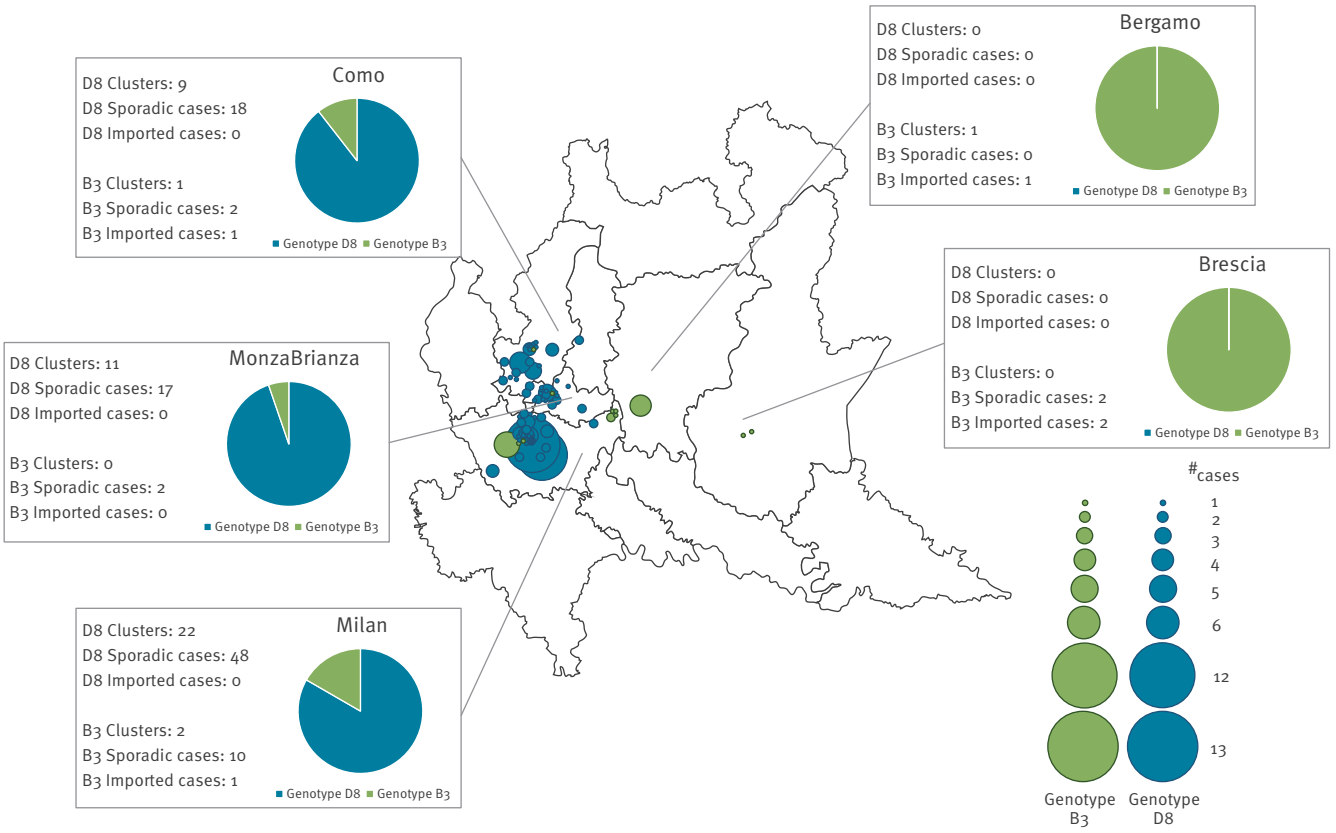
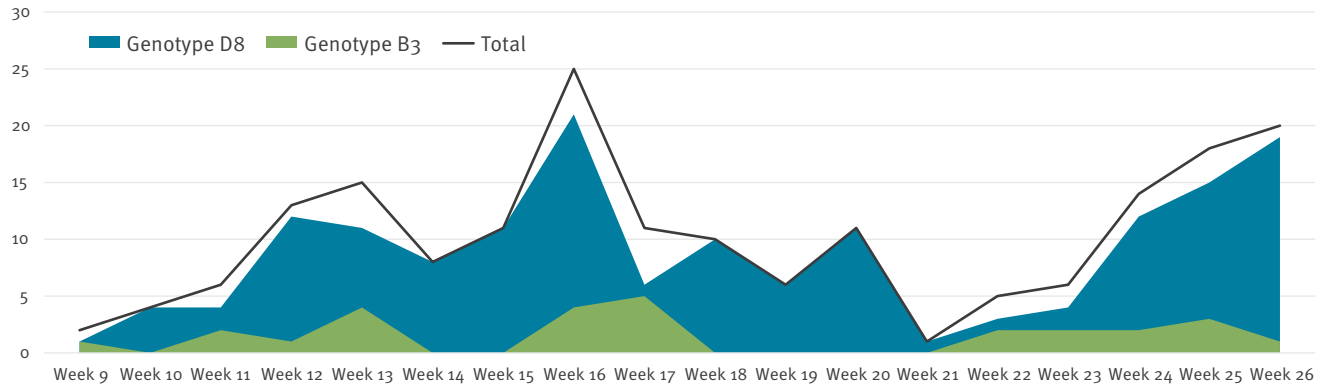


Figure 2

Temporal distribution of measles cases and genotypes detected, Milan, 1 March–30 June 2017 (n = 187)



on 27 March 2017, a serious family cluster affected three cases causing the death of one of them. The D8 MV strain was isolated from the biological samples of one of these cases.

