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ACKNOWLEDGEMENT

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Volume 1, Issue 2 (July-Dec 2021)

The Impact of Biotechnology on Agriculture and Food Production: A Promising Future

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Biotechnology has been playing a crucial role in the advancement of agriculture and food production for many years. The integration of cutting-edge technologies such as genetic engineering, molecular biology, and robotics has allowed for the development of new and improved methods for growing crops, producing livestock, and processing food. These innovations have the potential to revolutionize the way we produce food, making it more sustainable, efficient, and accessible for all. One of the key benefits of biotechnology in agriculture is the ability to develop crops that are more resilient to pests, disease, and environmental stressors. For example, genetically modified crops have been developed that are resistant to herbicides, which reduces the need for harmful chemicals in agriculture. This not only benefits the environment, but it also reduces the cost of production and increases the yield of crops. Additionally, genetically modified crops that are resistant to drought and extreme weather conditions can be grown in areas where traditional crops would not thrive, increasing food security in these regions [1]. Another significant impact of biotechnology on agriculture is the ability to produce crops with enhanced nutritional content. For example, crops such as rice and cassava have been modified to include increased levels of essential vitamins and minerals, providing a solution to micronutrient deficiencies in many parts of the world [2]. This technology has the potential to improve the health and well-being of millions of people, especially in developing countries where access to nutritious food is limited. The advancements in biotechnology have also had a positive impact on food production by improving processing methods and increasing the shelf life of food products. Biotechnology has allowed for the development of new food preservation techniques that keep food fresh for longer periods of time, reducing food waste and making food more accessible for consumers. Additionally, biotechnology has been used to improve the quality of food products by reducing spoilage, enhancing flavor, and improving texture. Despite the numerous benefits of biotechnology in agriculture and food production, there are also concerns that need to be addressed. For example, there is a growing concern about the potential health risks associated with consuming genetically modified crops. Additionally, there are concerns about the impact of biotechnology on traditional agriculture practices and the livelihoods of small farmers in developing countries. In conclusion, the impact of biotechnology on agriculture and food production is both promising and complex. While it has the potential to revolutionize the way we produce food, making it more sustainable, efficient, and accessible, it is important to consider the potential drawbacks and ethical implications of these technologies. As we move forward, it will be crucial for policymakers, researchers, and the public to engage in informed and meaningful discussions about the future of biotechnology in agriculture and food production, and to ensure that these technologies are used for the benefit of all.

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[2] Food and Agriculture Organization of the United Nations. The Role of Biotechnology in Improving Agricultural Productivity. 2017. Available at: http://www.fao.org/biotech/biotech-forum/en/.

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FUTURISTIC BIOTECHNOLOGY

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Mini Review

Dengue: An Overview of Pathogenesis and Analysis of Disease

Nida Naeem[1], Muhammad Obaid Tahir[1], Taha Mobeen[1], Lahrasb Khan[1] and Amna Mahmood[1*]

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ABSTRACT

Dengue as a viral infection was or is a serious issue. With the time this viral infection changes within it's environment. Researches are conducted to completely know the genome of dengue as well as it's long lasting treatment. Both flaviviruses and mammalian cells produce NS1 and induce strong humoral responses in circulation. NS1 levels correlate with viral titer and can be used as a viremia marker. The disappearance of NS1 at high concentrations between low nanograms per milliliter and micrograms per milliliter was determined using numerical ELISA detection. NS1 levels as high as 600 nanograms per milliliter during secondary infection have been found to indicate high levels of severe disease within his first 72 hours of illness.

INTRODUCTION

Dengue as a viral infection was or is a serious issue. With the time this viral infection changes within it's environment. Researches are conducted to completely know the genome of dengue as well as it's long lasting treatment. However biological science already solved many queries about dengue but still there is lot of work needed to be done on this viral infection.Viral dengue is the known viral contamination that affects human beings largely [1]. Historical perspectives relates the dengue fever with "poisen of water"to flying bugs in the clinical encyclopedia of China. The word dengue originates from the Swahili language word Ka-dinga pepi, means "hinder similar occupation" [2]. Equatorial and subtropical areas are the most exposed areas to dengue. Dengue virus DENV has four genetically and serologically different serotypes. 27 DENV has three structures and seven mon structural proteins. DENV are more fatal virus due to its secondary infection with hetrological virus [3]. Lack of awareness and social knowledge about dengue creates a disagreement among people [4]. Dispute begins with various questions, four dengue serotypes are further divides on the basis of nucleotides contrast among genotypes. Dengue pathogenesis and immune responses play a significant role in catching disease(5). After secondary infection severe disease is normal. Events take place in body including the fall of neutralizing antibodies and the complex between sub neutral antibodies and viruses results in more viral load leads to severe dengue [5]. Queries arised for the vaccine of dengue in the Philippines as the Children got new diseases after taking vaccines [6]. DENV is the lipid-covered particle and has structural proteins attached to it. Inside the envelope there is a complex of ribonucleoprotein attached to a single stranded RNA. The M protein is the precursor protein , With the C terminal the E proteins are attached to viral envelope. Viral genome entry route is through E- protein mediated membrane fusion [7]. Viral

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RNA involved in 3 steps of virus infected cell. Viral proteins formed by mRNA. With a 5'- cap and formation and a 3'-poly(A) tail viral RNAs are linked to poly A binding proteins and cap binding complex [8]. TRIZOL viral RNA that was removed from transfected cells of media of 200 µl. It was designed to louden not 1 to 1451 at the 5' end and not 10201 to 10723 at the 3' end in reverse transcriptase PCR (RT-PCR By using big dye terminator chemistry and ABI 377 automated DNA sequence RT-PCR products were sequenced [9].Freshly isolated platelets were fixed with 4% glutaric-aldehyde at °0 C in PBS. Overnight and washed once with PBS followed by three washes with pH 7.3 phosphate buffer (3444 minutes each). Platelets were then incubated with 2% phosphate-buffered osmium tetroxide for 45 minutes, washed with g of distilled water, and stained with 2% uranyl acetate in water at 25 degrees Celsius for 30 minutes. The samples were prepared at room temperature by successive incubations of dehydrated in 70% And 80% ethanol for 1.5 min, and 90% and 95% absolute ethanol and propylene oxide for 3 min (2-3 times for every step). The samples were then soaked with propylene oxide and epoxy resin mixture (50: 50) at 37°C for 30 minutes, followed by soaking with the epoxy resin Mixture alone at 37°C for 120 minutes. Samples embedded polypropylene capsules, polymerized overnight at 70°C. Identification of the dengue virus can be done mostly by the using method of real-time PCR. DENV can also be detected by several other methods such as viral antigen and genome detection, antibody detection, and ELISA. However, these techniques are not effective for DENV confirmation, so real-time reverse transcriptase RT-PCR is mostly usedThe circular motion of viral genome is observed during RNA-RNA interaction through atomic force microscope. The serootype confirmation of dengue virus RNA in 20 to 25 early serum samples while the past 30 samples with excessive anti-dengue lgt assembled but no viral RNA can be detected between 5 to 31 days. A sample was taken after 5 to 31 days when the RNA can be detected by observing through micro seize ELISA. DNEV identification is mostly done by real time pcr (RT-PCR) dengue virus serotypes can also be detected through it. Testing of DENV can be made through urine, serum, plasmDEN detection through urine involves the sample taking it's filtration and then the sample are cultured in a plate innoculated with Vero cells. After incubation, washing with phosphate buffered saline and with FCS samples are ready to check to the presence of DENV [10-12]. Virus lgM anti dengue antibodies are detected by Elaisa kit and detection of lgG antibodies by indirect Elaisa kit. The serological tests of DENV includes neutralization test, hemagglutination inhibition, indirect immunoflourescence antibodies test. These are easily detectable within 3 to 5 days. About 95% of patients develope lgM between 6 to 10 days. ELAISAs E protein are broadly used antigen for all the type of serotypes of DENV [13, 14]. The serological test consists of a fast immunochromatography test, an enzyme-linked immunosorbent assay, a neutralisation test, a hemagglutination inhibition test, an indirect immunofluorescence antibody test, and a complement fixation test [15, 16]. Both flaviviruses and mammalian cells produce NS1 and induce strong humoral responses in circulation. NS1 levels correlate with viral titer and can be used as a viremia marker. The disappearance of NS1 at high concentrations between low nanograms per milliliter and micrograms per milliliter was determined using numerical ELISA detection. NS1 levels as high as 600 nanograms per milliliter during secondary infection have been found to indicate high levels of severe disease within his first 72 hours of illness. With its high level of sensitivity and specificity, her NS1 as a diagnostic segment has revolutionized therapeutic approaches [17, 18]. In the secondary infections the presence of dengue viral antigens in serum is relatively low. The virus infects salivary gland in the hemocoel In lymphoid organs, such as the liver and lung, cells of the monocyte-macrophage lineage have been shown to contain dengue virus infection antigen. When dengue RNA from infected patients was used in reverse transcription, it confirmed liver involvement in the clinical presentation of DHF. The non-structural protein NS1 is necessary for the survival of DV. In the blood of DV-illness patients, the NS1 antigen has acted in the presence of an elevated level of enzyme-linked immunosorbent tests [19, 20].

