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Epidemiology of Parvovirus B19 in Türkiye: A Descriptive Analysis of National Surveillance Data (2020-2024)

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Background: Parvovirus B19 (B19V) infection occurs worldwide seasonally, especially in school-age children. Due to limited surveillance, clinicians report an increase of cases to identify outbreaks, while labs determine seropositivity rates. In 2024, B19V outbreak occurred in Türkiye and many other countries.

Aims: To estimate incidences of B19V infection in Türkiye from 2020 to 2024 using National Infectious Disease Surveillance and Early Warning System (IZCI) and to determine case fatality rate (CFR) during the 2024 outbreak period.

Study Design: Retrospective descriptive study.

Methods: The number of cases was obtained from the syndromic surveillance of rash diseases in national database. All notifications with International Classification of Diseases, 10th Revision diagnosis code "erythema infectiosum" within the syndromic surveillance were included in the study. All age groups were included in the study and no specific group was excluded. Annual estimated incidences were calculated for past 5 years. The distribution of cumulative incidence for the outbreak by age group and geographical regions was analysed. CFR was calculated for the outbreak period by using the proportion of people who have been diagnosed with B19V. Disease indicators were calculated as crude rates.

Results: The estimated incidence in 2024 was 15.24 per 100,000. The peak of the outbreak was in May. The regions with the highest cumulative incidences during the outbreak period were the Black Sea, Marmara, and Central Anatolia. The highest cumulative incidence was 102.64 per 100,000 in 5-9 age group. The CFR was calculated as 0.0184% in the outbreak with 2 deaths out of 10,898 cases.

Conclusion: Türkiye has experienced the largest B19V outbreak between February and June 2024. This study showed the unusual scale of B19V post-pandemic, suggesting that such outbreaks can be expected after pandemics. The establishment of syndromic surveillance has proved critical for early outbreak detection and response.

INTRODUCTION

Parvovirus B19 (B19V) is a single-stranded DNA virus. Although patients with B19V infection are usually asymptomatic or only exhibit mild flu-like symptoms, some patients may experience severe clinical symptoms. Clinical manifestations associated with B19V infection include erythema infectiosum (fifth disease), arthropathy, transient aplastic crisis, chronic red cell aplasia, papular or purpuric rashes on the hands and feet (often referred to as "glove and sock" syndrome), and hydrops fetalis. Less frequently, individuals may develop encephalopathy, epilepsy, meningitis, myocarditis, dilated cardiomyopathy, and autoimmune hepatitis.[1] There are no specific antivirals for B19V infection. While most B19V patients recover completely, cardiac B19V is associated with a significant mortality rate.[1,2] In a review of pediatric age group studies on B19V infection-associated myocarditis and dilated cardiomyopathy, the most prevalent symptoms were tachycardia, tachypnea, fever, and rash, respectively. Cardiac arrest, loss of consciousness, and systemic infection were linked to the most adverse prognosis.[2]

Historically, B19V has predominantly been associated with minor outbreaks worldwide, especially in elementary schools, and remained localized.[3-5] The prevalence of B19V in developed countries ranges from 2% to 10% in children under five years of age, 40% to 60% in adults over 20 years of age, and 85% or higher in individuals aged 70 years and older. Every three to four years, there are minor epidemics that primarily affect school-age children.[6] The virus is more widespread in late winter, spring, and early summer, with larger outbreaks occurring every 3-4 years. In 2017, a significant parvovirus outbreak with a seropositivity rate of 4.1% was documented in Denmark.[7] In a small outbreak in Türkiye in 2010, the B19V immunoglobulin G (IgG)

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seropositivity rates were 20.7% (112/542) in the under-18 age group and 36% (227/631) in the over-18 age group.[8]

Recent studies have indicated that during the coronavirus disease-2019 (COVID-19) pandemic, B19V was almost completely eradicated, resulting in lowered immunity levels, which may cause future outbreaks. It has been reported that there may be a rise in the number of B19V-susceptible individuals in the Netherlands in recent years.[9] A study conducted in Israel revealed that the previously existing seasonality of B19V outbreaks ended in 2023, with the largest outbreak to date occurring in 2024.[10] France has reported an increase in B19V IgM seropositivity from April 2023 to May 2024.[11] In Denmark, there were 3.5 times more cases than the peak of the B19V outbreak in 2017, and severe symptoms were noted.[7] Pediatric populations that have not previously been exposed to the virus may become more susceptible as a result of the COVID-19 pandemic, which could increase the number of cases and, in turn, the number of deaths from B19V infection.

