Prevalence of Human Parvovirus B19 and Associated Risk Factors in Women with Bad Obstetric History in Babylon Province, Iraq

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Abstract

Background: Parvovirus infection is an important cause of fetal loss during all three trimesters of pregnancy. **Objectives:** This study was conducted to investigate the prevalence, susceptibility rate, and risk factors of B19-V in women aged 15 to 45 in the Al-Hamza region of Babil, Iraq, considering the negative effects of the infection. **Materials and Methods:** Between January 2022 and March 2023, blood samples were taken from 116 women, including those with and those without a history of bad obstetric history (BOH). Enzyme-linked immunosorbent assay (ELISA) was used to test sera taken from the study participants for B19 IgM and immunoglobulin G (IgG) antibodies. Those samples tested positive for IgG B19 were further subjected to polymerase chain reaction amplification and sequencing, targeting partial gene sequences of the nonstructural viral protein 1 (VP1) gene. **Results:** For human parvovirus IgG and IgM, the seropositivity was 44% and 16.5%, respectively. The following variables were associated in this study with greater seroprevalence rates of IgG and IgM, respectively: age 36–45 years (72.7%, 36.4%); abortion (80%, 32.5%); education (82.2%, 33.3%); unemployment (61%, 22.2%); and overcrowding (73.3%, 31.1%). In this case–control study, positive amplicons (700 bp) were detected from 27 samples out of 40 women of childbearing age who tested positive for IgG. Sequence analysis of the partial sequence of the VP1 gene in all positive amplicons was 100% identical with each other and with human parvovirus B19 (NC: 00088.3). According to the current study, about 66% of women are serologically negative and at risk of contracting parvovirus B19, **Conclusion:** Our findings conclude that pregnant women in Iraq, particularly those with BOH, must undergo frequent serological screening for B19-V during all three trimesters and be given the necessary advice to avoid B19-V infection to improve their pregnancy outcomes.

Keywords: B19, B19-V, BOH, Iraq, parvovirus, PCR, pregnant

Introduction

Human parvovirus (B19-V) infection is a highly contagious childhood disease with a distinctive face rash for children. It is a cause of erythema infectiosum, aplastic crisis, and acute symmetric polyarthropathy in adults and children. It can also cause fetal complications, including spontaneous abortions and hydrops fetalis.[1] According to the UK Health Security Agency,[2] B19-V is among several viruses, such as cytomegalovirus (CMV), adversely affecting pregnancy outcomes and causing viral congenital infections. B19-V is transmitted principally through respiratory secretions, hand-to-mouth contact, transfusion of blood products, and from mother to fetus.[3]

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The diagnosis of parvovirus B19 infection is through serological assays. IgM antibodies can usually be measurable within a range of 7–10 days post-viral acquisition and can be detected for 2–3 months after contracting the virus. About 2 weeks post-viral exposure, immunoglobulin G (IgG) titer will usually rise, and the patient will develop lifelong

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immunity.[1] The presence of IgM and IgG antibodies is usually diagnostic of recent infections, while samples with IgG+ and IgM− suggest immunity. Samples with both IgG− and IgM− indicate susceptibility, while samples with IgG− and IgM+ suggest recent exposure to the virus.[1,3] Parvovirus is a single-stranded deoxyribonucleic acid (DNA) virus that selectively infects and lyses human erythroblasts.[3] Parvovirus is autonomous and does not require a helper virus and was, therefore, until recently, it was classified in the genus *Parvovirus*. Human Parvovirus B19 is now classified as a member of the *Erythroparvovirus* genus of the subfamily Parvovirinae.[4] Parvovirus B19 has three genotypes (1–3) and at least four subtypes (1a, 1b, 3a, and 3b), according to genome analyses. Currently, three genotypes with four subtypes correlated to genotypes 1 and 3 (a, 1b, 3a, and 3b) have been found, depending on the isolation year and the geographical location. The most prevalent B19-V is Genotype 1, which shows a widespread distribution. Genotype 2 is more common in patients from Europe, whereas Genotype 3 is common in South America, sub-Saharan Africa, and France.[5,6] Worldwide, about 2% of all pregnancies are affected by Parvovirus infection. The rate of infection increases significantly during epidemics to between 3% and 20%, with a seroconversion rate of 3%–34%.[7]

In Europe, around 60% of pregnant women are resistant to B19-V infection,[6] with a prevalence rate of about 1%–5% for pregnant women and with a risk of transmission of 25%–30% to the fetus.[8,9] In the United Kingdom, there was a remarkable increase in the incidence of B19-V in laboratory-confirmed cases among women of childbearing age in 2013, 2017, and 2018.[10] In the surrounding regions, B19 was detected among healthy blood donors of different nationalities residing in Qatar,[11] Iran,[12] and pregnant women in Marrakesh.[13] In Iraq, human parvovirus B19 has been recently detected in patients suffering from thalassemia[14] and hemophilia A.[15] Recent studies have detected the seroprevalence of human parvovirus among pregnant women in Kirkuk,[16] Erbil,[17] and the southern region of ThiQar.[18] There is currently no licensed vaccine and no preventive measures to date. Several studies have previously investigated B19-V among different target groups; however, there are paucity of data on the molecular and seroprevalence of human parvovirus B19 and associated risk factors in women with bad obstetric history (BOH) history, specifically in the current study area of Babil. Bearing in mind the significant consequences of the infection, this study was undertaken to determine the rate of Parvovirus B19 infection in women of childbearing age with BOH and the impact of sociodemographic variables among the target group in the Al-Hamza district of Babil, Iraq.

