RESEARCH PAPER

Diagnostic Accuracy of the Plotkin Score for Detecting Acquired Cytomegalovirus Infection in Children

Dody Abdullah Attamimi[1]*, Ninny Meutia Pelupessy[1,2], St. Aizah Lawang[1], Nadirah Rasyid Ridha[1,2], Ema Alasiry[1,2] and Mokhammad Ikhsan Nurkholis[1,2]

[1]*Department of Pediatrics, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia*
[2]*Dr. Wahidin Sudirohusodo General Hospital, Makassar, Indonesia*
Corresponding Author: *dodidul22@gmail.com*

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ABSTRACT

Objective: To evaluate the diagnostic performance of the Plotkin score for detecting acquired cytomegalovirus (CMV) infection in children using reverse transcription polymerase chain reaction (RT-PCR) as the reference standard.

Patients and Methods: A cross-sectional diagnostic accuracy study was conducted at a tertiary care center between January 2025 and January 2026. Eighty children aged 3 months to 18 years with suspected acquired CMV infection and positive CMV serology were consecutively recruited. Clinical and laboratory parameters were collected to calculate Plotkin scores. Diagnostic performance was evaluated using receiver operating characteristic (ROC) curve analysis and multivariable logistic regression.

Results: A total of 80 children were included in the study, comprising 40 RT-PCR-positive and 40 RT-PCR-negative patients. Median Plotkin scores were significantly higher in the RT-PCR-positive group than in the RT-PCR-negative group (4.0 vs. 3.0; $p = 0.039$). ROC analysis identified an optimal cut-off value of >5, with an area under the curve (AUC) of 0.631. A Plotkin score >5 independently predicted RT-PCR-confirmed CMV infection (OR = 3.97; 95% CI: 1.42–11.12; $p = 0.009$). Positive anti-CMV IgM also remained independently associated with CMV infection (OR = 4.93; 95% CI: 1.48–16.47; $p = 0.010$).

Conclusions: The Plotkin score demonstrated modest diagnostic performance for detecting acquired CMV infection in children and may serve as an initial screening and triage tool to identify pediatric patients requiring confirmatory RT-PCR testing, particularly in resource-limited healthcare settings.

Keywords: *Cytomegalovirus, Child, Polymerase Chain Reaction, Sensitivity and Specificity, Diagnostic Techniques and Procedures*

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INTRODUCTION

Cytomegalovirus (CMV) infection remains a significant cause of morbidity in pediatric populations due to its broad clinical spectrum and potential for multisystem involvement.[1,2] Early diagnosis is crucial for enabling timely antiviral therapy and reducing disease progression. However, diagnosing CMV in children is challenging because acquired CMV infection often presents with non-specific symptoms that overlap with other infectious diseases.[2,3] Pathophysiologically, CMV is a double-stranded DNA virus with broad cellular tropism that induces systemic inflammatory responses through the activation of cytokines and chemokines. This results in hematologic, hepatobiliary, neurological, respiratory, gastrointestinal, and systemic complications, particularly in vulnerable pediatric populations.[1,4]

Virological confirmation using polymerase chain reaction (PCR) is currently considered the reference standard for CMV diagnosis.[5,6] However, access to PCR remains limited in many healthcare settings due to high costs, restricted availability, and prolonged turnaround times, which may delay diagnosis and the initiation of antiviral treatment.[5,7] These limitations create an urgent need for practical clinical prediction tools that can help identify patients who require confirmatory testing and support more efficient allocation of diagnostic resources.[5,8,9]

The Plotkin score was initially developed to evaluate

**Author for Correspondence: dodidul22@gmail.com*

CMV-associated disease manifestations in kidney transplant recipients and was later refined in larger transplant cohorts.[10,11] This scoring system integrates clinical and laboratory parameters, including fever, leukopenia, thrombocytopenia, hepatitis, pneumonia, gastrointestinal involvement, neurological manifestations, renal dysfunction, musculoskeletal abnormalities, sepsis, and mortality outcomes.[12] Since these variables represent manifestations of systemic CMV infection, the Plotkin score may offer a feasible and cost-effective approach for identifying patients with a higher probability of CMV infection.[5,12]

Despite its potential utility, evidence regarding the diagnostic performance of the Plotkin score in acquired pediatric CMV infection remains limited, particularly in resource-limited settings.[5,13,14] To date, no study in Indonesia has evaluated the validity of this scoring system against RT-PCR-confirmed acquired CMV infection in children. Therefore, this study aimed to assess the diagnostic performance of the Plotkin score as a tool for diagnosing acquired CMV infection in pediatric patients and to determine its sensitivity and specificity using RT-PCR as the reference standard.

