

Risk of Vertical Transmission of Human Parvovirus B19 Among Pregnant Women Attending Antenatal Clinics in North-Central Nigeria

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Abstract:

➤ Background:

Human Parvovirus B19 (B19V) is a significant cause of foetal morbidity and mortality due to its ability to cross the placenta during maternal viraemia. Despite documented high seroprevalence in Nigeria, data on the molecular evidence of vertical transmission risk among pregnant women are limited.

➤ Objective:

To determine the seroprevalence, DNA detection rate, and associated risk factors for vertical transmission of B19V among pregnant women attending antenatal clinics in North Central Nigeria.

➤ Methods:

A cross-sectional study was conducted between 2018 and 2022 involving 276 pregnant women recruited from antenatal clinics of three tertiary health centres in Benue, Kogi and Plateau States, North-Central Nigeria. Demographic and clinical data were collected using a structured questionnaire. Participants' blood samples were analysed for anti-B19V IgG and IgM antibodies using ELISA. A subset of 38 serologically reactive samples was tested for B19V DNA using quantitative polymerase chain reaction. Statistical associations were analysed using SPSS (v26.0) at 95% confidence level.

➤ Results:

Anti-B19V IgG and IgM antibodies were detected in 12.7% and 7.7% of the pregnant women, respectively. B19V DNA was detected in 55.3% (21/38) of the sero-reactive pregnant women subset across all trimesters. Detection rate was highest in the second trimester. Tribe was marginally associated with both seroprevalence and DNA positivity; and between the number of previous pregnancies and IgG positivity.

➤ Conclusion:

This study reports serological and molecular evidence of B19V viraemia among pregnant women in North Central Nigeria, with DNA positivity suggesting risk of vertical transmission. Screening for B19V in antenatal care is recommended to prevent adverse foetal outcomes.

Keywords: Parvovirus B19, Vertical Transmission, Pregnancy, Nigeria, Hydrops Foetalis.

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I. INTRODUCTION

Human parvovirus B19 (B19V) is a small, non-enveloped, single-stranded DNA virus belonging to the *Parvoviridae* family and *Erythroparvovirus* genus. It is the primary pathogenic parvovirus in humans and exhibits a marked tropism for erythroid progenitor cells in the bone marrow and foetal liver (Heegaard & Brown, 2002; Young & Brown, 2004; Landry, 2016; Keramari et al., 2022). B19V is the causative agent of a wide spectrum of clinical manifestations, ranging from erythema infectiosum in children to severe complications such as transient aplastic crisis, chronic anaemia in immunocompromised individuals, and non-immune hydrops fetalis in pregnant women (Servey, Reamy, & Hodge, 2007; Brown, 2010; Qiu et al., 2017; Dittmer et al., 2024).

B19V is transmitted mainly through respiratory secretions and close contact, but may also spread through contaminated blood products and transplacentally, with viral infection of erythroid precursor cells disrupting erythropoiesis and potentially causing maternal and, particularly, fetal anaemia, hydrops fetalis, cardiac failure, spontaneous abortion, or intrauterine fetal death (Gallinella, 2014; Dittmer et al., 2024; Kagan et al., 2024). Vertical transmission rates are estimated to range from 17.0 to 33.0%, with the highest risk occurring between 9 and 20 weeks of gestation (Craboli et al., 2017; Women's Health & Education Centre [WHEC], 2009). Consequences of intrauterine B19V infection include spontaneous abortion, intrauterine foetal death, and hydrops fetalis due to foetal anaemia (Rodis et al., 1998; Enders et al., 2004).

The consequences of B19V infection during pregnancy should, however, be distinguished between maternal infection and confirmed fetal infection. Maternal infection does not necessarily result in fetal infection, and fetal infection does not invariably result in severe disease. This distinction is supported by recent evidence from a systematic review and meta-analysis of 44 studies involving 3,221 women and 748 fetuses with B19V infection. Sorrenti et al. (2026) reported an intrauterine demise rate of 7.3% among pregnancies with maternal infection compared with 38.7% among pregnancies with confirmed fetal infection. Among infected fetuses, ultrasound evidence of hydrops and cardiomegaly was also common, and intrauterine transfusion was required in a substantial proportion of cases. These findings emphasise the importance of early recognition of maternal infection and appropriate fetal surveillance rather than assuming that maternal infection inevitably results in adverse pregnancy outcome.

Early recognition of maternal B19V infection and timely fetal surveillance, including ultrasonographic monitoring and assessment of fetal anaemia, are essential for identifying pregnancies at risk and enabling interventions such as intrauterine transfusion in severe cases (Kagan et al., 2024; Prasad et al., 2025). Laboratory evaluation complements clinical monitoring, with B19V-specific IgM and IgG indicating recent and past exposure, respectively, while PCR/qPCR detection of viral DNA provides additional

evidence of infection, particularly when serological findings are inconclusive or recent infection is suspected (Dittmer et al., 2024; Malutan et al., 2024).