Materials and Methods

Study design

The total subjects of this descriptive case–control study involved 116 women of childbearing age (15 to 45 years old). Women with BOH were recognized and recruited from the primary healthcare centers located in the Al-Hamza district in Babil, Iraq. Twenty-five participants were excluded due to missing data. Of the residual (n = 91) study population members, 40 (44%) had BOH and were categorized as research group subjects, 51 (56%) had an average to good obstetric history and were classified as control group members.

Collection of data

For sample collection, members of the project team regularly visited primary health care centers in the Al-Hamza district. Possible participants were recognized, approached, interviewed, and involved in the project after obtaining informed consent. The exclusion criteria applied for the candidates were as follows: women with uterine or cervical abnormalities, chromosomal abnormalities in either spouse, hyperthyroidism, diabetes mellitus, hypertension, hypothyroidism, renal disorders, or a history of fetal chromosomal or genetic anomalies. The study population was classified into four classes; the first represents pregnant women with a good obstetric history. The second represents pregnant women with BOD. The third represents non-pregnant women with an average to good obstetric history. The fourth class represents non-pregnant women with BOD.

Collecting and handling of blood samples

A volume of approximately 10 mL of venous blood was taken from each individual between January 2022 and March 2023, and it was stored in sterile containers under aseptic conditions. After this, serum was divided and stored in aliquots at −20°C until it was processed further.

Enzyme-linked immunosorbent assay (ELISA) assay

Serum specimens from all participants were analyzed for B19 IgM and IgG antibodies using Vircell ELISA kits. The kit was purchased from Vircell S.L. Prague, Spain, G1031 and M1031 for IgG and IgM, respectively. The ELISA tests were performed in compliance with the manufacturer's recommendations from CALABIOTECH. A microwell ELISA reader was utilized to process the data, and an optical density of 450 nm was utilized for reading.

DNA extraction

Utilizing the Favor Prep Genomic DNA Mini Kit (Intronbio, Korea), viral genomic DNA was obtained from serum samples in a final total volume of 100 μL, as per the manufacturer's instructions. We measured the amount and quality of DNA using a NanoDrop 2000 spectrophotometer. Until it was needed, the eluted genomic DNA was kept at −20°C.

Table 1: Seroprevalence of B19-V immunoglobulin G among study population in regard to age, abortion, education, employability, and residential status

	Age groups				Abortion status		Education status		Occupation status		Residential status	
	Total	15–25 years old	26–35 years old	36–45 years old	Not aborted	Aborted	Uneducated	Educated	Unemployed	Employed	Not crowded	Crowded
B19-V IgG −ve	51	23	25	3	43	8	43	8	21	30	39	12
	56.0%	62.2%	58.1%	27.3%	84.3%	20.0%	93.5%	17.8%	38.9%	81.1%	84.8%	26.7%
B19-V IgG +ve	40	14	18	8	8	32	3	37	33	7	7	33
	44.0%	37.8%	41.9%	72.7%	15.7%	80.0%	6.5%	82.2%	61.1%	18.9%	15.2%	73.3%
Pearson Chi-square			4.33		**37.64**		**52.91**		**15.86**		**31.18**	
***P* value**			*NS*		***<0.01***		***<0.01***		***<0.01***		***<0.01***	

IgG, immunoglobulin G

NS refers to *P* values with insignificant difference

Bold values indicated a significant difference

Bold italic values indicate *P* values with a significant difference

Polymerase chain reaction

The partial gene sequence of the viral protein 1 (VP1) gene was amplified using the Macrogen, Korea, primers (K-1, 5′-ATAAATCCATATACTCATT-3′ and K-2, 5′-CTAAAGTATCCTGACCTTG-3′), in compliance with the protocol.[19] Using the Maxime PCR PreMix Kit (i-Taq) (Intronbio, Korea), DNA fragments were amplified using the polymerase chain reaction (PCR) in a total volume of 20 µL. The PCR tube containing Taq DNA polymerase, dNTP mixture, and reaction buffer was filled with 4 µL of template DNA, 2 µL of each forward and reverse primer, and 7 µL of RNase-free water. The target DNA was amplified using conventional PCR under the parameters given by Loy *et al.* (2002): annealing at 37°C for 120 s and elongation at 72°C for 180 s for 35 cycles. Positive control was provided by the Central Health Laboratory of the Ministry of Health, Iraq.

