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Patterns of Hematological Parameters among Dengue Fever Patients

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ABSTRACT

Introduction: Dengue is a disease caused by an arbovirus of the genus Flavivirus and belonging to the family Flaviviridae, transmitted by the bite of *Aedesaegypti* or *Aedesalbopictus*. The dengue virus is composed of a single strand of ribonucleic acid (RNA) that has an icosahedral capsid protein coat. Four main viral serotypes (DENV-1, DENV-2, DENV-3, and DENV-4) cocirculate among humans, and these are genetically related, but antigenically distinct.

Objectives: to study the patterns of hematological parameters among Dengue fever patients.

Materials and methods: by applying the cross-sectional comparative study, fifty blood samples of suspected dengue fever patients and fifty blood samples of healthy controls were collected, and submitted to the hematological (CBC) and serological (IgM and IgG for Dengue virus) investigations.

Results: the patterns of hematological parameters among cases revealed statistically significant differences when compared with those of controls. In the other hand, IgM and IgG results revealed significant differences among cases as compared with controls.

***Conclusion*:** Patterns of the studied hematological parameters (Hb, HCT, TWBC, Diff. lymph. count, and platelet count), IgM, and IgG revealed statistical significant differences among cases when compared with those of controls.

Key words: Hematological parameters, Dengue fever

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Introduction

Dengue is a disease caused by an arbovirus of the genus Flavivirus and belonging to the family Flaviviridae, transmitted by the bite of *Aedesaegypti* or *Aedesalbopictus* (Torres-Flores, J.M.;2022). The dengue virus is composed of a single strand of ribonucleic acid (RNA) that has an icosahedral capsid protein coat. Four main viral serotypes (DENV-1, DENV-2, DENV-3, and DENV-4) cocirculate among humans, and these are genetically related, but antigenically distinct (Alagarasu, K.; *et al*; 2021).

In 2013, data regarding a fifth serotype (DENV-5) were published based on an identification in Malaysia, Asia, which alerted the scientific community to new epidemiological and clinical aspects of the disease (Mustafa, M.S.; *et al*; 2015).Among the different dengue virus serotypes, DENV-1 stands out as the most virulent, since it has the potential to cause major epidemics in a short period of time. (Paixão, E.S.; *et al* ;2018).

Dengue fever, an infectious illness spread by mosquitoes, is raising alarm bells throughout the globe. More than thirty times as many cases of dengue fever have been documented in the last fifty years, with most outbreaks happening in tropical areas with warm, rainy climate (A clinical decision-support system 2022).One of the factors associated with this characteristic is the fact that dengue is a disease that manifests itself mainly in periods of heavy rainfall and, depending on the social determinants, can cause serious harm to the population; thus, public health actions become essential for its control (xavier,LL; *et al*; 2021).

Most mosquito-borne infectious illnesses, including Zika and dengue fever, are very sensitive to changes in both ambient temperature and rainfall. There is a favorable relationship between normal ambient temperature and vector features including bite rate and extinct incubation rate, as shown by previous laboratory and field study (Acceleratin 2018). Based on the correlation between weather and disease spread, many studies have predicted how dengue fever would spread in a warmer world. Research suggests that disease transmission and vectorial capability may increase in the future (climate change 2019).

Dengue fever (DF), a viral illness spread mostly by mosquitoes, is a major problem all over the world (componential 2022). Climate change is a potential contributor to the rising incidence of dengue fever and its geographic extension, as it may make conditions more favorable for mosquito breeding and increase the spread of the disease. DF may also be governed by seasonal precipitation as rainfall provides pockets of stagnant water around dwellings (Schmidt,C.A, 2018).

Although humid conditions generally coincide with rainfall, often ambient humidity is enough to create the necessary conditions for *Aedesaegypti* proliferation, by increasing the longevity of female mosquitoes and preventing the desiccation of mosquito ova. Hales et al., (2002) found that average annual vapor pressure was the strongest predictor of DF distribution. Favorable weather conditions can also help imported cases of DF to become local epidemics (Shang, C.-S.; *et al* ,2010). The World Health Organization (WHO) has emphasized the importance of identifying the factors, particularly weather variables that may act as leading indicators of DF outbreaks. Predictive models in other locations highlight the importance of these indicators and the potential of predictive modeling to minimize the burden of DF (Siddiq, A.; *et al* ,2022).