Since many countries lack regular surveillance programs, clinicians play a vital role in identifying outbreaks by reporting increases in case numbers, while laboratory studies help determine seropositivity rates.[11] In a study conducted in Türkiye, serum samples delivered to a microbiology laboratory between 2009 and 2012 for diagnosing various diseases were analyzed, and the prevalence of B19V IgM seropositivity was reported to be 8.5%.[12] Comparisons with prior years may not be feasible, however, because such a notification procedure lacks standardization. Passive gathering of International Classification of Diseases, 10th revision (ICD-10) diagnosis codes may allow comparison of the number of cases with those from previous years. Since 2015, ICD-10 diagnosis codes have been regularly collected from patient examination records in all clinics in Türkiye. The ICD-10 codes related to infectious diseases that pose a public health risk are identified and monitored by early warning units. Syndromic surveillance by combining similar ICD-10 codes can be employed to detect disease outbreaks. Therefore, starting 2019, a syndromic surveillance program has been implemented in Türkiye to identify spikes in cases of maculopapular rash-causing diseases, including measles, fifth disease, sixth disease and scarlet fever.[13] There is no national study on infectious disease prevalence in Türkiye; most research is done at the regional level. Additionally, no research has been conducted on the morbidity and mortality indicators of B19V.[14-16] This gap can be filled by our study.

Following the B19V outbreaks in 2024, the size of the susceptible population remains unclear. Therefore, it is essential to alert clinicians and set up nationwide early warning systems for potential new cases that may emerge during the 2025 B19V infection season. In Denmark, compared to the 2017 outbreak, the incidence of severe outcomes such as anemia, miscarriage, and fetal transfusion increased 3-5 times in 2024.[7] B19V-related mortality has also increased in France compared to prior years.[11] A heightened global awareness of this disease in 2024 may be attributed to a worsening prognosis. Hence, assessing disease indicators by analyzing the emerging trends is essential.

This study aimed to estimate the incidence of B19V infection in Türkiye between 2020 and 2024 utilizing the National Infectious Disease Surveillance and Early Warning System (IZCI) and to determine the case fatality rate (CFR) during the 2024 outbreak period.

MATERIALS AND METHODS

This retrospective descriptive study investigated the monthly distribution of cases with the ICD-10 code "B08.3 erythema infectiosum (fifth disease)" between January 1, 2020 and November 30, 2024 in Türkiye. The distribution of cumulative incidences by age group and geographical region during the outbreak period (February to June 2024) was examined.

We explored the outbreak using the syndromic surveillance data of the IZCI, which gathers information from all emergency departments nationwide. This system provides numerical data on the ICD-10 code, age, province, and district for all medical procedures performed across the country. The notifications were sent from all healthcare facilities countrywide. IZCI performs deduplication to accurately reflect the number of cases in case the same individual reapplies. To make sure the notifications were comprehensive, the information systems verified the number of cases. The personalized National Identification Number is used when registering patients with health institutions. Demographic information pertaining to the place of residence, gender, and date of birth linked to this ID is automatically anonymized and transferred to IZCI. Any missing demographic data were excluded. There was no sample selection; all notifications recorded in the system were included in the study. The event management system, which has been used to handle public health emergencies, provided notifications of mortality during the outbreak period. It is the system used to report all data obtained during the early detection, verification, and response stages of public health emergencies. Province-level public health emergencies are detected by early warning units with IZCI, and the related details are recorded in the event management system.[17]

To determine the CFR, the number of deaths due to B19V reported during the outbreak period was divided by the number of cases over the same timeframe. The estimated incidences were calculated by dividing the annual number of new cases by the midyear population of that year. The cumulative incidence per 100,000 people for each geographical region was estimated by dividing the number of cases for that region during the outbreak period by the midyear population of the same region. Disease indicators were calculated as crude rates. Population and demographic data from the Turkish Statistical Institute were utilized for calculations.[18] The geographical regions that were established in 1941 and are still in use today were used for classifying information pertaining to the geographical regions in which the provinces are located.[19]