Agarose gel electrophoresis

PCR products (5 µL) were separated on a 0.7% (w/v) agarose gel by electrophoresis using 1 × tris-borate-EDTA buffer containing 0.5 µg/mL of simply safe dye, run for 1 h and 30 min, and visualized under 320 nm ultra violet light. The size of the products was ascertained by means of comparison with Intronbio (Korea)'s 100 bp DNA ladder.

Sequencing

As described previously elsewhere,[20] positive PCR amplicons were gel purified and sequenced by a commercial service. Sequencing was conducted using the same forward and reverse primers used in the PCR. Upon downloading the sequences from the Eurofins Homepage, sequences were further compared with each other by the STADEN Package version 2003.0 Pregap4 and Gap4 programs as described earlier by Bonfield *et al.* (1995).[21] BLASTN and BLASTX options from the National Center for Biotechnology Information (NCBI) were used to compare the obtained sequences with data in GenBank. According to Hall (1999),[22] the BioEdit Sequence Alignment Editor program's ClustalW algorithm carried out several alignments of nucleotide sequences.

Data analyses

The data was collected and assembled using a Microsoft Excel spreadsheet. The relation between variables was examined using a Chi-squared test via SPSS (V.24). In order to calculate the odds ratio, the relation between categorical data was conducted by bivariate regression-line analysis.

Ethical approval

The Biotechnology ethics committee of Al-Qasim Green University, College of Medical Biotechnology, approved the research proposal to be conducted in its presented form.

Results

For this study, 116 women in total were pooled. For 91 of these women in the study sample, full data were documented. The research subjects were classified and subcategorized by sociodemographic variables; for example, education, employment, age, or living in overcrowded households. Overall, this study reported an infection rate of 44% with B19-IgG among the study population. Of the three different age groups illustrated in Table 1, IgG seropositivity increased with age, rising from 37.8% in the 15–25 years old to 41.9% in the 26 to 35 years old to reach the highest 72.7% among the 36–45-year old. There is, however, no significant correlation between B19-IgG and age group.

The aborted group (study group) had a higher seroprevalence of B19-IgG seropositivity of 80.0% compared to 15.7% in the non-aborted group (control group). The relation between B19-IgG and abortion status was significant ($P < 0.01$). The prevalence of B19-IgG among the unemployed was highest (61.1%) compared

to the employed (18.9%). The Chi-squared values and *P*-value between B19-IgG and employment status indicate a significant correlation at a *P*-value of <0.01 at a 95% confidence interval (CI). Education and overcrowding cohorts had a B19-IgG seroprevalence of 82.2% and 73.3% compared to the uneducated group (6.5%) and those living alone or in less crowded situations (15.2%). The relation between B19-IgG and education was significant ($P < 0.01$), and there was also a significant correlation between B19 and the crowding situation ($P < 0.01$).

This study also revealed an infection rate with B19 of 16.5% (B19-IgM +ve) among women of childbearing age. Of the three different age groups illustrated in Table 2, IgM seropositivity showed an increase with age, starting from 8.1% among 15–25 years old to 18.6% among the 26–35-year-old, to reach the highest level of 36.4% for the 36–45-year-old group. These results were, however, not statistically significant. The prevalence of B19-IgM among aborted women (32.5%) was higher than non-aborted (3.9%). The Pearson Chi-square test and the *P*-value indicate a significant correlation between B19-IgM and abortion status at a *P*-value below 0.01 at 95% CI. The prevalence of B19-IgM among were as follows: educated women (33.3%), unemployed (22.2%), and overcrowding families (31.1%), which were higher compared to non-educated (0.0%), employed (8.1%), and those living in non-crowded living arrangements (2.2%). The values of Chi-squared (χ^2) and *P*-values (*P*) indicate that the χ^2 figures for B19-IgM were significant both for education and residential status, with a *P*-value below 0.01 at a 95% CI. There is, however, no significant correlation between occupation status and the seroprevalence of B19-IgM [Table 2].

In order to confirm the infection with B19-V at the molecular level in the region, the sera from the IgG B19

Table 2: Seroprevalence of B19-V IgM among study population in regard to age, abortion, education, employability, and residential status

		Age groups			Abortion status		Education status		Occupation status		Residential status	
	Total	*15–25 years old*	*26–35 years old*	*36–45 years old*	*Not aborted*	*Aborted*	*Uneducated*	*Educated*	*Unemployed*	*Employed*	*Not crowded*	*crowded*
B19-V IgM −ve	76	34	35	7	49	27	46	30	42	34	45	31
	83.5%	91.9%	81.4%	63.6%	96.1%	67.5%	100.0%	66.7%	77.8%	91.9%	97.8%	68.9%
B19-V IgM +ve	15	3	8	4	2	13	0	15	12	3	1	14
	16.5%	8.1%	18.6%	36.4%	3.9%	32.5%	0.0%	33.3%	22.2%	8.1%	2.2%	31.1%
Pearson Chi-square		5.18			13.300		18.360		3.17		13.386	
***P* value**		*0.075*			***<0.01***		***<0.01***		*0.070*		***<0.01***	