Serological evidence of B19V exposure is common among women of reproductive age, with global anti-B19V IgG seroprevalence ranging from 35.0 to 65.0% depending on age and geography (Mosson et al., 2008; Sharifi et al., 2013). In Nigeria, studies have shown IgG seroprevalence of 41.5 to 62.8% among pregnant women, indicating widespread past exposure (Emiasegen et al., 2011; Musa et al., 2013; Jegede, Aminu, & Ella, 2014). However, seronegative women remain susceptible to primary infection, which is most dangerous during pregnancy due to the risk of vertical transmission (Brown et al., 2006). Combining serological and molecular testing improves detection of B19V infection because viral DNA may precede antibody development, although maternal B19V DNA alone indicates viraemia rather than confirmed fetal infection or vertical transmission, which requires appropriate fetal testing such as amniotic-fluid PCR when clinically indicated (Malutan et al., 2024).

The resurgence of B19V infections reported in several regions during 2023–2024 has renewed interest in its epidemiology and highlighted the importance of sustained surveillance, particularly among pregnant women, although available evidence suggests increased viral circulation rather than the emergence of a more virulent strain (Prasad et al., 2025; Sorrenti et al., 2026). Despite no significant increase in perinatal mortality, the recent rise in maternal infections has been associated with greater use of prenatal interventions, including repeated intrauterine transfusions for persistent fetal anaemia, indicating potential increased demands on maternal–fetal healthcare services (Prasad et al., 2025). In addition to serological surveillance, molecular characterisation is important for defining B19V genetic diversity and patterns of circulation; the three recognised genotypes differ in their geographical distribution, with genotype 1 predominating globally and genotypes 2 and 3 occurring more selectively, while sequencing and phylogenetic analyses provide valuable evidence for tracking circulating strains and their geographical relationships rather than predicting clinical severity (Servant et al., 2002; Qiu et al., 2017). However, contemporary epidemiological and molecular data remain limited in many African settings, including Nigeria, underscoring the need for locally generated evidence on B19V circulation and genetic characteristics.

Despite this risk, routine screening for B19V infection during antenatal care is not practiced in Nigeria. Moreover, most studies have focused on serological evidence without assessing active viraemia using molecular tools. The presence of B19V DNA in pregnant women during antenatal visits would provide definitive evidence of ongoing infection and potential risk to the foetus (Bonvicini et al., 2012; Gallinella et al., 2010).

This study was therefore designed to assess the risk of vertical transmission of B19V among pregnant women

attending antenatal clinics in North Central Nigeria through combined serological (IgM and IgG) and molecular (qPCR) approaches. By identifying the prevalence of active viraemia and associated risk factors, the study aims to inform policy on the need for routine antenatal screening and contribute to improved maternal-foetal health outcomes in the region.

II. METHODS

➤ *Study Design and Setting*

This was a descriptive cross-sectional study conducted between January 2018 and December 2022 in North Central Nigeria. The study sites included three tertiary health facilities: Plateau State Specialist Hospital, Jos (Plateau State); Federal Medical Centre, Lokoja (Kogi State); and Benue State University Teaching Hospital, Makurdi (Benue State). These centres were purposively selected to represent the major states in the region and to reflect diverse sociodemographic backgrounds. These facilities provide antenatal, obstetric and laboratory diagnostic services to pregnant women from different communities within the study area.

➤ *Study Population*

The study involved 276 pregnant women attending routine antenatal care at the selected hospitals. Participants were recruited consecutively after obtaining written informed consent. The inclusion criteria were age ≥ 15 years, confirmed pregnancy at any trimester, and willingness to provide informed consent. Women who declined consent were excluded. The study population was selected because primary B19V infection during pregnancy may result in maternal viraemia and potential transplacental transmission, with possible consequences for fetal health.

➤ *Ethical Considerations*

Ethical approval for this study was obtained from the Ethics Committees of the participating hospitals and the National Blood Transfusion Service Centre. The study objectives, procedures, potential risks and expected benefits were explained to eligible participants before enrolment. Informed consent was obtained from all participants before data and specimen collection. Confidentiality and anonymity were strictly maintained throughout the study.

➤ *Data Collection*

Sociodemographic and clinical data were collected using a structured, interviewer-administered questionnaire. Information gathered included age, gestational age, obstetric history (number of pregnancies, miscarriages, and stillbirths), history of blood transfusion, and relevant exposures.

➤ *Sample Collection and Processing*

Five millilitres of venous blood was collected aseptically from each participant using a sterile syringe. Serum was separated by centrifugation and stored at -20°C at the collection centre. Samples were transported in cold boxes to the Clinical Virology Laboratory at the University College Hospital (UCH), Ibadan, and stored at -20°C until analysis.