The CUSUM algorithms employed for outbreak identification during syndromic surveillance were utilized.[20] An outbreak was defined as a weekly case count 50% higher than the moving average of the previous 12 weeks. It was confirmed when there was an occurrence of 50% more cases than the average number of cases in the weeks corresponding to the same week in the preceding three years as well as from the feedback from early warning units in the provinces.[21]

While detecting outbreaks in the provinces, laboratory confirmations were conducted employing the polymerase chain reaction (PCR) test and ELISA-based IgM antibody titer determination. Relevant data usage permission and ethical approval were obtained. This study utilized anonymized data obtained from the National Notification System. As the data was anonymized and collected as part of routine public health surveillance, individual informed consent was not required.

Statistical analysis

The Microsoft Excel application was used to assess the descriptives. Data on the number of cases per week were expressed as mean ± standard deviation. Percentage distributions were used to examine the descriptive characteristics. The CFR and its 95% confidence interval (CI) were calculated utilizing the Wilson score interval method (prop.test function, R software, version 4.4.1).

RESULTS

Age data was complete, but 10% of notifications lacked address information (n = 1650). Therefore, regional estimates account for 90% of all notifications, while age distributions and national level disease indicators correspond to all available data. In the first week of February 2023 and the last week of January 2024, the weekly case counts (n = 16 and n = 102, respectively) exceeded the past 12-week moving averages (5.1 ± 1.3 and 37.3 ± 18.9, respectively) by 50%. In January 2024, there were 408 cases, which was 50% more than the average for the previous three years (15.0 ± 9.2). We contacted the early warning units in the provinces with the highest number of notifications and confirmed the outbreak by verifying the increase in the number of cases. Over the course of the five-year period, 15,836 cases were reported, 10,898 of which occurred during the outbreak period. The estimated incidence for 2024 was 15.24 per 100,000, an increase from 2.71 per 100,000 in 2023 (Figure 1).

The outbreak peaked in May, with the Marmara region recording the highest cumulative incidence recorded at 7.84 cases per 100,000. During the outbreak period, the regions with the highest cumulative incidences were the Black Sea, Marmara, and Central Anatolia, with rates of 20.57, 17.44, and 16.43 cases per 100,000, respectively (Figure 2, Table 1).

B19V cases were more common in individuals under 18 years of age compared with those aged 18 and above. The highest cumulative incidences were observed in the following age groups: 102.64 per 100,000 in the 5-9 age group, 51.10 per 100,000 in the 1-4 age group, and 29.28 per 100,000 in the 10-13 age group. The highest estimated incidence in the months from February to June was in the 5-9 age group. During the outbreak, the estimated incidence for each month was highest in the Black Sea and Marmara regions among all geographical regions (Table 1).

Between February and March, two B19V-related deaths in children under one year old were documented. One of them had a PCR-confirmed diagnosis of B19V. The other was the symptomatic sibling of another patient with PCR-confirmed B19V. Both patients experienced cardiac symptoms and elevated cardiac enzymes in addition to the rash. The CFR was 0.0184% (95% CI: 0.0032-0.0740%), with two deaths out of 10,898 cases. Both patients had no previous history of known disease or immune suppression.