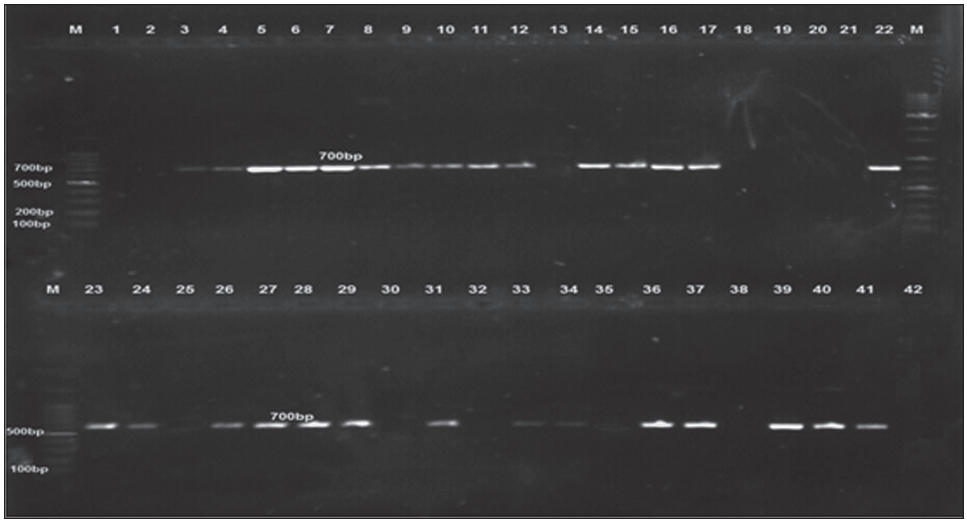

Figure 1: About 1.5% agarose gel electrophoresis (72 V/80 min) of PCR to amplify 700 bp partial sequence from VP1 gene of 1–42 represented samples; M deoxyribonucleic acid marker size (100bp), PC (positive control) (sample no 22), NC (negative control) (sample no 42), all of the rest represent those tested positive for PCR (patients' samples)

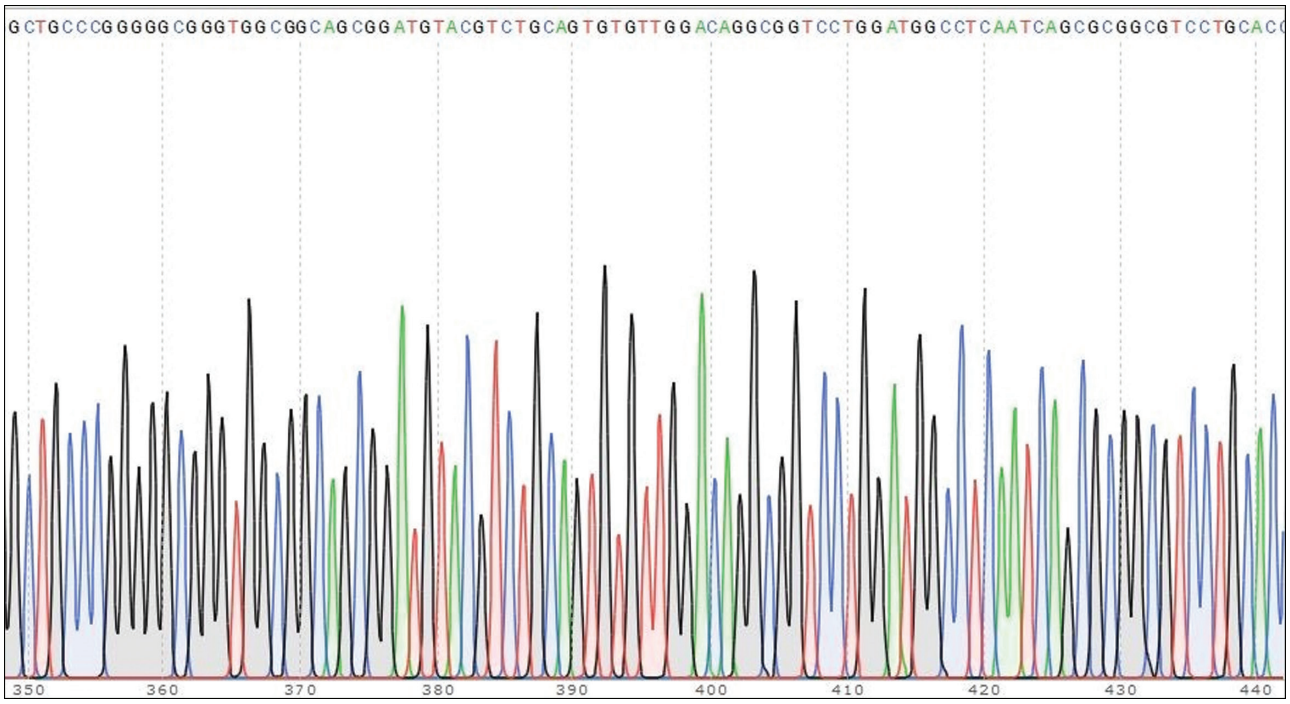

Figure 2: The pattern of deoxyribonucleic acid (DNA) chromatogram for DNA specimens of partial sequence of the 700 bp amplicon of the VP1 gene

