

# [Results chapter on cmv infection research](https://assignbuster.com/results-chapter-on-cmv-infection-research/)

Results

This study has been conducted on 366 patients with suspected CMV infection attending pediatric department at Zagazig University Hospital.

Table (1): Age distribution of the studied patients (except for neonates with congenital anomalies) (N= 344)

|  |  |  |
| --- | --- | --- |
| Studied patients (N= 344) | |  |
| No. | % |  |
| Age (years) | | |
| Mean ± SD | 9. 9 ± 3. 4 | |
| Median (Range) | 10. 0 (3. 5 – 18. 0) | |

The mean age and standard deviation (SD) of ages of the studied patients (except for neonates with congenital anomalies) in years as shown intable (1)was 9. 9 ± 3. 4.

Table (2): Age distribution of neonates with congenital anomalies (N= 22)

|  |  |  |
| --- | --- | --- |
| Studied patients (N= 22) | |  |
| No. | % |  |
| Age of neonateswith congenital anomalies group (days) | | |
| Mean ± SD  Median (Range) | 4. 1 ± 1. 6  4. 0 (2. 0 – 7. 0) | |

Table (2)shows that The mean age and standard deviation (SD) of ages ofneonates with congenital anomalieswere4. 1 ± 1. 6 days

Table (3): Sex distribution of the studied patients (N= 366)

|  |  |  |
| --- | --- | --- |
| Studied patients (N= 366) | |  |
| No. | % |  |
| Sex | | |
| Male | 202 | 55. 2% |
| Female | 164 | 44. 8% |

Table(3) shows that 55. 2% (202 out of 366) of the studied patients were males, while 44. 8% were females.

Figure (1): Pie diagram showing sex distribution of the studied patients (N= 366)

Table (4): Distribution of the risk factors among the studied patients (N= 366)

|  |  |  |
| --- | --- | --- |
| Risk factors | Studied patients  (N= 366) | |
| No. | % |
| * Malignant hematological disease with chemotherapy | 43 | 11. 7 % |
| * Receiving repeated blood transfusion | 164 | 44. 8 % |
| * Fever of unknown origin | 16 | 4. 4 % |
| * Critically ill patients lying in the ICUs with prolonged hospitalization | 28 | 7. 7 % |
| * Receiving corticosteroids or other immunosuppressives for long period | 22 | 6 % |
| * Chronic renal failure with haemodialysis | 64 | 17. 5 % |
| * Fever with pancytopenia | 7 | 1. 9 % |
| * Neonates with congenital anomalies | 22 | 6 % |

As shown intable (4)andfigure (2), 44. 8% of the studied patients were receiving repeated blood transfusion, 17. 5% were suffering from chronic renal failure and receiving haemodialysis, 11. 7% were suffering from Malignant hematological disease and receiving chemotherapy, 7. 7% were critically ill patients lying in the ICUs with prolonged hospitalization, 6% were receiving immunosuppressive agents for long period, 6% were  neonates with congenital anomalies, 4. 4% had fever of unknown origin, and 1. 9% suffered from fever with pancytopenia.

Figure (2): Pie diagram showing Distribution of the risk factors in the studied patients (N= 366).

Table (5): Results of ELISA IgM and IgG for CMV in the enrolled patients (N= 366)

|  |  |  |
| --- | --- | --- |
| ELISA results | Studied patients  (N= 366) | |
| IgM | | |
| * Positive | 60 | 16. 4 % |
| * Negative | 306 | 83. 6 % |
| IgG | | |
| * Positive | 93 | 25. 4 % |
| * Negative | 273 | 74. 6 % |
| Over all seropositivity | | |
| * Positive both IgM and IgG | 109 | 29. 8 % |

As shown intable (5), out of the 366 studied patients, 60 (16. 4%) and 93 (25. 4%) were positive for CMV IgM and IgG in an ELISA test respectively.

