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Molecular and serological markers of human parvovirus B19 infection in blood donors: A systematic review and meta-analysis

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Abstract:

BACKGROUND: Human parvovirus B19 (B19V) is one of the blood-borne viruses. The virus can be transmitted to susceptible individuals by blood or blood products. The virus is not associated with significant disease in general population, while people with underlying problems such as immunodeficiency can cause anemia and arthritis. The current systematic review and meta-analysis aimed to estimate the overall prevalence of B19V DNA, anti-B19V IgG, and anti-B19V IgM antibodies in blood donors worldwide.

METHODS: A systematic search was carried out in online databases for relevant studies from inception until March 30, 2019. Study selection was performed based on predesigned eligibility criteria. The proportion of B19V DNA, anti-B19V IgG, and anti-B19V IgM antibodies were pooled using the inverse variance method. All statistical analyses were performed using the R version 3.5.3, package "meta."

RESULTS: According to the random-effects model, the pool prevalence of B19V DNA, anti-B19V IgM, and anti-B19V IgG among blood donors was calculated to be 0.4% (95% confidence interval [CI] =0.3%–0.6%), 2.2% (95% CI = 1.3%–3.7%), and 50.1% (95% CI = 43.1%–57.1%), respectively.

CONCLUSION: For the transmission of B19V through blood, the presence of the virus genome is required, and the present study showed that the prevalence of the virus genome in blood donors is <1%. Therefore, there is no need to screen donated blood for B19V infection.

Keywords:

B19V DNA, blood donors, meta-analysis, parvovirus B19, seroprevalence

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Introduction

Over time, concerns regarding the safety of the blood supply have been dramatically decreased by adopting several precautionary strategies, such as virus removal or inactivation mechanisms, careful selection of donors, and implementation of nucleic acid testing (NAT), for common blood-borne viruses, including hepatitis C virus, hepatitis B virus, and human immunodeficiency virus type 1 in blood donors.[1] Nevertheless, there are other viruses such as human parvovirus B19 (B19V) that usually cause mild symptoms in healthy individuals, but they are associated with serious clinical implications in some high-risk groups and should be considered as a concern in transfusion medicine.[2]

B19V, a small, nonenveloped virus with a single-stranded, linear DNA genome, is a member of the genus *Erythroparvovirus*

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within the *Parvoviridae* family.[2,3] The primary route of B19V transmission is through respiratory droplets, and it can also be transmitted via hand-to-mouth contact, blood and blood-derived products, organ transplantation, and vertically from the infected mother to the fetus.[4] Infection with B19V is often asymptomatic in healthy immunocompetent individuals and is not associated with severe illness. However, it can lead to a wide spectrum of clinical features such as erythema infectiosum (fifth disease), arthropathy, chronic anemia, hydrops fetalis, transient aplastic crisis, and rash–fever illnesses that are influenced by the hematological and immunological status of host.[5] It has demonstrated that B19V is highly resistant to virucidal agents and commonly used viral inactivation procedures on the blood and plasma-derived products, which is considered as a risk to transfusion safety.[6] The *P* antigen or globoside is the major cellular receptor for B19V, which is expressed at higher levels on the cell surface of hematopoietic cells, such as bone marrow erythroid progenitors. Therefore, patients with hemolytic disorders are potentially more susceptible to acquiring life-threatening red blood cell aplasia and hemolysis following infection with B19V.[7,8]

The present study is the first systematic review and meta-analysis aiming to provide a precise estimate of the prevalence of B19V DNA, anti-B19V IgG, and anti-B19V IgM antibodies in the blood donor population in the world. These results offer new insights into the seroepidemiology and molecular prevalence of B19V.

Methods

This systematic review and meta-analysis was conducted in accordance with the Preferred Reporting Items for Systematic Reviews and Meta-Analyses guidelines.[9]

Search strategy

A comprehensive systematic search was performed in electronic databases, including Scopus, Institute of Scientific Information Web of Science, PubMed, Embase, and Google Scholar to identify articles reporting the prevalence of B19V infection in blood donors. Searches were carried out from database inception until March 30, 2019, with no limitation in language. The reference lists of all included articles were manually screened to identify more relevant articles. The keywords used for our search are listed in Appendix 1.

Study selection

All identified articles were imported to EndNote software version X8 (Thomson Reuters, California, USA) for removing duplicates. After removing duplicates, two trained research specialists independently reviewed all titles and abstracts of remained studies in parallel to exclude obvious irrelevant publications. Full text of relevant articles was then retrieved and reviewed, and any discrepancies that arose between the reviewers were resolved through discussion with a third reviewer.