PATIENTS AND METHODS

Study Design and Setting

This cross-sectional diagnostic accuracy study evaluated the performance of the Plotkin score in diagnosing acquired CMV infection in children, with reverse transcription polymerase chain reaction (RT-PCR) used as the reference standard. The study was conducted at a tertiary care hospital and its central laboratory from January 2025 until the target sample size was reached.

Study Population and Participants

The research targeted children aged from 3 months to 18 years who were clinically suspected of having acquired a CMV infection. To be included, participants needed to be pediatric inpatients or outpatients with positive CMV serology (anti-CMV IgM and/or IgG) and show clinical symptoms suggestive of CMV infection, which was then confirmed through RT-PCR testing. Individuals were eligible for inclusion if they: (1) were between 3 months and 18 years old; (2) showed serological proof of CMV infection along with relevant clinical symptoms; and (3) had obtained consent from a parent or guardian to participate in the study. The exclusion criteria were: (1) previous antiviral therapy with valganciclovir; (2) congenital conditions that might result in similar clinical symptoms (such as Edwards syndrome, fetal alcohol syndrome, metabolic disorders, Dandy–Walker malformation, Chiari malformation, Rett syndrome); and (3) immunocompromised states, including human immunodeficiency virus infection, autoimmune diseases, chronic kidney disease, diabetes mellitus, thyroid metabolic disorders, extended corticosteroid use, or other forms of immunodeficiency.

Sample Size and Sampling Technique

Participants were enrolled in succession until the required minimum sample size was met. The estimation of the sample size was conducted for the analysis of diagnostic accuracy, utilizing ROC curve evaluation with a 95% confidence interval and an anticipated prevalence of 87.8%, which determined that at least 60 participants were necessary.

Clinical Assessment and Data Collection

Standardized case report forms were utilized to document baseline demographic and clinical information, such as age, gender, body weight, nutritional condition, clinical symptoms, and laboratory results. The clinical symptoms evaluated encompassed fever, respiratory issues, neurological signs, hepatobiliary symptoms, gastrointestinal involvement, musculoskeletal complaints, and systemic manifestations. Laboratory tests conducted included a complete blood count, liver function assessments (AST/ALT), renal function evaluations (urea and creatinine), and inflammatory markers like erythrocyte sedimentation rate (ESR), C-reactive protein (CRP), procalcitonin, CMV serology (anti-CMV IgM and IgG), and RT-PCR analysis. Chest X-rays were performed solely when clinically necessary, especially in patients exhibiting fever, cough, respiratory distress, or suspected lung involvement.

Specimen Collection and Laboratory Procedures

Under sterile conditions, 3 mL of venous blood was drawn from either the median cubital or cephalic vein. The samples were then centrifuged to separate the serum, which was kept cold during transport and stored at −20°C until it was ready for analysis. The initial serological tests involved an enzyme-linked immunosorbent assay (ELISA) to detect anti-CMV IgM and IgG antibodies. Patients who showed positive serological results and had clinical symptoms consistent with CMV infection were further tested using RT-PCR for confirmation.

Plotkin Score Assessment

Clinical severity and disease manifestations were evaluated using the Plotkin scoring system developed by Plotkin et al. This system consists of 11 clinical and laboratory parameters, including fever, leukopenia, thrombocytopenia, hepatitis, pneumonitis, gastrointestinal involvement, central nervous system manifestations, renal insufficiency, musculoskeletal manifestations, sepsis, and mortality-related outcomes. Total Plotkin scores were calculated for each participant and compared with RT-PCR results.

Outcome Measures

The primary outcome was the diagnostic performance of

the Plotkin score in detecting acquired CMV infection, with RT-PCR serving as the reference standard. Diagnostic parameters included sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), and the area under the receiver operating characteristic curve (AUC).

