

Pathogenic Bacteria Isolated from House Flies and Compared with Pathogenic Bacteria Isolated from Children with Diarrhea

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Received: 2023-08-16, Revised: 2023-09-05, Accepted: 2023-09-06, Published: 2023-12-24

Abstract— House flies carry many disease-causing bacteria. Through this study, we will find the relationship between house flies and bacteria that cause diarrhea in children. A total of three hundred and fifty flies were collected from (butchers, chicken and fish shops, markets, house and hospitals) and 200 samples were collected from children with diarrhea from each of Shatrah and Nasiriyah Governorate during the research period from July 2022 to January 2023 in Thi-Qar Governorate. The current study showed that 126 (36.0 %) of the flies carried bacteria, while 224 (64.0 %) of them did not contain bacteria. The current study showed that the percentage of high isolated bacteria was from the internal content of flies (8.71%), followed by (5.57%), on the external surface of flies. the present study showed the high isolated bacteria were from butcher (4.29%), following in hospital (4.0%), while the lowest isolated bacteria from flies collected from houses (2.86%), The current study showed that the most isolated bacteria is *E. coli* with a percentage of (24.3%), followed by *S. aureus* (17.0%), followed by *Klebsiella. spp* (13.15%), while the least isolated bacteria is *Micrococcus* (3.94%). When comparing the bacteria present in flies with the bacteria isolated from pediatric patients with diarrhea, these bacteria, the current study showed that the predominant bacteria was *Escherichia coli* from diarrhea with a percentage of (44.63%), and *Escherichia coli* was (36.27%) in the dominant flies. *Staphylococcus aureus* in flies followed (25.49%), while diarrhea followed (16.53%). On the other hand, the least dominant bacterial species was *S. pyogen* in both diarrhea and diarrheal flies with (8.82%) and (9.09%), respectively. This study proved that house flies are carriers of pathological bacteria that cause diarrhea in children under the age of ten, and the infection rate was higher among children under one year of age. The proportion of bacteria was higher.

Keywords— Houseflies, Diarrhea, *Musca domestica* Fly, Relationships.

I. INTRODUCTION

The common name "house fly" comes from the fact that the *Musca domestica* L., a well-known cosmopolitan pest, is the most prevalent fly found in and around homes and is also a bothersome pest. It has pest. It has a wide geographic and delivery is present and delivery in close proximity to human endeavors [1]. house flies' role in the spread of pathogenic bacteria. House flies have been linked to the transmission of several human pathogens, including *Staphylococcus aureus*, *Vibrio Cholerae*, and *Pseudomonas spp.* Transmission occurs As many as 500000 germs may swarm over the fly's body and legs when it comes into contact with people or their meals [2]. Around the world, the common house fly is a significant insect in medicine. Numerous human infections, such as *Staphylococcus aureus* and *Pseudomonas spp.* and *Vibrio Cholerae* *Enterobacteriaceae* pathogens, have been linked to house flies as vectors or carriers. As 500000 or more germs could swarm all over the fly's body and legs during transmission when it comes into contact with people or their meals [2]. Many researchers have investigated and isolated pathogens reporting them as a potential source for the spread of these illnesses from house flies. The transmission and spread of various infections, such as *V. cholera*, *E. coli* 0157:H7, *Salmonella spp.*, and *Compylobacter spp.*, have been linked to house flies [2], [3]. House flies frequently urinate while feeding or resting, leaving behind fly specks and other organisms that have passed via their digestive system. This is a straightforward mechanical transmission of germs by a vector, whose behavior deposits the pollutants from diseased and decomposed sources they visit ([4] House flies have hundreds of related species, many of which are tissue- and dysentery-causing agents, and can contaminate clean surfaces with about 0.1mg of food per landing. as *Bacillus*



spp; *Staphylococcus* sp; *Enterococcus* spp; *Shigella* spp; *E. coli*; *Bacillus anthracis*; *Chlamydiales*; *Corynebacterium* spp; and other parasitic organisms [5]. In underdeveloped nations, synanthropic flies play a significant epidemiological role in the transmission of trachoma among newborns and young children as well as severe gastroenteritis. In addition, synanthropic house flies play an epidemiologically significant role in the transmission of nosocomial infections, including (MDR) bacteria pathogens, in unhygienic healthcare settings among newborns and young children, particularly in developing countries [6].