Eligibility criteria

Studies were included in this meta-analysis if they met the following criteria: (1) studies using a cross-sectional design examining the prevalence of B19V infection in blood donors; (2) studies published in any language in peer-reviewed journals with an available English abstract published; (3) studies using diagnostic methods including ELISA and different types of polymerase chain reaction (PCR) techniques to assess the presence of anti-B19V IgM/IgG and B19V DNA; and (4) studies using the serum or plasma samples from healthy blood donors.

The following studies were excluded: (1) studies using diagnostic methods other than ELISA and PCR such as receptor-mediated hemagglutination assay; (2) studies examining the prevalence of B19V infection in blood donors through viral antigen detection; (3) studies examining the incidence rate of B19V infection in blood donors; (4) studies examining the prevalence of B19V infection using the serum or plasma samples from blood donors with underlying conditions; (5) studies published in any language without an available English abstract; and (6) reviews, letters to the editor, conference abstracts, and case reports.

Data extraction and quality assessment

Data extraction for all eligible studies was carried out independently by two reviewers in a prepiloted data extraction spreadsheet using Microsoft Excel 2013 (Microsoft Corporation, Redmond, Washington, USA). The following specific information and data were extracted from all included studies: First author's name, study location, year of publication, total sample size, type of specimen, detection method, molecular detection index, positive rate of anti-B19V IgG and anti-B19V IgM antibodies, and positive rate of B19 DNA. Based on a modified checklist extracted from the Strengthening The Reporting of OBservational studies in Epidemiology, a quality assessment of the identified studies was conducted.[10,11] The checklist consisted of 12 questions including different methodological aspects. Studies were considered eligible for the main meta-analysis if they reached a validity score of at least 8 out of a maximum of 12.

Statistical analysis

The proportion of B19V viremia, B19V IgM-positive, and B19V IgG-positive was pooled using the inverse

variance method, according to a random-effects model (DerSimonian–Laird weights method).[12] Logit transformation was used to stabilize the variation of proportions, and the Clopper–Pearson method was used to estimate confidence interval (CI) for each study.[13] Continuity correction of 0.5 was applied in studies with zero cell frequencies. The meta-analysis was carried out using the Mantel–Haenszel and DerSimonian–Laird methods to calculate heterogeneity among the results of the studies which was assessed by the I^2 statistic, and the $P < 0.1$ was considered statistically significant. To find the potential sources of heterogeneity between studies, subgroup analysis was performed by study location, detection method, sample type, and molecular detection index. All statistical analyses were done using the R version 3.5.3 (2019-03-11),[14] package "meta,"[15] and $P < 0.05$ was considered statistically significant.

Results

Literature selection and study characteristics

A total number of 269 papers were identified from the five databases and bibliographic hand searching. Collectively, 118 duplicates were excluded and 151 papers were remained for screening the title and abstract. Of these, 102 papers were excluded. A total of 49 full-text papers were assessed for eligibility; of these, 8 were excluded. All studies could reach to validity score and no study was not excluded due to quality assessment. Finally, 41 papers met the inclusion criteria and were included in this meta-analysis. The process of literature retrieval and screening is illustrated in Figure 1. The characteristics of eligible studies included in this systematic review and meta-analysis are summarized in Table 1. The publication date of articles ranged from 1993 to 2019. The included studies were divided into three groups for meta-analysis: those with data regarding B19V DNA, those regarding anti-B19V IgM, and those regarding anti-B19V IgG in the blood donor population. All of the 41 selected articles were cross-sectional studies.

Prevalence of molecular marker of B19V in blood donors

The overall prevalence of B19V DNA was calculated among 93,636 blood donors from 17 countries in the world. According to the random-effects model, the pool prevalence of B19V DNA in blood donors was 0.4% (95% CI = 0.3–0.6%; I^2 = 89.7%). Figure 2 represents the forest plot and results of the meta-analysis for estimating the pooled prevalence of B19V DNA in blood donors with a 95% CI. The results of the subgroup analysis of the prevalence of B19V DNA in blood donors are presented in Table 2. Subgroup analysis by geographical region showed that the lowest pooled prevalence of B19V DNA was in Polish (0.1%; 95% CI = 0.01%–0.7%) and South Korean (0.1%; 95% CI = 0.05%–0.2%) population, while the highest prevalence was in the Sudanese population (7.2%; 95% CI = 3.6%–13.8%). Most studies on the prevalence of B19V DNA have been conducted in Brazil with six studies. More details on the prevalence of B19V DNA for subgroups among blood donors are shown in Table 2.