Statistical Analysis

Statistical analyses were performed using IBM SPSS Statistics version 29.0. Continuous variables were presented as mean ± standard deviation or median (interquartile range), while categorical variables were expressed as frequency and percentage. Diagnostic accuracy was evaluated using contingency tables and Chi-square tests where appropriate. Receiver operating characteristic (ROC) analysis was performed to determine the optimal cut-off value of the Plotkin score based on sensitivity and specificity. Optimal cut-off was determined using the maximum Youden Index. Diagnostic performance was interpreted using the area under the curve (AUC), with higher values indicating better discriminatory ability. Statistical significance was defined as $p < 0.05$. All estimates were reported with 95% confidence intervals.

Ethical Considerations

This study received approval from the Biomedical Research Ethics Committee, Faculty of Medicine, Hasanuddin University, Makassar, Indonesia (Approval No. 398/UN4.6.4.5.31/PP36/2026; Protocol No. UH25100859; approval date: March 23, 2026). Written informed consent was obtained from parents or legal guardians before study participation. All study procedures were conducted in accordance with applicable ethical guidelines and regulations.

RESULTS

Clinical and Laboratory Characteristics of Study Participants According to RT-PCR Status

A cross-sectional diagnostic accuracy study evaluated the predictive performance of the Plotkin score for acquired CMV infection among pediatric patients treated at a tertiary care hospital between January 2025 and January 2026. Eighty eligible patients were included: 40 with RT-PCR-confirmed CMV infection and 40 with negative RT-PCR results. All participants underwent standardized clinical and laboratory evaluation for Plotkin score calculation. Collected variables included demographic characteristics, clinical manifestations, and laboratory abnormalities within the Plotkin system: fever, wasting, jaundice, hematologic, gastrointestinal, neurological, and serological findings.

Table 1 presents bivariate analysis of clinical and laboratory characteristics by RT-PCR-confirmed CMV status. Fever distribution differed between groups ($p = 0.033$): PCR-positive patients more often had no documented fever (87.5% vs. 62.5%), whereas mild (7.5% vs. 22.5%) and moderate fever (5.0% vs. 15.0%) were more frequent in PCR-negative patients. No patient had severe fever lasting >21 days. Jaundice was more frequent in PCR-positive patients (50.0% vs. 30.0%; $p = 0.068$). Elevated transaminases were associated with infection (72.5% vs. 42.5%; $p = 0.007$). No significant differences were observed across complications, including thrombocytopenia (22.5% vs. 10.0%; $p = 0.130$), leukopenia (5.0% vs. 0%; $p = 0.494$), acute kidney injury (0% vs. 10%; $p = 0.314$), sepsis (17.5% vs. 7.5%; $p = 0.176$), pneumonia (82.5% vs. 55.0%; $p = 0.080$), gastrointestinal bleeding, arthritis, central nervous system involvement, and mortality. Wasting inversely correlated with RT-PCR-confirmed CMV infection (60.0% vs. 22.5%; $p = 0.001$). anti-CMV IgM, not IgG, positivity was associated with RT-PCR-confirmed infection (35.0% vs. 12.5%; $p = 0.018$; 15.0% vs. 5.0%; $p = 0.263$).

Comparison of Plotkin Scores Between RT-PCR Positive and RT-PCR Negative Groups

Comparative analysis of Plotkin scores was performed among pediatric patients with seropositive acquired CMV infection in both RT-PCR-positive (n = 40) and RT-PCR-negative (n = 40) groups. Normality testing using the Kolmogorov–Smirnov test demonstrated non-normal distribution of Plotkin scores in both the RT-PCR-positive group ($p = 0.023$) and RT-PCR-negative group ($p = 0.005$); therefore, comparisons were performed using the Mann–Whitney U test.

As shown in Table 2, patients with RT-PCR-confirmed CMV infection demonstrated significantly higher Plotkin scores than PCR-negative patients. The median Plotkin score was 4.0 (range: 1–10) in the PCR-positive group compared with 3.0 (range: 1–7) in the PCR-negative group ($U = 590.000$; $Z = -2.062$; $p = 0.039$). Mean rank values were also higher among PCR-positive patients (4.55 vs. 3.65), indicating greater cumulative clinical burden in patients with confirmed CMV infection.

Determination of the Optimal Cut-off Value of the Plotkin Score

Receiver operating characteristic (ROC) curve analysis was performed to determine the optimal cut-off value of the Plotkin score for distinguishing pediatric patients with RT-PCR-confirmed acquired CMV infection. As illustrated in Figure 1 and summarized in Table 4, the ROC analysis yielded an area under the curve (AUC) of 0.631 (95% CI: 0.508–0.754; standard error = 0.063; $p = 0.043$), indicating weak but statistically significant discriminatory performance and suggesting that the Plotkin score performed better than random classification (AUC = 0.50).