Additionally, it is noted that, even in more favorable socioeconomic conditions, the absence of environmental awareness associated with the frequent habits in the cities of the country, such as the cultivation of aquatic plants and improper disposal of recyclable waste, may present risks for the emergence of the disease (da Silva, J.C.B.; Machado, C.J.S. 2018). Therefore, from epidemiological studies, it is noted that different risk factors that can lead to the susceptibility to and transmission of dengue are related to the social determinants of health. Internal migration, violence, poverty, disorderly growth, illegal deforestation, and deficiencies in environmental management may indirectly promote the proliferation and spread of dengue (Ortiz Guerrero, L.M.; *et al* 2020).

Epidemiological studies not only provide an overview of dengue, but are also relevant in specific studies on genotypic variations that map viral changes that can trigger new epidemics, especially in the most severe manifestation of the disease (dengue haemorrhagic fever), resulting in an increase in the number of deaths (Angelo, M.; *et al*, 2020).

Prevalence of the dengue fever in the world

Current situation

The global incidence of dengue has markedly increased over the past two decades, posing a substantial public health challenge. From 2000 to 2019, the World Health Organization (WHO) documented a ten-fold surge in reported cases worldwide increasing from 500 000 to 5.2 million. The year 2019 marked an unprecedented peak, with reported instances spreading across 129 countries. After a slight decline of cases between the year 2020-2022 due to the COVID-19 pandemic and lower reporting rate, in 2023, an upsurge in dengue cases have been observed globally, characterized by a significant increase in the number, scale, and simultaneous occurrence of multiple outbreaks, spreading into regions previously unaffected by dengue.

Dengue transmission is cyclic and large outbreaks every 3-4 years can be expected. During the COVID-19 pandemic we saw moderate transmission of dengue in some regions and low transmission in others leading to an accumulation of people without immunity to certain dengue virus serotypes. However, the data on the circulating dengue serotypes is limited.

Since the beginning of 2023, ongoing transmission, combined with an unexpected spike in dengue cases have resulted in close to a historic high of over five million cases and more than 5000 dengue-related deaths reported in over 80 countries/territories and five WHO regions: Africa, Americas, South-

East Asia, Western Pacific and Eastern Mediterranean Regions globally . Close to 80% of these cases, or 4.1 million, have been reported in the region of the Americas. Dengue is the most widespread arbovirus and causes the highest number of arboviral disease cases in the region of the Americas, with cyclic epidemics recurring every 3 to 5 years. Countries/territories/areas reporting autochthonous dengue cases (November 2022- November 2023)

Regional overview

WHO Region of Africa:

Africa is among the top four regions most affected by arboviral diseases, including yellow fever, dengue, chikungunya, O'nyongnyong, Rift Valley fever, and Zika. In 2023, 171 991 dengue cases have been reported in countries in the region and 753 deaths. Evidence of dengue circulation has been detected in local populations and/or among travelers returning from more than 30 African countries. Outbreaks have been reported from 15 of the 47 countries including Benin, Burkina Faso, Cape Verde, Chad, Côte d'Ivoire, Ethiopia, Ghana, Guinea, Mali, Mauritius, Niger, Nigeria, São Tomé and Principe, Senegal and Togo. The outbreaks in most of these countries began in 2023, except in São Tomé and Príncipe, where it was a continuation of an outbreak that started in April 2022. As of 19 December 2023, outbreaks are still ongoing in 11 countries and were declared over in Chad, Guinea, Mauritius, and São Tomé and Príncipe. The most affected country in the region in 2023 is Burkina Faso.