CONCLUSION

NS1 levels as high as 600 nanograms per milliliter during secondary infection have been found to indicate high levels of severe disease within his first 72 hours of illness.

Conflicts of Interest

The authors declare no conflict of interest

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Original Article

Sensitivity and Resistance Pattern of 18 Commercially Available Antibiotics against Pseudomonas Species Isolated from Cloacal Swab of Domestic Pigeons

Ahmad Azeem[1*], Hafiz Shahzad Muzammil[2], Hina Asif[3] and Sadia Sarwar[4]

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ABSTRACT

Antibiotic resistance is a growing concern globally, leading to increased morbidity and mortality due to bacterial infections. **Objective:** To determine the sensitivity of *pseudomonas* species against various antibiotics. **Methods:** A total of 120 cloacal swab samples were collected from domesticated pigeons in the Narowal district of Pakistan and examined in a laboratory. After that gram staining was performed. Motility test, oxidase, Indole, catalase, coagulation and antibiotic susceptibility test was performed. **Results:** The results showed that Amikacin, Trimethoprime, and Clarithromycin were the most effective antibiotics against pseudomonas *species*, with 93.94% sensitivity to each. On the other hand, 54.55% of the *pseudomonas* strains showed sensitivity to Gentamicin, while 18.18% showed resistance. **Conclusion:** The domestic pigeons are *pseudomonas species* carriers and spread the disease to people and other animals via their faeces. The findings highlight the need for ongoing monitoring and research to understand the development and spread of antibiotic resistance and to ensure the effective treatment of bacterial infections.

INTRODUCTION

Antibiotics are an essential group of therapeutic drugs used to kill bacteria on various levels (tissues, organs, organ systems) in the human body against different bacterial infections. These antibiotics had played a significant role for the treatment as well as the prevention of bacterial diseases. The effectiveness of antibiotics against bacterial infections cannot be denied [1]. Karimzadeh *et al.*, finds that overall 50 to 60 percent of all nosocomial infections in the United States were caused by antibiotic-resistant bacteria [2]. Antibacterial resistance in the United States had resulted in approximately 23,000 deaths per year. The direct and indirect overall public costs of antibacterial resistance in the US had been estimated to be 20 million dollar and 35 billion dollar, respectively. In the countries of European Union, likely 25,000 deaths were expected due to antibiotic resistant bacteria, costing 1.5 billion dollar annually in both direct and indirect costs. The availability of new antibiotics had significantly increased our ability to treat complex infections Bacterial infections are among the most important causes of morbidity and mortality worldwide [3, 4]. Spread of resistant microorganisms is playing a significant role in this regard. Previous studies showed that Pakistan is a developing country with poor healthcare facilities and economic resources [5, 6]. Lack of access to basic healthcare facilities, unhygienic lifestyle and misuse of substandard

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antibiotics by the patients added up to deteriorate the antibiotic resistance situation. Misuse of antibiotics are directly linked to the resistance in bacteria and multi drug resistant (MDR) bacteria are becoming more significant. Scientists refer that antibacterial resistance or antibiotic resistance is a very serious issue for the health of both humans and animals [7, 8]. The cost of United States human health care system was estimated to be 100 million dollars to 30 billion dollars annually due to antibacterial resistance. The Study conducted in Germany to prevail the antibiotic resistance had shown that there was a 75% increase in resistance of *E. coli* to tetracycline, 80% increase to Ampicillin and 90% increase to sulfonamides [9-11]. Furthermore, for *S. Aureus,* resistance increased by 50% to 60% to penicillin and by 400% to Gentamicin. Hsueh *et al.,* showed that the antibiotic resistance results in bacteria due to change by some approach that eliminates or reduces the effectiveness of antibacterial agents apply for treatment of infections [12, 13]. The bacteria cause more damage to human body by survival and continuous multiplication. In this analytical experimental study, a total of 120 Cloacal swab samples of domesticated Pigeons were collected from different areas of District Narowal. The experimental work was carried out at the Department of Microbiology, Sughra Shafi Medical Complex Narowal, Pakistan over a period of one year.

METHODS

Within an hour of collection, cloacal swab samples were sent to a lab for examination in a sterile container labelled with the source, date, and time of collection. Samples were grown on specific medium such as Blood Agar, MacConkey Agar, and Chocolate Agar after sample collection. The agar plates were then incubated at 37°C for 24 hours. Following incubation, isolated colonies were seen, and the cfu/ml value was determined. To obtain a pure culture for storage, the colonies were then streaked on agar plates. Colonial morphology of the isolates was identified by their growth on MacConkey agar and Blood agar base. On MacConkey agar, *Pseudomonas* species form flat and smooth colonies while on Blood agar they produce smooth and mucoid colonies. After that gram staining was performed. Motility test, oxidase, Indole, catalase, coagulation and antibiotic susceptibility test was performed. Data were analyzed using SPSS.

RESULTS

Figure 1 is showing the sensitivity of *pseudomonas species* against different tested antibiotics. Amikacin (AK), Trimethoprime (TMP) and Clarithromycin (CLR) are most effective against concerned bacteria. *Pseudomonas* showed 6.06% resistance and 93.94% were showing sensitivity against TMP antibiotic. Clarithromycin (CLR)) showed 93.94% sensitivity *against Pseudomonas*. 18.18% *Pseudomonas* were showing resistance and 54.55% were showing sensitivity against Gentamicin(CN).