Table (6): Agreement between ELISA IgM and IgG in the studied patients (N= 366)

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ELISA IgM | | | ELISA IgG | | Total | #Test | P-value |
| Negative | Positive |
| Negative | No. | 257 | 49 | 306 | 0. 469 | 0. 000\*  (HS) |  |
| % | 94. 1 % | 52. 7 % | 83. 6 % |  |
| Positive | No. | 16 | 44 | 60 |  |
| % | 5. 9 % | 47. 3 % | 16. 4 % |  |
| Total | | No. | 273 | 93 | 366 |
| % | 100. 0 % | 100. 0 % | 100. 0 % |

#   Kappa measure of agreement

P < 0. 05 is significant.

Statistical Significance

Standards for strength of agreement for the kappa coefficient:

≤0= poor,

. 01-. 20= slight,

. 21-. 40= fair,

. 41-. 60= moderate,

. 61-. 80= substantial, and

. 81-1= almost perfect.

Table 6shows that there is a moderate agreement between ELISA IgM and IgG in the detection of CMV in children with high statistical significance.

Table (7): Prevalence of CMV IgM seropositivity among different risk groups

|  |  |  |  |
| --- | --- | --- | --- |
| Risk Factors | No. | Studied patients  (N= 366) | |
| Positive IgM | |
| No. | % |
| * Malignant hematological disease with chemotherapy | (43) | 8 | 18. 6 % |
| * Receiving repeated blood transfusion | (164) | 36 | 21. 9 % |
| * Fever of unknown origin | (16) | 8 | 50 % |
| * Critically ill patients lying in the ICUs with prolonged hospitalization | (28) | 0 | 0 % |
| * Receiving corticosteroids or other immunosuppressives for long period | (22) | 0 | 0 % |
| * Chronic renal failure with haemodialysis | (64) | 8 | 12. 5 % |
| * Fever with pancytopenia | (7) | 0 | 0 % |
| * Neonates with congenital anomalies | (22) | 0 | 0 % |

Table (7)andfigure (3)show that the highest prevalence (50%) of CMV IgM seropositivity was reported from patients suffering from fever of unknown origin.

Figure (3): Bar chart showing prevalence of CMV IgM seropositivity among different risk groups

Table (8): Association between CMV IgM seropositivity and different risk factors

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Risk factors | No. | Studied patients  (N= 366) | | | | Test | p-value |
| ELISA IgM | | | |
| Positive  (N= 60) | | Negative  (N= 306) | |
| No. | % | No. | % |
| * Malignant hematological disease with chemotherapy | (43) | 8 | 18. 6 % | 35 | 81. 4% | #11. 17 | 0. 010  (S) |
| * Receiving repeated blood transfusion | (164) | 36 | 21. 9 % | 128 | 78% |
| * Fever of unknown origin | (16) | 8 | 50 % | 8 | 50% |
| * Chronic renal failure with haemodialysis | (64) | 8 | 12. 5 % | 56 | 87. 5% |

#   chi square test

P < 0. 05 is significant.

\*statistical Significance

Table (9): Prevalence of CMV IgG seropositivity among different risk groups

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Risk factors | No. | Studied patients  (N= 366) | | | |
| Positive IgG | | | |
| No. | | % | |
| * Malignant hematological disease with chemotherapy | (43) | | 0 | | 0 % |
| * Receiving repeated blood transfusion | (164) | | 63 | | 38. 4 % |
| * Fever of unknown origin | (16) | | 0 | | 0 % |
| * Critically ill patients lying in the ICUs with prolonged hospitalization | (28) | | 0 | | 0 % |
| * Receiving corticosteroids or other immunosuppressives for long period | (22) | | 0 | | 0 % |
| * Chronic renal failure with haemodialysis | (64) | | 8 | | 12. 5 % |
| * Fever with pancytopenia | (7) | | 0 | | 0 % |
| * Neonates with congenital anomalies | (22) | | 22 | | 100 % |

Table (9)andfigure (4)show that the highest prevalence (100%) of CMV IgG seropositivity was reported from neonates with congenital anomalies.

Figure (4): Bar chart showing prevalence of CMV IgG seropositivity among different risk groups.