WHO Region of the America:

Between 1 January 2023 and 11 December 2023, a total of 4.1 million suspected dengue cases (cumulative incidence of 419 cases per 100 000 population), including 6710 severe cases (0.16% of suspected cases) and 2049 deaths (CFR 0.05%) were reported from 42 countries and territories in the Region of the Americas, with 15 countries reporting active outbreak. Of the total number of dengue cases until 12 November 2023 (EW 48 of 2023), 1 895 122 (45%) were laboratory confirmed. Currently, 46 countries and territories systematically report, through the Health Information Platform for the Americas, on a weekly basis, the total number of cases, incidence, number of severe cases, number of deaths and lethality due to dengue, as well as entomological surveillance data. As of EW 48, Brazil has reported the highest number of suspected cases in the Region (n = 2 909 404; 1359 cases per 100 000 population), followed by Peru (n= 271 279; 813 cases per 100 000 population), and Mexico (n = 235 616; 179 cases per 100 000 population). In terms of severe dengue, Colombia reported the most cases (1504; 1.35% of cases), followed by Brazil (1474; 0.05% of cases), Mexico (1272; 0.54% of cases), Peru (1065; 0.39% of cases), and Bolivia (640; 0.44% of cases).

Although dengue is endemic in most countries of South America, Mexico and Central America, and the Caribbean countries, the second half of 2023 has witnessed an alarming increase in cases, with cumulative cases for the year surpassing all previous yearly totals and in some countries extending beyond historically affected areas of transmission. Dengue cases have increased in the Americas over the past four decades, from 1.5 million cases from 1980 to 1989 to 17.5 million in 2010-2019. Before 2023, the highest historical dengue caseload was in 2019, with over 3.18 million cases, 28 208 severe cases, and 1823 deaths (CFR 0.06).

WHO Eastern Mediterranean Region:

Dengue and severe dengue epidemics were first reported in the region in 1998, and since then, their frequency and geographical spread have increased, with outbreaks occurring in all nine endemic countries: Afghanistan, Djibouti, Egypt, Oman, Pakistan, Saudi Arabia, Somalia, Sudan, and Yemen.

Among these are fragile, conflict affected and vulnerable countries such as Afghanistan, Pakistan, Sudan, Somalia and Yemen. The outbreaks are exacerbated due to disruption of health services (Sudan), fragile health systems (Afghanistan, Somalia, Sudan, Pakistan and Yemen), mass population movements, poor water and sanitation infrastructure, and recurring natural disasters such as floods affecting Somalia, Sudan, Pakistan, and Yemen, along with earthquakes in Afghanistan. Outbreaks are also reported in middle- and high-income countries such as Egypt, Oman and Saudi Arabia due to climate change leading to unusual rainfalls. Pakistan (n= 20 072), Saudi Arabia and Oman have reported the highest number of confirmed cases thus far in 2023.

WHO European Region:

Dengue is not endemic in the WHO European Region and cases are mainly travel-related; however, since 2010, there have been reports of autochthonous cases in a number of countries in the region, including Croatia, France, Israel, Italy, Portugal and Spain. In 2018, the year with the most comprehensive data available, a total of 2500 cases of dengue were reported to WHO through the regional annual surveillance data collection mechanism with Germany, France, and the United Kingdom contributing the majority of cases. The vast majority of these cases were imported. However, it should be noted that data completeness remains challenging.

Between 1 January and 5 December 2023, sporadic autochthonous cases and outbreaks have been reported in three countries: Italy (n = 82), France (n = 43) and Spain (n = 3).

WHO South-East Asia Region:

In the WHO Southeast Asia region, 10 out of 11 Member States are known to be endemic for dengue virus. In 2023, several countries, including Bangladesh and Thailand, have reported a notable surge in dengue cases compared to previous years. In particular, India, Indonesia, Myanmar, Sri Lanka and Thailand rank among the world's 30 most highly endemic countries. Compared to 2022, in 2023, Bangladesh and Thailand recorded a larger number of dengue cases . By November 2023, Bangladesh experienced a substantial rise in cases reaching 308 167 compared to 62 382 reported for the entirety of 2022. Thailand saw an increase of over 300%, with dengue cases rising from 46 678 in 2022 to 136 655 in 2023 (as of 22 November 2023). During the same period, the death toll in Bangladesh rose from 281 (CFR 0.45%) to 1598 (CFR 0.52%), while in Thailand, it increased from 34 (CFR 0.07%) to 147 (CFR 0.11%). In other countries, the CFR ranged from 0.04% in Nepal to 0.72% in Indonesia. It's important to interpret these values cautiously due to variations in the case definition used across countries, with some systems primarily focused on reporting hospitalized or severe dengue cases. (WHO,21 Dec 2023)