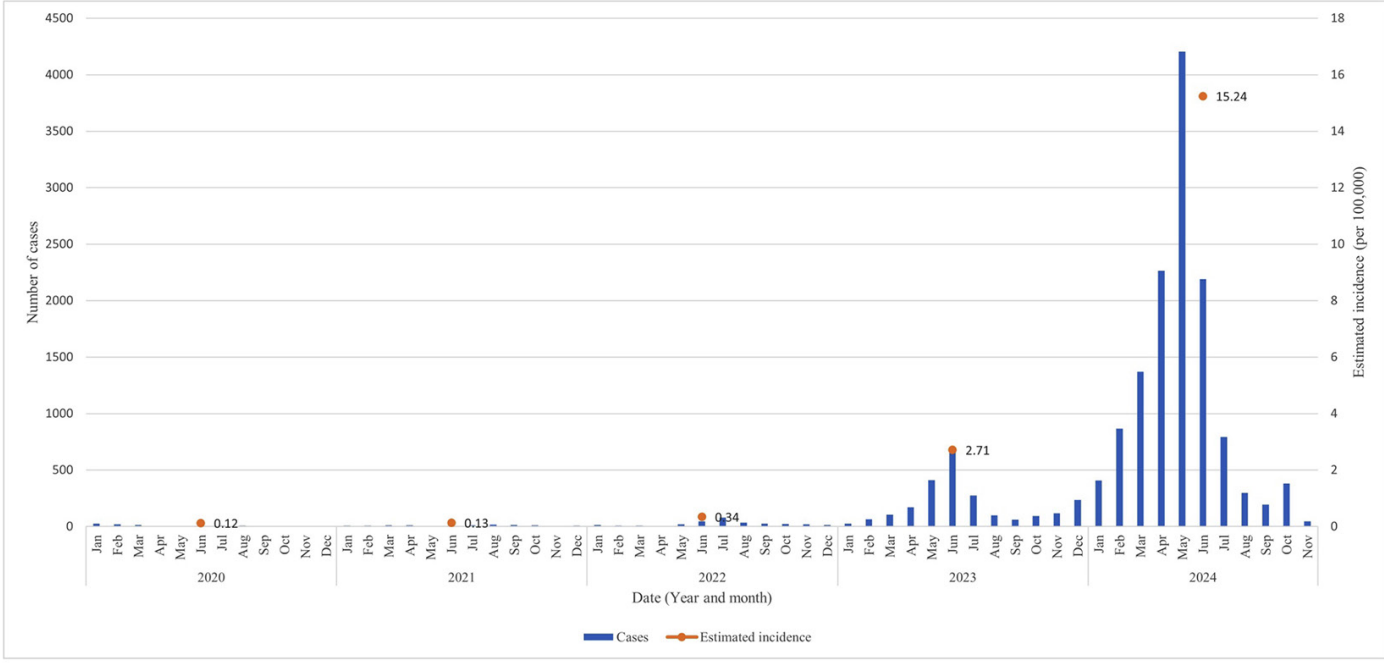
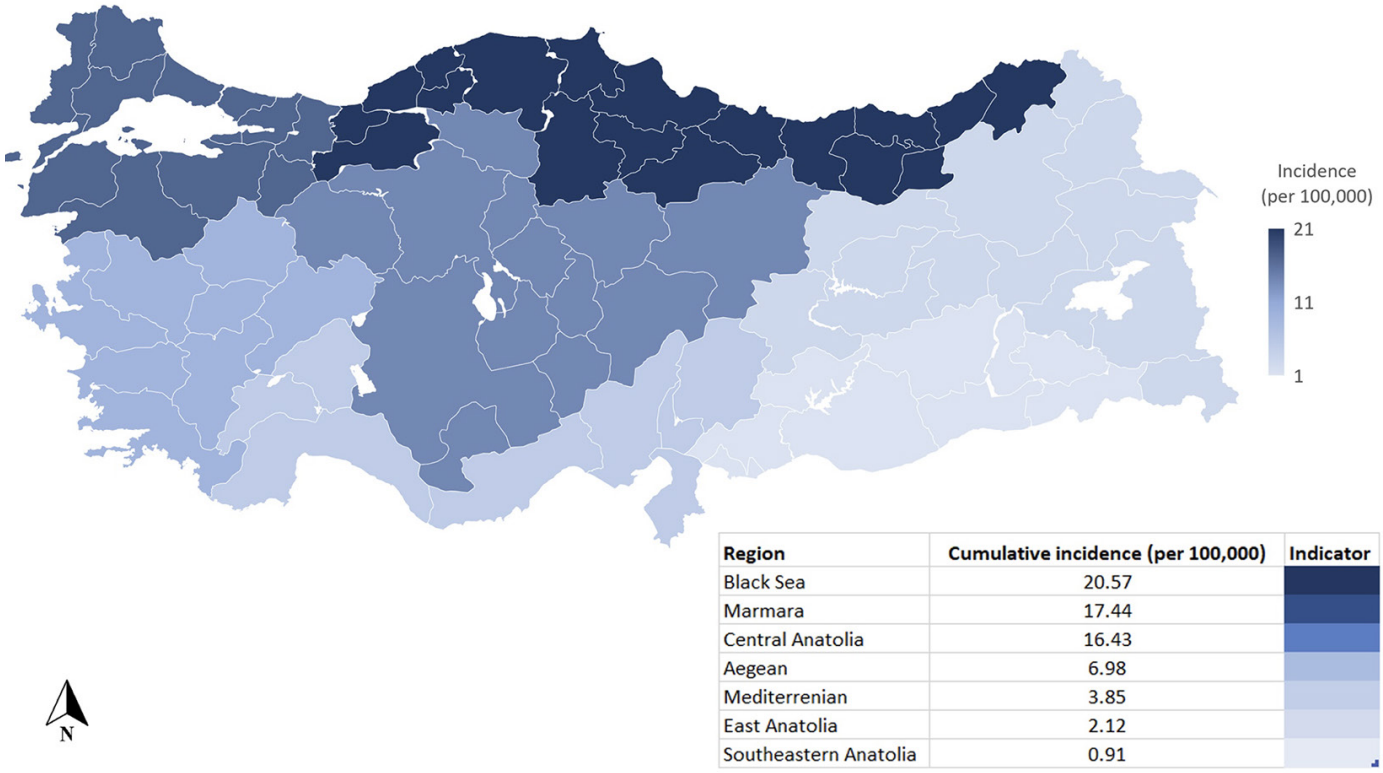