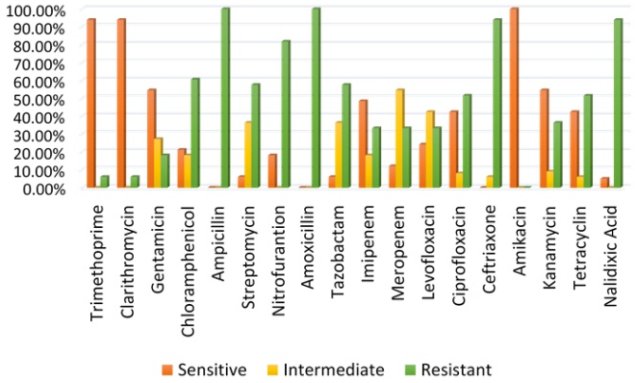

Figure 1: Antibiotic resistance and sensitivity of *P. aeruginosa*

DISCUSSION

In a related study using domestic bird samples, Varriale *et al.,* found that *P. aeruginosa* was present in 59/75 samples, whereas *E. coli* was present in 231/755 samples [14]. A few species of Gram-negative bacteria, including *Citrobacter* spp., *Pantoea* spp., *Serratia* spp., and *Morganella* spp., were furthermore sometimes identified. *P. aeruginosa* bacteria were resistant to sulfamethoxazole-trimethoprim and amoxycicillin/clavulanic acid in 45/59 (76.3%) cases. Doxycycline resistance was seen in 42/59 (71.2%) cases, enrofloxacin resistance in 46/59 (78%) cases, gentamicin resistance in 17/59 (28.9%) cases, and oxytetracicline resistance in 48/59 (81.3%) cases. Many of the strains exhibited multidrug resistance. A total of 118/231 (51.1% of the *E. coli* isolates) were resistant to amoxycicillin/clavulanic acid, 127/231 (55%) were resistant to sulfamethoxazole-trimethoprim, 132/231 (57.1%) were resistant to doxycycline, 92/231 (40%) were resistant to enrofloxacin, 61/231 (26.4%) were resistant to gentamicin The majority of strains *P. aeruginosa* also exhibited multidrug resistance [15, 16]. Perwaiz *et al.,* elaborate in their study that all clinical isolates (Gram positive) showed complete sensitivity to Vancomycin (VA), Klaricid (KL), Fusidic acid (FU), Vibramycin (VI), Erythromycin (ER), Linezolid (LI), Oxicillin (OX) and Nalidixic Acid (NA) while Amoxicillin (AM), Cefotaxime (CE), Ciprofloxacin (CI), Ampicillin (AMP). All clinical isolates (Gram negative) showed complete sensitivity to Tazocin (TA), Meteronidazole (ME), Ciprofloxacin (CI), Ofloxacin (OF), Gentamycin (GA), Levofloxacin (LE), Gatifloxacin (GA) while complete resistance to Cefotaxime (CE), Nalidixic Acid (NA), Oxicillin (OX), Norfloxacin (NO) [17].Vancomycin, Klaricid and Fusidic acid showed excellent antibacterial activity against gram positive bacteria and no resistant isolate was detected against these antibiotics in this study.

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Taj *et al.,* also had been reported resistance in other areas of Pakistan for Vancomycin, Klaricid and for Linezolid [18, 19]. They also showed in their study that Gram negative bacteria had also been found sensitive to Fusidic acid, Vibramycin and erythromycin. Long and Hammer showed in their research that all gram-negative isolates was resistant to Amoxicillin, Cefotaxime, Ciprofloxacin and Ampicillin and showed no therapeutic activity against bacterial infections [19]. Similar results had been obtained in other areas of Pakistan. Bhatiani and Chandna showed in their study that gram positive isolates (MRSA) were totally resistant to Amoxicillin and Cefotaxime in this study [20]. MRSA had showed complete resistance to Oxicillin and Penicillin. Similar reports had also obtained for the antibacterial activity of Cefotaxime.

CONCLUSIONS

The domestic pigeons are pseudomonas species carriers and spread the disease to people and other animals via their faeces. Transmission must be prevented using preventative measures. Before recommending antibiotics to patients, an antibiotic susceptibility test (AST) should be conducted.

Conflicts of Interest

The authors declare no conflict of interest.

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Original Article

Conversion of Potato Peels into Single Cell Protein

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ABSTRACT

The economic expansion in developing countries can be achieved by converting their low cost industrial and agricultural wastes into more valuable resultants with the help of emerging scientific approaches. **Objective:** to produce single cell protein from microorganism (fungus) through the process of submerged fermentation utilizing the agro-industrial waste (potato peel) as substrate. **Methods:** Four broths (control, glucose broth, potato peel broth and mix broth) were prepared. The maximum dry cell biomass (0.523 g/100 ml) was obtained with mix broth which was unitized for further research. All the broths were supplemented with potassium dihydrogen phosphate, magnesium sulphate, sodium chloride, and yeast extract. **Result:** The growth of fungal biomass in stirred tank and bubble column fermenter was compared and optimum yield was obtained with bubble column fermenter (5.45 g/100ml). This bioconversion will not only supply protein rich food but also help in control of environmental pollution. **Conclusion:** It is concluded that potato peels can be an attractive substrate for the production of single cell protein as they are good source of sugar and other nutrients required for the support of microorganisms.

INTRODUCTION

In developing countries, the economic expansion can be achieved by using their low cost industrial and agricultural wastes into more profitable resultants with the aid of emerging scientific approaches. In the same way, potato peel waste can be converted into various value-added compounds such as enzymes, biogas, bio-sorbents, biohydrogen and various other products as this waste is increasing due to increased usage of manufactured edible potato products [1]. Biodegradable wastes can be an important source for making of highly nutritious and high-quality products without any harm. Different types of waste materials add pollution to the environment; however, they can be transformed into low quality products. Many approaches have been appearing to convert these waste materials into high quality products [2, 3]. Increasing aquaculture farming practices has been putting pressure on the greater demand of protein in animals feed which is reduced by converting low-cost agricultural waste into single cell protein (SCP) by using the bacteria or yeast [4, 5]. A large amount of waste and by-products from food industries are not only a source of environmental pollution but also dangerous for all living organisms. Alongside, a huge number of people around the world have been suffering from malnourishment [6, 7]. To fulfill the global protein deficiency, different kinds of wastes can be bio-converted into single cell protein which can be used as a solution to environmental pollution as well as feed for animals [8]. Potato peels are weighty material in potato-processing industries that are not much used and considered as waste, while they can be a good source of lignin, protein, lipids, cellulose, ash, starch and non-starch carbohydrates (pectin, cellulose and hemicellulose), although the fermentable sugars are low in quantity [9-11]. Potato is the 4th basic crop being cultivated thought out the globe after, wheat, rice and maize. The fast-growing chips and fries' industries are involved in making of huge

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piles of potato peels waste which is highly considered a pollution issue since it can spread, the leaf roll and late blight like diseases in adjacent plants in close vicinity, due to high moisture content. This waste has anti-inflammatory, antioxidant, apoptotic, antibacterial and chemo preventive like extraordinary properties [9-12]. The breed, variety and composition of potato varies to some extent depending on the geographical region but usually its composition shows that the raw potato peel consists of 83.3–85.1% of water, 1.2–2.3% of protein, 8.7–12.4% of carbohydrates, 0.1–0.4% of lipids, 7.8% of starch, 1.02–2.92% of phenolic compounds, 2.5% of dietary fiber, 0.51–0.96% of flavonoids and 0.9–1.6% of ash [1, 11]. The peeling methods also affect the potato peels composition, since the abrasion peeling results in more starch and less lignin content while the opposite case exists in steam peeling [1]. With increasing demand of protein, the pressure on conventional protein sources has been increased which urges the researchers to find alternate protein sources to meet the demand. The aim of this experimental work is to obtain single cell protein from microorganism using cheap and easily available low-cost substrate that are of no use but cause environmental pollution.