In Yemen: Dengue Outbreak - Dec 2019

In 2019 there were 76,768 suspected cases across the country and 271 deaths, 71 per cent of all cases were in Al Hodeidah, and in the first two weeks of January, there were 5,524 with 11 associated deaths. The number of suspected cases has reduced in some areas, but there are still hotspot districts, and the highest incidence per 10,000 of the population are in Al Hodeidah (10.7), Aden (2.36), Marib (2.12) and Lahj (1.63). (OCHA, 31 Jan 2020)

Since the onset of the outbreak in Yemen, dengue suspected cases to date continue to increase during 2020 compared with 2019, the suspected cases up to week 28 are four times the cases in comparison 2019, and six times the reported numbers in 2018, according to the Yemen Health Cluster. According to the latest epidemiological bulletin Issue 28 (covering week 28 up 6-12 July, epi week 28), Hodeidah remains the most affected, recording 31,241 cases out of the total caseload. (IFRC, 28 Aug 2020)

From 1 January to 27 September 2020, a total of 38,516 suspected Dengue Fever cases were reported from northern governorates, with 76 associated deaths. Within the reporting period, 50 districts reported suspected cases with 92 per cent of suspected cases were reported from four governorates: Mareb (52 per cent), Al-Hodeidah (22 per cent), Hajjah (12 per cent) and Taizz (7 per cent). A dengue fever control campaign in Aden city's eight districts was launched on 13 September by the Ministry of Public Health and population, with the support of the WHO and KSRelief. The campaign included indoor and outdoor fogging, community awareness activities, vector surveillance and environmental management of all mosquitoes breeding sources, to provide direct protection to 430,000 people and indirectly to the 1.7 million total population of Aden city.(WHO,19 oct 2020)

Pathogenesis is linked to the host immune response, which is triggered by infection with the virus. Primary infection is usually benign but secondary infection with different serotypes cause severe infection.(Torres-Flores, J.M.; *et al* ,2022) Antigen-presenting dendritic cells, the humoral immune response, and the cell-mediated immune response are involved in pathogenesis. The proliferation of memory T cells and production of proinflammatory cytokines (Cytokine Tsunami) leads to dysfunction of the luminal surface of the vascular endothelium which has a layer of glycocalyx which results in plasma leakage.(Paixão, E.S.; *et al,*2 018)

There is also abundant replication of DENV’s in liver parenchymal cells, in macrophages, in lymph nodes, liver and spleen, and peripheral blood monocytes. Antibody-dependent enhancement (ADE) occurs when mononuclear phagocytes are infected through their Fc receptors by immune complexes that form between DENV’s and non-neutralizing antibodies. These non-neutralizing antibodies result from previous heterotypic dengue infections or from low concentrations of dengue antibodies of maternal origin in infant sera. Hence ADE theory can cause DHF in both primary infection in infants and secondary infection at any age. (Senenayake AM Kularatne. 2016.) Severe dengue has a mortality rate of 50% if untreated; however, this is reduced to less than 5% if appropriately treated. Medical care by experienced teams decreases mortality rates to less than 1% in majority of the countries. Most severe dengue and most deaths occur in children aged under 15 years.(WHO;2022).

DENV not only indirectly or directly escapes immune surveillance, but also specifically targets immune mediators to prevent intracellular antiviral signal transduction(Kao *et al*. 2018).After successful infection, DENV primarily attacks and replicates in dendritic cells and infects macrophages, monocytes, and lymphocytes (Wan et al. 2018).Thereafter, the nucleocapsid (NC) is released into the cytoplasm, the RNA genome is uncoated, and viral materials are transported to the ER by the cytoskeletal transport machinery (Cuartas-López*et al*. 2018).