FIG. 1. Parvovirus B19 infection cases by months and estimated incidences by years, Türkiye, 2020-2024.



Region	Cumulative incidence (per 100,000)	Indicator
Black Sea	20.57	
Marmara	17.44	
Central Anatolia	16.43	
Aegean	6.98	
Mediterrenian	3.85	
East Anatolia	2.12	
Southeastern Anatolia	0.91	

FIG. 2. Cumulative incidences of parvovirus B19 infection during the outbreak period from February to June 2024 by geographical regions of Türkiye.

TABLE 1. Estimated Monthly Incidences of Parvovirus B19 Infection During the Outbreak Period by Geographical Regions and Age Groups, Türkiye, February-June 2024.

		Population	Incidences per hundred thousand individuals (n)					
		Months						
			Feb	Mar	Apr	May	Jun	Sum
Region*	Mediterranean	10,851,089	0.45 (49)	0.48 (52)	0.68 (74)	1.32 (143)	0.92 (100)	3.85 (418)
	East Anatolia	5,982,493	0.32 (19)	0.38 (23)	0.27 (16)	0.72 (43)	0.43 (26)	2.12 (127)
	Aegean	10,946,780	0.59 (62)	0.97 (102)	1.22 (133)	2.45 (263)	1.74 (186)	6.98 (764)
	Southeastern Anatolia	9,410,624	0.2 (19)	0.16 (15)	0.07 (7)	0.33 (31)	0.15 (14)	0.91 (86)
	Central Anatolia	13,689,886	1.87 (256)	2.18 (298)	3.6 (493)	5.51 (754)	3.27 (448)	16.43 (2,249)
	Black Sea	8,079,004	2.33 (188)	3.54 (286)	5.2 (420)	6.51 (526)	3 (242)	20.57 (1,662)
	Marmara	26,412,501	0.77 (204)	1.78 (469)	3.52 (930)	7.84 (2,071)	3.53 (933)	17.44 (4,607)
	Total	85,372,377	0.94 (800)	1.46 (1,249)	2.43 (2,074)	4.49 (3,836)	2.29 (1,954)	11.61 (9,913)
Age group	<1	934,215	0.75 (7)	1.18 (11)	2.57 (24)	3.64 (34)	4.92 (46)	13.06 (122)
	1 to 4	4,413,839	3.62 (160)	5.75 (254)	9.47 (418)	19.67 (868)	12.98 (573)	51.5 (2,273)
	5 to 9	6,566,486	8.25 (542)	13.05 (857)	22.16 (1,455)	39.7 (2,607)	19.48 (1,279)	102.64 (6,740)
	10 to 13	5,122,388	2.75 (141)	4.39 (225)	6.15 (315)	11.34 (581)	4.65 (238)	29.28 (1,500)
	14 to 17	5,169,106	0.14 (7)	0.12 (6)	0.41 (21)	0.85 (44)	0.41 (21)	1.92 (99)
	18≤	63,166,343	0.02 (10)	0.03 (16)	0.05 (33)	0.11 (72)	0.05 (33)	0.26 (164)
	Total	85,372,377	1.02 (867)	1.6 (1,369)	2.66 (2,266)	4.93 (4,206)	2.57 (2,190)	12.77 (10,898)

*: Regional calculations account for 90% of all notifications.