Diarrhea disease estimates 525,000 children die from diarrhea each year, which is the second greatest cause of death in children under the age of five. There are 1.7 billion occurrences of childhood diarrhea worldwide each year. The majority of this death can be avoided by getting access to care and using rehydration therapy. After the initial illness has passed, complications that affect a child's growth can be observed, such as the succeeding malabsorption. Infections caused by foodborne contamination account for 80% of the estimated 5.2 million cases of bacterial diarrhea that occur in the United States each year [7]. According to global estimates, the prevalence of certain types of bacterial diarrhea among all causes of diarrhoea ranges from 10% for *Shigella*, from 10% to 6%, and from 25% to 50% for *E. coli*, *Shigella*, *Salmonella*, and *Campylobacter*. [8]. In the US, it was estimated that bacteria were to blame for 31% of all instances of diarrhea. According to estimates, *Salmonella* accounts for 15.4%, *Campylobacter* for 11.8%, *Shigella* for 4.6%, and *Shiga*-producing *E. coli* (STEC) for around 3% of the bacteria that cause foodborne diarrheal illness in the United States.

II. MATERIALS AND METHODS

A. Samples Collection

Estimation of the number of adult houseflies carrying pathogenic bacteria

Flies were collected from (butchers, chicken and fish shops, markets hospitals and houses). of the cities of Shatrah city and Nasiriyah 152 samples were collected in the Thi-Qar province between July 2022 and January 2023 for the study after transferring it to the laboratory, we did the following steps .he flies were placed in the refrigerator for 3 minutes and at a temperature of 0 °C to inactivate their activity; in order to isolate bacteria from them [9].

B. House fly morphological identification

Following the identification keys, identification of flies was carried out using morphologic criteria to the family taxon level [10].The specimens were sent to the Iraq Natural History Research Center and Museum in Basra to confirm identification. Isolation of pathogen bacteria from the outer surface of flies: In order to isolate bacteria from them (flies), the samples were washed twice in 1 ml of sterile water for one minute each, then placed in 2 ml of normal saline with a concentration of 0.85%. Finally, 0.1 ml of this solution was transferred to the plates containing the appropriate culture medium, and the plates throughout a 24-hour incubation period at 37 °C [9].

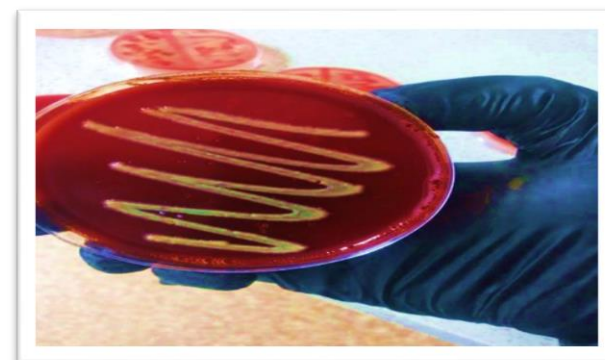
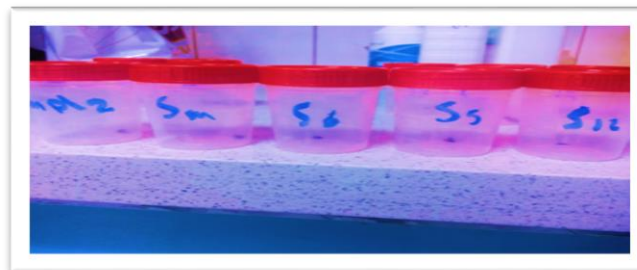
C. Pathogen Bacteria were Isolated in the Guts of the Flies

Using a dissecting microscope, the samples of flies were first sterilized by being washed in ethyl alcohol at a 70% concentration, then gently washed with sterile water, and finally dissected to remove the intestine. The insect's intestine was then crushed using a tapering tool with a head, mixed with 2 ml of saline solution for steeping, and finally 0.1 ml of the infusion was taken and planted [11].

D. Pathogenic Bacteria Isolated from House Flies.

The bacteria were cultured on two different mediums after being removed from the flies' exterior and inner surfaces. Additionally, the presence of the bacterium was determined in diarrheal samples taken from children under the age of 10 from Shatra General Hospital and grown on specialized culture media (blood agar; MacConkey agar).

Then phenotypic and microscopic diagnosis, and then a stain Gram, Then conduct biochemical tests and API , Vitek verification tests. [1].