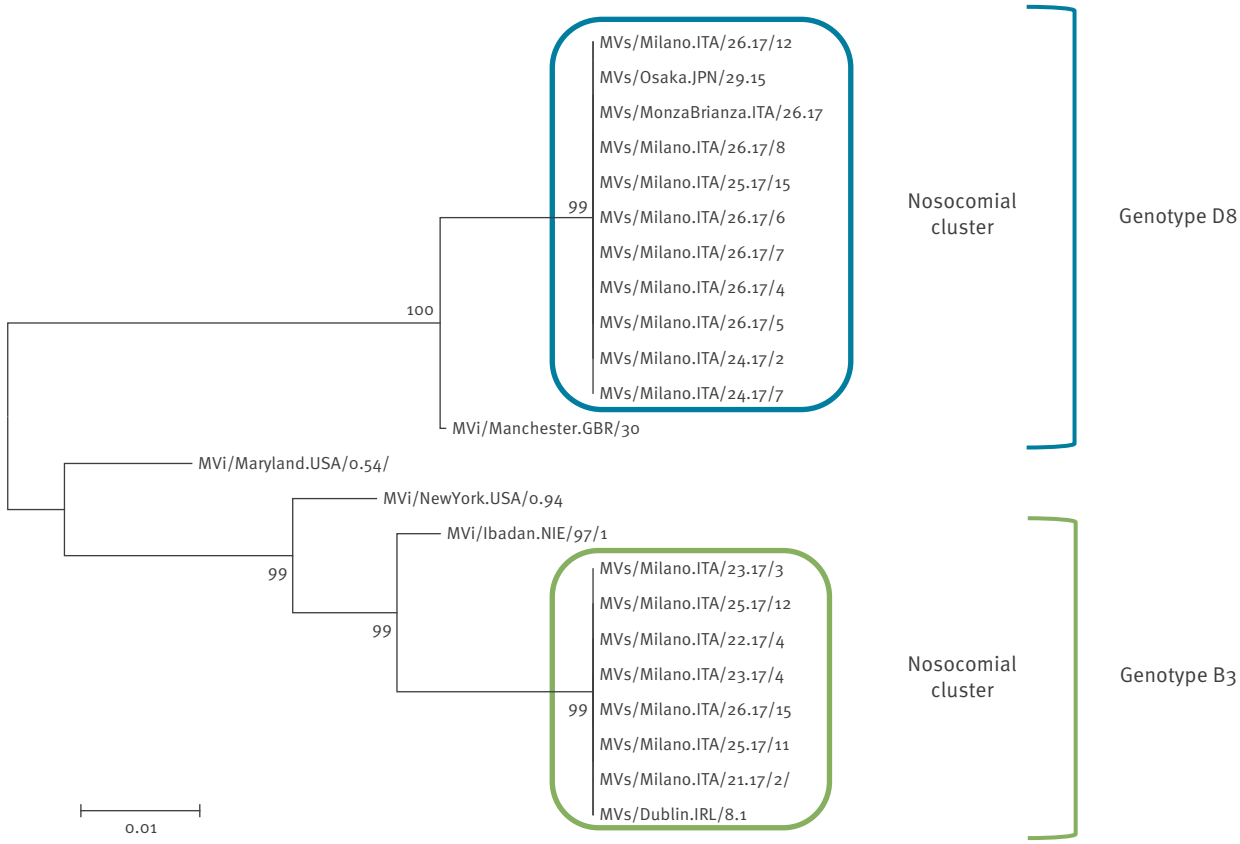
In June 2017, the D8 Osaka variant spread through the city of Milan and caused a nosocomial cluster in a hospital. Based on epidemiological data, a link was established between 12 cases: eight healthcare workers (HCWs), three patients and one visitor. Phylogenetic analysis showed that the nine sequences obtained were 100% identical. The match of epidemiological data and phylogenetic analysis highlighted a single transmission chain for all cases (Figure 3).

Measles virus genotype B3

Phylogenetic analysis showed that all B3 sequences (n = 27) were identical to the variant Dublin (MVs/Dublin.IRL/8.16; similarity: 100%) which is circulating in European countries and responsible for an ongoing epidemic in Romania [3].

Figure 3

Neighbour-joining tree for nucleotide sequences of measles virus D8 and B3 variants causing nosocomial clusters in two hospitals, Milan, 1 March–30 June 2017 (n = 16)



The evolutionary history was inferred using the neighbour-joining method. The evolutionary distances were computed using the Kimura 2-parameter method. Evolutionary analyses were conducted in MEGA6.

The B3 Dublin variant was first introduced in the east of Milan at the beginning of March 2017, and there was an epidemiological link to the Roma community in France. By the end of March, this variant was detected in a sporadic case returning from Piedmont (northern Italy). Subsequently, the same variant was isolated in a cluster caused by an index case returning from the Apulia Region (southern Italy) and in a cluster that was imported from Romania. In April 2017, genotype B3 was identified in a sporadic case returning from the Lazio Region (central Italy).

During May and June 2017, 12 autochthonous cases were notified in the eastern and south-eastern suburbs of Milan. In June, three nosocomial clusters were identified in an emergency department. Although initially reported as unrelated clusters, the phylogenetic analysis showed a single source of transmission (n = 7, two HCWs, four patients, and one visitor) (Figure 3).

Conclusions

Eliminating measles and rubella is a core goal of World Health Organization European Region Member States. Effective surveillance is essential for eliminating measles and rubella and its verification [4]. Since the beginning of 2017 and up to 6 August, the Italian Ministry of Health has reported 4,087 cases of measles and three deaths. Most cases occurred in Piedmont and Lombardy (northern Italy), Tuscany, Lazio and Abruzzo (central Italy) and Sicily (southern Italy). Most were older than 15 years (median age: 27 years) and 89% of the cases were not vaccinated. Overall, 42% of the cases were hospitalised and 277 cases were reported among HCWs [5].

Timely measles surveillance is critical to disease control. Identifying and confirming suspected measles cases through surveillance allows early detection of outbreaks and analysis of ongoing transmission in order to mount more effective vaccination measures. MV genotyping can play an important role in tracking transmission pathways during outbreak investigations [6].

From March to June 2017, the genotypes D8 and B3 co-circulated in Milan and surrounding areas. The most common genotype detected was genotype D8, related to 83 sporadic cases and 42 clusters. The high

similarity between the D8 MV strains, all belonging to the Osaka lineage, suggests a unique initiating transmission event. This is the first evidence of the Osaka D8 variant in northern Italy, which seems to be replacing the D8 variants that had been circulating in this area since 2013 [7,8].

Moreover, our data show multiple imported cases of B3 MV strains which subsequently spread across Italy and caused several autochthonous cases and clusters. The B3 Dublin variant has replaced the B3 variant Como that had been present in this Italian area from August 2015 to November 2016 [9].

By the end of June 2017, D8 MV strains and B3 MV strains had caused clusters in two major Milanese hospitals. In August (current month), the epidemic is still ongoing and the number of notified cases during the month of July was almost twice the number of cases notified in June. Other authors have already reported that where there is evidence of both nosocomial and community transmission of measles, nosocomial transmission appeared to precede community transmission with a peak of hospital-acquired cases occurring almost two weeks before the peak of the community outbreak [10].

In conclusion, the suboptimal immunisation level (92.5% vaccination coverage rate in Lombardy Region; [11]) and the consequent accumulation of susceptible population have led to an increase in the transmission of measles in northern Italy with detrimental effects on both public health and ongoing measles elimination efforts. Furthermore, the nosocomial outbreaks highlight the importance of improving measles vaccination coverage of healthcare workers.

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Conflict of interest

None declared.

Authors' contributions

A Amendola coordinated virological/epidemiological investigation and laboratory activities and wrote the manuscript. S Bianchi, ER Frati, G Ciceri and D Colzani confirmed measles cases and performed genotyping and phylogenetic analysis of the measles virus sequences isolated from cases in the Lombardy region and interpreted the results. M Faccini, S Senatore, A Lamberti investigated measles cases. M Gramegna and D Cereda coordinated surveillance and control activities in Lombardy region. F Magurano, M Baggieri, L Nicoletti (MoRoNet National Reference Laboratory) coordinated the virological investigation and supervised phylogenetic analyses. E Tanzi supervised virological/epidemiological investigation and laboratory activities and wrote the manuscript. All the authors reviewed and approved the final manuscript.

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A nosocomial measles outbreak in Italy, February-April 2017

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We describe a nosocomial outbreak of measles that occurred in an Italian hospital during the first months of 2017, involving 35 persons and including healthcare workers, support personnel working in the hospital, visitors and community contacts. Late diagnosis of the first case, support personnel not being promptly recognised as hospital workers and diffusion of the infection in the emergency department had a major role in sustaining this outbreak.