METHODS

Potato peels were collected to use as substrate from local market Lahore. Initially, potato peels were washed with tap water to remove dust particles, dried at room temperature and stored in zipper bag at 4 °C. The fungus, *Rhizopus oligosporous* was obtained from PCSIR testing laboratories complex, Lahore and used to produce single cell protein. The *R. oligosporus* was grown and maintained on potato dextrose agar (PDA) plates and then slants were stored at 4 °C. Potato peels were chopped/ cut into small pieces then, 20 g potato peels were taken in 250 ml Erlenmyer flask and 100 ml distilled water was added. The pH of this mixture was adjusted 3.5 with conc. HCl and then autoclaved at 121 °C for 15 minutes. After cooling, it was filtered with muslin cloth to separate potato chunks. The filtrate was designated as potato peel extract (PPE). For fermentationn, innoculum was prepared from subculture of *R. oligosporous* grown on PDA slants. The slants were flodded with 20 ml sterilzed distilled water to dislodge spores from the fungal hyphae. The inoculum size was adjusted to 10^{6-7} spore/ml with the help of hemocytometer for inoculation in all experiments. The fresh inoculum was prepared every time for the investigation of each parameter. Four broths were prepared named as control, potato peels extract broth, glucose broth and mix broth. The control broth comprising of yeast extract, peptone, glucose, sodium chloride and magnesium sulphate prepared. The pH of this solution was kept at 6.5 with HCl/NaOH. This control was then shifted to fermentor and autoclved alongwith fermentor at 121 ℃ for 15 min. The control was inoculated with 2% (v/v) *Rhizopus oligosporus*. After 3 days fermented material was harvested and measured the wet weight of biomass. It was dried by keeping in oven for 24 hrs at less than 80 ℃ until constant mass was achieved. Then dried biomass was recorded. Potato peels extract broth contains 100 ml of previously described pretreated potato peel extract. Glucose broth (100ml) was prepared by adding 3 g glucose in 100ml distilled water. Mix broth comprising of 100 ml potato peels extract broth and 1.2 g glucose. The potato peels extract, glucose and mix broth were supplemented with chemicals mentioned in The pH of all broths were adjusted with dil. HCl/ NaOH at 5.5. These broths were autoclaved at 121 °C for 15 min. After cooling, the broth were inoculated with 2% (v/v) freshly prepared inoculum of *R. oligosporous*. These culture were placed in incubator at 35 °C for 3 days. After three days, biomass was filtered by using Whatmann filter paper and weighed the wet biomass by using digital balance. The biomass was kept in oven at 80 °C for 24 hours until constistant weight. All the experiments were carried out in triplicates. Fermenters are the vessels that provide optimum conditions for the growth of microorganisms and are used to produce a variety of products. Stirred tank fermenters are better known for their property of agitation with the help of impellers while the airlift fermenter lacks the impeller system for agitation and use air for the purpose of mixing [13]. The temperature in both the fermenter types was maintained at 35 ℃ with aeration speed of 1.0 vvm. The mix media was fermented with *Rhizopus oligosporus* for upto 3-4 days in each fermenter. After that cell biomass was separated from filtrate by filtering the fermented media. This wet cell biomass was then kept in oven at 70-75 °C temperature until the constant weight was achieved. All the experiments were carried out in triplicates. For determinition of reducing sugars Benedict's quantitaive test was used [14]. The crude protein of single cell protein was determined by the Kjeldhal procedure [15]. The total protein in the growth media was estimated by following the Lowrey method [16].

RESULTS

The purpose of utilizing waste potato peels was to reduce the burden on conventional protein sources. Based on this fact, a series of experiments were conducted to produce single cell protein from *Rhizopus oligosporos* from waste potato peels through submerged fermentation. This waste is selected beacuse it is easily available in enormous qauntity and cheap source to utilize for developmental purposes. Three broths (glucose broth, potato peels broth

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and mix broth containing both potato peels as well as glucose) were formulated with slight difference in their composition and same suplements were added in all of them. The results described in table 1, that maximum product of SCP (0.523 g/100 ml) was achieved with mix media which is followed by potato peels media. The crude protein content of dried biomass was in range of 45-55%. The results of control medium was 0.045 g/100 ml dry cell biomass. The purpose of control was to compare the results of mix broth with it. The comparison showed that potato peels were better substrate to provide necessary elements for the fungus. The statistical analysis showed that dry biomass yield produced with all of the three media was significantly different ($p < 0.001$).

Media	Dry biomass (%) Mean ± SD	Consumed sugar (%) Mean ± SD	Biomass yield (g/g) Mean ± SD
Glucose media	$0.29^{c} \pm 0.006$	$1.37^{c} \pm 0.008$	$0.21^{c} \pm 0.002$
Potato peel media	$0.42^{b} \pm 0.003$	$1.42^{b} \pm 0.003$	$0.30^{b} \pm 0.005$
Mix media	$0.52^{a} \pm 0.002$	$1.65^{a} \pm 0.004$	$0.32^{a} \pm 0.004$
Significance level (95%)	$P < 0.001$		

Table 1: Screening of best yield giving media based on total biomass quantity

Means that do not share a letter are significantly different in a column. Initial sugar: Glucose=3%, Potato peel media=1.8%, Mix media=3% Mix medium and potato peels medium yielded more biomass as compared to the glucose medium and mix medium was selected as best yield-producing medum. The clustered bar graph respresenting the total dry biomass, biomass yield and consumed sugar of each medium was shown in figure 1.

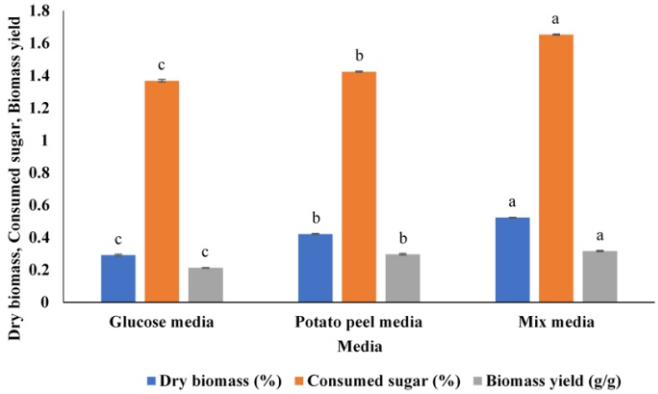

Figure 1: Screening of medium with different carbon sources for biomass production.

The effect of fermenter type on the growth of SCP was studied by fermenting one litre of mix media in both STR and Bubble column fermenter shown in Figure 2.3. and 2.4, respectively. The biomass from both fermenters were harvested after three days. The maximum yield of dry cell biomass (5.452 g/L) was obtained from Airlift fermenter. The results were mentioned in table 2.

Biomass	Stirred-Tank Bioreactor	Bubble Column Fermenter
Dry mass (g/L) ± SD	$4.52^{b} \pm 0.020$	$5.45^{a} \pm 0.010$
Significance level (95%)	$P < 0.001$	

Table 2: Effect of fermenter type on the yield of biomass

Means that do not share a letter are significantly different

The total quantity of dry cell biomass was significantly different with STR and bubble column fermenter ($p < 0.001$). The change in total dry biomass with respect to the fermenter type depicted in Figure 2.

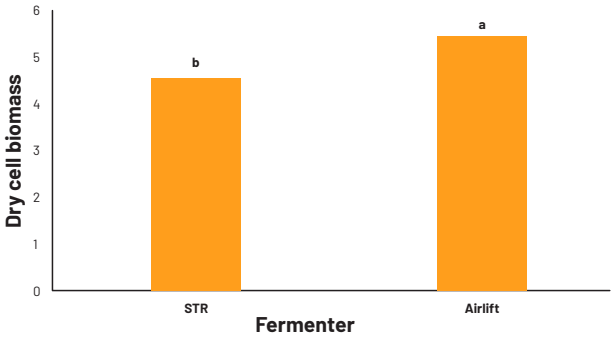

Figure 2: Dry cell biomass production in different bioreactors

Total nitrogen and crude protein in *Rhizopus oligosporous* fungal biomass was determined with micro-Kjeldhal method and it was found that it was found that the dry mass contained 50% crude protein.