The diagnostic characteristics across multiple threshold

values are presented in Table 3 and Figure 2. The highest Youden Index (0.250) was achieved at a cut-off value of >5 (corresponding to threshold ≥4.5), indicating the best balance between sensitivity and specificity. At this threshold, sensitivity was 47.5% and specificity reached 77.5%. Higher cut-off values increased specificity but substantially reduced sensitivity.

Diagnostic Performance and Optimal Cut-off of the Plotkin Score

Based on ROC analysis, a Plotkin score >5 was identified as the optimal threshold for distinguishing pediatric patients with RT-PCR-confirmed CMV infection from those with negative RT-PCR findings. Table 5 demonstrated a significant association between Plotkin score classification and RT-PCR-confirmed CMV infection ($p = 0.019$). Among patients with Plotkin scores <5, 40.4% were PCR-positive and 59.6% were PCR-negative. In contrast, among patients with Plotkin scores ≥5, PCR positivity increased to 67.9%, whereas PCR negativity decreased to 32.1%. Patients with Plotkin scores above the threshold had significantly increased odds of RT-PCR-confirmed CMV infection (OR = 3.12; 95% CI: 1.18–8.20). These findings suggest that although the overall discriminatory ability remained modest, the Plotkin score may function as a practical initial screening and triage tool to identify pediatric patients requiring confirmatory RT-PCR testing.

Multivariable Logistic Regression Analysis

Multivariable logistic regression analysis was performed to evaluate the independent predictive value of anti-CMV IgM serology and Plotkin score for RT-PCR-confirmed CMV infection (Table 6). Positive anti-CMV IgM demonstrated the strongest predictive effect and was independently associated with an approximately five-fold increase in the odds of RT-PCR-confirmed CMV infection ($B = 1.595$; $SE = 0.615$; OR = 4.93; 95% CI: 1.48–16.47; $p = 0.010$). Likewise, a Plotkin score ≥5 remained an independent predictor and was associated with an approximately four-fold increase in CMV infection odds ($B = 1.378$; $SE = 0.526$; OR = 3.97; 95% CI: 1.42–11.12; $p = 0.009$). The model intercept was −2.135 ($SE = 0.701$; $p = 0.002$). These findings indicate that combining serological and clinical scoring variables improved prediction performance compared with either parameter alone.

DISCUSSION

Among the individual components of the Plotkin score, elevated transaminase levels demonstrated a significant association with RT-PCR-confirmed CMV infection. In this study, elevated transaminase levels were observed more frequently among PCR-positive patients than PCR-negative patients, suggesting that hepatobiliary involvement may represent an important indicator of active viral replication. This finding is biologically plausible because CMV exhibits marked hepatotropism and may induce hepatocellular injury through direct viral replication and T-cell–mediated inflammatory responses. Similar observations were reported by Tezer et al. (2016), who described liver enzyme elevation as one of the most frequent manifestations of pediatric CMV hepatitis and emphasized that hepatic involvement may occur even among immunocompetent children.[15] Likewise, Min et al. (2017), in a retrospective cohort involving 132 pediatric patients with CMV infection, reported simultaneous elevation of AST and ALT in approximately 97% of cases, supporting the importance of transaminase abnormalities as markers of active disease.[16] These findings further support the inclusion of hepatic involvement within the Plotkin scoring framework originally developed to evaluate CMV disease severity.

Wasting also emerged as an important parameter in this study. However, an unexpected pattern was observed, with wasting being more common among PCR-negative patients than PCR-positive patients. This finding contrasts with the observations reported by Ferrua et al. (2023), who evaluated 43 children with CMV-associated protein-losing enteropathy and demonstrated that nutritional deterioration was a prominent manifestation of active disease, with 66.7% of immunocompetent patients presenting with anorexia and 52.4% experiencing asthenia contributing to worsening nutritional status.[17] The discrepancy between studies may reflect differences in disease phenotype, patient population, and underlying mechanisms of nutritional impairment. Whereas Ferrua et al. (2023) focused on gastrointestinal CMV manifestations directly affecting nutritional intake and protein loss, the present study evaluated broader acquired CMV presentations in which wasting may instead represent chronic illness burden, delayed referral, or alternative underlying conditions rather than active viral replication itself.[17]