Measles vaccination coverage is suboptimal in Italy (ranging between 85.4% and 90.6% for one dose during the period 2007–2016) [1], which has led to large pockets of susceptible adults. We describe an outbreak in an Italian hospital between February and April 2017 among healthcare workers (HCW), hospital support personnel (hospital workers in activities not involving direct contact with patients), hospital visitors and community contacts. This outbreak was part of a wider epidemic in Italy that started in January 2017 and has, as at 30 July 2017, led to 4,001 cases nationwide (275 in HCW) [2].

Outbreak description

A HCW was referred to the emergency department (ED) of an Italian hospital for a rash developed after taking antibiotics for a mild cough and coryza. The rash was considered an allergic reaction to the antibiotic and the HCW was admitted to the hospital inpatient clinic. Three days later, the HCW's child was admitted to hospital for a rash diagnosed as due to a non-communicable systemic disease.

Subsequent serology showed that both the HCW and the child had measles. The origin of the infection for the index case is still unknown. It should be noted, however, that at least 10 community cases of measles occurred in the same period in the area of residence of the HCW.

Using the standard case definition of the European Commission [3], a total of 34 measles cases during the following weeks were identified by tracing the contacts of the index case. Among them, 15 were HCWs, five were support personnel, four were hospital visitors and 11 were community contacts of the above cases.

The secondary cases to the index (n = 8) occurred in two of the HCW's relatives, in four other HCWs, and in two support workers who were not immediately recognised as belonging to the hospital outbreak. One of the secondary cases, a HCW, was in service until the onset of symptoms, accessing all rooms on two inpatient wards.

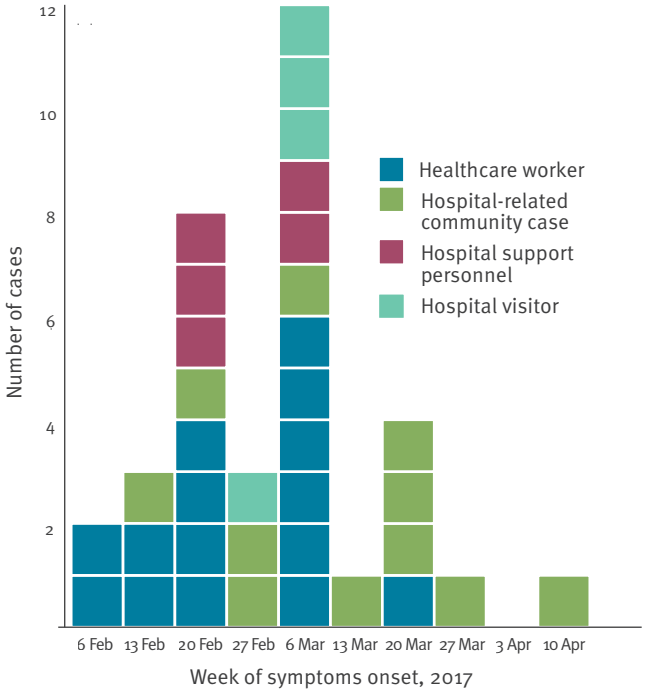
Tertiary cases (n = 6) involved the family of this HCW, three HCWs and a member of support personnel.

Two weeks after the admission of the index case, two of the HCWs belonging to tertiary cases presented during the night to the ED where they stayed for nearly 10 hours. An additional 15 cases could be traced following this single exposure window, namely seven HCWs, two support workers, three relatives of theirs and three visitors to the ED during the time the two HCWs were present. One more community case was related to contact outside hospital with one of the tertiary HCW cases.

Additional cases were related to a visitor at one of the involved inpatient wards, who probably got in contact with one of the tertiary cases who were HCW during

Figure 1

Confirmed measles cases by week of symptom onset and role in hospital setting, nosocomial outbreak, Italy, 5 February–13 April 2017 (n = 35)



the incubation period and generated three cases in the community, among them a family paediatrician.

Figure 1 and Figure 2 show the epidemic curve and the outbreak tree.

Characteristics of cases

Six cases occurred in children up to nine years of age, while two occurred in adolescents between 10 and 17 years and the majority of cases (n = 27) in adults 18 years and older. Figure 3 describes the age distribution among different categories of cases.

Vaccination status was known for 24 cases. Sixteen were unvaccinated (two children, 14 adults), two had received one dose, one a full course of two doses, and five cases occurred in contacts who received one dose of post-exposure vaccination. Of the five contacts who received post exposure vaccine, one was an infant younger than 1 year for whom information about the date of vaccination is not available; for the other four, the delay between presumed contact date and immunisation was 3 days in two cases, 6 and 12 days for the remaining two cases. Among the HCWs, two were vaccinated, 11 were unvaccinated and for two of them the data was unavailable. Among the five cases belonging to support personnel two were unvaccinated and the status was unknown for the remaining three.

Genotyping was available for three cases: genotype B3, subtype 3.1 was found in all of them.

Control measures

For each case recorded in the hospital, exposed contacts among personnel and patients were identified and offered a post-exposure vaccination. The Hospital Occupational Health Unit reviewed the immunisation status of all the personnel of the involved units, with an active offer of vaccination for those who were negative. At present, data on the results of this intervention cannot be provided and will be described in a further publication from our occupational health unit. An internal hospital procedure was issued, mandating that all cases with measles-like symptoms were to be assessed in the infectious diseases unit directly rather than passing through the ED.

Regular communication about the epidemiological investigation between the local health authority and the hospital's epidemiology unit was established in order to share information about all cases occurring in the community. This allowed identification of additional cases among hospital visitors.

Conclusion and recommendations

Measles elimination in Europe, despite the immunisation efforts, is still jeopardised by recurrent outbreaks in susceptible populations [4-7]. Nosocomial transmission of measles is an important and emerging way of spreading the infection [8-11]. Anyone staying in the hospital environment, regardless of role, can be affected because measles is highly contagious and persists in the environment for up to 2 hours, thus requiring appropriate and timely infection control measures [12,13].

Considering that transmission may occur 3 days before the onset of rash, early diagnosis when only non-specific preliminary symptoms (cough, coryza and conjunctivitis) are present is crucial for containing the outbreak [14].