DISCUSSION

Fermentation is the process by which single cell protein can be yielded and there are three types of fermentation: solid state, semi-solid and submerged fermentation. The main difference in all types is of moisture content of substrate being fermented. Each type has its own pros and cons [2, 3]. The process of fermentation is often followed by the harvesting, filtration, centrifugation, washing, cell disruption, protein extraction and purification steps [2]. Substrates provide nutrition for microorganism which participate in the fermentation process because these are rich in organic compounds essential for the fermentation. In submerged fermentation all the nutrients are completely dissolved in liquid medium and factors like pH and temperature can be controlled easily [17]. In our study, potato peels were used as substrate in submerged type of fermentation and the process of single cell protein (SCP) production was carried out at 35 ℃ temperature as well as at 5.5 pH. One study reported that different fungi produced different quantity of crude protein (*A. niger*-6.26%, *R. stolonifera*-7.25%, *R. pusillus*-6.63%, *A. fumigatus*-6.28%) on jackfruit peels [18]. According to many studies, the 1.0 vvm rate of oxygen flow accounts for better output. According to this review the most frequently used temperature and pH are in the range of 25-38 ℃ as well as 3.5-5.0 respectively [19]. This study is also conducted with

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1vvm aeration rate in both STR and airlift fermenter at 35 ℃ and pH 5.5. The results of our study indicates that maximum yield of dry biomass (0.523 g/100 ml) was obtained when the potato peel media was supplemented with glucose. Similar results were reported by Mondal *et al*. (2012) where glucose was added in fruit hydrolysate to enhance the biomass production from *S. cerevisiae* because glucose acts as a carbon source [20]. The total crude protein obtained from orange peels (30 %) was lower than that of obtained with cucumber peels which was 53.4 %. In our study almost 50 % crude protein was obtained with *Rhizopus oligosporus*. The findings of our study were in line with that of Khan *et al*. (2009) who obtained the crude protein of 59.5 mg from papaya waste, 57.3 mg from cucumber peels, 51.6 mg from pomegranate waste, 48 mg from pineapple skin and 43.2 mg from skin of watermelon through the process of fermentation by using *Rhizopus oligosporus* [21]. In one research conducted by Yousufi (2012a), Okara and wheat grit were used as substrates to produce SCP by using *Rhizopus oligosporus* and *Aspergillus oryzae* [22]. The substrates were managed in ratio 3: 1, 1: 1 and 1: 3 and fermented at different pH (3,4,5,6,7) at 30 C. The results showed that maximum SCP was achieved at pH 5. Oshoma *et al*. (2017), made three media: glucose banana peel medium, supplemented banana peel medium and un-supplemented banana peel medium [23]. Media were autoclaved and inoculated with *Aspergillus niger*. After that the media were fermented for 8 days at 28 ℃. The highest biomass obtained was 3.05 g/L in supplemented banana peel media. The protein content of supplemented banana peel medium was 0.68 g/L, that of glucose banana peel medium was 0.67 g/L and of un-supplemented medium was 0.57 g/L. The results of this study are contrary to our research work as we obtained a good yield of biomass and total crude protein. The reason may be a difference of substrate or microorganism (fungus) as the factors that influence the production of dry cell biomass are mainly the type of substrate and the type of microorganisms [18].

CONCLUSIONS

It is concluded that potato peels can be an attractive substrate for the production of single cell protein as they are good source of sugar and other nutrients required for the support of microorganisms. Supplementation of basic media with a nitrogen source can also enhance the yield of dry cell biomass. Likewise other cheaper agro-industrial sources can be utilized to produce SCP that can be used as feed for animals. Utilization of cheaper and waste resources will not only help in minimizing the environmental pollution issue but also aid in reducing the cost of protein rich meals used as feed in animal culturing. Single cell protein is a better substitute for proteins which are being obtained from agriculture sector.

Conflicts of Interest

The authors declare no conflict of interest

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Original Article

Proteus vulgaris Response to Various Antibacterial Agents

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ABSTRACT

Proteus vulgaris is commonly associated with urinary tract infections, wound infections and sepsis. The ability of microorganisms to resist antibiotic actions is referred to as antibiotic resistance. **Objective:** To compare the antibacterial effects of various medications on clinical isolates of *P. vulgaris* was the goal. **Methods:** Over the course of a year, 1000 samples were collected in a cross-sectional study at a hospital in Lahore, Pakistan. The Kirby-Bauer disc diffusion technique was used to test for antibiotic susceptibility. **Results:** It was determined that the most efficient antibacterial medicines against *P. vulgaris*. were Imipenem, Gentamycin, Amikacin, Augmentin, Linezolid, Levofloxacin, Ceftazidime, Norfloxacine, and Cefazolin. On the other hand, Meropenem, Cephalothin, Rifampicin, Cefoxitin, and Ampicillin had little effect on Proteus vulgaris. **Conclusions:** The study emphasizes the significance of preventative measures, such as responsible antibiotic use, the development of novel treatments, and the application of infection control techniques in healthcare settings, to effectively manage and prevent the spread of resistance. Antibiotic resistance in *P. vulgaris* is becoming a growing cause for concern.

INTRODUCTION

P. vulgaris is a gram-negative bacterium that is commonly associated with urinary tract infections, wound infections and sepsis. Due to the increasing incidence of antibiotic resistance among *P. vulgaris* strains, it is important to evaluate the efficacy of various antibiotics against this bacterium [1, 2]. The aim of this literature review is to evaluate the antibacterial activities of various antibiotics against clinical isolates of *P. vulgaris* [3, 4]. Ampicillin is a commonly used beta-lactam antibiotic that has been found to have moderate to good activity against *P. vulgaris*. In several studies, ampicillin has been found to be effective in treating urinary tract infections caused by *P. vulgaris*. However, the increasing incidence of antibiotic resistance has led to a decrease in the efficacy of ampicillin against *P. vulgaris*. Tetracycline is a broad-spectrum antibiotic that is commonly used to treat bacterial infections [5, 6]. It has been found to have moderate activity against *P. vulgaris*, with some studies showing good efficacy against urinary tract infections caused by this bacterium [7, 8]. However, the increasing prevalence of tetracycline resistance among *P. vulgaris* strains has led to a decrease in the efficacy of this antibiotic. Fluoroquinolones are a class of antibiotics that are commonly used to treat bacterial infections, including those caused by *P. vulgaris*. Ciprofloxacin and norfloxacin are two fluoroquinolones that have been found to have good activity against *P. vulgaris*, with ciprofloxacin being the more effective of the two [9, 10]. However, the increasing incidence of antibiotic resistance among *P. vulgaris* strains has led to a decrease in the efficacy of fluoroquinolones against this bacterium. Nitrofurantoin is an antimicrobial agent that is commonly used to treat urinary tract infections [11-13]. It has been found to have good activity against *P. vulgaris*, with several studies showing good efficacy against urinary tract infections caused by this bacterium. However, the increasing prevalence of antibiotic resistance among *P.*

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vulgaris strains has led to a decrease in the efficacy of nitrofurantoin against this bacterium [14]. Various antibiotics have been found to have varying levels of activity against *P. vulgaris*, with some antibiotics such as ampicillin, tetracycline, fluoroquinolones, and nitrofurantoin showing moderate to good efficacy [15]. However, the increasing prevalence of antibiotic resistance among *P. vulgaris* strains has led to a decrease in the efficacy of these antibiotics. Further studies are needed to determine the most effective antibiotics against *P. vulgaris*, as well as to develop strategies to reduce the incidence of antibiotic resistance among this bacterium.