Prevalence of serological markers of B19V in blood donors

The prevalence of anti-B19V IgM was calculated among 10228 blood donors from 11 countries, and the range was from 0% to 15.6%. According to the random-effects model, the pool prevalence of anti-B19V IgM in blood donors was 2.2% (95% CI = 1.3%–3.7%; I^2 = 93.5%) [Figure 3]. The lowest and the highest pooled prevalence of anti-B19V IgM was calculated in the Spanish and Zambian population, respectively (0.3%, 95% CI = 0.02%–5.5% vs. 15.6%, 95% CI = 11.1%–21.4%). Most studies on the seroprevalence of anti-B19V IgM have been conducted in China and Iran, each with three studies. There was no statistically significant difference in the seroprevalence rate of anti-B19V IgM in the ordering of type of specimen between serum and plasma. More details on the seroprevalence of anti-B19V IgM among blood donors for subgroups are presented in Table 3.

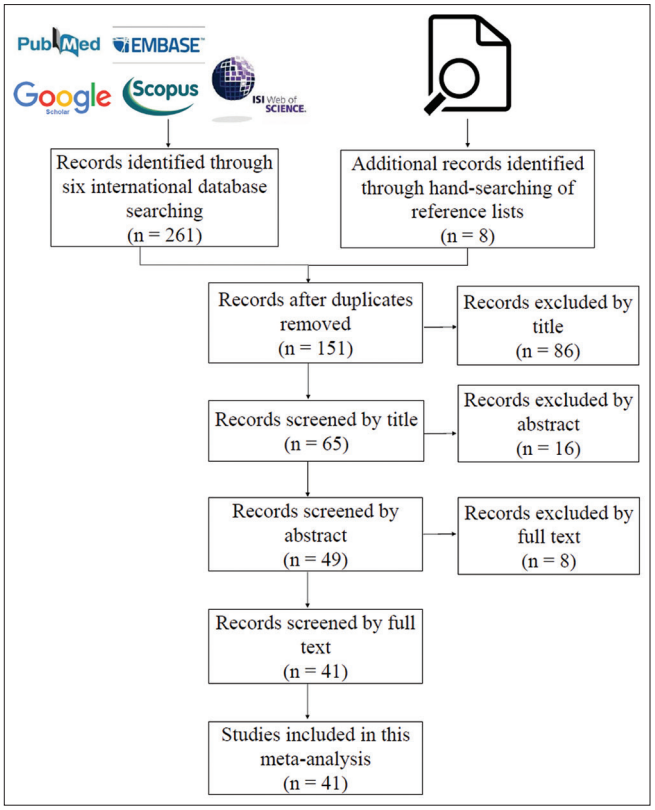

Figure 1: Flowchart presenting the results of the literature search

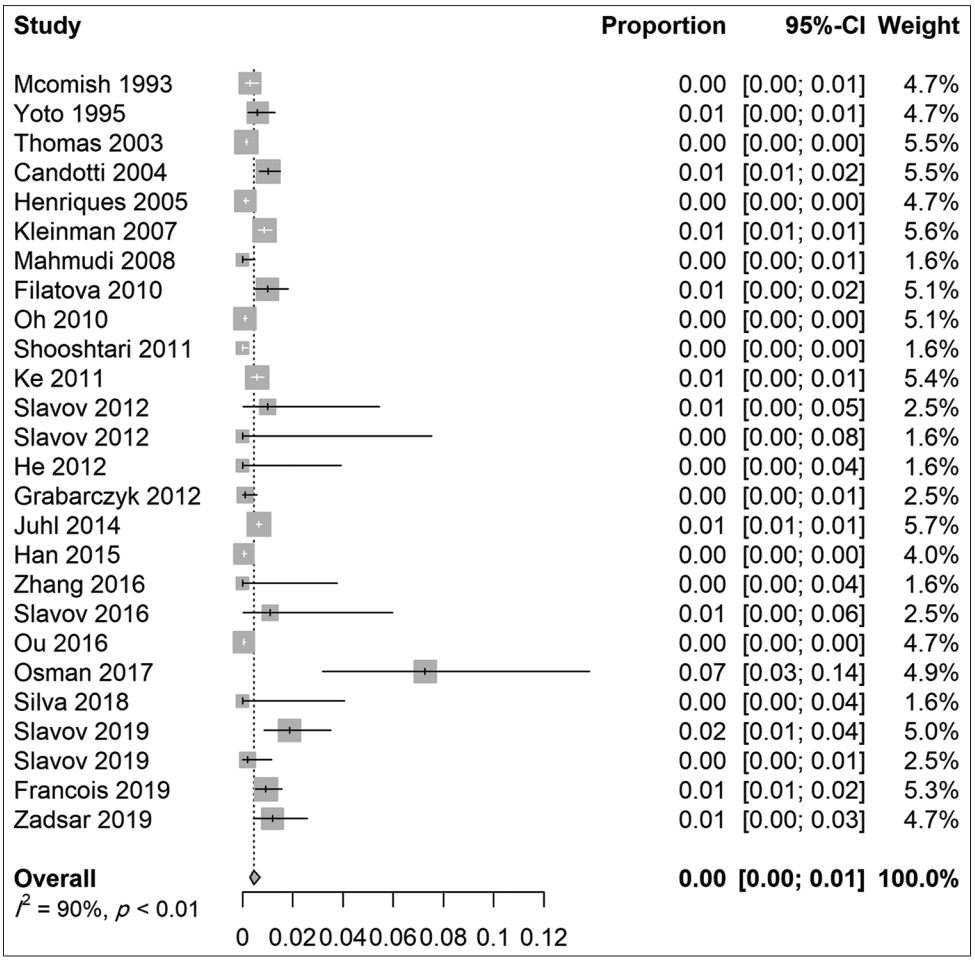

Figure 2: Forest plot of the prevalence of B19V DNA among blood donors

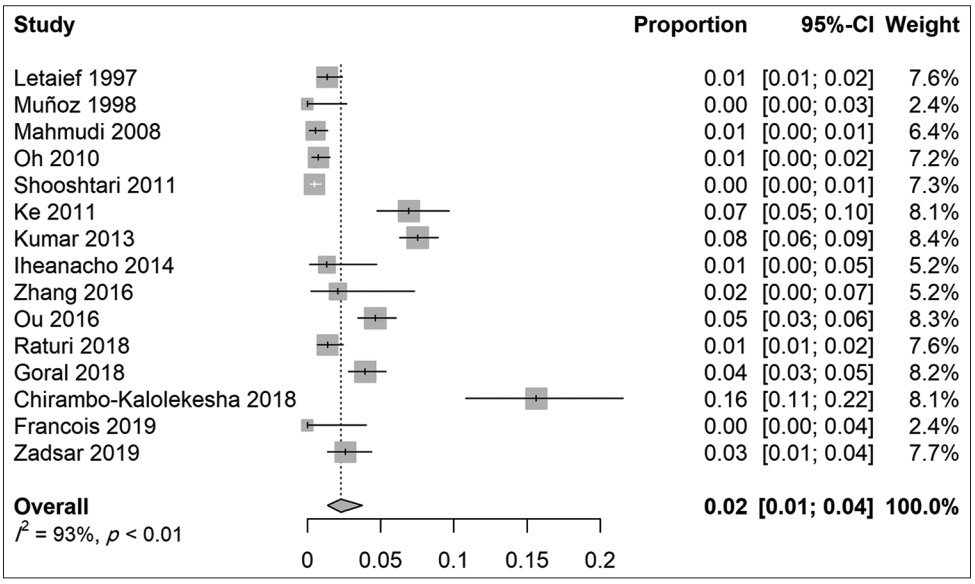

Figure 3: Forest plot of the seroprevalence of anti-B19V IgM among blood donors

The prevalence of anti-B19V IgG was calculated among 13594 blood donors from 17 countries, and the range was from 9.7% to 79.1%. According to the random-effects model, the pool prevalence of anti-B19V IgG in blood donors was 50.1% (95% CI = 43.1%–57.1%; I^2 = 98.2%) [Figure 4]. The lowest and the highest pooled prevalence of anti-B19V IgG was estimated in the Chinese and Italian populations, respectively