Figures (1): Collect houseflies and culture media (blood agar; MacConkey agar)

E. Morphological Tests

Colony properties was tested such as shape of the colonies, size, color, borders and texture of colonies.

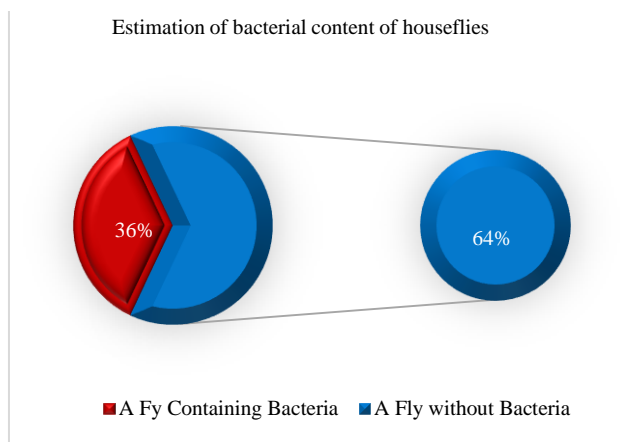
F. The Diagnosis is the Following Steps

- Microscopic Examination
- Biochemical Test
- API-system (Analytical profile index for Enterobacteriaceae Test ,*Stapholococcia* Test and *streptococcia* Test)
- Vitek 2 compact
- Antibiotic Susceptibility

III. RESULTS

1. Estimation of Bacterial Content of House Flies

A total of three hundred and fifty flies were collected from (butchers, chicken and fish shops, markets and hospitals and houses) from both Al-Shatra and Nasiriyah districts in Province of Thi-Qar throughout the time of the study from July 2022 to January 2023. the present study showed 126 (36.0%) of flies carrying bacteria, while 224 (%64.0) of which have not bacteria, the present study also noticed a significant difference in the amount of bacteria in the flies, as illustrated in figure (2), at a p value less than 0.05.



CalX ² = 37.362	TabX ² =3.84	DF=1	p. value < 0.001
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Figure (2): Estimation of bacterial content of houseflies

2. Estimation of Bacterial Content of house flies according to Site of Swab Collection

The present study showed the high isolated bacteria were from internal content of flies 8.71%, followed in the outer surface of flies 5.57%, also, noted 3.71% of flies have a bacterium in both outer surface and internal content, while the study showed 40.71% of outer surface have not bacterial infection, and 37.57% of internal content have not bacterial infection. In contrast, 3.71% of flies have not bacterial infection in both outer surface and internal content. The study as demonstrated in table (1), there was a considerable difference in the amount of bacteria present in the flies depending on the source of the swab.

Table (1): Estimation of bacterial content of houseflies according to site of swab collection

Culture Result Source of Swab	Positive		Negative		Total	
	No.	%	No.	%	No.	%
Outer Surface only	39	5.5	285	40.7	324	46.2
Internal Content only	61	8.7	263	37.5	324	46.2
Both	26	3.7	26	3.7	52	7.4
Total	126	18	574	82	700	100
CalX ² = 20.762	TabX ² =5.99		DF=2		p. value < 0.001	

3. Estimation of Bacterial Content of House flies according to Place of Collection

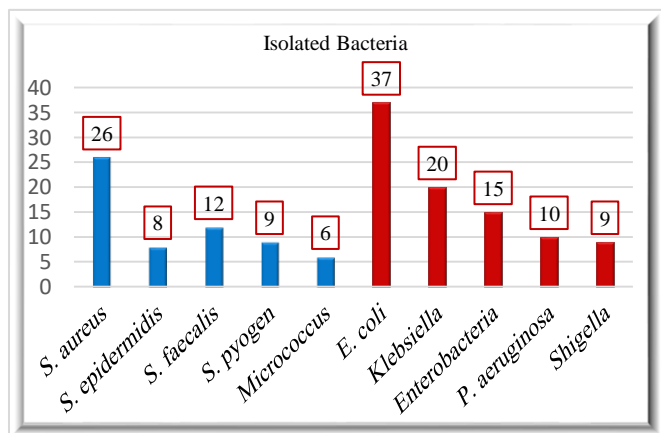
The present study showed the high isolated bacteria were from butcher 4.29%, following in hospital 4.0%, while the lowest isolated bacteria from flies collected from houses 2.86%. In contrast, the high flies have not bacterial infection were collected from houses 17.14%. Depending to the location of collection, there was a non-significant difference in the number of bacteria present in the flies, as indicated in table (2).