➤ *Serological Analysis*

All serum samples were screened for anti-human parvovirus B19 (B19V) IgM and IgG antibodies using commercially available Enzyme-Linked Immunosorbent Assay (ELISA) kits (DeMeditec Diagnostic GmbH, Germany) following the manufacturer's protocol. Optical density was measured at 450 nm, and interpretation of results was based on the provided cut-off values. Appropriate positive and negative controls were included in each assay run. For the IgG assay, all 276 serum samples were tested. The IgM assay was performed on 273 participants. The difference in denominator between the IgG and IgM analyses resulted from the assay configuration, which included an additional control in the IgM testing. Serological results were interpreted according to the manufacturer's recommended criteria. IgG positivity was considered evidence of previous exposure to B19V, whereas IgM positivity was considered evidence consistent with recent or current infection.

➤ *Molecular Analysis (qPCR)*

A total of 38 serologically reactive samples (either IgM-positive, IgG-positive, or both) from pregnant women were selected for molecular testing. Molecular investigation was conducted on a subset of 38 pregnant women selected from the serologically investigated participants. The molecular subset represented participants with serological reactivity and adequate serum specimens available for molecular analysis. The molecular sample was therefore not an independently selected random sample of all 276 pregnant women. Consequently, the proportion of B19V DNA-positive samples among the 38 tested participants was interpreted as the detection rate within the molecularly investigated subset and not as the population prevalence of B19V DNA among all pregnant women. This distinction was maintained throughout the analysis and interpretation of the molecular findings. DNA extraction was performed using QIAamp DNA Mini Kit (QIAGEN, Germany) according to the manufacturer's instructions. Quantitative real-time polymerase chain reaction (qPCR) targeting the NS1 region of B19V DNA was carried out using a Rotor-Gene Q platform (QIAGEN). Amplification conditions included initial denaturation at 95°C for five minutes, followed by 45 cycles of 95°C for 15 seconds, 55°C for 30 seconds, and 72°C for 30 seconds. Positive and negative controls were included in each run.

➤ *Quality Control*

Quality assurance measures included use of internal controls, proper calibration of equipment, and adherence to standard operating procedures. Quality assurance procedures were implemented throughout specimen collection, serum processing, serological testing, DNA extraction, qPCR, conventional PCR, gel electrophoresis and sequencing. Appropriate positive and negative controls were included during laboratory assays. For molecular testing, pre-amplification and post-amplification activities were conducted separately to minimise contamination. Sterile consumables and aerosol-resistant pipette tips were used throughout DNA extraction and PCR procedures. The qPCR system, thermocycler, spectrophotometer and other laboratory equipment were operated according to

manufacturers' recommendations. All biological specimens were handled using appropriate personal protective equipment and standard laboratory biosafety procedures. Biological waste was disposed of according to institutional biomedical-waste management procedures.

➤ Statistical Analysis

Data generated from the structured questionnaires and laboratory investigations were entered into Microsoft Excel for data cleaning, coding and verification and subsequently analysed in Statistical Package for Social Sciences (SPSS) version 26.0 (IBM Corp., Armonk, NY, USA) using descriptive and inferential statistics. Categorical variables were expressed as frequencies and percentages. For the serological analysis, B19V IgG positivity was calculated using 276 as the denominator, whereas IgM positivity was calculated using 273, corresponding to the number of participants tested for each antibody. For the molecular analysis, the denominator was restricted to the 38 pregnant women tested by qPCR. Associations between B19V serological or molecular status and selected socio-demographic, obstetric and clinical characteristics were

assessed using the Pearson chi-square test. Fisher's exact test was applied where expected cell frequencies were inadequate for the chi-square test. A two-tailed p -value of <0.05 was considered statistically significant. For trimester-specific analyses, participants were classified according to their recorded trimester of pregnancy. Serological and molecular findings were expressed as frequencies and percentages based on the number of participants tested within each relevant trimester or analytical category.

III. RESULTS

➤ Sociodemographic Characteristics of Participants

A total of 276 pregnant women were enrolled in the study across the three tertiary health facilities in North Central Nigeria. The mean age was 30.8 years ($SD \pm 6.6$), with the majority aged between 26 and 35 years (55.1%). Most participants were married (97.1%), had a tertiary education (49.6%), and were self-employed (44.6%). The highest number of participants was from the Igala ethnic group (32.6%). (Table 1)

Table 1 Sociodemographic Characteristics of Pregnant Women in North Central Nigeria. (n=276)

Variable	Frequency (n)	Percent (%)
Age group (years)		
≤25	53	19.2
26–35	152	55.1
>35	71	25.7
Education level		
Variable	Frequency (n)	Percent (%)
None/Primary	35	12.7
Secondary	104	37.7
Tertiary	137	49.6
Occupation		
Civil servant	66	23.9
Self-employed	123	44.6
Unemployed	48	17.4
Others	39	14.1
Ethnic group		
Igala	32	32.6
Tiv	49	21.4
Idoma	11	19.2
Berom	13	4.7
Ngas	7	2.5
Mwaghavul	9	3.3
Others	45	16.3

➤ Seroprevalence of Human Parvovirus B19 Among Pregnant Women in North Central Nigeria

Of 276 serum samples tested, anti-B19V IgM antibodies were detected in 21 participants (7.6%), and IgG antibodies in 35 (12.7%). Dual IgM/IgG positivity was found in 2.0% of the study population.