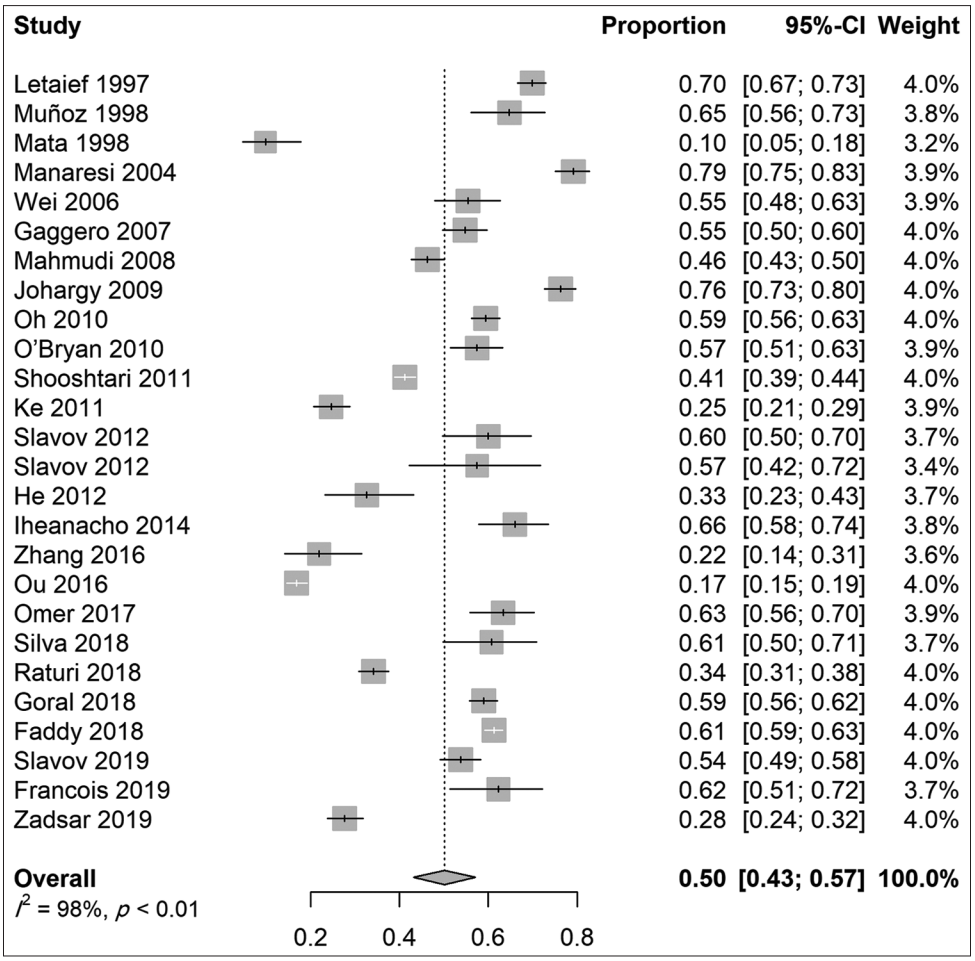

Figure 4: Forest plot of the seroprevalence of anti-B19V IgG among blood donors

Table 1: Characteristics of the included studies in this systematic review and meta-analysis (original)

Author, year (reference)	Location	Total sample size	Type of sample	Detection method	Molecular target	Number of positive for B19V DNA	Number of positive for anti-B19V IgM	Number of positive for anti-B19V IgG
Mcomish *et al.*, 1993[16]	Scotland	2000	Plasma	Nested PCR	NR	6	-	-
Yoto *et al.*, 1995[17]	Japan	1000	Serum	Nested PCR	VP1	6	-	-
Letaïef *et al.*, 1997[18]	Belgium and Tunisia	819	Serum	ELISA	-	-	11	572
Mata Rebón *et al.*, 1998[19]	Spain	92	Serum	ELISA	-	-	-	9
Muñoz *et al.*, 1998[20]	Spain	136	Serum	ELISA	-	-	0	88
Thomas *et al.*, 2003[21]	Belgium	16,859	Plasma	Nested PCR	NS1	27	-	-
Candotti *et al.*, 2004[22]	UK, Ghana, South Africa, and Malawi	2440	Plasma	Nested PCR and real-time PCR	NS1	25	-	-
Manaresi *et al.*, 2004[23]	Italy	446	Serum	ELISA	-	-	-	353
Henriques *et al.*, 2005[24]	Portugal	5025	Plasma	Real-time PCR	NR	6	-	-
Wei *et al.*, 2006[25]	China	184	Serum	ELISA	-	-	-	102
Kleinman *et al.*, 2007[26]	USA	5020	Plasma	Real-time PCR	VP1	44	-	-
Gaggero *et al.*, 2007[27]	Chile	400	Serum	ELISA	-	-	-	219
Mahmoudi *et al.*, 2008[28]	Iran	730	Serum	Semi-nestedPCRandELISA	NS1, NS2, VP1	0	4	338
Johargy, 2009[29]	Saudi Arabia	578	Serum	ELISA	-	-	-	441
O'BryanandWright,2010[30]	USA	282	Serum	ELISA	-	-	-	162

Contd...

Table 1: Contd...