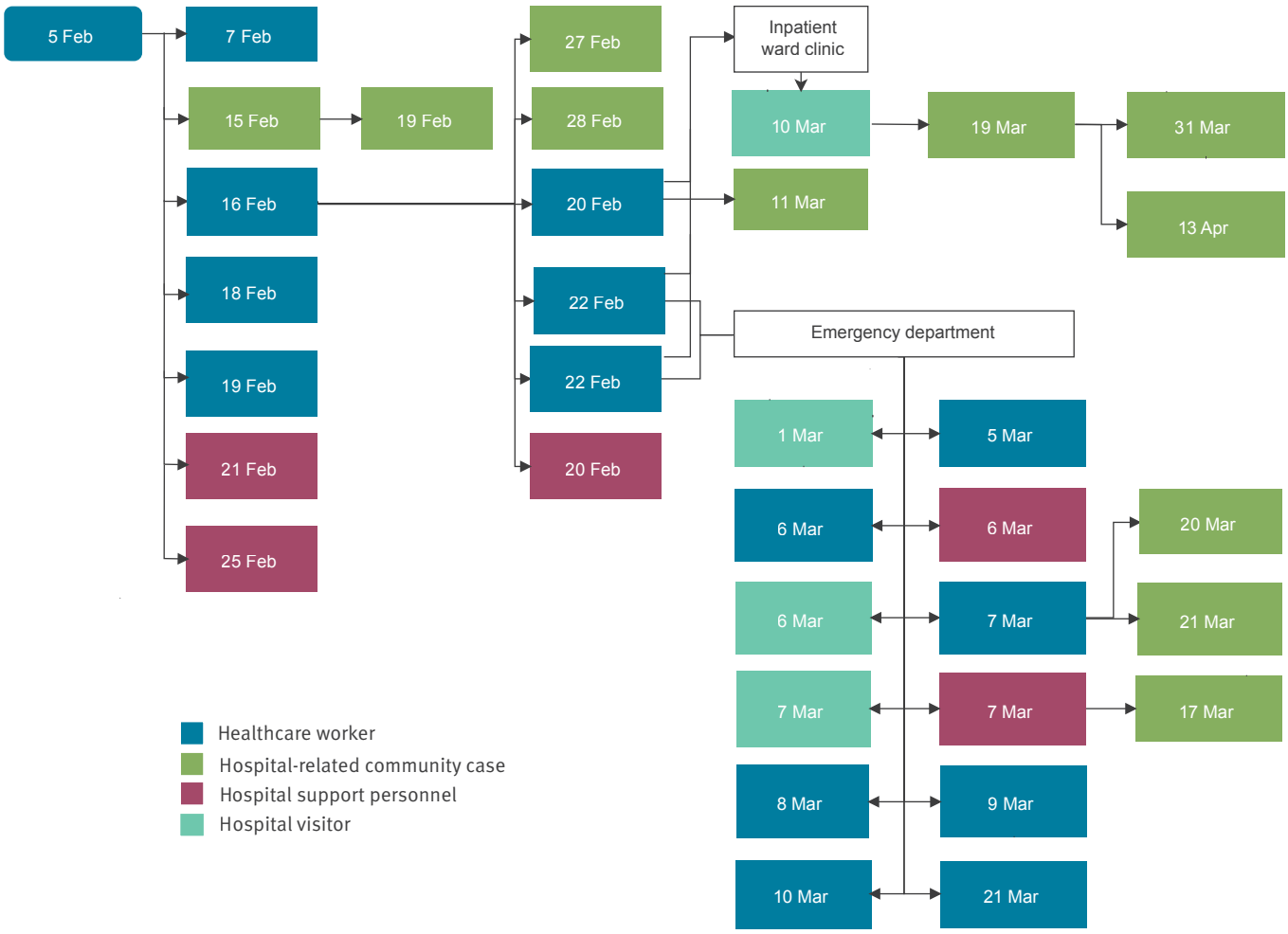
A single exposure window, that occurred two weeks after the admission of the index case, when two cases were present in the ED, resulted in further 15 cases. Appropriate procedures are needed for patients with suspect transmissible infection in the ED, an issue not limited to measles but shared with several other highly infective conditions [13].

A two-dose vaccination is the most effective measure to prevent measles [15]. This is of crucial importance for HCWs, with a view to their higher risk of exposure and of transmission to vulnerable patients.

However, it should be noted that in at least five cases in this outbreak, measles occurred in personnel working in the hospital environment in support functions, highlighting the need to take into consideration the role of such personnel in the spread of the infection. Given that most of the support personnel belong to outsourced services, coordination is needed between occupational health unit and occupational health responsible of outsourced services.

Figure 2

Measles nosocomial outbreak tree with date of symptom onset and role in hospital setting, nosocomial outbreak, Italy, 5 February–13 April 2017 (n = 35)



Conflict of interest

None declared.

Authors' contributions

AP and FQ designed the study, analysed data, drafted and revised the manuscript. GPP and PLL advised on analysis, drafted and revised the manuscript. AP FA GP BB and GG performed the epidemiological investigation and collected data. MLV and MP performed the genotyping of biological samples and revised the manuscript. All Authors contributed to the final approval of the version to be published.

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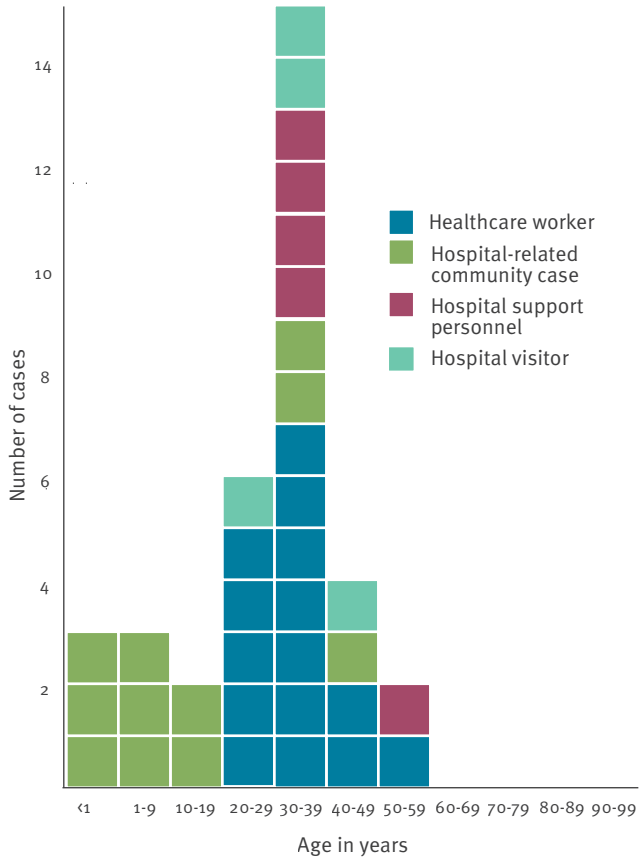
Figure 3

Confirmed measles cases by age group and role in hospital setting, nosocomial outbreak, Italy, 5 February–13 April 2017 (n = 35)



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Imported case of Middle East respiratory syndrome coronavirus (MERS-CoV) infection from Oman to Thailand, June 2015

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Thailand reported the first Middle East respiratory syndrome (MERS) case on 18 June 2015 (day 4) in an Omani patient with heart condition who was diagnosed with pneumonia on hospital admission on 15 June 2015 (day 1). Two false negative RT-PCR on upper respiratory tract samples on days 2 and 3 led to a 48-hour diagnosis delay and a decision to transfer the patient out of the negative pressure unit (NPU). Subsequent examination of sputum later on day 3 confirmed MERS coronavirus (MERS-CoV) infection. The patient was immediately moved back into the NPU and then transferred to Bamrasnaradura Infectious Disease Institute. Over 170 contacts were traced; 48 were quarantined and 122 self-monitored for symptoms. High-risk close contacts exhibiting no symptoms, and whose laboratory testing on the 12th day after exposure was negative, were released on the 14th day. The Omani Ministry of Health (MOH) was immediately notified using the International Health Regulation (IHR) mechanism. Outbreak investigation was conducted in Oman, and was both published on the World Health Organization (WHO) intranet and shared with Thailand's IHR focal point. The key to successful infection control, with no secondary transmission, were the collaborative efforts among hospitals, laboratories and MOHs of both countries.