➤ Seroprevalence by Gestational Age of Pregnancy

The highest seroprevalence of IgM (indicating recent infection) was recorded in the second trimester (8.2%),

followed by the third (7.5%) and first (6.5%) trimesters. IgG seroprevalence (indicating past exposure) was also highest in the second trimester (13.5%). (Table 2)

Table 2 B19V IgM and IgG Antibody Distribution by Gestational Age in North Central Nigeria. (N = 276)

Trimester	No. of Women	IgM Positive (%)	IgG Positive (%)
First (≤ 13 weeks)	62	4 (6.5%)	7 (11.3%)
Second (14–27 weeks)	134	11 (8.2%)	18 (13.5%)
Third (≥ 28 weeks)	80	6 (7.5%)	10 (12.5%)
Total	276	21 (7.6%)	35 (12.7%)

➤ Detection of B19V DNA in Pregnant Women

B19V DNA was tested in a subset of 38 seropositive pregnant women (IgM- and/or IgG-positive). Of these, 21

(55.3%) tested positive for B19V DNA, confirming active viraemia. (Table 3)

Table 3 Distribution of B19V DNA Positivity by Gestational Age in North Central Nigeria (n = 38)

Trimester	DNA Tested	DNA Positive (%)
First trimester	6	4 (66.7%)
Second trimester	19	10 (52.6%)
Third trimester	13	7 (53.8%)
Total	38	21 (55.3%)

➤ Association with Obstetric Risk Factors

There was a marginally significant association between pregnancy history and IgG positivity ($p = 0.054$), with higher IgG seropositivity among multigravidae. However, no

statistically significant association was observed between B19V seropositivity or DNA positivity and history of miscarriage or stillbirth ($p > 0.05$). (Table 4)

Table 4 Association between Selected Obstetric Factors and B19V Infection Among Pregnant Women in North Central Nigeria.

Risk Factor	IgG Positive (%)	p-value	DNA Positive (%)	p-value
Previous miscarriage	10.2%	0.081	47.6%	0.463
Stillbirth history	5.7%	0.140	28.6%	0.242
Previous pregnancies ≥ 3	15.6%	0.054	62.5%	0.370

IV. DISCUSSION

This study provides complementary serological and molecular evidence of human parvovirus B19 (B19V) infection among pregnant women attending antenatal clinics in North-Central Nigeria and highlights the potential for maternal–fetal transmission. B19V DNA was detected in 21 of 38 (55.3%) pregnant women selected for molecular investigation, providing evidence of detectable viral DNA

among serologically investigated women; however, this proportion should not be interpreted as the prevalence of viraemia among all pregnant women because the molecular subset was not independently representative of the full study population.

Maternal B19V infection is clinically important because transplacental infection can result in fetal erythroid suppression, severe anaemia, non-immune hydrops fetalis,

miscarriage and intrauterine fetal death (Bonvicini et al., 2012; Puccetti et al., 2014; Gigi & Anumba, 2021). The observed anti-B19V IgM and IgG seroprevalences of 7.7% and 12.7%, respectively, were lower than several estimates previously reported among Nigerian pregnant women, including IgG prevalences of 27.5% in Central Nigeria (Emiasengen et al., 2011), 20.0% in Oyo State (Iyanda et al., 2013), and 44.3% in Ido-Ekiti (Akele et al., 2021). These differences may reflect variation in geographical setting, population characteristics, cumulative exposure, timing of sampling, circulating viral activity and laboratory methodology. Although the relatively low IgG prevalence observed in this study should not be interpreted as evidence of lower B19V transmission in North-Central Nigeria, it indicates that most participants had no detectable IgG at the time of testing and were therefore potentially susceptible to primary infection. This is particularly relevant during pregnancy because primary maternal B19V infection can result in transplacental transmission and fetal disease through infection of erythroid precursor cells and suppression of fetal erythropoiesis (Gigi & Anumba, 2021; Kagan et al., 2024). The marked heterogeneity among Nigerian studies, including the 40.7% overall antibody positivity reported by Emiasengen et al. (2011) and the substantially higher IgG and IgM prevalences reported by Akele et al. (2021), underscores the need for caution when making direct comparisons between populations studied at different times and in different settings. Taken together, the evidence of substantial serological susceptibility, recent infection and detectable B19V DNA supports the epidemiological importance of B19V during pregnancy in North-Central Nigeria and provides a rationale for geographically representative surveillance and improved recognition of maternal infection, particularly because identification of recent infection can facilitate appropriate fetal monitoring for anaemia and hydrops (Gigi & Anumba, 2021; Kagan et al., 2024).