Author, year (reference)	Location	Total sample size	Type of sample	Detection method	Molecular target	Number of positive for B19V DNA	Number of positive for anti-B19V IgM	Number of positive for anti-B19V IgG
Oh *et al*., 2010[31]	South Korea	10,032	Plasma	Real-time PCR	NR	10	-	-
	South Korea	928	Plasma	ELISA	-	-	7	551
Filatova *et al*., 2010[32]	Russian federation	1000	Serum	Real-time PCR	NR	10	-	-
Ke *et al*., 2011[33]	China	3957	Plasma	Real-time PCR	NS1	23	-	-
	China	448	Plasma	ELISA	-	-	31	110
Mahmoodian-Shooshtari and Sharifi, 2011[34]	Iran	1640	Serum	Semi-nestedPCRandELISA	NS1, NS2, VP1	0	8	676
Grabarczyk *et al*., 2012[35]	Poland	980	Plasma	Real-time PCR	NR	1	-	-
He *et al*., 2012[36]	China	92	Plasma	Real-time PCR and ELISA	NS1	0	-	30
Slavov *et al*., 2012[37]	Brazil	47	Plasma	Real-time PCR and ELISA	VP1	0	-	27
Slavov *et al*., 2012[38]	Brazil	100	Plasma	Real-time PCR and ELISA	VP1	1	-	60
Kumar *et al*., 2013[39]	India	1633	Serum	ELISA	-	-	123	-
Iheanacho *et al*., 2014[40]	Nigeria	150	Serum	ELISA	-	-	2	99
Juhl *et al*., 2014[41]	Germany	23,889	Plasma	Real-time PCR	NR	157	-	-
Han *et al*., 2015[42]	China	5030	Plasma	Real-time PCR	NR	3	-	-
Ou *et al*., 2016[43]	China	10,452	Plasma	Real-time PCR	NR	6	-	-
	China	1078	Plasma	ELISA	-	-	50	181
Slavov *et al*., 2016[44]	Brazil	91	Plasma	Real-time PCR	VP1	1	-	-
Zhang *et al*., 2016[45]	China	96	Plasma	Real-time PCR and ELISA	NS1	0	2	21
Osman *et al*., 2017[46]	Sudan	110	Plasma	Nested PCR	VP1	8	-	-
Omer *et al*., 2017[47]	Sudan	180	Serum	ELISA	-	-	-	114
Chirambo-Kalolekesha *et al*., 2018[48]	Zambia	192	Serum	ELISA	-	-	30	-
Faddy *et al*., 2018[49]	Australia	2221	Plasma	ELISA	-	-	-	1360
Göral *et al*., 2018[50]	Turkey	988	Serum	ELISA	-	-	39	582
Raturi *et al*., 2018[51]	India	800	Serum	ELISA	-	-	11	273
Silva *et al*., 2018[52]	Brazil	89	Serum	Real-time PCR and ELISA	VP1	0	-	54
Zadsar *et al*., 2019[6]	Iran	500	Plasma	Nested PCR and ELISA	VP2	6	13	138
Francois *et al*., 2019[53]	South Africa	1500	Plasma	Real-time PCR	NS1	14	-	-
	South Africa	90	Plasma	ELISA	-	-	0	56
Slavov *et al*., 2019[54]	Brazil	477	Plasma	Real-time PCR	VP1	1	-	-
Slavov *et al*., 2019[55]	Brazil	480	Plasma	Real-time PCR and ELISA	VP1	9	-	258

PCR=Polymerase chain reaction, ELISA=Enzyme-linked immunosorbent assay

(28.8%, 95% CI = 17.3%–44.0% vs. 79.1%, 95% CI = 75.1%–82.6%). Most studies on the seroprevalence of anti-B19V IgG have been conducted in China, with five studies [Table 4].

Discussion

Human B19V is one of the blood-borne viruses, which could be transmitted to susceptible individuals by blood or blood products. B19V infection is important in pregnant women and in people who receive blood regularly, such as thalassemia patients and immunocompromised patients. B19V can cause hydrops fetalis in pregnant women. It can also lead to anemia and arthritis in thalassemia patients and immunocompromised patients.[56]

To date, there was no overall estimation of B19V DNA prevalence, as well as seroprevalence of IgG and IgM antibodies against B19V in the blood donor population, and the current meta-analysis was conducted to address this gap. The results of our meta-analysis demonstrated an overall prevalence of 0.4% for B19V DNA among blood donors in the world. The pooled prevalence was calculated from studies using real-time PCR, nested PCR, and semi-nested PCR. Our subgroup analysis has shown that the nested PCR could be more sensitive for detection of B19V

Table 2: Subgroup analysis of the prevalence of B19V DNA in blood donors

Characteristics	Categories	Number of studies	Pooled prevalence (%) (95% CI)	Heterogeneity test (I^2%, *P*)	Differences between subgroups; Chi-square test (*P*)
Overall	-	26	0.4 (0.3-0.6)	89.7, <0.01	-
Sample type	Serum	5	0.4 (0.1-1.1)	56.0, 0.04	*P*=0.94
	Plasma	21	0.4 (0.2-0.7)	91.4, <0.01	
Detection method	Real-time PCR	18	0.4 (0.2-0.6)	86.6, <0.01	*P*=0.04*
	Nested PCR	6	0.8 (0.2-2.3)	95.4, <0.01	
	Semi-nested PCR	2	0.05 (0.01-0.3)	0, 0.69	
Detection index	VP1	9	1.1 (0.5-2.4)	79.1, <0.01	*P*=0.01*
	NS1	6	0.5 (0.2-1.2)	90.8, <0.01	
	NS1 and NS2	2	0.05 (0.01-0.3)	0, 0.69	
	VP2	1	1.2 (0.5-2.6)	0, NA	
Study location	Brazil	6	1.3 (0.7-2.3)	1.1, 0.41	*P*<0.01*
	China	5	0.2 (0.05-0.8)	88.5, <0.01	
	Iran	3	0.2 (0.01-2.4)	78.7, <0.01	
	South Africa	2	0.8 (0.5-1.4)	0, 0.49	
	Belgium	1	0.1 (0.1-0.2)	0, NA	
	Germany	1	0.6 (0.5-0.7)	0, NA	
	Ghana	1	1.3 (0.7-2.2)	0, NA	
	Japan	1	0.6 (0.2-1.3)	0, NA	
	Malawi	1	1.2 (0.2-8.3)	0, NA	
	Poland	1	0.1 (0.01-0.7)	0, NA	
	Portugal	1	0.1 (0.05-0.2)	0, NA	
	Russian Federation	1	1.0 (0.5-1.8)	0, NA	
	Scotland	1	0.3 (0.1-0.6)	0, NA	
	South Korea	1	0.1 (0.05-0.2)	0, NA	
	Sudan	1	7.2 (3.6-13.8)	0, NA	
	United Kingdom	1	0.9 (0.47-1.72)	0, NA	
	USA	1	0.9 (0.6-1.1)	0, NA	