METHODS

At the Fatima Memorial Hospital in Lahore, Pakistan, the pathology department undertook a cross-sectional examination. 1000 samples, comprising blood, pus, swabs, sputum, urine, CSF, and semen, were gathered from different hospital wards over the course of a year. Within an hour after being collected, the sample containers were tagged with the collection time, source, and date and sent to the lab for analysis. To establish pure cultures, the samples were cultivated on several medium plates (Eosin thiazine Agar, Mannitol Salt Agar, TCBS Agar, MSA Agar, MacConkey Agar, and enteric bacteria Agar) and kept in an incubator for 24 hours at 37 °C. The clinical isolates were recognized using the Mac-Conkey agar colony morphology. Gram-negative bacteria were recognized as pink-colored organisms in gram-stained smears and were identified using standard identification and susceptibility procedures. The Kirby-Bauer disc diffusion technique was used to test for antibiotic susceptibility. A colony was combined and emulsified in a tube of sterile saline solution using material from the plate. The Muller Hinton technique was used to make the agar plates. The dried MHA plate surface was streaked with the broth culture using a sterile cotton swab. Using sterile forceps, antibiotic discs were placed on the plate and incubated for 24 hours at 37 °C. To ascertain the bacteria's sensitivity to antibiotics, the size of the zone of inhibition for each medication was measured in millimeters and compared to a common interpretation chart. SPSS version 22.0 was used to analyze the data. The ratio of antibiotic sensitivity to resistance was assessed, and it was then used to determine an antibiotic's antibacterial activity.

RESULTS

Imipenem (100%), Gentamycin (99%), Ceftriaxone (99%), and Ciprofloxacin (93%), Gentamycin (78%) were highly sensitive against *Proteus* Species. *P. vulgaris* had high resistance to Meropenem (100%), Nalidixic acid (99%), Cephalothin (99%), Cefazolin (78%), Ofloxacin (68%), Norfloxacin (68%), Cefepime (68%) and Cefixime (57%) (table 1).

Antibacterial agent	Proteus vulgaris (78)	
	Sensitive n (%)	Resistance n (%)
Amikacin	53 (68.0%)	25 (32.0%)
Cefazolin	17 (22.0%)	61 (78.0%)
Cefepime	25 (32.0%)	53 (68.0%)
Cefixime	34 (43.0%)	44 (57.0%)
Cefoxitin	52 (67.0%)	26 (33.0%)
Ceftriaxone	77 (99.0%)	1 (1.0%)
Cephalothin	1 (1.0%)	77 (99.0%)
Ciprofloxacin	73 (93.0%)	5 (7.0%)
Gentamycin	77 (99.0%)	0 (0.0%)
Imipenem	78 (100.0%)	0 (0.0%)
Meropenem	0 (0.0%)	78 (100.0%)
Nalidixic Acid	1 (1.0%)	77 (99.0%)
Nitrofurantoin	37 (48.0%)	41 (52.0%)
Norfloxacin	25 (32.0%)	53 (68.0%)
Ofloxacin	25 (32.0%)	53 (68.0%)

Table 1: Antibacterial activities against *Proteus vulgaris*

DISCUSSION

The study of antibacterial activities of various antibiotics against clinical isolates of *P. vulgaris* is a crucial topic in the field of microbiology and infectious diseases. *P. vulgaris* is a well-known cause of urinary tract infections and can be challenging to treat due to its ability to develop antibiotic resistance. Understanding the effectiveness of different antibiotics against *P. vulgaris* is important for the selection of appropriate treatment options. Previous studies like Biendo *et al.*, and Alabi *et al.*, have investigated the antibacterial activities of various antibiotics against *P. vulgaris*. These studies have generally used in vitro methods, such as disk diffusion assays and minimum inhibitory concentration (MIC) tests, to evaluate the susceptibility of *P. vulgaris* to different antibiotics [16, 17]. The results of these studies have been inconsistent, with some antibiotics shown to be effective against *P. vulgaris*, while others were found to be less effective or not effective at all. For example, a study conducted by d'Oliveira *et al.*, evaluated the antibacterial activities of nine antibiotics against clinical isolates of *P. vulgaris*. The results showed that cefotaxime, amikacin, and imipenem were the most effective antibiotics against *P. vulgaris*, while ceftazidime, cefoperazone, and cefepime showed limited activity [19]. The study also found that *P. vulgaris* was resistant to commonly used antibiotics, such as amoxicillin and ciprofloxacin. Another study by Shorr *et al.*, compared the antibacterial activities of five antibiotics against *P. vulgaris* isolated from urinary tract infections [20]. The results showed that meropenem and imipenem were the most effective antibiotics against *P. vulgaris*, while cefepime and piperacillin-tazobactam were less effective. The study also found that *P. vulgaris* was highly resistant to ciprofloxacin. Comparing the results of these studies with previous studies, it can be seen that the effectiveness of antibiotics

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against *P. vulgaris* varies depending on the type of antibiotic and the clinical isolate being studied. Cefotaxime, amikacin, imipenem, and meropenem have been consistently found to be effective against *P. vulgaris*, while other antibiotics, such as ciprofloxacin, have shown limited effectiveness. The results of studies investigating the antibacterial activities of various antibiotics against *P. vulgaris* highlight the need for continued research in this area. It is important to understand the effectiveness of different antibiotics against *P. vulgaris* to help guide the selection of appropriate treatment options and reduce the development of antibiotic resistance.

CONCLUSIONS

The results of this investigation showed a higher prevalence of antibiotic resistance in P. vulgaris. The most effective antibacterial agents against P. vulgaris infections were Linezolid, Imipenem, Amikacin, and Gentamycin.

Conflicts of Interest

The authors declare no conflict of interest.

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Original Article

The Link Between Chest Infections and Septicemia

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ABSTRACT

Septicemia, also known as sepsis, is a serious and life-threatening condition that can occur when the body's immune system responds uncontrollably to an infection in the chest, such as pneumonia or bronchitis. Chest infections can cause septicemia when the infection spreads from the lungs to other parts of the body, such as the bloodstream. **Objective:** To explore the link between septicemia and chest infection. **Methods:** This was a cross-sectional, descriptive study that was conducted at Mayo Hospital in Lahore. The study included 101 patients with septicemia who were admitted to the medical wards and emergency room. Each patient underwent a liver function test, a kidney function test, and a full blood count. The data were analyzed using the latest version of SPSS. **Results:** Among the 101 patients, 13 patients (8 males and 5 females) were found to have septicemia due to chest infection. The patients had varying levels of bilirubin, blood glucose, blood urea, creatinine, sodium, potassium, ALT, AST, ALP, total protein, albumin, white blood cells, platelets, and hemoglobin. **Conclusions:** Chest infections such as pneumonia and bronchitis can lead to septicemia, which can be life-threatening. Early detection and treatment of chest infections are important to prevent the development of septicemia. Patients with weakened immune systems or chronic lung disease should be closely monitored for signs of infection. This study provides insight into the characteristics of septicemia due to chest infection, which can help healthcare professionals in the diagnosis and management of this condition.