➤ *B19V DNA Detection According to Gestational Age*

B19V DNA was detected across all three trimesters in the present study, with the highest frequency observed among women in the second trimester. This finding is biologically plausible because the fetal liver undergoes active erythropoiesis during mid-gestation, resulting in an abundance of erythroid progenitor cells that are particularly susceptible to B19V infection (Brown, 2010; Young & Brown, 2004). Consequently, infection during this period may have greater potential to produce clinically significant fetal anaemia, consistent with evidence that severe fetal complications are particularly associated with maternal infection during periods of active fetal erythropoiesis (Bonvicini et al., 2012; Kagan et al., 2024). Nevertheless, detection of B19V DNA in all trimesters indicates that the potential for maternal–fetal transmission is not confined to a specific gestational period. Transplacental transmission can occur throughout pregnancy, although the likelihood and severity of fetal disease depend on factors including gestational age at infection, establishment of fetal infection and subsequent development of fetal anaemia or hydrops (Craboli et al., 2017; Kagan et al., 2024).

The trimester-specific serological findings require somewhat different interpretation. Although IgG positivity increased from 26.0% in the first trimester to 57.0% in the second and 47.8% in the third trimester, the cross-sectional design does not permit determination of when infection occurred relative to the trimester in which a woman was sampled. The observed differences may instead reflect cumulative exposure, age, parity, social contact, occupational exposure, population composition or differences in the timing of infection relative to enrolment. The relatively high frequency of equivocal IgG results in the third trimester may also reflect borderline antibody reactivity or other assay-related factors and should not, in isolation, be interpreted as evidence of active infection. Thus, although gestational age is important when interpreting B19V infection during pregnancy, prospective longitudinal studies beginning early in pregnancy would provide stronger evidence regarding the incidence and timing of primary infection and its relationship with fetal outcomes.

➤ *Obstetric History and Potential Exposure-Related Factors*

No statistically significant association was observed between B19V seropositivity or DNA detection and reported previous miscarriage or stillbirth. This absence of association should be interpreted cautiously because previous obstetric outcomes were obtained retrospectively and may be affected by incomplete documentation, underreporting or recall bias. Moreover, miscarriage and stillbirth are multifactorial outcomes involving genetic, infectious, maternal and obstetric factors; therefore, the absence of an association in this study does not exclude the possibility that B19V contributed to individual adverse pregnancy outcomes.

The marginal association between higher gravidity and B19V IgG positivity is nevertheless epidemiologically plausible. Women with multiple previous pregnancies may have experienced greater cumulative opportunities for exposure to B19V through repeated contact with children, household members and wider social networks. Such exposure may increase the likelihood of previous infection and subsequent development of detectable IgG antibodies (Heegaard & Brown, 2002). However, gravidity is also closely related to age and cumulative lifetime exposure, and the observed relationship should therefore not be interpreted as an independent causal effect of pregnancy number. Further studies incorporating multivariable analyses of age, parity, occupation, household exposure and other potential determinants would be necessary to establish whether gravidity independently predicts B19V serostatus.

➤ *B19V IgM Seropositivity and Evidence of Recent Infection*

B19V-specific IgM was detected in 21 of 273 pregnant women (7.7%), providing serological evidence compatible with recent infection when interpreted in conjunction with clinical and molecular findings. This prevalence was lower than the 13.2% reported among pregnant women in Central Nigeria by Emiasengen et al. (2011), but higher than the 4.0% reported in Oyo State by Iyanda et al. (2013), and substantially lower than the 41.8% reported in Ido-Ekiti by Akele et al. (2021). The considerable variation among these estimates is unlikely to represent a uniform national

epidemiological pattern and may instead reflect differences in population characteristics, geographical setting, recruitment periods, viral circulation, exposure intensity and diagnostic methodology.

Unlike IgG, which generally reflects cumulative previous exposure and may persist for prolonged periods, IgM is more closely associated with the recent phase of B19V infection and is therefore expected to show greater temporal variation. A cross-sectional study captures only a relatively narrow window of recent infection, meaning that estimates of IgM prevalence can vary substantially according to when and where participants are recruited.

Differences in circulating viral activity and local transmission patterns may further contribute to this variation. Accordingly, the 7.7% IgM prevalence observed in this study should be interpreted as evidence of recent exposure within the sampled antenatal population rather than as an estimate of the incidence of B19V infection during pregnancy.