Introduction

Background

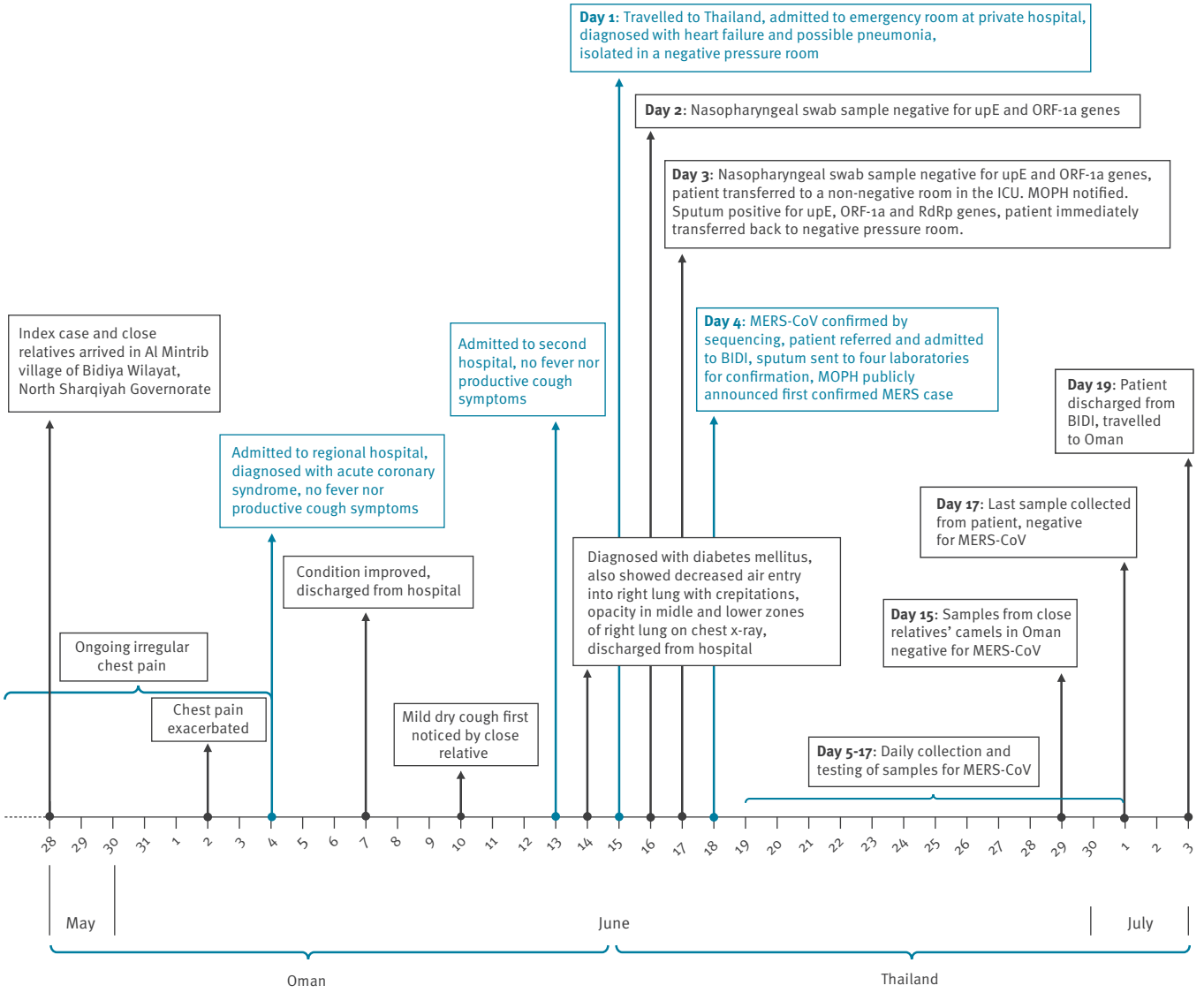
From 2012 to 21 July 2017, there have been 2,040 reported laboratory-confirmed cases and 712 deaths from Middle East respiratory syndrome coronavirus (MERS-CoV) infection in 27 countries [1]. A single imported case of Middle East respiratory syndrome (MERS) in South Korea, identified on 20 May 2015, resulted in 150 laboratory-confirmed cases, amplified by infection in hospitals and the transfer of patients within and between hospitals, and caused 15 deaths within 26 days, mainly among patients, visitors and healthcare personnel [2]. This highlighted the need for vigilant surveillance and the importance of swift and thorough contact tracing.

The Thai Ministry of Public Health (MOPH) launched MERS surveillance and made MERS a notifiable disease in 2012, particularly targeting people travelling into Thailand from affected countries. It also initiated a nationwide public education campaign [3]. In 2015, MERS-CoV infection was classified as a dangerous communicable disease in Thailand according to the Communicable Act B.E. 2523 (AD 1980). Being added to this Act required all probable and confirmed cases and their close contacts to be quarantined in a designated area for the duration of the maximum incubation period of 14 days [4].

There have been increasing numbers of incoming travellers from the Middle East seeking medical care in Thailand in the past decade. More than 1.3 million medical tourists travelled to Thailand in 2015, of which 14.2% were from United Arab Emirates (UAE) and Oman [5]. Despite that, only three cases of MERS have been confirmed as of July 2017 [6].

Figure 1

Timeline of events for the first imported case of MERS in Thailand, Thailand and Oman, May–July 2015



BIDI: Bamrasnaradura Infectious Disease Institute; MERS: Middle East respiratory syndrome; MERS-CoV: Middle East respiratory syndrome coronavirus; MOPH: Thai Ministry of Public Health; ORF-1a: open reading frame 1a; RdRp: RNA-dependent RNA polymerase; UpE: upstream of envelope.

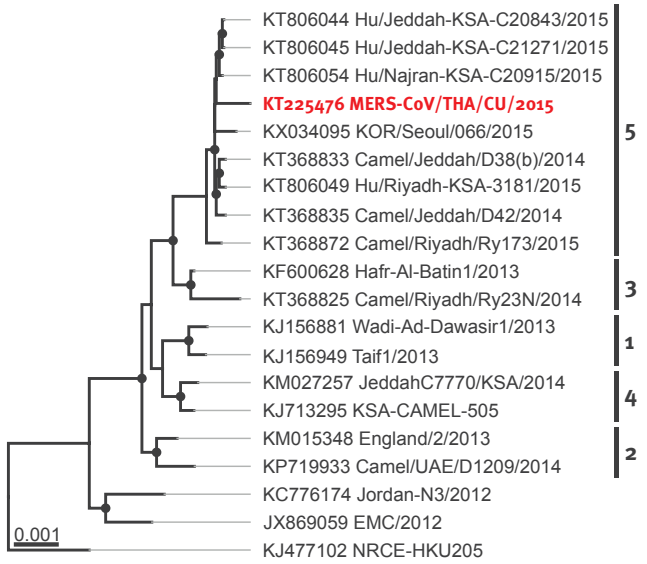
This study shows that, in addition to needing collaboration among different organisations during an outbreak, diagnosis cannot rely only on laboratory examination alone, especially when the specimen was not suitable. A negative laboratory result in a patient from an endemic region with MERS-like clinical signs still demands cautious infection control measures in an isolation unit.