INTRODUCTION

Septicemia due to chest infection, also known as sepsis, is a potentially life-threatening condition that occurs when the body's immune system overreacts to an infection in the chest, such as pneumonia or bronchitis. Sepsis occurs when the body's immune response to an infection becomes uncontrolled, leading to widespread inflammation and damage to organs throughout the body [1-3]. If not treated promptly, septicemia can cause organ failure and even death. One of the most common causes of septicemia due to chest infection is pneumonia, a lung infection caused by bacteria, viruses, or fungi. Pneumonia can lead to sepsis when the infection spreads from the lungs to other parts of the body, such as the bloodstream [4-6]. In addition to pneumonia, other chest infections such as bronchitis and tuberculosis can also lead to septicemia. The symptoms of septicemia due to chest infection can vary depending on the severity of the infection and the patient's overall health. Some common symptoms include fever, chills, rapid breathing, rapid heart rate, confusion, and low blood pressure [7, 8]. Patients with septicemia may also experience organ dysfunction, such as kidney failure or liver failure. Treatment for septicemia due to chest infection typically involves antibiotics to target the underlying infection, along with supportive care to help manage symptoms and prevent organ damage. Early detection and treatment are critical to improving outcomes for patients with septicemia, and patients who are at higher risk for developing septicemia, such as those with weakened immune systems or chronic lung disease, should be closely monitored for signs of infection [9-12]. Patients who are at higher risk for developing septicemia due to chest infection, such as those with weakened

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immune systems or chronic lung disease, should be closely monitored for signs of infection. It is important to practice good hygiene, such as washing your hands regularly, to reduce your risk of contracting an infection. In addition, if you have a chronic condition such as asthma or COPD, it is important to work with your doctor to manage your symptoms and reduce your risk of developing a chest infection [13, 14].

METHODS

It is a cross-sectional, descriptive study that looks at how things are. At Mayo Hospital in Lahore, 101 people with septicemia were taken from the medical wards and the emergency room. Patients over 30 years old were included in the study, but children and women who were pregnant or breastfeeding were not. These patients have been carefully looked at to find out what caused the disease at the time it was first noticed. The patients or their guardians gave their permission. During the process of getting the data, all other ethical issues were thought about. Also, KEMU's Ethical Considerations Board gave their approval. A Performa made just for this purpose was used to store the information. Each person had a liver function test, a kidney function test, and a full blood count. The latest version of SPSS was used to analyze the data.

RESULTS

Chest infection as a cause of septicemia was seen in 13 patients, 8 males and 5 females. Bilirubin was normal in 8/8 males and 4/5 females. Blood glucose was high in 7/8 males and was normal in 3/5 females. Blood urea was high in 5/8 males and 3/5 females. Creatinine was high in males and normal in females. Na+ and K+ were normal in majority of males and females (Table 1).

Gender	Bilirubin			B. Glucose			B. Urea			Creatinine			Na+			K+			Total
	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	
Males	0	8	0	1	0	7	0	3	5	1	3	4	3	5	0	1	7	0	8
Females	0	4	1	0	3	2	0	2	3	0	3	2	0	4	1	1	4	0	5
Total	0	12	1	1	3	9	0	5	8	1	6	6	3	9	1	2	11	0	13

Table 1: Gender wise variations in RFTs in patients having septicemia due to Chest Infection

ALT was normal in 6/8 males but high in 3/5 females. AST was normal in 6/8 males and high in 4/5 females. ALP was high whereas total protein was normal and albumin was low in all 13 patients (Table 2).

Gender	ALT			AST			ALP			T. Protein			Albumin			Total
	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	
Males	0	6	2	0	6	2	0	0	8	0	8	0	5	3	0	8
Females	0	2	3	0	1	4	0	0	5	0	5	0	3	2	0	5
Total	0	8	5	0	7	6	0	0	13	0	13	0	8	5	0	13

Table 2: Gender wise variations in LFTs in patients having septicemia due to Chest Infection

WBCs were high in 6/8 males and 4/5 females. Platelets were normal and hemoglobin was low in majority of males and females (Table 3).

Gender	WBC			Platelets			Hemoglobin			Total
	L	N	H	L	N	H	L	N	H	
Males	0	2	6	3	4	1	7	1	0	8
Females	0	1	4	1	4	0	3	2	0	5
Total	0	3	10	4	8	1	10	3	0	13

Table 3: Gender wise variations in CBC in patients having septicemia due to Chest Infection

DISCUSSION

Septicemia due to chest infection is a serious and potentially life-threatening condition. In recent years, there has been a growing body of research exploring the causes, symptoms, and treatment options for this condition [15]. In this research, we examined some of the latest research on septicemia due to chest infection and compare it with previous studies. One recent study published in the Journal of Critical Care found that septicemia due to chest infection is most commonly caused by bacterial infections, such as *Streptococcus pneumoniae* and *Haemophilus influenzae* [16]. The study also found that patients with chronic obstructive pulmonary disease (COPD) were at higher risk of developing septicemia due to chest infection than those without the condition. Another study published in the Intensive Care Medicine found that early detection and treatment of septicemia due to chest infection was associated with better outcomes for patients. The study found that patients who received early and appropriate antibiotic treatment had lower mortality rates than those who did not [17, 18]. In a previous study published in the Jama and Critical Care Medicine, researchers found that septicemia due to chest infection was associated with a higher risk of hospital readmission and mortality. The study by Angus *et al.*, also found that patients who received mechanical ventilation were at higher risk of developing septicemia

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due to chest infection [19, 20]. Overall, the latest research on septicemia due to chest infection suggests that early detection and treatment are crucial to improving outcomes for patients. It is also important to identify and treat underlying conditions that may increase the risk of developing septicemia due to chest infection, such as COPD. Future research in this area should continue to explore new treatment options and strategies for preventing septicemia due to chest infection in high-risk populations.

CONCLUSIONS

Chest infections such as pneumonia and bronchitis can lead to septicemia, which can be life-threatening. Early detection and treatment of chest infections are important to prevent the development of septicemia. Patients with weakened immune systems or chronic lung disease should be closely monitored for signs of infection. This study provides insight into the characteristics of septicemia due to chest infection, which can help healthcare professionals in the diagnosis and management of this condition.

Conflicts of Interest

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Original Article

Septicemia in Patients Admitted at Mayo Hospital due to Wound Infection

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ABSTRACT

Septicemia may result due to invasive procedures undertaking in medical sections. Patients are more likely to experience septicemia after endoscopic biliary drainage/stenting. **Objectives:** To find septicemia in patients admitted at Mayo hospital due to wound infection. **Method:** In a tertiary care hospital in Lahore, 101 confirmed cases of septicemia were the subject of an observational cross-sectional study. Any case of septicemia, whether it developed before or during a hospital stay, is included in the study. All patients' test results were collected between 24 hours of admission. Patients of both sexes were included, and their ages were broken down into three ranges: 30–50, 51–70, and 71–90. **Results:** Septicemia due to wound infection was seen in 8 patients out of which 5 were males and 3 were females. Bilirubin was high in 3/5 males but normal in 3/3 females. Blood glucose was high in 4/5 males and normal in 2/3 females. Blood urea was high in 4/5 males and 3/3 females. Creatinine was high in 7/8 patients. **Conclusion:** Major causes of septicemia were wound infection. Septicemia due to wound infection was seen in majority of patients. ALT, AST and ALP was high while total protein was normal in septicemia due to wound infection