Table (10): Association between CMV IgG seropositivity and different risk factors

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Risk factors | No. | | Studied patients  (N= 366) | | | | | | | | Test | | p-value |
| ELISA IgG | | | | | | | |
| Positive  (N= 93) | | | | Negative  (N= 273) | | | |
| No. | | % | | No. | | % | |
| * Receiving repeated blood transfusion | (164) | 63 | | 38. 4% | | 101 | | 61. 6% | | 53. 96 | | 0. 000\*  (HS) | |
| * Chronic renal failure with haemodialysis | (64) | 8 | | 12. 5% | | 56 | | 87. 5% | |
| * Neonates with congenital anomalies | (22) | 22 | | 100% | | 0 | | 0% | |

#   chi square test

P < 0. 05 is significant.

\*highly statistical Significance

Table (11): Results of real time PCR for CMV in the enrolled patients (N= 366)

|  |  |  |
| --- | --- | --- |
| Real time PCR | Studied patients (N= 366) | |
| * Positive | 36 | 9. 8% |
| * Negative | 330 | 90. 2% |

Table (11)shows that 9. 8% (36 out of 366) of the studied patients were positive for CMV in real time PCR test.

Table (12): Results of nested PCR for CMV in the enrolled patients (N= 366)

|  |  |  |
| --- | --- | --- |
| Nested PCR | Studied patients (N= 366) | |
| * Positive | 29 | 7. 9% |
| * Negative | 337 | 92. 1% |

Table (12)shows that 7. 9% (29 out of 366) of the studied patients were positive for CMV in nested PCR test.

Figure (4): Results of real time PCR and nested PCR for CMV in the enrolled patients.

Figure (5): 1 st run nested PCR showing band at 435 bp.

Figure (6): 2 nd run nested PCR showing band at 159 bp.

Table (13): Prevalence of CMV infection in the studied patients (using real time PCR as a gold standard test)

|  |  |  |  |
| --- | --- | --- | --- |
| Risk factors | No. | Studied patients  (N= 366) | |
| Positive | |
| No. | % |
| * Malignant hematological disease with chemotherapy | (43) | 36 | 83. 7% |
| * Receiving repeated blood transfusion | (164) | 0 | 0% |
| * Fever of unknown origin | (16) | 0 | 0% |
| * Critically ill patients lying in the ICUs with prolonged hospitalization | (28) | 0 | 0% |
| * Receiving corticosteroids or other immunosuppressives for long period | (22) | 0 | 0% |
| * Chronic renal failure with haemodialysis | (64) | 0 | 0% |
| * Fever with pancytopenia | (7) | 0 | 0% |
| * Neonates with congenital anomalies | (22) | 0 | 0% |

As shown intable (13), CMV infection (using real time PCR as a gold standard test) was only reported from patients suffering from malignant hematological disease and receiving chemotherapy, where  83. 7% of these patients were positive for CMV.

Figure (7):

Figure (8):

Table (14): Titer of CMV viremia in patients with malignant hematological disease receiving chemotherapy

|  |  |
| --- | --- |
| Quantitative PCR | Studied patients (N= 366) |
| Mean ± SD | 6907. 30 ± 15846. 04 |
| Median (Range) | 623. 50 (3. 70 – 57500) |

The mean titer and SD of titers of CMV viremia in patients with malignant hematological disease receiving chemotherapy as shown intable (14)was 6907. 30 ± 15846. 04.

Table (15): Results of Nested PCR for CMV among different risk groups

|  |  |  |  |
| --- | --- | --- | --- |
| Risk factors | No. | Studied patients  (N= 366) | |
| Positive | |
| No. | % |
| * Malignant hematological disease with chemotherapy | (43) | 29 | 67. 4% |
| * Receiving repeated blood transfusion | (164) | 0 | 0% |
| * Fever of unknown origin | (16) | 0 | 0% |
| * Critically ill patients lying in the ICUs with prolonged hospitalization | (28) | 0 | 0% |
| * Receiving corticosteroids or other immunosuppressives for long period | (22) | 0 | 0% |
| * Chronic renal failure with haemodialysis | (64) | 0 | 0% |
| * Fever with pancytopenia | (7) | 0 | 0% |
| * Neonates with congenital anomalies | (22) | 0 | 0% |

Twenty nine out of 43 patients suffering from malignant hematological disease with chemotherapy with a percentage of 67. 4 were positive for CMV in a nested PCR test as shown intable (15).