Fever demonstrated another unexpected distribution pattern. Despite being traditionally considered a hallmark manifestation of viral infection, a higher proportion of afebrile patients was observed among PCR-positive children in this study. This finding suggests that acquired CMV infection in pediatric populations may frequently present with subtle or non-specific clinical manifestations and may remain clinically underrecognized. These findings are consistent with Takehara et al. (2023), who highlighted that CMV infection may occur with minimal systemic manifestations and variable hematologic abnormalities.[5] However, the present findings differ from those reported by Min et al. (2017), where fever represented the most common presenting symptom and was observed in 39.4% of immunocompetent children with CMV hepatitis.[16] Similar findings were also reported by Na (2012), who documented fever in approximately

60% of infants with CMV hepatitis, with a median duration of three days.[18] Taken together, these observations suggest substantial heterogeneity in the clinical expression of pediatric acquired CMV and reinforce the limited utility of isolated symptoms for diagnostic decision-making.

Serological findings further strengthened the predictive model developed in this study. Positive anti-CMV IgM remained independently associated with RT-PCR-confirmed infection, whereas anti-CMV IgG positivity demonstrated limited discriminatory value. This observation is biologically plausible because IgM generally reflects recent infection or viral reactivation, while IgG may persist after previous exposure or represent residual maternal antibodies in younger children. Similar findings have been reported by Jain et al. (2023), who emphasized that concurrent IgM positivity and molecular confirmation are more representative of active CMV infection than serological testing alone.[19] Therefore, combining clinical scoring with serological evaluation may improve identification of pediatric patients requiring confirmatory molecular testing.

LIMITATIONS

This study has several limitations. First, it was conducted at a single tertiary center with a relatively small sample size. Second, the Plotkin score was originally developed in transplant recipients, which may limit generalizability to immunocompetent pediatric populations. Third, external validation was not performed.

CONCLUSIONS

This study demonstrated that the Plotkin score was significantly associated with RT-PCR-confirmed acquired CMV infection in pediatric patients. Children with confirmed CMV infection had significantly higher Plotkin scores than those with negative RT-PCR results, and a cut-off value of >5 was identified as the optimal threshold for clinical discrimination. Although the overall diagnostic performance of the Plotkin score was modest (AUC = 0.631), patients with Plotkin scores >5 showed significantly increased odds of RT-PCR-confirmed CMV infection. Positive anti-CMV IgM also remained an independent predictor and showed stronger predictive value than clinical scoring alone. The combination of anti-CMV IgM and Plotkin score further improved risk estimation and enabled stratification of patients according to the probability of CMV infection. These findings suggest that the Plotkin score should not replace RT-PCR as the reference standard for diagnosis; however, it may serve as a practical initial screening and triage tool to support early identification of pediatric patients requiring confirmatory molecular testing, particularly in resource-limited healthcare settings.

DECLARATIONS

Consent for Publication

Written informed consent for publication of anonymized clinical and research data was obtained from the parents or legal guardians of study participants. No identifiable personal information is included in this manuscript.

Availability of Data and Materials

The datasets generated and/or analyzed during the current study are not publicly available due to institutional and participant confidentiality policies but are available from the corresponding author on reasonable request.

Conflict of Interest

The authors declare that they have no competing interests.

Financial Disclosure

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Authors' Contributions

DAA conceptualized and designed the study, coordinated data collection, performed data interpretation, and drafted the manuscript. NMP, SAL, and NRR contributed to study design, clinical supervision, and manuscript revision. EA and MIN contributed to laboratory procedures, data validation, and critical revision of the manuscript. All authors reviewed and approved the final version of the manuscript.

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Declaration AI

In the course of preparing this document, we utilized ChatGPT (OpenAI) for minor edits related to language and grammar. The authors thoroughly reviewed and amended all sections and assume complete responsibility for the final version of the manuscript.