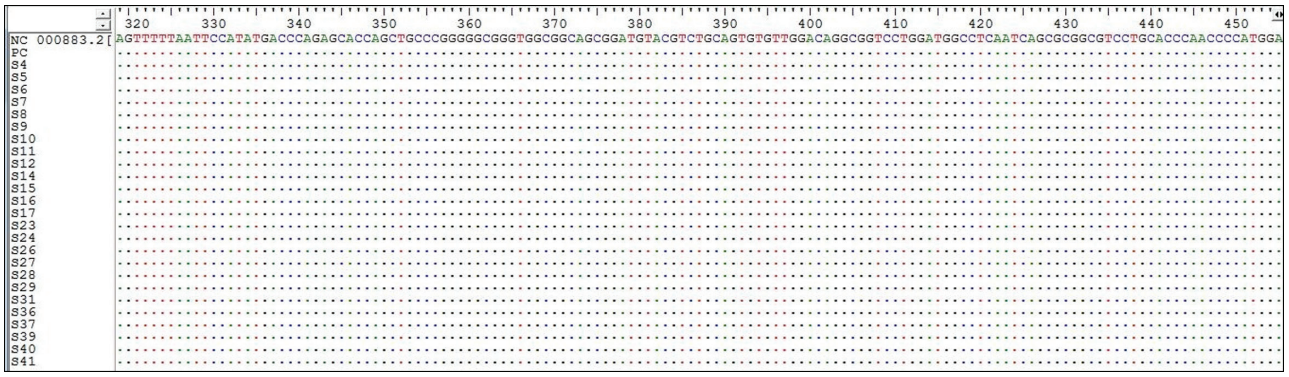

Figure 3: Partial Multiple deoxyribonucleic acid alignment of the 700 bp of the VP1 gene of human parvovirus B19

positively tested women ($n = 40$) were subjected to PCR targeting a partial sequence of the VP1 gene. Positive amplicons (700 bp) were detected from 27 samples of these women, as illustrated in Figure 1.

Upon sending the PCR products to Macrogen, Korea, for nucleotide sequencing, chromatograms derived from patients and positive control were obtained, as shown in Figure 2.

All nucleotide sequences obtained from patients and positive control were aligned using the DNA Star BioEdit program and found to be 100% identical among each other and to the reference "Human Parvovirus B19 (NC: 00088.3)." The numbers S4–S41 represent those 25 patients tested positive via PCR while PC represents the positive control [Figure 3].

Nucleotide sequences of the VP1 gene for all 26 positive PCR products (resembling 25 patients and one from PC) were 100% identical among each other and to the reference "Human Parvovirus B19 (NC: 00088.3)." Dots indicate identical letters to the reference sequence (NC: 00088.3). The alignment was performed according to EditSeq DNA STAR software.

The obtained nucleotide sequence of the partial gene sequence of VP1 (700bp) was subjected to blast N in NCBI and found to be 100% identical to the human parvovirus viral protein (VPI) gene (ID._000883.2) [Figure 4].

Discussion

Globally, according to recently published reports, the seroprevalence of B19-V among pregnant women in Europe is around 60%; in Italy, for instance, it is 69.5%.[23] This is higher than that detected among pregnant women

Figure 4: BLASTN alignment results of 700 bp partial gene sequence of viral protein (VP1) gene indicate 100% similarity to human parvovirus VPI gene (ID._000883.2)

in Africa (20%),[24] and among pregnant women in the Middle East, such as Iran, it is 54%.[23]

Previous research conducted in several parts of Iraq has found high seroprevalence rates of 93% in Kirkuk among women with BOH,[16] lower prevalence rates were reported in Erbil (40%),[17] and for ThiQar (38%)[18] in women with spontaneous abortion. Within this study, the overall seroprevalence of B19-V was 44%; this study found B19-V seroprevalence with the lowest rates among the youngest group (15–26) years old and increasing with age. The susceptibility rate of 66% identified in this study is within the national average. A significantly considerable link between the infection with abortion and BOH (control group) was also shown by our findings. Our study also revealed greater seroprevalence rates in overcrowded households, unemployed, educated, and aborted populations. This study found 44.0% seroprevalence of B19-IgG antibodies among the study population, which is in alignment with those in ThiQar (38%),[18] Erbil (40%),[17] and considered lower than that reported for Kirkuk (93%).[16] Our findings are also comparable to that documented in the surrounding regions as in Iran (40%)[12] and Makkah, Saudi Arabia (46.6%).[25] The findings of this study are also in alignment with a previous study from Erbil, Iraq, which also documented a 40% seroprevalence rate of B19 IgG among women of childbearing age.[17] This study also found the seroprevalence of B19-IgG increased with age. There was also a higher seroprevalence of IgG among the aborted women (study group) (80%) and among those living in overcrowded situations (73.3%); our findings are also in accordance with the previous report from Kirkuk.[16]