Table (2): Estimation of bacterial content of house flies according to place of collection

Culture Result Source of Swab	Positive		Negative		Total	
	No.	%	No.	%	No.	%
Butchers						
Fish and Chicken Shops	30	4.29	110	15.71	140	20.00
Vegetable Stores	24	3.43	116	16.57	140	20.00
Houses	24	3.43	116	16.57	140	20.00
Hospitals	20	2.86	120	17.14	140	20.00
Total	28	4.00	112	16.00	140	20.00
Butchers	126	18.00	574	82.00	700	100
CalX ² = 2.942	TabX ² = 9.49		DF=4		p. value 0.568	

4. Identification of Isolated Bacteria from Flies

The present study showed the high isolated bacteria was *E. coli* 24.3%, followed *S. aureus* 17.0%, followed *Klebsiella Spp* 13.15%, while the lowest isolated bacteria was *Micrococcus* 3.94%. as show in figure (3).



Figure(3): Identification of isolated bacteria from flies

5. Distribution of Isolated Bacteria from Flies According to Swab Sites

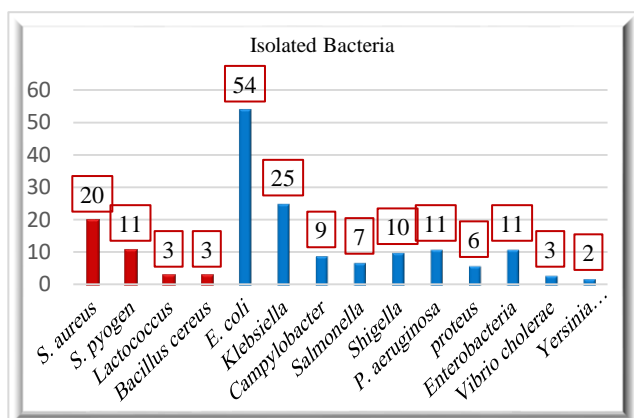
The present study showed the high isolated bacteria was *E. coli* from internal content 11.84%, followed *S. aureus* from both outer surface and internal content 6.58%, followed *E. coli* from outer surface 5.92%, followed *Klebsiella Spp* from internal content, and from outer surface and internal content 5.26%, while the lowest isolated bacteria was *S. pyogen* from outer surface 0.66%. the study also, p. value 0.05 was used to as indicated in table (3), it was possible to conclude that there was a substantial difference at the swab location.

Table (3): Distribution of isolated bacteria from flies according to swab sites

Culture Result Source of Swab	Outer		Internal		Both		Total		
	No	%	No	%	No	%	No.	%	
<i>S. aureus</i>	9	5.9	7	4.6	10	6.5	26	17.1	
<i>S. epidermidis</i>	8	5.2	0	0	0	0	8	5.2	
<i>S. faecalis</i>	2	1.3	6	3.9	4	2.6	12	7.8	
<i>S. pyogen</i>	1	0.6	4	2.6	4	2.6	9	5.9	
<i>Micrococcus</i>	0	0	4	2.6	2	1.3	6	3.9	
<i>E. coli</i>	9	5.9	18	11.8	10	6.5	37	24.3	
<i>Klebsiella</i>	4	2.6	8	5.2	8	5.2	20	13.1	
<i>Enterobacter ia</i>	2	1.3	7	4.6	6	3.9	15	9.8	
<i>P. aeruginosa</i>	2	1.3	4	2.6	4	2.6	10	6.5	
<i>Shigella</i>	2	1.3	3	1.9	4	2.6	9	5.9	
Total	39	25.6	61	40.1	52	34.2	152	100	
CalX ² = 33.121		TabX ² = 28.87		DF=18		p. value 0.016			

7. Identification of Isolated Bacteria from Pediatric Stool

The present study showed the high isolated bacteria was *E. coli* 30.85%, followed *Klebsiella Spp* 14.28%, followed *S. aureus* 11.42%, while the lowest isolated bacteria was *Y. enterocolitica* 1.14%. as show in figure (4).