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TABLES AND FIGURES

Table 1. Analysis of the Plotkin Scoring System in the Study Sample

Characteristics	PCR Positive (n = 40) n (%)	PCR Negative (n = 40) n (%)	p-value
Fever			0.033*
No fever	35 (87.5%)	25 (62.5%)	
Mild (2–4 days)	3 (7.5%)	9 (22.5%)	
Moderate (5–20 days)	2 (5.0%)	6 (15.0%)	
Severe (>21 days)	0 (0%)	0 (0%)	
Jaundice			0.068**
Jaundice	20 (50%)	12 (30%)	
No jaundice	20 (50%)	28 (70%)	
Thrombocytopenia			0.130**
Thrombocytopenia	9 (22.5%)	4 (10%)	
No thrombocytopenia	31 (77.5%)	36 (90%)	
Leukopenia			0.494*
Leukopenia	2 (5%)	0 (0%)	
No leukopenia	38 (95%)	40 (100%)	
Elevated transaminase enzymes			0.007**
Elevated transaminase enzymes	29 (72.5%)	17 (42.5%)	
No elevation of transaminase enzymes	11 (27.5%)	23 (57.5%)	
Acute kidney injury			0.314*
Acute kidney injury	0 (0%)	1 (10%)	
No acute kidney injury	40 (100%)	39 (90%)	
Sepsis			0.176**
Sepsis	7 (17.5%)	3 (7.5%)	
No sepsis	33 (82.5%)	37 (92.5%)	
Pneumonia			0.08**
Pneumonia	33 (82.5%)	22 (55%)	
No pneumonia	7 (17.5%)	18 (45%)	
Gastrointestinal bleeding			0.494*
Gastrointestinal bleeding	2 (5.0%)	0 (0%)	
No gastrointestinal bleeding	38 (95%)	40 (100%)	
Arthritis			1.000*
Arthritis	1 (2.5%)	0 (0%)	
No arthritis	39 (97.5%)	40 (100%)	
Wasting			0.001**
Wasting	9 (22.5%)	24 (60%)	
No wasting	31 (77.5%)	16 (40%)	
Central nervous system involvement			0.568*
Lethargy	4 (10%)	3 (7.5%)	
Stupor	1 (2.5%)	0 (0%)	
Coma	1 (2.5%)	0 (0%)	
No impaired consciousness	34 (85%)	37 (92.5%)	
Mortality			0.494**
Died	2 (5%)	0 (0%)	
Survived	38 (95%)	40 (100%)	
Serological IgM			0.018**
IgM positive	14 (35%)	5 (12.5%)	
IgM negative	26 (65%)	35 (87.5%)	
Serological IgG			0.263*
IgG positive	6 (15%)	2 (5%)	
IgG negative	34 (85%)	38 (95%)	

*Fisher's Exact test; **Chi-square test.

Table 2. Comparison of Plotkin Scores Between PCR-Positive and PCR-Negative Patients

Variable	PCR Positive (n = 40)	PCR Negative (n = 40)	p-value
Plotkin Score, Median (Range)	4 (1–10)	3 (1–7)	0.039*
Mean Rank	4.55	3.65	

PCR = Polymerase Chain Reaction. Data are presented as Median (Range). Mann–Whitney test was used because the data were not normally distributed (Shapiro–Wilk test, $p < 0.05$). Mann–Whitney test results: $U = 590.000$; $Z = -2.062$.

Table 3. Cut-off Values, Sensitivity, and Specificity of the Plotkin Score Compared with PCR Examination

Positive if ≥	Sensitivity	1 − Specificity	Youden Index
0.00	1.000	1.000	0.000
1.50	0.975	0.975	0.000
2.50	0.850	0.825	0.025
3.50	0.650	0.450	0.200
4.50	0.475	0.225	0.250
5.50	0.275	0.100	0.175
6.50	0.175	0.075	0.100
7.50	0.075	0.000	0.075
8.50	0.050	0.000	0.050
9.50	0.025	0.000	0.025
11.00	0.000	0.000	0.000

PCR = Polymerase Chain Reaction. The optimal cut-off point was determined based on the highest Youden Index.

Table 4. AUC of the Plotkin Score Based on PCR Results

Area Under the Curve (AUC)	Std. Error	p-value	95% Confidence Interval Lower Bound	95% Confidence Interval Upper Bound
0.631	0.063	0.043*	0.508	0.754

PCR = Polymerase Chain Reaction. AUC values were analyzed using receiver operating characteristic (ROC) curve analysis. Statistical significance was defined as $p < 0.05$.