DISCUSSION

Between February and June 2024, an unexpected B19V outbreak occurred in Türkiye. We determined the annual incidences of the previous five years. The incidence in 2024 was 14 times higher than it had been in the prior years. In 2023, there was a smaller outbreak of B19V. Some factors may have contributed to the B19V outbreaks in the past two years, such as the increase in the vulnerable population, decline in mask use, and rise in social interactions following the COVID-19 pandemic.[9,22] The first cases of COVID-19 were reported in Türkiye in March 2020.[23] The increase in B19V cases in Türkiye in 2023 corresponds to the transition period from the COVID-19 pandemic to a state of normalization. Social mobility may have improved, and workplaces, schools, and social activities may have fully recovered by 2024. In the 2023 B19V outbreak, the continued high prevalence of taking personal protective measures may be one of the factors affecting the variation in B19V incidences over the previous two years.[24,25] Microbial exposure enhances the immune system development and function by promoting immune cell diversity.[26,27] The greater exposure of susceptible individuals who were not infected in previous years may have contributed to the higher incidence. In addition, during the pandemic, healthcare workers focused more on COVID-19 and there was a decline in the reporting of other diseases.[28,29] The incidence of B19V infection, which increased during and after the normalization period, may have been investigated more than usual. In addition, health-seeking behavior increased during the pandemic period.[30,31] Increased B19V exposure following the normalization period may have resulted in increased hospital admissions. This could have been the cause of the widespread outbreak. Gradually lowering protection and control measures after pandemics could help contain subsequent outbreaks caused by similar pathogens. The impact of interventions during the transitional periods of disease control can be evaluated through SIR model studies.

An increase in the incidence of B19V infections was reported to the ECDC by Denmark, Ireland, Lithuania, the Netherlands, Norway, Latvia, the Czech Republic, France, and Austria in 2023 and in the first half of 2024.[32] Five B19V-related deaths in children under one year old were reported during the April 2023-May 2024 outbreak in France, although the average annual number of B19V-related deaths is 1.8.[11] Two deaths due to B19V infection among children under one year of age were documented during the outbreak period (February-June 2024) in Türkiye. Türkiye and France differ in terms of the B19V-related CFR. In France, the number of B19V-related deaths was calculated by filtering notifications with the ICD-10 diagnosis code B08.3 and B19V-related comments in texts from a system where all deaths were examined. In Türkiye, the number of fatalities was calculated based on the notifications that were sent out. The recorded deaths in Türkiye were among patients who were admitted to hospitals. However, the number of deaths could not accurately represent the actual numbers if the patient had no record of hospitalization or if the death happened outside the medical facility. The number of deaths filtered from death notifications might not reflect the actual number of deaths. This is due to a failure to inquire about the disease history of the deceased. By improving the quality of death registries, both systems can be combined, and duplicates reviewed to produce more accurate death counts. Denmark experienced an increase in B19V cases beginning in January 2024, with the incidence peaking at 5.93 per 100,000 in April, while it peaked in Türkiye at 4.93 per 100,000 in May 2024. They observed that 12.3% of pregnant women experienced at least one severe adverse event, such as anemia, hydrops fetalis, or miscarriages.[7] The epidemic period, peak period, and incidences are comparable in Denmark and Türkiye. Both studies were based on patient records. There may have been similar epidemics in other nations; however, these incidents may have gone unreported in the literature.