PCR=Polymerase chain reaction, CI=Confidence interval, NA=Not available

Table 3: Subgroup analysis of the seroprevalence of anti-B19V IgM in blood donors (original)

Characteristics	Categories	Number of studies	Pooled prevalence (%) (95% CI)	Heterogeneity test (I^2%, *P*)	Differences between subgroups; Chi-square test (*P*)
Overall	-	16	2.2 (1.3-3.7)		-
Study location	Iran	3	0.9 (0.2-3.0)	88.2, <0.01	*P*<0.01*
	China	3	5.1 (3.4-7.7)	60.7, 0.08	
	India	2	3.3 (0.6-16.2)	96.8, <0.01	
	Belgium	1	0.9 (0.3-2.3)	0, NA	
	Nigeria	1	1.3 (0.3-5.1)	0, NA	
	South Africa	1	0.5 (0.03-8.1)	0, NA	
	South Korea	1	0.7 (0.3-1.5)	0, NA	
	Spain	1	0.3 (0.02-5.5)	0, NA	
	Tunisia	1	1.8 (0.8-3.8)	0, NA	
	Turkey	1	3.9 (2.9-5.3)	0, NA	
	Zambia	1	15.6 (11.1-21.4)	0, NA	
Sample type	Serum	9	2.0 (0.9-4.3)	95.4, *P*<0.01	*P*=0.5
	Plasma	6	2.6 (1.4-5.0)	86.2, *P*<0.01	

CI=Confidence interval, NA=Not available

DNA in all kinds of samples (0.8, 95% CI = 0.2%–2.3%) when compared to the real-time PCR and semi-nested PCR methods, and the differences were statistically significant ($P = 0.04$) [Table 2]. This reflects the fact that the nested PCR is more sensitive than other methods commonly used for the detection of B19V DNA since this technique is based on two rounds of PCR reactions conducted on a DNA template.

Our analysis has also revealed that B19V DNA contamination of donated blood in developing countries and some Sub-Saharan African countries such as Ghana,

Table 4: Subgroup analysis of the seroprevalence of anti-B19V IgG in blood donors (original)

Characteristics	Categories	Number of studies	Pooled prevalence (%) (95% CI)	Heterogeneity test (I^2%, *P*)	Differences between subgroups; χ^2 test (*P*)
Overall	-	26	50.1 (43.1-57.1)	98.2, <0.01	-
Study location	China	5	28.8 (17.3-44.0)	96.7, <0.01	*P*<0.01*
	Brazil	4	55.7 (52.0-59.3)	0, 0.49	
	Iran	3	38.1 (29.5-47.5)	95.5, <0.01	
	Spain	2	31.1 (2.7-87.8)	98.1, <0.01	
	Australia	1	61.2 (59.1-63.2)	0, NA	
	Belgium	1	73.9 (69.6-77.8)	0, NA	
	Chile	1	54.7 (49.8-59.5)	0, NA	
	India	1	34.1 (30.9-37.4)	0, NA	
	Italy	1	79.1 (75.1-82.6)	0, NA	
	Nigeria	1	66.0 (58.0-73.1)	0, NA	
	Saudi Arabia	1	76.3 (72.6-79.5)	0, NA	
	South Africa	1	62.2 (51.8-71.6)	0, NA	
	South Korea	1	59.3 (56.1-62.4)	0, NA	
	Sudan	1	63.3 (56.0-70.0)	0, NA	
	Tunisia	1	56.0 (60.1-69.7)	0, NA	
	Turkey	1	58.9 (55.8-61.9)	0, NA	
	USA	1	57.4 (51.6-63.0)	0, NA	
Sample type	Serum	15	56.1 (48.0-64.0)	97.7, <0.01	*P*=0.07
	Plasma	11	42.0 (30.0-55.0)	98.7, <0.01	