The rising of B19 IgG seroprevalence with age among women in this study is consistent with findings from a previous study, which reported a rise from 5.8% in women under 20 years of age to a peak of 32.4% in those aged

between 30 and 40 years of age. These rates, however, were lower than that documented in our study: 37.8% for those aged 15–25 years old, 41.9% for 26–35 years old, and approximately 72.7% for the geriatric group. Similar findings have come out from studies in other countries such as the USA, Australia, and Iran.[26,27] In the current study, B19-IgG seroprevalence continued to increase among the 36–45 year olds, reaching the highest at 72.7%. Indeed, this finding is comparable with other studies that have reported levels of approximately 60%–80% B19-IgG seropositivity among the geriatric age groups.[26] Seropositivity of IgG is believed to confer lifelong immunity. The finding of a seropositivity rate of 44.0% to B19-V infection among recruited women in the Al-Hamza district in Iraq in this study is noteworthy. This finding shows a difference of approximately 4% from Ahga *et al.* (2020),[28] who found a seropositivity rate of approximately 40% in Erbil, Iraq. This descriptive case–control study reported a higher seroprevalence of IgM among the aborted (32.5%), educated (33.3%), unemployed (22.2%), and overcrowded (31.1%). The role of sociodemographic factors in the epidemiology of B19 is well documented.[29] The increasing levels of B19 IgM antibodies increased from 8.1% among the youngest group (15–25 years) to 18.6% among the second age group (26–35 years) to reach the highest levels at 36.4% among the older group (36–45 years) is aligned with the high levels of current infections among the aborted women. This rise of IgM seroprevalence from those below 20 years of age to a peak among 36–45 years old age group is aligned with other studies.[26-30]

The high seroprevalence of B19-IgM among those living in overcrowded households and among homemakers (unemployed) aligns with the results of similar studies. Women whose social activities expose them to young children are noted in studies to be at higher risk of B19 infections. Women in their late 20s or 30s are more likely to be multiparous, have children of their own, engage in school runs, and engage with children from other families through the social activities of their children.[30] The interaction of large numbers of seronegative children within these contexts creates infection pools of active shedding episodes, which can persist for prolonged periods.[31] Similar to other viral infections such as CMV,[32] B19 is usually transmitted through body secretions, for example, nasal secretions, and women involved in cleaning and other sanitary activities. For similar reasons, women who work in after-school clubs, day-care centers, or nurseries have also been documented to be at higher risk for such viruses. Women with para-one are at three times greater risk than the nulliparous woman, while the risk of B19 infection increases to 7–8 times for those with 3 or more children at home.[33]

Fetal loss from congenital B19 infection is the most common in the first 20 weeks of pregnancy, with fetal death occurring approximately 28–42 days post B19-V infection.[9,34] In the current study, among aborted women in Babil, Iraq, 80.0% IgG and 32.5% IgM seropositivity were detected. Our data revealed a highly significant correlation between the seroprevalence of B19-IgG and IgM with abortion ($P < 0.01$). This is comparable to other studies in the region; for example, Khameneh *et al.* reported an 88.0% IgG seroprevalence among aborted women in Iran.[35] The high seroprevalence of IgG and IgM of B19-V found in this study among those individuals with BOH supports the advice to screen pregnant women on a regular basis, particularly if they may have been exposed to the virus through interactions with their own or other families' children.

Based on sequencing analysis of the partial gene sequence of VP1 from B19-V, the nucleotide sequences were 100% identical to the human parvovirus VPI gene (ID._000883.2), and this, in turn, confirms the infection with B19-V among Iraqi women at childbearing age. A previous study from Iran[12] has recorded B19-V, Genotype 1, subtype 1a, as a circulating B19-V in the region. Further studies molecularly characterizing B19-V and determining the genotype and subtype are needed in the region.