Table 5. Association Between the Plotkin Scoring System and PCR Results

Plotkin Score	PCR Positive n (%)	PCR Negative n (%)	Total n (%)	p-value	OR (95% CI)
< 5	21 (40.4%)	31 (59.6%)	52 (65.0%)	0.019*	3.12 (1.18–8.20)
≥ 5	19 (67.9%)	9 (32.1%)	28 (35.0%)		
Total	**40**	**40**	**80 (100%)**		

Chi-square test. OR = Odds Ratio; CI = Confidence Interval. The optimal cut-off point was determined based on the highest Youden Index obtained from ROC curve analysis.

Table 6. Multivariate Analysis of the Predictive Value of the Plotkin Score for CMV Infection

Variable	B	S.E.	p-value	OR (95% CI)
Positive IgM Serology	1.595	0.615	0.010*	4.929 (1.475–16.468)
Plotkin Score ≥ 5	1.378	0.526	0.009*	3.967 (1.415–11.117)
Constant	−2.135	0.701	0.002*	

B = regression coefficient; S.E. = standard error; OR = Odds Ratio; CI = Confidence Interval.

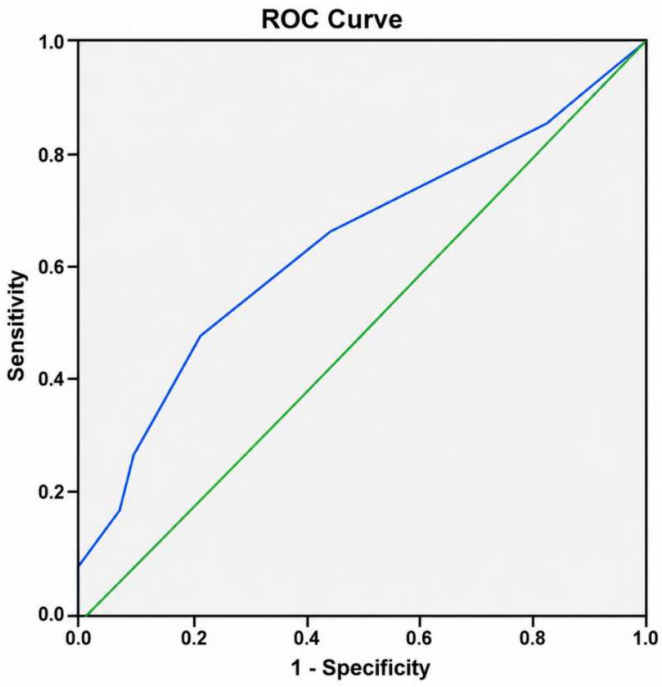

Figure 1. ROC Curve of the Plotkin Score

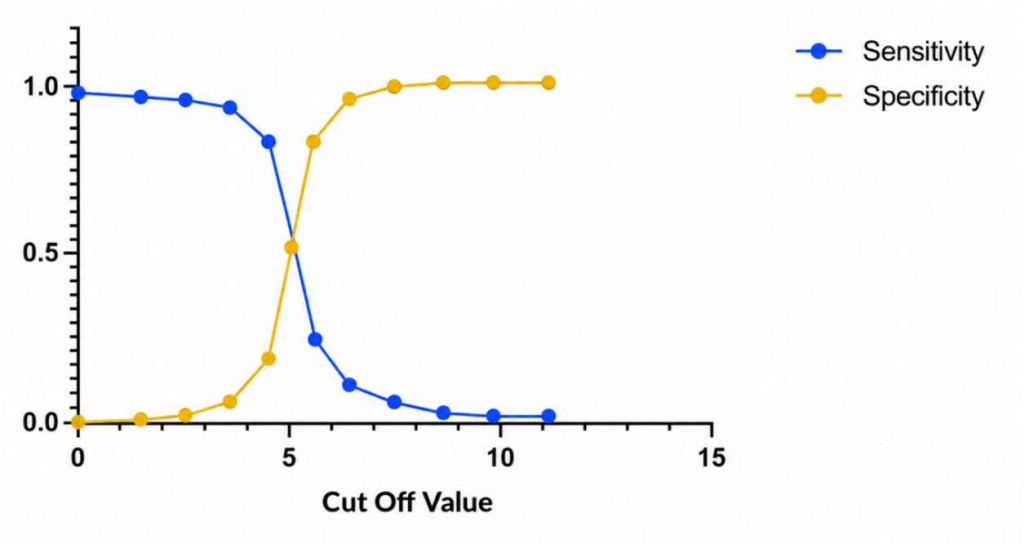

Figure 2. ROC-Based Cut-off Point of the Plotkin Score in Children with CMV Infection