CI=Confidence interval, NA=Not available

Malawi, and Sudan is higher than that in developed countries, with prevalence of >1%. The European regulatory requirements and the US Food and Drug Administration have proposed a limit of 10^4 IU/mL of B19V DNA for the manufacturing pooled plasma to further decrease the potential risk of transmission. In this line, the German Red Cross Centers have been screened B19V mini-pool NAT in all blood donors in 2000.[57] Testing for B19V DNA for all pools is also recommended in the US.[42] Further, about 6.5 million blood donations between 2003 and 2009 have been screened for B19V DNA in the Netherlands.[58] However, it is nearly impossible for developing countries with limited financial resources to spend money just for B19V DNA screening of blood donations.

Our meta-analysis has shown that the pooled prevalence of anti-B19V IgM and IgG in blood donors was 2.2% and 50.1%, respectively. These prevalence rates were estimated from studies using ELISA assay. Approximately 10–14 days after the exposure, anti-B19V IgM is detectable in blood and usually lasts until the 5th month, and hence, the presence of IgM may be associated with the current or recent infection with B19V. On the other hand, about 15 days after infection, anti-B19V IgG appears in blood and lasts for months.[50] Similar to molecular prevalence rate, the seroprevalence rate of anti-B19V IgG and anti-B19V IgM varies among different countries, and the discrepancy between these reports can be attributed, in part, to geographic region, seasonal variation, demographic characteristics, target, and sensitivity of the assay used.

Although the B19V can be transmitted through blood and blood products, the risk of transmitting the virus and causing the disease is very low due to the low prevalence of this viral infection in blood donors. Because of the low prevalence of B19V infection and the high cost of molecular testing, screening donated blood for B19V infection is not recommended.

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Nil.

Conflicts of interest

There are no conflicts of interest.

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Appendix 1

Embase

('blood donor'/exp OR 'blood donation' OR 'blood donor' OR 'blood donors' OR 'plasma donor') AND ('human parvovirus b19'/exp OR 'human parvovirus b19' OR 'parvovirus b19' OR 'parvovirus b19, human') AND ('prevalence'/exp OR 'prevalence' OR 'prevalence study' OR 'epidemiology'/exp OR 'clinical epidemiology' OR 'cohort effect' OR 'confounding factors (epidemiology)' OR 'controlled before after studies' OR 'controlled before and after studies' OR 'controlled before and after study' OR 'controlled before-after studies' OR 'effect modifier, epidemiologic' OR 'effect modifiers (epidemiology)' OR 'effect modifiers (psychology)' OR 'environmental epidemiology' OR 'epidemiologic factors' OR 'epidemiologic methods' OR 'epidemiologic research' OR 'epidemiologic research design' OR 'epidemiologic studies' OR 'epidemiologic study characteristics' OR 'epidemiologic study characteristics as topic' OR 'epidemiologic survey' OR 'epidemiological research' OR 'epidemiology' OR 'epidemiology model' OR 'epidemiometry' OR 'healthy worker effect' OR 'historically controlled study' OR 'interrupted time series analysis' OR 'precipitating factors' OR 'sampling studies' OR 'virus detection'/exp OR 'detection, virus' OR 'viral detection' OR 'virus detection') AND 'article'/it

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Search ((((((“Prevalence”[Mesh] OR “Cross-Sectional Studies”[Mesh] OR “Epidemiology”[Mesh])))) AND ((“Parvovirus B19, Human”[Mesh] OR B19 virus OR B19 viruses OR Human Parvovirus B19))) AND ((“Blood Donors”[Mesh] OR Blood Donor OR Donor, Blood OR Donors, Blood OR Blood Donation OR Blood Donations OR Donation, Blood OR Donations, Blood)))

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TITLE-ABS-KEY ((“Prevalence” OR “Cross-Sectional Studies” OR “Epidemiology”) AND (“Parvovirus B19, Human” OR “B19 virus” OR “B19 viruses” OR “Human Parvovirus B19”) AND (“Blood Donors” OR “Blood Donor” OR “Donor, Blood” OR “Donors, Blood” OR “Blood Donation” OR “Blood Donations” OR “Donation, Blood” OR “Donations, Blood”)) AND (LIMIT-TO (DOCTYPE, “ar”))

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(TS=((“Prevalence” OR “Cross-Sectional Studies” OR “Epidemiology”) AND (“Parvovirus B19, Human” OR “B19 virus” OR “B19 viruses” OR “Human Parvovirus B19”) AND (“Blood Donors” OR “Blood Donor” OR “Donor, Blood” OR “Donors, Blood” OR “Blood Donation” OR “Blood Donations” OR “Donation, Blood” OR “Donations, Blood”))) AND LANGUAGE: (English) AND DOCUMENT TYPES: (Article)