Induction of IFN-α/β through TLR7/8/9 is also mediated by the adaptor molecule myeloid differentiation primary response protein 88 (MyD88) through the MAPK and NF-κB pathways. (Kao; *et al*. 2018) IFN-α/β, secreted from DENV-infected cells, triggers a signal to nearby cells and inhibits DENV infection (Tremblay *et al*. 2019).In a given region, periodic outbreaks occur due to different serotypes over decades, thus development of complete herd immunity for all four serotypes in the community is not achievable and the disease may remain without natural elimination. The abnormal immune response results in increased microvascular permeability without inflammation or vasculitis, and leads to altered thromboregulatorymechanisms.(Hasan *et al*. 2016)

DENV is usually greater in tropical and subtropical environments throughout the world, frequently in urban and semiurban zones. People, exposed to infected mosquitoes of all ages are susceptible to DENV infection. DENV infection causes dandy fever, breakbone fever, and dengue hemorrhagic fever; and in severe cases, dengue shock syndrome has occurred. The rainy season is the most favorable climate for DENV infection outbreaks in tropical countries in Asia and South America. Generally, the infected female *Aedes* mosquitoes transmit DENV in humans. Although humans are not capable of transmitting DENV, it can be transmitted during the blood transfusion between an infected person to a non-infected (healthy) person (1. S. M. Eick, A. P. Dale, B. McKay *et al*.,2019).(1. R. Kulkarni, D.*et al* .,2019).

The symptoms of Dengue fever infection are diffuse skin flushing of the face, neck, and chest develops early in the infection. This evolves into a maculopapular or rubelliform rash of the whole body on day 3 or 4 of fever, which is associated with blanching when pressed.(Senenayake AM Kularatne ,2015) Other common symptoms noted were myalgia , joint pain , headache, vomiting pain abdomen rash hepatomegaly bleeding and shock. Hess test was positive. (Farhan Fazal, SangramBiradarJ ;2015)

Plasma leakage-Ascites, postural dizziness, or pleural effusion leading to respiratory distress. These are seen in DHF(Senenayake AM Kularatne ,2015) Damaged blood vessels cause severe dengue (Hasan *et al*. 2016) and the number of clot-forming cells (platelets) in the bloodstream decreases. This can lead to shock, internal bleeding, organ failure, and even death. Hepatomegaly Plasma leakage- dizziness, or pleural effusion leading to respiratory distress. These are seen in DHF. Circulatory collapse-cold clammy skin, rapid and weak pulse with narrowing of pulse pressure to <20 mm Hg with decreased diastolic pressure, a postural drop of blood pressure >20 mmHg, capillary refill time greater than 3 seconds, reduced urine output, indicates the presence of shock and supports the diagnosis of dengue shock syndrome. (Senenayake AM Kularatne ,2015).

On assessment, the patient's heart rate was 112 beats per minute (bpm), normal blood pressure (BP) was 92/60 mmHg, respiratory rate was 24 breaths per minute (bpm), and oxygen saturation when breathing room air was 98% (Singh et al. 2018). Circulatory collapse-cold clammy skin, rapid and weak pulse with narrowing of pulse pressure to <20 mm Hg with decreased diastolic pressure, a postural drop of blood pressure >20 mmHg, capillary refill time greater than 3 seconds, reduced urine output, indicates the presence of shock and supports the diagnosis of dengue shock syndrome (Senenayake AM Kularatne ,2015).

Hemorrhagic signs-Minor hemorrhage includes petechiae, purpura, positive tourniquet test (BP cuff is inflated to a point midway between systolic and diastolic blood pressures for 5 minutes. The test is positive if >10 petechiae per square inch or per 2.5 square cm appear on the forearm (Senenayake AM Kularatne ,2015). Major hemorrhage includes epistaxis, gingival bleeding, and hematemesis. Malena, metromenorrhagia, bleeding from venepuncture site. These signs can occur either in DF or DHF.(Senenayake AM Kularatne ,2015).

Of these manifestations bleeding and hepatomegaly are highly correlated with the progression of DF into severe dengue disease (SDD).Damaged blood vessels cause severe dengue (Hasan *et al*., 2016) and the number of clot-forming cells (platelets) in the bloodstream decreases. This can lead to shock, internal bleeding, organ failure, and even death. Hepatomegaly Plasma leakage - dizziness, or pleural effusion leading to respiratory distress. These are seen in DHF. The warning signs of severe DF can develop quickly (Hasan *et al*. 2016).