Figure(4): Identification of Isolated Bacteria from Pediatric Stool

8. A comparison between Dominant Bacteria Isolated from Flies and Stool

The present study showed the high dominant bacteria were *E. coli* from diarrhea 44.63%, also in flies the high dominant was *E. coli* 36.27%. followed *S. aureus* in flies 25.49%, while in diarrhea 16.53%. in the other hand the lowest dominant bacteria were *S. pyogen* in both flies and diarrhea 8.82%, and 9.09% respectively. The study also, found a non-significant difference between flies and stool with a 0.05 p value, as displayed in table (4).

Table (4): A comparison between dominant bacteria isolated from flies and stool

Source Bacteria	Flies		Diarrhea		Total	
	No.	%	No.	%	No.	%
<i>S. aureus</i>	26	25.4	20	16.5	46	20.6
<i>S. pyogen</i>	9	8.8	11	9.0	20	8.9
<i>E. coli</i>	37	36.2	54	44.6	91	40.8
<i>Klebsiella</i>	20	19.6	25	20.6	45	20.1
<i>P. aeruginosa</i>	10	9.8	11	9.0	21	9.4
Total	102	45.7	121	54.2	223	100
CalX ² = 2.596		TabX ² = 9.49		DF=4		p. value 0.628

IV. DISCUSSION

A total of three hundred and fifty flies were collected from (butchers, chicken and fish shops, markets hospitals and house) from both Al-Shatra and Nasiriyah districts while conducting research in the province of Thi-Qar, July 2022 to January 2023, the present study showed 126 (36.0%) of flies carrying bacteria, while 224 (64.0%) of which have not bacteria. *Musca. domestica* is a perfect mechanical vector for transmitting human and animal infections due to its biology and ecology. Houseflies can multiply in garbage, livestock barns, poultry houses, slaughterhouses, and hospitals.

These results are consistent with the following studies Ahmed *et al.*[10] and Hussny *et al* [12] at Thi-Qar University, College of Science, whether in the internal or external parts. Baker *et al.* [13] In Iraq; at the University of Tikrit; the house flies are the source of the vector of contamination in bacterial infections; where the study showed the isolation of 9 types of bacteria which are harmful to people. Kababian *et al.* [14], This research was conducted in Central Iran's Qom Province .Because the location and manner of collecting the flies, as well as the same health system and collection times, are all to blame for the results' convergence.

These results are not consistent with both Park *et al.* [15]; Over 400 flies from Belgium and Rwanda, where the percentage of bacteria presence was 85%. collected and examined in study Together; Where a difference appeared in the results between the two studies due to the difference in the environment, as well as the method of selling in the markets, the method of selling fish and meat, and health monitoring. Our findings demonstrate that *M. domestica* is connected to a remarkably diversified micro biome. Another study by Reedha, [16], revealed that house flies carried a significant number of bacteria on their external surface and gut, 482 parasites were isolated from their external surfaces, and 422 from their digestive tracts. this indicates the

obvious effect of this insect on the general health of humans as a result of the important role it plays in carrying and transmitting bacterial pathogens that cause various diseases for humans especially intestinal diseases, this study shows that house flies are considered as a typical mechanic carrier for human and animal pathogens, The findings of this research suggest that the house fly the results of this study indicate that the house fly is more harmful than being an annoying insect as it represents a definite health risk through its role in the transfer of bacteria among humans and animals.

Through the comparisons above, we find that the number of bacteria transferred to the flies varies from one place to another and from one country to another, depending on the method of sale, the use of health conditions, and the use of pesticides and sterilizers.

1- Estimation of Bacterial Content of House flies according to Site of Swab Collection

The present study showed the high isolated bacteria were from internal content of flies 8.71%, followed in the outer surface of flies 5.57%. also, noted 3.71% of flies have a bacterium in both outer surface and internal content, while the study showed 40.71% of outer surface have not bacterial infection. 37.57% of internal content have not bacterial infection, in contrast 3.71% of flies have not bacterial infection in both outer surface and internal content as shown in table(1).

This agrees with Hussny et al.[12] at Thi-Qar University, College of Science in Iraq Kababian et al. [14], in Iran this study in Qom Province; Central Iran, Hemmatinezhad et al. [17] in Iran and, all studies had a greater percentage of bacterial contamination in the digestive system than in the external surface. This shows that the inner surface may be most crucial for vectoring a wide range of ambient as well as harmful microorganisms. The inner body is more restricted to bacteria that can survive in these settings and may operate as fly symbionts. The internal and external populations changed depending on the region and habitat, indicating that the discovered fungi may not actually be commensals but rather transient microbes. To clarify the potential roles of these microorganisms, their origins, and transmission patterns, more research is required.