The event

On 15 June 2015 (day 1), A 75-year old Omani man travelled to Thailand, seeking treatment for his heart condition. Upon arriving at the airport, the patient took a taxi to a hotel and checked in before leaving to a private hospital in another taxi. Upon presentation at the emergency room at the private hospital, the patient was promptly diagnosed with heart failure and possible pneumonia. As the patient had travelled from the Middle East that day, MERS was suspected and he was isolated in a negative pressure room (NPU). On day 3, the private hospital notified the Bureau of Epidemiology, under the Thai MOPH, of the Omani patient. RT-PCR for MERS-CoV on upper respiratory tract samples (nasopharyngeal swabs) that were sent on days 2 and 3 resulted in false negatives, leading to a 48-hour delay in diagnosis and a decision to transfer the patient out of the negative pressure unit (NPU) on day 3. Subsequent examination of a sputum sample later on day 3 confirmed MERS-CoV infection in the patient. The patient was immediately transferred back into the NPU. On day 4, Thailand's MOPH officially reported the first imported MERS case and the

Figure 2

Maximum-likelihood phylogeny of representative MERS-CoV genomes and the complete MERS-CoV genome obtained for this study, first imported case of MERS in Thailand, June 2015



MERS-CoV: Middle East respiratory syndrome coronavirus.

Filled circles at nodes indicate bootstrap supports above 75% (1,000 replicates). The virus sequence obtained from the case described in this manuscript (THA/CU/2015, GenBank accession number KT225476) is shown in red. The trees were rooted by Camel/Egypt/NRCE-HKU205 (GenBank accession number KJ477102). MERS-CoV lineages defined by Sabir et al. [12] are given on the right.

patient was transferred from the private hospital to Bamrasnaradura Infectious Disease Institute (BIDI).

The Omani Ministry of Health (MOH) was immediately notified as per the International Health Regulation (IHR) mechanism (day 4). Outbreak investigation was conducted in Oman, and the Oman IHR focal point published the results of this investigation on the World Health Organization (WHO)'s intranet to which all IHR focal points worldwide, including the one in Thailand, have access. The following report provides a brief patient history and clinical report, detailed laboratory findings and the diagnostic challenges faced in the first imported case of MERS in Thailand.

Methods

Over 170 individuals, including 48 with high-risk of exposure were traced. Thirty-six high-risk close contacts were quarantined in Thailand and 40 low-risk contacts were monitored in Oman. Another 12 high-risk close contacts (airline crew members) were quarantined in the country they were situated when traced. Medical records from the private hospital and BIDI under the Department of Disease Control, under the Thai MOPH, were reviewed [7]. Further, the patient and their family members were asked to elaborate on the clinical presentations and previous medical care in Oman by Thai investigators. Information from the Omani MOH was obtained via the IHR mechanism during investigation.

Laboratory investigation: PCR assay

In accordance with WHO interim guidelines for laboratory testing for MERS-CoV [8], MERS-CoV RNA was tested in sputum (pre-treated with *N*-acetylcysteine) and via nasopharyngeal swab (when sputum was not available), using QIAamp viral RNA mini kit (Qiagen, Hilden, Germany) for extraction. Two real-time RT-PCR assays targeting upstream of envelope (UpE) and open reading frame 1a (ORF-1a) genes [9,10], and one RT-PCR assay for generating amplicons for sequencing, targeting the betacoronavirus RNA-dependent RNA polymerase (RdRp) gene (RdRpSeq assay) [10], were performed simultaneously by WHO Collaborating Centre for Research and Training on Viral Zoonoses, Faculty of Medicine, Chulalongkorn University (WHOCC) to increase efficiency and allow reporting of results within 24 hours of receiving the samples.

Case monitoring

Respiratory specimens (sputum, nasopharyngeal and throat swabs) were collected daily from the index case from the time of patient isolation on day 5 through to day 17. The respiratory samples were sent to three centres, the BIDI, the Thai National Institute of Health (NIH) and WHOCC, for parallel real-time PCR testing of MERS-CoV. Additional molecular sequencing was performed by WHOCC.

Whole genome sequencing and phylogenetic analyses

The whole genome amplification of MERS-CoV was carried out from extracted viral RNA from collected sputum of the index case. Seventy sets of specific primer pairs were used to amplify the complete genome as previously described [11], followed by Sanger sequencing.

For the analysis, all MERS-CoV genomes with complete coding sequences available in GenBank as of 30 December 2016 (n = 233), were compared with the MERS-CoV genome obtained in this study. Sequences showing less than 35 divergent nt positions and two representatives of the five lineages defined by Sabir et al. [12], were selected and used for phylogenetic analysis. A phylogenetic tree was constructed using the maximum likelihood method based on the general time reversible model and 1,000 bootstrap replicates in MEGA7 [13].

Contact tracing, active case finding, quarantine and isolation

Contact tracing was immediately implemented by the Thai MOPH. Contacts were divided into two categories; high-risk and low-risk. A high-risk close-contact was defined as any person who was within 1 m of contact with the index case while the patient was symptomatic, regardless of duration of contact. Airline passengers

Table 1

RT-PCR results for the first imported case of MERS, Thailand, June 2015

Date	Day	Specimen type	Real-time RT-PCR (Ct)		RT-PCR and partial sequencing
			UpE gene	ORF-1a gene	RdRp gene
16 Jun 2015	2	Nasopharyngeal swab[a]	ND	ND	NA
17 Jun 2015 (AM)	3	Nasopharyngeal swab[a]	ND	ND	NA
17 Jun 2015 (PM)	**3**	**Sputum**	**Detected (33.75)**	**Detected (34.23)**	**Positive[b]**
18 Jun 2015	**4**	**Sputum**	**Detected (30.97)**	**Detected (30.55)**	**Positive[b]**
20 Jun 2015	6	Sputum and nasopharyngeal swab	ND	ND	ND
21 Jun 2015	7	Nasopharyngeal swab[a]	ND	ND	ND
22 Jun 2015	8	Nasopharyngeal swab[a]	ND	ND	ND
1 July 2015	17	Nasopharyngeal swab[a]	ND	ND	ND

Ct: cycle threshold; MERS: Middle East respiratory syndrome; NA: not available; ND: not detected; ORF-1a: open reading frame 1a; RdRp: RNA-dependent RNA polymerase; UpE: upstream of envelope.

[a] Sputum not available.

[b] Partial sequencing of 185 nt of RdRp gene showed 99% (185/186 bp) identity to the 2015 MERS-CoV isolate from a human case in Riyadh (GenBank accession number KT026454).

Table 2

Tracing contacts of the first imported case of MERS in Thailand, Thailand and Oman, June 2015 (n = 211)

Type of contact	Number of contacts	Course of action
High-risk close contacts in Thailand (n = 48)		
Close relatives travelling with the patient	3	Quarantined. Laboratory testing results for MERS-CoV were negative.
Airline passengers who sat in the two rows around the patient	14[a]	Quarantined. Laboratory testing results for MERS-CoV were negative.
Airline crew members	12	Identified, but left Thailand for their return flight on 15 June 2015 (day 1). Self-quarantined and self-monitored for symptoms, being off-service for the duration of the quarantine period. None reported to have developed any illness.
Healthcare workers at the private hospital	17	All were immediately quarantined in the hospital. Their laboratory testing were negative for MERS-CoV.
Taxi drivers	2	Quarantined. Laboratory testing for MERS-CoV were negative.
Low-risk contacts in Thailand (n = 122)		
Airline passengers	63	Self-monitored for symptoms, with social distancing.
Hotel staff	6	
Healthcare workers	53	
Low-risk contacts in Oman (n = 41)		
Close relatives	11	Assigned for two weeks of follow-up from the last date of exposure. One close-contact was assigned to be tested for MERS-CoV infection, but refused to cooperate.
Healthcare contacts at the first hospital	20	
Healthcare contacts at the second hospital	10	

MERS: Middle East respiratory syndrome; MERS-CoV: Middle East respiratory syndrome coronavirus.