Table (16): Relation between ELISA IgM and real time PCR and nested PCR in the studied patients (N= 366)

Agreement between ELISA IgM and real time PCR and nested PCR in the studied patients (N= 366)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Laboratory findings | ELISA | | | | Test | P-value |
| Positive IgM  (N= 60) | | Negative IgM  (N= 306) | |
| No. | % | No. | % |
| Real time PCR | | | | | | |
| * Positive (n= 36) | 8 | 22. 2 % | 28 | 77. 8 % | # 0. 05 | 0. 320  (NS) |
| * Negative (n= 330) | 52 | 15. 8 % | 278 | 84. 2 % |
| Nested PCR | | | | | | |
| * Positive | 8 | 27. 6 % | 21 | 72. 4 % | #0. 082 | 0. 090  (NS) |
| * Negative | 52 | 15. 4 % | 285 | 84. 6 % |

#   Kappa measure of agreement

P < 0. 05 is significant.

Statistical Significance

Standards for strength of agreement for the kappa coefficient:

≤0= poor,

. 01-. 20= slight,

. 21-. 40= fair,

. 41-. 60= moderate,

. 61-. 80= substantial, and

. 81-1= almost perfect.

As shown intable 16, there is poor statistical agreement between ELISA IgM and PCR reactions in the detection of CMV in children with no significance.

Table (17): Relation between ELISA IgG and real time PCR and nested PCR in the studied patients (N= 366)

Agreement between ELISA IgG and real time PCR and nested PCR in the studied patients (N= 366)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Laboratory findings | ELISA | | | | Test | P-value |
| Positive IgG  (N= 93) | | Negative IgG  (N= 273) | |
| No. | % | No. | % |
| Real time PCR | | | | | | |
| * Positive (n= 36) | 0 | 0 % | 36 | 100 % | # -0. 137 | 0. 001\*  (HS) |
| * Negative (n= 330) | 93 | 28. 2 % | 237 | 71. 8 % |
| Nested PCR | | | | | | |
| * Positive | 0 | 0 % | 29 | 100 % | #-0. 165 | 0. 000\*  (HS) |
| * Negative | 93 | 27. 6 % | 244 | 72. 4 % |

#   Kappa measure of agreement

P < 0. 05 is significant.

\*highly statistical Significance

Standards for strength of agreement for the kappa coefficient:

≤0= poor,

. 01-. 20= slight,

. 21-. 40= fair,

. 41-. 60= moderate,

. 61-. 80= substantial, and . 81-1= almost perfect.

A high statistically significant non-agreement is present between ELISA IgG and PCR reactions in the detection of CMV in childrenas shown intable 17.

Table (18): Relation between real time PCR and nested PCR in the studied patients (N= 366)

Agreement between real time PCR and nested PCR in the studied patients (N= 366)

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Laboratory findings | Nested PCR | | | | Test | P-value |
| Positive  (N= 29) | | Negative (N= 337) | |
| No. | % | No. | % |
| Real time PCR | | | | | | |
| * Positive (n= 36) | 29 | 100 % | 7 | 2. 1 % | # 0. 882 | 0. 000\*  (HS) |
| * Negative (n= 330) | 0 | 0 % | 330 | 97. 9 % |

#   Kappa measure of agreement

P < 0. 05 is significant.

\*highly statistical Significance

Standards for strength of agreement for the kappa coefficient:

≤0= poor,

. 01-. 20= slight,

. 21-. 40= fair,

. 41-. 60= moderate,

. 61-. 80= substantial, and . 81-1= almost perfect.

Table 18shows that there is an almost perfect statistical agreement between real time PCR and nested PCR in the detection of CMV in children with high significance.

Table (19): Relation between real time PCR and nested