Subjects and Methods

- **Study design**

A comparative cross-sectional study was carried out in Hodiedahgovernorate.

- **Study Population**

All individuals admitted to the Al-thowrah Hospital, and General Hospital of Zabied, came with fever and suspected Dengue infection were enrolled in the present study.

- **Inclusion criteria**

Any admitted individuals and above 5 years in both sexes with suspected dengue infection were included in the study.

- **Exclusion criteria**

Individuals less than 5 years and those who had no fever or symptoms related to Dengue virus infection were excluded.

- **Sample size**

About 100 participants (50 of them with suspected Dengue infection and 50 age and sex matched controls were recruited in the study).

- **Methods**

- **Sample collection**

About 5ml of blood sample was collected from 50 participants who had fever and suspected Dengue fever infection, and 5ml of the same sample was collected from 50 apparent healthy individuals to be as a control group.

The collected samples for both (cases and controls) were divided into two parts, one part for performing complete blood count (CBC) and the other part for detecting IgM and IgG of Dengue virus.

- **Laboratory tests**

- **Performing the hematological parameters or complete blood count (CBC)** (Fig. 1; A & B)

A complete blood count (CBC) tests including hemoglobin (Hb) and hematocrit (HCT) or packed cell volume (PCV), Total white blood cell count (TWBC), differential lymphocyte count, and platelet count were analyzed by using 3- diff hematology analyzer (Zybio, Zybio Incorporation, Chongqing, China) with in 4 hour blood collection.

- **Detecting IgM , and IgG of Dengue virus by ELISA**

1- *Detecting Dengue virus IgM antibodies:*-

By using the Dengue IgM ELISA kit and according to the manufacturing instructions of the kit, the titer of Dengue IgM was determined by using the ELISA reader (PKL, LettoreMicropiastra, Italy) (Fig. 2 A and B) and the result was reported as positive if the titer was > 1.1 U/L and negative if the titer was < 1.1 U/L.

2- *Detecting Dengue virus IgG antibodies*:-

By using the Dengue IgM ELISA kit and according to the manufacturing instructions of the kit, the titer of Dengue IgG was determined by using the ELISA reader (PKL, LettoreMicropiastra, Italy) (Fig. 3 A and B) and the result was reported as positive if the titer was > 1.1 U/L and negative if the titer was < 1.1

Results

1- Patterns of hematological parameters among participants (cases and controls)

Table (1) shows the pattern of hematological parameters among cases and controls, where all the studied hematological parameters (Hb, HCT, TWBC, Diff. lymph. count, and platelet count) of cases revealed a statistically significant differences (*P*- < 0.05) when compared with controls.

Table (1): Patterns of hematological parameters among participants (cases and controls)

Variable		**Type of Participants**		***P. value*****
		Cases Median (IQR*)	**Controls Median (IQR*)**	
Hematological Parameters	Hb	10.6 (8.0 -11.9)	13.8 (12.7- 15.4)	**0.001**
	HCT	32.5 (25 – 36)	40.4 (37.8 – 44.8)	**0.001**
	TWBC count	3.8 (2.9 – 4.9)	6.4 (5.2 – 8.0)	**0.001**
	Diff. Lym count %	42.2 ± 12.4	48.4 ± 14.8	**0.026**
	Plt. Count	115 (73.2 – 146)	332.5 (283.5 – 361.2)	**0.001**

*****IQR; interquartile range**.** ******P value is significant at <0.05, and was calculated by Mann-Witney test

2- The difference of Dengue IgM results among participants (cases and controls)

Table (2) shows the difference of Dengue IgM results among cases and controls, where the results of IgM (positive and negative) among cases revealed a statistically significant difference (*P*- < 0.05) when compared with those among controls.

Table (2):The difference of Dengue IgM results among participants (cases and *controls)*

Variable		**Type of participants**		***P. value****
		Cases	Controls	
IgM of Dengue virus	Positive	37	0	**0.001**
	Negative	13	50	

**P*. value is significant at < 0.05 and was calculated by Chi-Square test

3-The difference of Dengue IgG results among participants (cases and controls)

Table (3) shows the difference of Dengue IgG results among cases and controls, where the results of IgG (positive and negative) among cases revealed a statistically significant difference (*P*- < 0.05) when compared with those among controls.