Post-pandemic outbreaks of respiratory infections and related deaths underscore the critical need for effective surveillance and prevention measures.[33-35] We have contacted health authorities in areas with an increase in cases for implementing appropriate prevention measures during the B19V outbreak. Since the B19V vaccination was not available, we concentrated on general respiratory precautions in collective living environments. For instance, we contacted the kindergarten and primary school administrators and educated them about the symptoms. We informed the clinicians and ensured that throat swab samples were collected and subjected to PCR testing when symptoms consistent with B19V were observed.

In the years following the 1957-1958 influenza A/H2N2 pandemic, outbreaks caused by other pathogens were reported in some countries. For example, an outbreak called summer flu occurred in the USA, and it was believed that the coxsackie B-2 virus might have been the dominant agent in the samples.[33] In 2020, following the malaria outbreak in the African region, Sudan reported a rise in arboviral diseases and alerted clinicians about outbreaks caused by additional pathogens once the health system was overburdened by the epidemic.[34] The authors discussed that the incidence of respiratory illnesses such as invasive pneumococcal disease and measles decreased during the COVID-19 pandemic.[36,37] A measles outbreak occurred in the US state of Ohio after the COVID-19 pandemic, and it was reported that the increase in cases may be due to the decline in vaccination rates.[35] A measles outbreak was reported to have started in Romania after March 2023.[38] This implies that major pandemics may be followed by outbreaks caused by other respiratory pathogens. Therefore, countries that have not yet encountered any outbreaks of respiratory pathogens such as B19V should be prepared for outbreaks, especially in the winter, spring, and early summer of 2025. The ICD-10 codes gathered in the national syndromic surveillance to track infectious diseases that cause rash could be used to identify a B19V infection outbreak. In several European countries, there appears to be a limited focus on B19V surveillance and the absence of standardized protocols. This may be attributed to the generally self-limiting and milder nature of the infection.[39] Regularly monitoring the reporting of ICD-10 codes related to respiratory pathogens, developing syndromic surveillance programs, and updating diagnostic codes may help in identifying outbreaks.

The calculation of cumulative incidences for each region enabled a comparative analysis of the outbreak data. The results indicated that the cumulative incidences in the Marmara, Black Sea, and

Central Anatolia regions were significantly greater than those in other regions during the outbreak period. Furthermore, an analysis of the average temperatures in the geographical regions of Türkiye between February and June 2024 revealed that the Eastern Anatolia and Southeastern Anatolia regions had lower average temperatures than the other regions.[40] However, in our study, the B19V cumulative incidence was lower in these regions. Lee and Yoon[41] estimated the association between respiratory diseases and air temperature using the national health system data from 2008 to 2017. The study reported that cold weather raised the risk of most respiratory diseases.[41] Sohn et al.[42] found that warmer temperatures were protective against pneumonia. Qiu et al.[43] associated cold weather with an increase in respiratory tract infection symptoms and hospital admissions. Similarly, B19V is most infectious in winter and spring.[7,10,11,44] The disease incidence between regions could be influenced by diverse factors. It is known that infectious diseases are more common in regions with a higher number of migrants.[45,46] According to national statistical data, the Black Sea region, Marmara region, and Central Anatolia region (0.019%, 0.017%, and 0.015%, respectively) were the regions of Türkiye with the highest migration in 2023.[47] Therefore, population density could be a factor that may contribute to higher incidences in densely populated provinces such as the Marmara region, which includes İstanbul, and the Central Anatolia region, which includes Ankara.[18] Education, economic standing, and the number of physicians may also be factors influencing the incidence of B19V in different regions. According to the 2023 National Health Statistics Yearbook, the total number of physicians per 100,000 people was highest in the Central Anatolia, Marmara, Aegean, Mediterranean, Black Sea, Eastern Anatolia, and Southeastern Anatolia regions, respectively. These regions differ in terms of socioeconomic status. The economic development of the Southeastern Anatolia and Eastern Anatolia regions was lower than the national average in 2023.[18] Also, a 2020 study and national data from 2022 showed that they had the lowest degree of schooling.[18] Health-seeking behavior might have declined as economic status and education level decreased.[48] This may have contributed to the low detection rate of B19V cases by the surveillance system.