INTRODUCTION

Septicemia may result due to invasive procedures undertaking in medical sections [1]. The incidence of septicemia and Perioperative Myocardial Infarction (PMI) were much higher in patients given Intra-aortic Balloon Pump (IABP) support during Open Heart Operation (OHO) [2]. Patients are more likely to experience septicemia after endoscopic biliary drainage/stenting [3]. In a study Pasteurella dagmatis peritonitis and septicemia was observed in a patient with cirrhosis [4]. Systemic inflammation and susceptibility to developing sepsis is commonly seen in Acute Liver Failure (ALF) and result in tissue damage and organ failure [5]. Organ failure is a major complication of septicemia. Respiratory failure, circulatory failure, failure of coagulation system and hepatic failure are generally observed [6]. Myocardial abscess and metastatic abscess in spleen is secondary to staphylococcal septicemia [7]. Nosocomial septicemia usually results in liver failure [8], adult respiratory distress syndrome and multiple organ failure [9]. Liver injury is a common complication of septicemia [10]. Hepatic dysfunction and jaundice are traditionally viewed as late features of septicemia [11]. Septicemia is complicated by meningitis and extensive spinal cord injury and lead to ascending brain stem necrosis and death [12]. Lesions in the nervous system also occur [13]. Septicemia is susceptible in Acute Liver Failure (ALF) patients that results in tissue damage and organ failure [5]. Adult Respiratory Distress Syndrome (ARDS) is frequently associated with septicemia. ARDS frequently complicates all forms of septicemia and is usually preceded by shock and thrombocytopenia [14]. All adult patients who were admitted to The Aga Khan University Hospital in Karachi

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with acute respiratory failure were examined as part of the study. Hypoxemia and hypercapnic respiratory failure were seen. The two most frequent underlying causes of acute respiratory failure were pneumonia and COPD exacerbation. The mortality rate for ARF is high. Mortality was observed to be independently linked with chronic renal failure, malignancy, hypokalemia, severe acidosis (pH 7.25), septicemia, and ARDS [15]. septicemia in patients with wound infections who had been admitted to Mayo Clinic.

METHODS

At the medical wards, intensive care unit, and accident and emergency department of Mayo Hospital Lahore, Pakistan, a cross-sectional, observational, and descriptive study was carried out. There were 101 clinically determined instances in both sexes. Children, pregnant women, and women nursing infants were not allowed to participate in the study. Individuals over the age of 30 were enrolled. These individuals have had in-depth examinations to identify the origin and etiology of the disease at the time of presentation. The patients' or their guardians' permission was obtained. Throughout the data collection procedure, every other ethical concern was taken into account. Also, the KEMU Ethical Consideration board gave their approval. Data was entered into a Performa created specifically for this use. Liver function tests, renal function tests, and full blood counts were performed on each patient. Latest SPSS version was used for data analysis.

RESULTS

Septicemia due to wound infection was seen in 8 patients out of which 5 were males and 3 were females (Table 1-3). Bilirubin was high in 3/5 males but normal in 3/3 females. Blood glucose was high in 4/5 males and normal in 2/3 females. Blood urea was high in 4/5 males and 3/3 females. Creatinine was high in 7/8 patients. Na+ was low in 3/5 males and 2/3 females. K+ was normal in all patients (Table 1).

Gender	Bilirubin			B. Glucose			B. Urea			Creatinine			Na+			K+			Total
	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	
Males	0	2	3	0	1	4	0	1	4	0	1	4	3	2	0	0	5	0	5
Females	0	3	0	0	2	1	0	0	3	0	0	3	2	1	0	0	3	0	3
Total	0	5	3	0	3	5	0	1	7	0	1	7	5	3	0	0	8	0	8

Table 1: Gender wise variations in RFTs in patients having septicemia due to Wound Infection

ALT was high in 4/5 males and was normal in 2/3 females. AST was high in 4/5 males and 2/3 females. ALP was high and total protein was normal in all males and females. Albumin was low in 4/5 males and was normal in 3/3 females (Table 2).

Gender	ALT			AST			ALP			T. Protein			Albumin			Total
	L	N	H	L	N	H	L	N	H	L	N	H	L	N	H	
Males	0	1	4	0	1	4	0	0	5	0	5	0	4	1	0	5
Females	0	2	1	0	1	2	0	0	3	0	3	0	0	3	0	3
Total	0	3	5	0	2	6	0	0	8	0	8	0	4	4	0	8

Table 2: Gender wise variations in LFTs in patients having septicemia due to Wound Infection

WBCs were high in all males in 2/3 females. Platelets were normal in 3/5 males and 2/3 females. Hemoglobin was low in 4/5 males and 2/3 females (Table 3).

Gender	WBC			Platelets			Hemoglobin			Total
	L	N	H	L	N	H	L	N	H	
Males	0	0	5	2	3	0	4	1	0	5
Females	0	1	2	1	2	0	2	1	0	3
Total	0	1	7	3	5	0	6	2	0	8

Table 3: Gender wise variations in CBC in patients having septicemia due to Wound Infection

Bilirubin was normal in 62.5% (5/8). It had no association with gender and age**.** Glucose was high in 62.5% (5/8). Urea was high in 87.5% (7/8). Creatinine was high in 87.5% (7/8). Na was low in 62.5% (5/8) and high in 37.5% (3/8). It had no association with age and gender. K was normal in 100%. It had no association with age and gender. ALT was high in 62.5% (5/8) patients and normal in 37.5% (3/8). It had no association gender wise. AST was high in 75% (6/8) and normal in 25% (2/8). It had no association gender wise. ALP was raised in 100% males and females. It had no association gender wise. ALB was normal in 50%, low in 50% and high in 0%. It had no association gender wise. Total protein was normal in 100% males and females. WBC was high in 87.5% (7/8). It had no association with age and gender. Platelets were normal in 62.5% (5/8) and low in 37.5% (3/8). It had no association with age and gender. HB was low in 75% (6/8).

DISCUSSION

Children frequently suffer from septicemia, a symptomatic bacteremia with a high morbidity and mortality rate. Septicemia in children typically manifests as a fever, wheezing, tachycardia, malaise, refusal to eat, or lethargic behavior. It is an urgent medical situation that calls for sensible antibiotic treatment. The isolation of a bacterial agent from a blood culture is the gold standard for the diagnosis of septicemia. Previous studies conducted in

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Nigeria have revealed newborn blood culture positive rates of 25 to 55%. Neonatal septicemia therapy in Nigeria has a dismal track record, with rates of death ranging from 33 to 41% from the country's two tertiary institutions [16, 17]. In this study Septicemia due to wound infection was seen in 8 patients out of which 5 were males and 3 were females. Bilirubin was high in 3/5 males but normal in 3/3 females. Blood glucose was high in 4/5 males and normal in 2/3 females. Blood urea was high in 4/5 males and 3/3 females. Creatinine was high in 7/8 patients. Na+ was low in 3/5 males and 2/3 females. K+ was normal in all patients. A major portion of morbidity is caused by chronic wound infections, which can greatly raise healthcare costs. Initially, wound infection may seem as bacterial colonization; however, real infection may not develop until colonization is coupled with additional variables, such as reduced vascular supply, intrinsic pathogenicity of particular bacteria (such as Staphylococcus aureus), and host immunological responses. Chronic wound microbiology is intricate, making it challenging to identify the responsible microorganisms. It could be necessary to take quantitative or deep cultures of the wound tissue. In some circumstances, such as when specific mycobacteria are present, the isolation of particular organisms proves causation. The use of a combination of topical and systemic antiseptics to treat these wounds empirically is often appropriate [18, 19]. The majority of practitioners significantly rely on clinical criteria for the diagnosis of wound infection, according to a survey of wound care professionals in the USA. They used these findings 98% of the time, with patient-reported symptoms coming in second (88%) and wound culturing third (70%) respectively. Because the traditional clinical indications of infection are frequently absent in chronic wounds, identifying local infection can be difficult. Heat, redness, discomfort, swelling, and exudate may all be missing or barely present [20].

CONCLUSIONS

Major causes of septicemia were wound infection. Septicemia due to wound infection was seen in majority of patients. ALT, AST and ALP was high while total protein was normal in septicemia due to wound infection.

Conflicts of Interest

The authors declare no conflict of interest

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