Locally, previous studies conducted found an infection rate with B19-V of 30.4% and 31% among women with adverse pregnancy outcomes.[36,37] In the current study, the main goal of the PCR tool was to amplify a partial sequence of the VPI gene to establish the infection with B19-V among the Iraqi population, and it was not to be correlated with the serological results. The 27 patients' samples showed positive PCR amplicons out of the $n = 40$ positively tested women (67.5%) for B19-V IgG do not represent infection rate simply because PCR was performed only for samples tested positive for B19-IgG and not for the entire study population. The explanation of B19 viral DNA detection in our patient group remains ambiguous basically because of the persistence of low-level viremia post-viral infection.[24,25] This might explain the less than 100% detection rate via PCR from those women who tested positive for B19-V IgG through ELISA. Case–control studies are, therefore, useful in estimating the association between DNA detection of B19V and the disease. Using internal positive controls was of significant value to examine the existence of inhibitory substances during PCR and sequencing procedures.[38]

Conclusion

This is the first study into the molecular and serological detection of B19-V among women with BOD in the Al-Hamza district of Hilla, Iraq. Based on the results of this study, B19-V is endemic in Babil, Iraq. The study found about 66% of women with BOH were susceptible to B19-V infection, which indicates a need for screening of all pregnancies for B19 immunity at the earliest

possible opportunity. Such screening will help to identify susceptibility and evidence of any seroconversion at a later stage of the pregnancy. Lifelong immunity is believed to result from B19 infection demonstrated by IgG prevalence. To conclude, this paper highlights the need for B19-V seroprevalence and molecular data to be further researched and explored in local populations. This will subsequently inform proactive intervention measures on regional levels.

Author contribution

Maha Diekan Abbas collected the data and wrote the manuscript, Haider Turky Mousa Al-Mousawi revised the manuscript, Nadhim Mushtaq Hashim Al-Bderee designed the experiment and assisted in molecular analyses, and Rasha M.A. Al-Humairi conducted the statistical analyses.

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Nil.

Conflicts of interest

There is no conflict of interest.