The detection of IgM remains clinically relevant because some IgM-positive women may have experienced primary B19V infection during pregnancy. However, maternal infection does not necessarily result in fetal infection or adverse fetal outcome. Recent evidence supports an important distinction between maternal infection and confirmed fetal infection when assessing prognosis. Sorrenti et al. (2026) reported substantially higher fetal mortality among pregnancies with confirmed fetal infection than among those in which maternal infection alone was documented, emphasising that maternal seropositivity should not be equated with fetal disease. Thus, IgM positivity in the present study identifies women who may warrant further assessment but cannot, by itself, establish fetal infection or predict an adverse pregnancy outcome.

➤ *Molecular Detection of B19V DNA*

An important finding of the present study was the detection of B19V DNA in 21 of 38 pregnant women investigated molecularly (55.3%). Of these, six samples (15.8%) were detected during Normal Amplification Time (NAT), while an additional 15 samples (39.5%) became detectable during Extended Amplification Time (EAT). The increased detection achieved through EAT indicates that a proportion of the investigated samples contained B19V DNA at levels below the detection threshold of the initial amplification protocol.

The 55.3% molecular detection rate must, however, be interpreted within the context of the study design. The 38 women who underwent molecular testing were not independently sampled from the entire cohort of 276 pregnant women; rather, molecular testing was undertaken in a selected subset, largely based on serological reactivity. Consequently, the 55.3% figure represents B19V DNA detection among the molecularly investigated subset and should not be interpreted as the prevalence of B19V viraemia among all pregnant women in the study population. This distinction is important because selection on the basis of serological findings may enrich the molecular subset for

participants with evidence of previous or recent infection.

Despite this limitation, the molecular findings provide important complementary evidence to the serological results. Serological testing provides information on the host immune response and can assist in identifying susceptible, previously exposed and recently infected individuals, whereas PCR provides direct evidence of detectable viral genetic material. The detection of B19V DNA among a substantial proportion of the selected participants therefore strengthens the evidence of B19V circulation within the investigated antenatal population. Combining serological and molecular approaches is particularly valuable because viral DNA and antibody responses vary according to the stage of infection, and reliance on a single diagnostic marker may therefore provide an incomplete assessment of infection status (Gallinella et al., 2014; Gigi & Anumba, 2021).

➤ *Significance and Interpretation of Extended Amplification-Time Detection*

The detection of 15 additional DNA-positive samples during EAT is a noteworthy methodological finding. It suggests that some participants had relatively low levels of B19V DNA that were not detected during the initial amplification period but became detectable following additional amplification. Low-level B19V DNA detection may occur at different stages of infection and should therefore be interpreted in conjunction with IgM, IgG, clinical history and other laboratory findings. Importantly, EAT positivity should not automatically be interpreted as evidence of high-level or clinically significant viraemia. Although extended amplification may increase analytical sensitivity, prolonged amplification may also increase the opportunity for nonspecific amplification if assay specificity is not adequately controlled. In the present study, this concern was addressed through subsequent conventional PCR amplification, agarose gel electrophoresis and sequence confirmation of successfully amplified products. The EAT findings are therefore best interpreted as evidence of detectable low-level B19V DNA, rather than as independent evidence of clinically significant infectious viraemia.

This observation also highlights the importance of clearly defining molecular positivity according to the analytical characteristics of the assay used. Differences in amplification thresholds, target regions, cycle numbers and criteria for positivity can substantially influence reported B19V DNA detection rates. Comparisons between molecular studies should therefore take into account differences in specimen selection, PCR targets, amplification protocols and interpretation criteria.

➤ *Geographic Variation in B19V DNA Detection*

Marked differences in B19V DNA detection were observed across the three study locations. Positivity was highest in Jos (11/13; 84.6%), followed by Lokoja (7/9; 77.8%), and was lowest in Makurdi (3/16; 18.8%). This geographical pattern is potentially important because it suggests heterogeneity in B19V circulation within the study region. However, these findings should not be interpreted as definitive evidence that B19V transmission is intrinsically

higher in Jos or Lokoja.

Several methodological factors may have contributed to the observed differences. First, the molecular sample sizes at the individual locations were relatively small, particularly in Jos and Lokoja. Second, participants were not randomly selected for molecular testing from the antenatal populations at each site. Third, the proportion of serologically reactive women selected for molecular investigation may have differed between locations. Consequently, selection effects and small denominators could have magnified the apparent geographical differences in DNA detection.

Nevertheless, the findings are consistent with the broader observation that B19V epidemiology can vary geographically according to population structure, social contact patterns, occupational exposure, household density, urbanisation and temporal patterns of viral circulation. The geographical variation observed in this study, together with differences reported among previous Nigerian studies (Emiasengen et al., 2011; Iyanda et al., 2013; Akele et al., 2021), supports the need for multicentre surveillance rather than extrapolation of prevalence estimates from one location to the entire country.