This is not consistent results. Al-Khozaei et al., (2021) at the University of Tikrit in Iraq; at the College of Science at Thi-Qar University Baker et al., (2018), where the difference between the two studies, where the two case studies, the percentage of bacteria on the inner surface is more than the outer surface, unlike our study, The reason for the difference is due to the place where the flies are collected, where some collection places use sterilizers that affect the amount of bacteria present on the outer surface.

2- Identification of Isolated Bacteria from Flies

The present study showed the high isolated bacteria was *E. coli* 24.3%, followed *S. aureus* 17.0%, followed *Klebsiella Spp* 13.15%, while the lowest isolated bacteria was *Micrococcus* 3.94%. as show in Figure(3).

The present study showed the high isolated bacteria was *E. coli* from internal content 11.84%, followed *S. aureus* from both outer surface and internal content 6.58%, followed *E. coli* from outer surface 5.92%, followed *Klebsiella Spp* from internal content, and from outer surface and internal content 5.26%, while the lowest isolated

bacteria was *S. pyogen* from outer surface 0.66%. the study also, as show in Table(4).

This results agreed with both at the University of Tikrit, and Hussny et al; (2012) At Thi-Qar University, Kalpana et al.,(2004), Boonchu et al.,(2004), Almeida et al; (2014), Baker et al ;(2018) In Iraq; there are studies that are close to the results we obtained Hemmatinezhad et al ; (2015),and Al-Khozaei ; (2021), at Thi-Qar University, College of Science, the highest bacteria were *E. coli*; while the lowest isolated bacteria in mouth content and the most isolated bacteria were *S. aureus*. Holt et al.,(2007) showed that *Salmonella typhi* bacteria ranked of pollution, and *Salmonella typhi* one of the world most dangerous food-borne bacteria that threaten human.

The reasons for the similarity of the results showed that open environments such as animal populations and massacres are more susceptible to contamination than protected environments because flies are frequented in contrast to protected environments such as hospitals and homes, which showed less pollution. Most of this bacteria is found naturally in these areas, and the frequent pollution, is due to this bacteria, poor health management, and the abundance of waste in areas near hospitals, homes, and butcher shops. Humans and animals are at danger of infection as a result of the house fly's continual movement from animal waste (or other excrement) to food and drinking water. It is conceivable that house flies simply serve as mechanical vectors when transmitting infections given the frequency with which pathogens have been isolated from the body surfaces of the flies (Fisher et al., 2017).

This result does not match the findings of the studies (Zhang et al., 2010; Ramirez-Blanco et al., 2017), where the study ratios were 36.9% have no bacterial infection where. Also the current study investigated microorganisms that are most isolated *E. coli* 26.59 is listed first, then *S. aureus*. 25.43%; *E. fecalis* 17.34 %; *P. aeruoginosa* 8.09 %; *S. epidermidis* %6.94; *K. pneumonia* %6.36; *S. pyogen* 4.05%; *S. pneumonia* 3.47%; *Proteus spp* 1.73%. is not consistent (Abduljabbar et al; 2020).

The difference in results is due to The difference in percentages of pollution and isolation of house flies depended on months of year was due to the difference in temperature and humidity during the months of the year that effect on the rate of growth and presence of bacteria and the rate of spread of flies, the temperatures reached for where no bacteria were seen under study due to the decrease in temperature, which affects bacteria growth , Also the reason for the difference between Nasiriyah and Shatrah is due to the place of collecting samples and some areas that are protected, such as butcher shops and hospitals, more than the shops of Shatrah district, as well as the lack of waste, the existence of designated places and the speed of their destruction.

3- Estimation of bacteria in children with diarrhea, and comparison with flies

The present study showed the high isolated bacteria was *E. coli* 30.85%, followed *Klebsiella Spp* 14.28%, followed *S. aureus* 11.42%, while the lowest isolated bacteria was *Y. enterocolitica* 1.14%. as show in figure (4-4). The present study showed the high dominant bacteria were *E. coli* from diarrhea 44.63%, also in flies the high dominant was *E. coli*

36.27%. followed *S. aureus* in flies 25.49%, while in diarrhea 16.53%. in the other hand the lowest dominant bacteria were *S. pyogen* in both flies and diarrhea 8.82%, and 9.09% respectively. The study also, found a non-significant difference between flies and stool with a p value of 0.05, as shown in table (4-4).