References

1. Bertoldi A, Salbetti MBC, Rodríguez G, Tenaglia M, Hernández G. Human parvovirus B19 infection in a pregnant patient resulting in severe hydrops, foetal death and persistent infection. Acc Microbiol 2022;4:000428.
2. UK Health Security Agency, 2022. Guidance on the investigation, diagnosis and management of viral illness, or exposure to viral rash illness, in pregnancy. Available from: viral-rash-in-pregnancy-guidance UK.pdf, [Last accessed on 15 Oct 2023].
3. Kostolansky S, Waymack JR. Erythema Infectiosum. 2023. In: StatPearls [Internet]. Treasure Island, FL: StatPearls Publishing; 2024. PMID: 30020681.
4. Susan CF. https://jgv.microbiologyresearch.org/content/journal/jgv/10.1099/jgv.0.001212" \t "_blank" ICTV virus taxonomy profile: Parvoviridae. J Gener Virol 2019;100:367-8.
5. Ekman A, Hokynar K, Kakkola L, Kantola K, Hedman L, Bondén H, *et al*. Biological and immunological relations among human parvovirus B19 genotypes 1 to 3. J Virol 2007;81:6927-6935.
6. Ornoy A, Ergaz Z. Parvovirus B19 infection during pregnancy and risks to the fetus. Birth Defects Res 2017;109:311-23.
7. Ergaz Z, Ornoy A. Parvovirus B19 in pregnancy. Reprod Toxicol 2006;21:421-35.
8. Grubman O, Hussain FN, Nelson Z, Brustman L. Maternal parvovirus B19 infection causing first-trimester increased nuchal translucency and fetal hydrops. Case Rep Obstet Gynecol 2019;3259760:1-4. doi:10.1155/2019/3259760.
9. Kielaite D, Paliulyte V. Parvovirus (B19) infection during pregnancy: Possible effect on the course of pregnancy and rare fetal outcomes. A case report and literature review. Medicina (Kaunas) 2022;58:664.
10. PHE. Increased parvovirus activity in England. 2018. Health Protection Report 12 issue 20, August 2018. Available from: www.gov.uk [Last accessed on 2024 Jan].
11. Abdelrahman D, Al-Sadeq DW, Smatti MK, Taleb SA, Abu Odeh RO, *et al*. Prevalence and phylogenetic analysis of parvovirus (B19V) among blood donors with different nationalities residing in Qatar. MDPI Viruses 2021;13:540.
12. Taherkhani R, Farshadpour F, Norozi M. Molecular evaluation of human parvovirus B19 infection and associated risk factors among pregnant women in Bushehr Province, Southern Iran. Am J Trop Med Hyg 2022;106:1539-46.
13. Bouraddane M, Warda K, Elkamouni Y, Arsalane L, Zouhair S. Parvovirus B19 in Morocco: Seroprevalence of immunoglobulin G antibody in pregnant women in Marrakesh. Clin Exp Obstet Gyneco 2023;50:25.
14. Alnassar AWD, Shallal MJM. Serological study of human parvovirus (B19) detected among patients with Thalassemia. J Pop Ther Clin Pharmacol 2023;30:e26-31.
15. Al-khegane MA, Wijdan NI, Meaad KH. Human parvovirus B19 among hemophilia A patients in Basrah, Southern Iraq,. Iraqi J Hematol 2022;IP:109.224.55.22.
16. Samarai AM, Hassan HM, Al samarai MA, Aljumaili ZK. Parvovirus B19 seroprevalence in women with bad obstetric history in Kirkuk. Antiinflamm Antiallergy Agents Med Chem 2021;20:359-66.
17. Nyan JM. Association of autoimmunity and parvovirus B19 infection among spontaneous miscarriage women in Erbil/ Iraq. Raf. J. Sci 2020;29:29-38.
18. Majeed KR. The seroprevalence of parvovirus B19 among pregnant women with spontaneous abortion in Thi-Qar province, Iraq. J Glob Pharma Technol 2018;10:1038-44.
19. Loy A, Lehner A, Lee N, Adamczyk J, Meier H, Ernst J, *et al*. Oligonucleotide microarray for 16S rRNA gene-based detection of all recognized lineages of sulfate-reducing prokaryotes in the environment. Appl Environ Microbiol 2002;68:5064-81.
20. Nadhim MH, Al-Mousawi HT, Al-Saad NFN, QabasNeamalt AL. Vitamin D receptor polymorphism and correlated with some chronic diseases among Iraqi women. Indian J Public Health Res Dev 2019;10:P1163.
21. Bonfield JK, Smith KF, Staden R. A new DNA sequence assembly program. Nucl Acids Res 1995;24:4992-9.
22. Hall TA. BioEdit: A user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucl Acids Symp Series 1999;41:95-8.
23. De Paschale M, Pavia C, Cerulli T, Cagnin D, Manco MT, Belvisi L, *et al*. Prevalence of anti-parvovirus B19 IgG and IgM and parvovirus B19 viremia in pregnant women in an urban area of Northern Italy. J Med Virol 2022;94:5409-14.
24. Moosazadeh M, Alimohammadi M, Mousavi T. Seroprevalence and geographical distribution of parvovirus B19 antibodies in pregnant women: A meta analysis. J Immunoassay Immunochem 2023;44:103-16.
25. Ghazi HO. Prevalence of antibodies to human parvovirus b19 in Saudi women of childbearing age in Makkah. J Family Comm Med 2007;14:15-7.
26. Kelly HA, Siebert D, Hammond R, Leydon J, Kiely P, Maskill W. The age-specific prevalence of human parvovirus immunity in Victoria. Epidemiol Infect 2000;124:449-57.
27. Sharifi P, Khodabandehloo M, Rahimiyan-Zarif BS. Seroprevalence of parvovirus B19 antibodies in young women Sanandaj Iran. Iranian J V 2013;7:1-6.
28. Ahga N, Alharmni K, Alkhayat Z. Seroepidemiology of human parvovirus B19 among pregnant women in Erbil, Iraq. Med J Babylon 2020;17:64-8.
29. Alanen A, Kahala K, Vahlberg T, Koskela P, Vainionpää R. Seroprevalence, incidence of prenatal infections and reliability of maternal history of varicella zoster virus, cytomegalovirus, herpes simplex virus and parvovirus B19 infection in South-Western Finland. Inter J Obst Gynaecol 2005;112:50-6.
30. Al-Hajjar QN, Al-Mousawi HTM. Immunological and molecular diagnosis of cytomegalovirus infection between aborted & pregnant women in Babylon City. Baghdad Sci J 2021;18:1086-94.
31. Savings mothers lives, The Seventh Report of the Confidential Enquiries into Maternal Deaths in the United Kingdom, Reviewing maternal deaths to make motherhood safer - 2003-2005, Confidential Enquiry into Maternal and Child Health 2007; Available from: https://www.publichealth.hscni.net/sites/default/files/Saving%20Mothers%27%20Lives%202003-05%20.pdf. [Last accessed on 10 Apr 2021]
32. Abbas MD, Egbe SS. Seroprevalence of CMV in women with bad obstetric history in Babil/ Iraq. Iraqi J Pharm Sci 2021;30:106-12.

33. Public Health England, protecting and improving the nation's health, Guidance on infection control in schools and other childcare setting. 2017; 1-15. Available from https://cks.nice.org.uk/topics/parvovirus-b19-infection/management/children-adults-not-pregnant/ [Last accessed on 10 Apr 2021].
34. Staroselsky A, Klieger-Grossmann C, Garcia-Bournissen F, Koren G. Exposure to fifth disease in pregnancy. Can Fam Phys 2009;55:1195-8.
35. Khameneh ZR, Hanifian H, Barzegari R, Sepehrvand N. Human parvovirus B19 in Iranian pregnant women: A serologic survey. Indian J Pathol Microbiol 2014;57:442-4.
36. Abdulhassan LF, Hathal HD, Abdullah TH. Detection of parvovirus B19 in bad obstetric history by using real time PCR. Iraqi JMS 2017;15:350-7.
37. Hussein AA. Detection of human parvovirus B19 antibodies in pregnant women with spontaneous abortion. J Faculty Med Baghdad 2016;58:80-4.
38. Abbas, MD. Diagnosis of ferlaviruses in snakes and characterization of isolates based on gene sequences. PhD dissertation, Faculty of Agricultural science, Institute of Environmental and Animal Hygiene, Hohenheim University, Stuttgart, Germany, 2013.