➤ Association between Ethnicity and B19V DNA Positivity

Ethnic group was significantly associated with B19V DNA detection among the 38 molecularly investigated pregnant women ($\chi^2 = 16.8$, $p < 0.001$), with the highest frequency of DNA positivity observed among women of Igala ethnicity. Although statistically significant, this finding should not be interpreted as evidence that ethnicity itself confers biological susceptibility to B19V infection. Ethnicity is a social and population descriptor that may be correlated with geographical residence, occupation, mobility, household composition, socioeconomic circumstances and patterns of interpersonal contact, any of which may influence opportunities for exposure to B19V.

The relatively small molecular sample also limits the extent to which an independent effect of ethnicity can be inferred. In particular, it is difficult to determine whether the observed association persists after accounting for study location and other potential confounders. The finding is therefore better regarded as an epidemiological association that warrants further investigation rather than evidence of ethnicity-specific biological susceptibility. Larger studies using representative sampling and multivariable modelling would be required to determine whether the association remains after adjustment for age, geographical location, occupation, gravidity, household exposure and other relevant factors.

➤ Implications for Maternal-Fetal Transmission and Pregnancy Outcome

The combined serological and molecular findings indicate that B19V infection occurs among pregnant women in the study population and that a proportion had evidence compatible with recent infection or detectable viral DNA. These findings are clinically relevant because B19V can cross the placenta and infect the fetus, where its tropism for

erythroid precursor cells may result in severe fetal anaemia and, in severe cases, hydrops fetalis and fetal death (Kagan et al., 2024). Nevertheless, maternal infection should not be equated with fetal disease, because not all maternal infections result in fetal infection or clinically significant complications.

Recent evidence reinforces this distinction. Sorrenti et al. (2026) reported substantially

greater fetal mortality among confirmed fetal infections than among maternal infections alone, highlighting the importance of establishing fetal involvement when assessing prognosis.

Similarly, a multicentre study of pregnancies affected during the 2023–2024 B19V upsurge found no significant increase in perinatal mortality compared with earlier periods, although affected pregnancies were more likely to require repeated intrauterine transfusion because of persistent fetal anaemia, and fetal hydrops at presentation was associated with increased perinatal mortality (Prasad et al., 2025). These findings indicate that the principal clinical value of identifying maternal infection is to recognise pregnancies that may benefit from appropriate fetal assessment and surveillance rather than to assume that maternal infection inevitably results in fetal loss.

➤ Molecular Characterisation of B19V among Pregnant Women

The successful amplification and sequencing of the B19V VP1/VP2 region provided molecular confirmation of infection and enabled assessment of the genetic characteristics of circulating virus among the investigated pregnant women. The high nucleotide similarity observed among the successfully sequenced isolates indicates substantial conservation within the analysed genomic region and supports close genetic relatedness among the circulating strains.

The molecular epidemiology of B19V is important because three major genotypes—genotypes 1, 2 and 3—have been recognised, with genotype 1 predominating globally and genotype 3 having particular relevance in several African populations. Previous molecular studies have demonstrated geographical differences in genotype distribution, highlighting the importance of sequence-based surveillance in regions where molecular data remain limited. The present findings therefore contribute useful baseline molecular information on B19V circulating among pregnant women in North-Central Nigeria.

For this pregnancy-focused article, however, genotype distribution should be presented specifically for the pregnant-women sequence dataset. Because the broader thesis included isolates from both blood donors and pregnant women, the denominator for genotype distribution in this article should comprise only successfully sequenced isolates derived from pregnant women. Maintaining this distinction will prevent findings from the broader study population from being inadvertently generalised to the antenatal population.

➤ *Strength of the Combined Diagnostic Approach*

A major strength of this study is the integration of serological and molecular diagnostic approaches. IgM provided evidence compatible with recent infection, IgG identified previous exposure, while PCR demonstrated detectable B19V DNA in the molecularly investigated subset. The complementary nature of these methods is particularly important because viral DNA and antibody responses change dynamically during infection; consequently, reliance on a single diagnostic marker may provide an incomplete assessment of infection status (Gallinella et al., 2014).

The molecular component also strengthens the epidemiological interpretation of the serological findings by demonstrating detectable viral genetic material among selected participants. This is particularly relevant in pregnancy, where evidence of recent maternal infection may prompt consideration of fetal surveillance. However, PCR positivity should not be interpreted as synonymous with fetal infection, infectiousness or adverse pregnancy outcome. Establishing fetal infection requires appropriate fetal investigations, while determining pregnancy outcome requires prospective follow-up. The cross-sectional design of the present study did not permit either of these assessments.