This results agreed with, in a Study conducted in Al-Nasiryah city by(Lhwak &Abbas .,2018) also convergent with our findings ; Al-Hilali .,(2015)isolated the following species *K. pneumoniae* , *S. aureus* , *P. aeruginosa*, *P. mirabilis*, *Enterococcus spp.* , *S. saprophyticus* , and *Citrobacter spp.* (N.T. Pham et al;2010) , (J. Liu et al;2012), This result agreement with quondam studies in by (Blazar et al;2011) reported The isolated bacteria species Pediatric Patients with Diarrhea *Escherichia. Coli* (36.58%) The least frequent bacteria were *Pseudomonas* species (2.44%) and *Salmonella species* (2.44%), followed by *Staphylococcus species* (26.83%), *Shigella species* (14.64%), and *Streptococcus species* (17.07%). This investigation was conducted in Qom Province in Central Iran. The external surfaces of house flies have been linked to *E. coli*, *Pseudomonas aeruginosa*, *Klebsiella pneumonia*, *Proteus mirabilis*, and *Staphylococci aureus* infections.

In a recent study, Abduljabbar *et al.* (2020) examined the prevalence of aerobic pathogenic bacteria isolated from burn patients in Al-Najaf region. Their study found that a high incidence of multidrug resistant bacteria existed in their study, with 57.5% of patients infected having both gram positive and gram-negative bacterial infections. The infection rate in their study was also virtually equal to the infection rate of the current study. was *P. aeruginosa* 27.6%, followed by *S. aureus* 20.7%, and among this finding percentage 76.2% were mixed bacterial infections and the other bacterial types consist 9.2%. The number and type of isolated bacteria in their study were incompatible with the isolated bacteria ,These findings Baker *et al.*,(2018) from the University of Tikrit in Iraq are in line with the research. Al-khozaei and Ali, [18] At Thi-Qar University, College of Science, the current results illustrated the most infected with *Staph. aureus* bacteria 33.8%; followed by *E. coli* 32.3%. while the lowest burn patients infected with *S. epidermidis* 3.1% followed by *Proteus spp.*

This indicates the obvious effect of this insect on the general health of humans as a result of the important role it plays in carrying and transmitting bacterial pathogens that cause various diseases for humans especially diseases, this study shows that house flies are considered as a typical mechanic carrier for human and animal pathogens, The findings of this study show that house flies are more dangerous than just bothersome insects. as it represents a definite health risk through its role in the transfer of bacteria among humans and animals.

This result disagreement with study by Pava-Ripoll *et al* .[19]. The study's findings were somewhat similar to those reported by Sime *et al.*[20], who stated that among Of the 292 bacteria, it was the lowest percentage, *E. coli*, *K. pneumoniae* and *Citrobacter* divers us; other study conducted by Arshad and Yousaf, [21] also disagreement with our findings depended on location was due to many reasons including the differences of sewage systems in houses, hospitals and vegetable market sites, in addition to the increase of waste in each of the above sites, which all

lead to the spread of houseflies carrying these bacteria as well as the spread of bacteria itself. The reason may be due to the appropriate temperatures for the growth and presence of bacteria, in addition to the abundance of flies during certain months of a year. Temperature may influence the spread of bacteria through a variety of mechanisms, including direct effects on bacterial growth and indirect effects. Insects carrying germs are common, and they become more active in the warmer months.

V. CONCLUSIONS

The current study confirmed the following: The number of contaminated bacteria on the inner surface is more than the outer surface,, the percentage of flies contaminated with bacteria in Nasiryah is more than in Shatrah, and the most polluted areas were butcher shops, The current study recorded that bacterial isolates contaminated with houseflies and diarrhea samples recorded the highest percentage of *Escherichia coli* and *Staphylococcus aureus*. The current study demonstrated that there is a positive relationship between fly contamination and diarrhea samples.

Acknowledge

I thank Thi -Qar Health Department and Hossa Al Shatrah General Hospital, and I do not forget the College of Science, Thi -Qar University, for completing this research paper.

CONFLICT OF INTEREST

Authors declare that they have no conflict of interest.

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