Table (3):The difference of Dengue IgG results among participants (cases and controls)

Variable		**Type of participants**		***P. value****
		Cases	Controls	
IgG of Dengue virus	Positive	30	0	**0.001**
	Negative	20	50	

**P*. value is significant at < 0.05 and was calculated by Chi-Square test

4-Correlation between hematological parameters and the IgM among cases

Table (4) shows the correlation between hematological parameters and the IgM among cases, where all the studied hematological parameters (Hb, HCT, TWBC, Diff. lymph. count, and platelet count) of cases revealed no significant correlation (*P*-> 0.05) between the two variables.

Table (4): Correlation between hematological parameters and the IgM among *cases*

Variable		IgM results		*P. value**
		Positive	Negative	
Hematological Parameters	Hb	37	13	0.172
	HCT(PCV)	37	13	0.232
	TWBC	37	13	0.622
	Diff. count of Lym.	37	13	0.098
	Platelet count	37	13	0.458

**P.* value is significant at <0.05 and was calculated by Pearson correlation test

5- Correlation between hematological parameters and the IgG among cases

Table (5) shows the correlation between hematological parameters and the IgG among cases, where all the studied hematological parameters (Hb, HCT, TWBC, Diff. lymph. count, and platelet count) of cases revealed no significant correlation (*P*-> 0.05) between the two variables.

Table (5): Correlation between hematological parameters and the IgG among cases

Variable		IgG results		*P. value**
		Positive	Negative	
Hematological Parameters	Hb	30	20	0.066
	HCT(PCV)	30	20	0.102
	TWBC	30	20	0.682
	Diff. count of Lym.	30	20	0.422
	Platelet count	30	20	0.551

**P.* value is significant at <0.05 and was calculated by Pearson correlation test

Discussion

Dengue is a disease caused by an arbovirus of the genus Flavivirus and belonging to the family Flaviviridae, transmitted by the bite of *Aedesaegypti* or *Aedesalbopictus* (Torres-Flores, J.M.;2022). The most interesting character and life threatening problem is that this virus has four main viral serotypes (DENV-1, DENV-2, DENV-3, and DENV-4) cocirculate among humans, and these are genetically related, but antigenically distinct (Alagarasu, K.; et al; 2021).

Laboratory diagnosis of Dengue viral infection has been developingsince the emergence of new accurate and reliable methods. However and unfortunately these methods are not cost effective or very expensive and not reachable especially in developing countries. Therefore, the specialists of tropical diseases (including Dengue fever infection) are looking for other options (cost effective and less expensive) for diagnosing such infections.

Among the available options are some hematological parameters as; hemoglobin, hematocrit, total & differential count of white blood cells, and platelet count. Therefore, the present study concentrated on the study of patterns of the above mentioned hematological parameters of suspected cases and comparing them with healthy control individuals.

In the present study, patterns of hematological parameters (Hb, HCT, TWBC, Diff. lymph. count, and platelet count) among cases revealed statistically significant differences (*P*- < 0.05) when compared with the same parameters of control individuals. Similar findings in a similar study, (Senenayake AM Kularatne;2015), reported significant differences of hematological parameters in cases when compared with controls.

In the current study, the results of IgM and IgG (positive and negative) among cases revealed a statistically significant difference (*P*- < 0.05) when compared with those of controls. These findings went in line with findings in a similar study, (Vongsouvath M, *et al* ; 2016), where values of IgM and IgG revealed a significant difference.

In this study, the correlation between the hematological parameters and IgM or IgG results among cases revealed no significant correlation (*P*- >0.05). Likewise,similar studies;(Ananda Nisalak; 2015), and (Felix AC ;*et al* ,2017) revealed no correlation with the hematological parameters although there was correlation with the clinical symptoms.

Conclusion: Patterns of the studied hematological parameters revealed a statistical significant difference among cases when compared with those of controls. The studied hematological parameters are of value for diagnosing Dengue fever infection especially in medical centers with less diagnostic equipment or facilities.

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