➤ *Public Health and Clinical Implications*

The findings have important implications for antenatal care and B19V surveillance in Nigeria. The detection of B19V IgM and DNA among pregnant women demonstrates that recent exposure and detectable viral infection occur within the antenatal population and should be considered when evaluating women with compatible symptoms, known exposure or ultrasound findings suggestive of fetal anaemia or hydrops. Maternal B19V infection is clinically important because fetal complications can be severe even though many maternal infections do not result in clinically significant fetal disease (Gigi & Anumba, 2021; Kagan et al., 2024).

From a clinical perspective, the findings support a targeted and evidence-based approach to B19V testing rather than assuming that every pregnant woman with serological evidence of exposure has an increased risk of adverse fetal outcome. Women with suspected recent infection may benefit from confirmatory serological or molecular assessment and, when maternal infection is established, appropriate fetal surveillance for evidence of anaemia or hydrops. The potential clinical value of such surveillance is supported by evidence that severe fetal anaemia may require intrauterine transfusion and that fetal hydrops is associated with poorer perinatal outcomes (Prasad et al., 2025).

From a public-health perspective, the geographical variation observed in this study and the substantial differences between Nigerian seroprevalence estimates support the development of geographically representative B19V surveillance. Such surveillance would help define the magnitude and temporal distribution of infection, identify populations with greater susceptibility and provide evidence for determining whether targeted antenatal testing and enhanced fetal monitoring would be feasible and cost-effective in Nigeria. Strengthening laboratory capacity for

reliable serological testing, molecular detection and sequence-based characterisation would further improve the ability to monitor B19V circulation and recognise future increases in transmission.

Overall, this study demonstrates that B19V infection is an important and potentially under-recognised infection among pregnant women attending antenatal clinics in North-Central Nigeria. The coexistence of substantial serological susceptibility, evidence of recent infection and detectable B19V DNA highlights the potential for maternal-fetal transmission and supports greater clinical and epidemiological attention to B19V during pregnancy. However, because the molecular subset was selected, the study was cross-sectional and fetal infection and pregnancy outcomes were not prospectively assessed, the findings should not be interpreted as demonstrating the population prevalence of viraemia or a direct causal relationship between maternal B19V infection and adverse fetal outcomes. Future multicentre prospective studies should combine serial maternal serology with quantitative molecular testing, systematic fetal ultrasound and Doppler surveillance, documentation of pregnancy outcomes and, where clinically indicated, fetal diagnostic investigations to establish the incidence, timing and determinants of clinically significant B19V infection and vertical transmission in Nigeria.

V. LIMITATION OF THE STUDY

Despite its strengths, the study has some limitations. Foetal outcomes were not tracked, making it difficult to establish a direct link between maternal viraemia and adverse pregnancy outcomes. Prospective cohort studies with longitudinal follow-up of mother-infant pairs are recommended to more effectively quantify the risk of foetal loss and congenital anomalies associated with B19V.

VI. CONCLUSION

This study provides compelling evidence that human parvovirus B19 (B19V) infection is a significant and under-recognized public health concern among pregnant women in North Central Nigeria. The detection of anti-B19V IgM and IgG antibodies in 7.6% and 12.7% of participants, respectively, indicates both recent and past exposure within this vulnerable population. More importantly, the detection of B19V DNA in 55.3% of Sero-reactive pregnant women confirms active viraemia, a strong indicator of the risk for vertical transmission.

The findings are of health importance, given the known consequences of maternal B19V infection, including miscarriage, intrauterine foetal death, hydrops fetalis, and severe foetal anaemia. The observed higher DNA positivity in the second trimester reinforces existing global evidence that this gestational window poses a heightened risk for transplacental transmission and foetal compromise. The absence of significant associations with miscarriage and stillbirth histories may reflect the cross-sectional nature of the study or underreporting and not be interpreted as a lack of foetal impact.

Given that B19V infection is not currently part of routine antenatal screening in Nigeria, this study underscores an urgent need for a policy shift. Routine screening, especially during the second trimester alongside appropriate diagnostic support, including qPCR, can facilitate early detection, risk stratification, and timely interventions to protect both maternal and foetal health. Health care workers, particularly obstetricians and antenatal care providers, must be sensitized to the risk and clinical implications of B19V in pregnancy.

Furthermore, public health education aimed at women of reproductive age, particularly in high-burden regions, should be prioritized to reduce susceptibility and promote early healthcare-seeking behaviour when symptoms suggestive of viral illness occur during pregnancy. Community-based surveillance and longitudinal research are also recommended to establish causal links between maternal infection and specific pregnancy outcomes.

In conclusion, this study adds to the growing body of evidence calling for heightened attention to parvovirus B19 in pregnancy. Highlighting the serological and molecular burden of infection among Nigerian pregnant women, it provides critical baseline data for public health planning and clinical management aimed at reducing preventable pregnancy complications associated with B19V.

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