[a] Only one of whom was a Thai national.

seated in the two rows surrounding the index case's seat were also considered high-risk close contacts as per WHO guidelines [14]. A low-risk contact was any person who had been in contact with the patient while the patient was symptomatic, but from a distance of more than 1 m. People were considered non-contacts if there was no evidence of direct contact with the patient or if they were not likely to be in contact with respiratory droplets, the means of transmission for MERS-CoV.

Several methods of contact tracing and active case finding were applied depending on the nature of contact, contact location, degree of symptoms at the time of contact, etc. At the hospital, attending physicians' and nurses' contact status was determined via

interview and the hospital surveillance camera. At the hotel, potential contacts were identified by interviewing the personnel on-duty when the patient checked in and by using the hotel's surveillance camera. The investigation team from the Department of Disease Control (DDC) at the Thai MOPH identified the airport-to-hotel taxi driver using the airport taxi booking slip and the hotel-to-hospital taxi driver by looking at the surveillance camera from the Traffic Control Department. The airline provided the investigation team with the passenger manifest and the Thai authorities identified passengers' local address using immigration arrival cards. Local health authorities in relevant provinces were informed and asked by the investigation team to locate and contact the identified passengers in their jurisdiction. Some passengers voluntarily reported to a hospital or health authority in response to the MOPH's announcement of first imported MERS case in Thailand. Central authorities were responsible for locating all high-risk close-contacts, while local authorities were responsible for low-risk contacts. The time lapse between the affirmed diagnosis and each contact-tracing varied. Contacts at the hospital were identified within a day, while other high-risk close contacts, such as passengers on the flight, were identified within 3 days. Other low-risk contacts were traced within 7 days.

Patients who were in the same NPU ward as the index case at the private hospital on day 1 were monitored despite being considered non-contacts because: i) the room for each patient was separated, ii) they had no direct contact with the index case and iii) the known mode of transmission of MERS-CoV is respiratory droplet. Further, patients in the ICU, which is where the index case was moved after being taken out of the NPU 8 hours before diagnosis on day 3, were monitored, despite being non-contacts. In the event they developed a new episode of fever or respiratory symptoms, samples were collected and sent for testing to rule out MERS-CoV infection. Another concern was ICU healthcare workers' simultaneous care of several patients. Prompt quarantine and monitoring of patients in the ICU was to be implemented if any ICU healthcare worker developed any symptoms or was diagnosed with MERS-CoV infection.

Most high-risk close contacts were quarantined and all were continuously monitored for 14 days. Nasopharyngeal and throat swabs, stored in single viral transport media, from 36 high-risk close contacts were collected on two occasions as per the Bureau of Epidemiology guidelines [15]: first upon identification as being a high-risk close contact and second on day 12 during the quarantine period. Specimens were duplicated and sent to any two of three laboratories (BIDI, NIH and WHOCC) for parallel real-time PCR testing of MERS-CoV, using both WHO and commercial primers for any given sample. In line with the Thai Communicable Disease Act, high-risk close contacts were only released after completing 14 days of quarantine and if laboratory testing on the 12th day of quarantine was negative.

Sera from three high-risk close contacts (the close relatives who travelled with the patient to Thailand) were sent to the Institute of Virology, University of Bonn Medical Centre, Bonn, Germany to test for anti-MERS IgG and IgM using MERS-CoV infected Vero cells for immunofluorescence assay (Anti-MERS-CoV IIFT, EUROIMMUN, Lübeck, Germany).

Results

Laboratory diagnosis and clinical picture

The real-time RT-PCR results on the patient's nasopharyngeal swabs were negative for UpE and ORF-1a gene targets on days 2 and 3 (Table 1), and the patient was thus transferred to a non-NPU in the ICU. However, the third sample from sputum that was taken later on day 3 as the patient's condition deteriorated and that underwent three simultaneous RT-PCR assays at the WHOCC, was positive for UpE, ORF-1a and RdRp gene targets. When WHOCC confirmed sputum was positive for MERS-CoV infection, the patient was immediately transferred back to the NPU that night. MERS-CoV was confirmed via sequencing within 24 hours by WHOCC.

The patient was referred to and isolated at BIDI on the morning day 4. The patient's clinical presentation at that time was diffused bilateral pneumonia with pending acute respiratory distress syndrome [7]. He did not report any previous illnesses pertaining to these symptoms.

Later the same day, sputum was collected from the patient for reconfirmation, which tested positive for UpE and ORF-1a genes by four different laboratories: the NIH, Ramathibodi Hospital, BIDI and WHOCC. The Thai MOPH proceeded to publicly announce the first confirmed imported MERS case in the evening of 18 June 2015 (day 4). The patient was monitored for MERS until 1 July 2015 (day 17) and was discharged on 3 July 2015 (day 19).

Retrospective case history

Upon laboratory confirmation on day 3, the case was immediately notified to the WHO. In order to support local handling of the outbreak, an epidemiologist and a risk communication expert were deployed from the WHO South-East Asia Regional Office and WHO Headquarters, respectively.

The epidemiological investigation revealed retrospectively that on 4 June 2015, 11 days before the admission to the private hospital in Thailand, the patient was admitted to a regional hospital in Oman, with retrosternal and left-sided chest pain, which was radiating to his left arm (Figure 1). The condition was associated with shortness of breath on exertion and was considered typical cardiac pain. The patient was diagnosed with acute coronary syndrome. Three days later, on 7

Table 3

Serology testing of anti-MERS-CoV IgM and IgG in three close relatives travelling with the patient using MERS-CoV infected Vero cells for immunofluorescence assay, first imported MERS case in Thailand, June–July 2015

Close relatives at high-risk	First sera 19 Jun 2015 (day 5)	Second sera 1 Jul 2015 (day 17)
Relative 1, 45 years of age	Negative	Negative
Relative 2, 30 years of age	Negative	Negative
Relative 3, 25 years of age	Negative	Negative

MERS-CoV: Middle East respiratory syndrome coronavirus.

June 2015, his condition had improved and he was discharged. A close relative of the patient observed a dry cough of mild degree in the patient since 10 June 2015. On 13 June 2015, he was admitted to a second hospital, displaying signs of somnolence, fatigue and elevated blood sugar level; he was diagnosed with diabetes mellitus on 14 June 2015. There was also decreased air entry in the right lung with fine crepitations. Chest X-ray showed opacity in middle and lower zones of right lung. Both hospitals' medical records confirmed the patient did not exhibit any fever or cough symptoms. The patient was discharged that day with a follow-up appointment at a regional hospital scheduled for 16 June 2015; however, the patient wished to seek medical care in Thailand and flew there on 15 June 2016.