Additionally, conditions related to mild infections, such as individuals' immune system responses, can play a role. If not associated with health-seeking behavior, there may still be vulnerable populations in the Mediterranean, Eastern Anatolia, Southeastern Anatolia, and Aegean regions, which experienced low cumulative incidences throughout the outbreak period. A B19V outbreak could yet occur in these areas due to susceptible populations. However, because our study was not designed as an analytical study, additional studies are required to examine differences based on these variables.

In our study, B19V infection was more prevalent in individuals under 18 years of age compared with those aged 18 and older. Upon analyzing the age groups, we discovered that the highest cumulative incidences occurred in the 5-9 age group. This age range is equivalent to primary school children in Türkiye, where the susceptible population frequently interacts closely with one another. Additionally, the health behaviors of this age group may have contributed to the increased disease incidence.[49]

Our study has certain limitations. First, the incidence was deduced, which implies there may be patients who were unwell but chose not to seek treatment at any health institution. This may have been influenced by the socioeconomic level and the number of physicians per 100,000. However, despite this possibility, the World Health Organization has stated that the estimated incidence figures accurately reflect the actual incidence rates in situations where there is no disruption in the data flow.[50]

Second, the CFR was calculated based on the number of deaths attributed to B19V infection and reported to the Ministry of Health during the outbreak. It is important to note that this calculation did not include deaths that were not notified or occurred outside the hospital. Since there is a lack of studies on B19V-related fatalities in literature, our study will make a valuable contribution. During the COVID-19 pandemic, B19V's virulence might have changed significantly. Notably, cardiac involvement has been observed in the reported deaths in our country. Therefore, we recommend analyzing the virus's genomic sequence and regularly monitoring its mutations. In addition to genomic sequencing information to be obtained from clinical samples during outbreaks, the clinical conditions of people admitted to the hospital, the geographical region where the outbreak occurred, climatic conditions, and criteria such as CFR should be documented. Thus, if variations between outbreaks are detected, alterations in the genome of the pathogen can also be investigated. We anticipate an increase in B19V cases, particularly from February onwards in the late winter, spring, and early summer of 2025. It is vital for clinicians to be prepared for this. Additionally, clinical trials may also be conducted in hospitals during these periods to investigate the virus's virulence, clinical status, and prognosis of the infection.

Third, we were unable to compare the number of B19V cases that occurred before and after the pandemic since the syndromic surveillance program, which allowed us to detect the B19V outbreak, has been in use only for the past five years in Türkiye. However, based on both the surveillance experience of the early warning units and the number of B19V cases manually tracked before syndromic surveillance, the B19V outbreak period in Türkiye in 2024 had a higher number of cases compared to previous B19V seasonal periods. We excluded old data to ensure data standardization and completeness. In populations where data is routinely collected, this allows for the generation of novel hypotheses, such as comparing disease indicators before and after a pandemic.

Fourth, PCR or serologic tests are used diagnosing B19V infection.[6] Because our study employed clinical diagnoses and ICD-10 codes, it might not accurately reflect the reality due to confusion with comparable rash-associated diseases and misclassification due to incorrect use of ICD-10. The séroconversion rates of B19V are not routinely monitored in Türkiye. Clinical diagnoses can be confirmed by PCR in all regions. Additionally, in areas with limited diagnostic capacity, the national reference laboratory facilitates diagnosis confirmation. However, as there is no specific treatment for B19V disease, some patients can be treated symptomatically without laboratory confirmation.

We experienced the largest B19V outbreak with a CFR of 0.0184% between February and June 2024 in Türkiye with two deaths among 10,898 patients. Cases were more common in the northern geographical regions of the Black Sea, Central Anatolia, and the Marmara region. This study revealed the unusual scale of B19V using estimated incidences and CFR indicators. Therefore, the use of existing syndromic surveillance is crucial for early detection and intervention. Policymakers should consider establishing screening programs for vulnerable populations (e.g., pregnant women and the under-5 population) and low-income regions. In low socioeconomic regions, health promotion can be achieved through health education, especially for the population at risk.

Ethics Committee Approval: The study protocol was approved by the Ethics Committee of the Bilkent City Hospital Medical Research Scientific and Ethical Evaluation Board (approval number: TABED 1/845/2024, date: 18.12.2024).

Informed Consent: Not applicable.

Data Sharing Statement: The datasets analyzed during the current study are available from the corresponding author upon reasonable request.

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