Phylogenetic analysis

The virus sequence (THA/CU/2015) obtained from the patient was submitted to GenBank (GenBank accession number KT225476). THA/CU/2015 showed closest relations (99.91% nt identity) to three human MERS-CoV strains isolated in Saudi Arabia in 2015 (GenBank accession numbers KT806044, KT806045 and KT806054). Figure 2 shows the phylogenetic tree constructed from the MERS-CoV whole genome obtained from the patient (THA/CU/2015, 29,809 bp), among the closest relatives and representatives for each MERS-CoV lineage defined by Sabir et al. [12].

Exposure history in Oman

Correspondences with a close relative of the patient and the Omani MOH revealed that the patient was a fisherman from Ghasil village, South Sharqiya Governorate, but spent June–August in Al Mintrib village of Bidiya Wilayat, North Sharqiyah Governorate. The patient neither had any history of travel outside Oman nor contact with anyone with a history of travel outside Oman within the 14 days preceding his travel to Thailand. Further, the patient had no contact with any person with acute respiratory infection or confirmed MERS before developing symptoms. The family used to own one camel but had not had contact with that camel for few months. A close relative who lived near the patient, but did not travel to Thailand with the patient, owned and cared for three camels. Samples collected from these camels tested negative in Oman for MERS-CoV by RT-PCR on day 15. It is also noteworthy that the patient and the patient's close relatives never consumed raw camel milk or camel urine.

Contact tracing and active case finding

A total of 211 contacts of the index case were identified after the patient was confirmed to have MERS. In Thailand, 170 contacts (excluding the 42 healthcare personnel at BIDI, investigated separately in the report by Wiboonchutikul et al. [7]) were identified. Of these 170, 48 were high-risk close contacts and 122 were low-risk contacts (Table 2). All patients treated in the same ward (ICU) at the private hospital of first admission of index case before MERS diagnosis were identified as non-contact, however they were fully monitored and followed up for 14 days, as per the Thai MOPH's protocol, as a precautionary measure. In Oman, the outbreak investigation determined there to be 41 low-risk contacts and this information was published on the dedicated WHO system. Fortunately, there was no secondary transmission associated with this case.

High-risk close contacts

Three of the patient's close relatives who (45, 30 and 25 years of age) travelled with the patient to Thailand and took care of the patient. They were also isolated at BIDI on the morning of 18 June 2015 (day 4) along with the patient. Their RT-PCR tests (each person tested four times) were negative for MERS-CoV. However, they were closely monitored for symptoms until 1 July 2015 (day 17). Sera from these three close relatives collected on 19 June and 1 July 2015 (days 5 and 17), were sent to the Institute of Virology at University of Bonn Medical Centre, Bonn, Germany, and all tested negative for anti-MERS IgG and IgM using MERS-CoV infected Vero cells for immunofluorescence assay (Anti-MERS-CoV IIFT, EUROIMMUN, Lübeck, Germany) (Table 3).

The Thai outbreak investigation identified 45 other high-risk close contacts, including 14 airline passengers who sat in the two rows around the index case's seat, 12 airline crew members, 17 healthcare workers at the private hospital (first hospital of admission) in Bangkok and two taxi drivers. All but the 12 airline crew members were quarantined as the crew members left the country for their return flight operation on 15 June 2015 (day 1). However, once the diagnosis was confirmed, the crew members were notified and self-quarantined for 14 days. Laboratory testing carried out on samples collected from 36 high-risk close contacts all tested negative at least twice for MERS-CoV by real-time PCR. Further, none of the high-risk close contacts, including the airline crew members and healthcare workers, reported to have developed symptoms compatible with MERS-CoV infection during the quarantine period.

Discussion

This study demonstrates the challenges faced by physicians and the cross-border threats that exist with increasing international medical tourism. Although

precautions such as ThermoScan are in place at airports in light of the MERS-CoV outbreak in the Middle East and South Korea, cases can slip through checkpoints due to atypical presentations. The patient flew on a commercial airline despite his sickness and was not detected by the ThermoScan at the immigration checkpoint in Bangkok as he was afebrile. He only had a mild, non-productive cough. This case report also provides important lessons regarding clinical case identification. The clinical diagnosis was complicated due to the existence of congestive heart failure, a condition that predisposes to either community-acquired or nosocomial pneumonia of various aetiologies. Furthermore, initial chest radiographs did not show clear signs of interstitial pneumonia as expected with MERS-CoV infection. Various contact tracing methods involving the cooperation of several authorities and business institutes, such as the border control, airline, hotel management, traffic control, local authorities and hospitals, were used to track-down all potential contacts in order to prevent an outbreak. Phone calls, passenger manifests, surveillance videos and immigration cards were essential tools for the successful contact tracing.

Upper respiratory tract samples, such as nasopharyngeal and oropharyngeal, are often used to detect upper respiratory tract illnesses during the acute phase. In MERS-CoV infection, however, higher viral loads have been found in specimens from the lower respiratory tract [16], with sputum or endotracheal secretion samples yielding better results [17]. This aligns with the WHO interim guidelines, which encourage using lower respiratory tract samples if available [8]. Physicians, surveillance staff and laboratory personnel must be well-informed about the procedures, reliability and limitations of diagnostic tests, and should be able to recognise signs of mismatch between laboratory results and clinical presentations. In this case, the initial diagnostic testing of upper respiratory tract samples on days 2 and 3 caused a delay in diagnosis that could have facilitated onward transmission. Fortunately, the patient was isolated in a NPU upon initial admission; however, he could have exposed other patients and hospital workers during the 8 hours he spent in regular ICU after the initial false negative test results. The decision to conduct repeated laboratory testing, as well as to test lower respiratory tract samples, was driven by clinical assessment and knowledge of the virus excretion pattern reported in earlier cases.

The algorithm for diagnosing MERS in the current WHO interim guidelines for laboratory testing indicates that two positive real-time PCR tests are sufficient in diagnosing MERS, i.e. ORF-1a and UpE. However, we found that performing three simultaneous assays and sequencing for UpE, ORF-1a and RdRp genes in parallel, allowed for swift in-country confirmation of the presence of MERS-CoV and reporting within 24 hours, facilitating prompt outbreak control measures. There was no secondary transmission, not even to close relatives or the healthcare workers at BIDI where the patient was transferred after the diagnosis was confirmed, despite 170 contacts, including 48 high-risk close contacts [7].

Despite the successful outcome of infection control measures, the case provides an example of the risk of MERS-CoV infection importation. Aside from providing technical support through the MOPH Emergency Operations Centre, deployments of experts from the WHO South-East Asian Regional Office also greatly facilitated the exchange of information on possible modalities of MERS-CoV infection with the Omani MOH through the IHR (2005) mechanism [18]. This study therefore emphasises how important hospital and organisation collaboration, as well as cross-border cooperation, is to successful infection control in the event of an outbreak.

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Conflict of interest

None declared.

Authors' contributions

TPl, RB, PS and CP were responsible for the case investigation, sample handling and coordination of sample tests. They were also responsible for contact tracing and quarantine. CS was responsible for the clinical case management and hospital quarantine authority. SW, TK, SP, TPo, JJ, YJ, AJ, SK and DRS were responsible for the laboratory testing and sequencing of MERS-CoV. AR and SG analysed the sequence and submitted it to GenBank. RB, SW, SG and TH wrote the original manuscript. CD, VMC, RB, SW, SG and TH critically reviewed the original manuscript. SG, RB, SW and TH critically reviewed the revised manuscript.

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