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PREVALENCE AND RISK FACTORS OF HEPATITIS B IN THE TWIN CITIES OF RAWALPINDI-ISLAMABAD

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ABSTRACT

Countries with poor economies tend to have higher rates of hepatitis B and C. Rawalpidi has a very high ratio (2.16), indicating a very type-specific language. At Bilal Hospital Rawalpindi, 2.16 percent of both replacement and voluntary blood donors were positive for HBV. Our study's results suggest to a rising prevalence rate, which, if not handled, might balloon out of control. Therapeutic injections, dental procedures, and barbershop shaving may all increase the risk of transmitting Hepatitis B Virus (HBV). It is suggested that public healthcare facilities switch from employing immunochromatographic tests (ICT) to using enzyme-linked immunosorbent assays (ELISA) to reduce the spread of Hepatitis B. It is also critical to educate the population at large about the prevalence of Hepatitis B in specific metropolitan regions.

INTRODUCTION

Classification

Hepatitis B virus' DNA origin was uncovered in the 1960s. According to the system established by the International Committee on Taxonomy of Viruses (ICT), this virus is in the family of orthopa DNA viruses known as Hepadnaviridae. Only one animal virus, from the spumaretrovirinae subfamily of the retroviridae family, uses viral RNA as an intermediate in the process of replicating its DNA genome. The estimated rate of hepatitis B transmission is 75-200 times greater than that of HIV. Hepatitis B is most often spread by skin-to-blood contact.

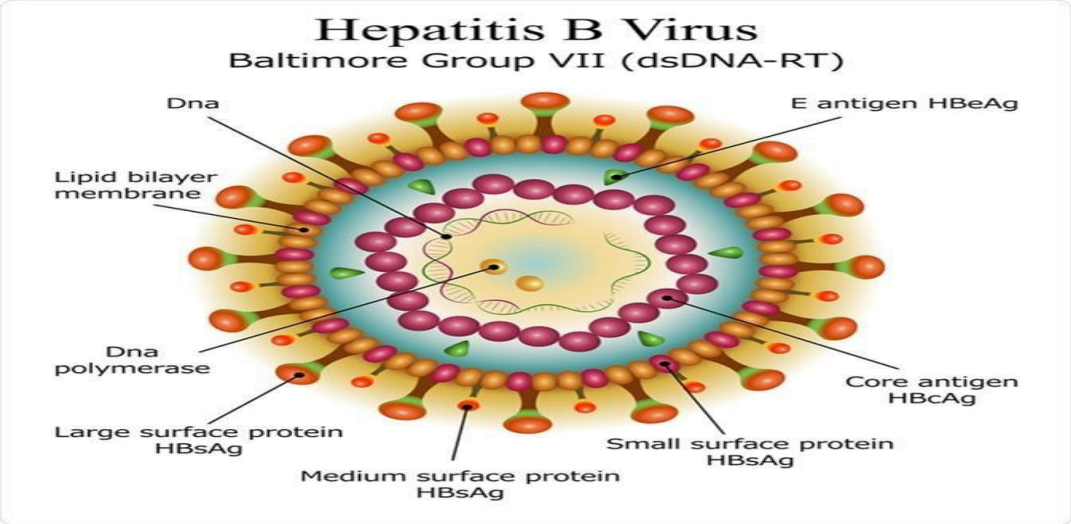
Hepatitis E, or HEV

Hepatitis B virus (HBV) has a lipid envelope and a spherical shape, with a diameter of 42–47 nanometers. As can be seen in figure 1.1, the virion consists of the nucleocapsid, the viral envelope, and an incomplete double-stranded DNA genome. The big L, small S, and intermediate M surface proteins make up

the nucleocapsid core protein dimers, which were discovered in 2007 research

by Seeger et al., 2007. Infected hepatocytes have a minus-strand covering the whole genome and a plus-strand covering around two-thirds of the genome.

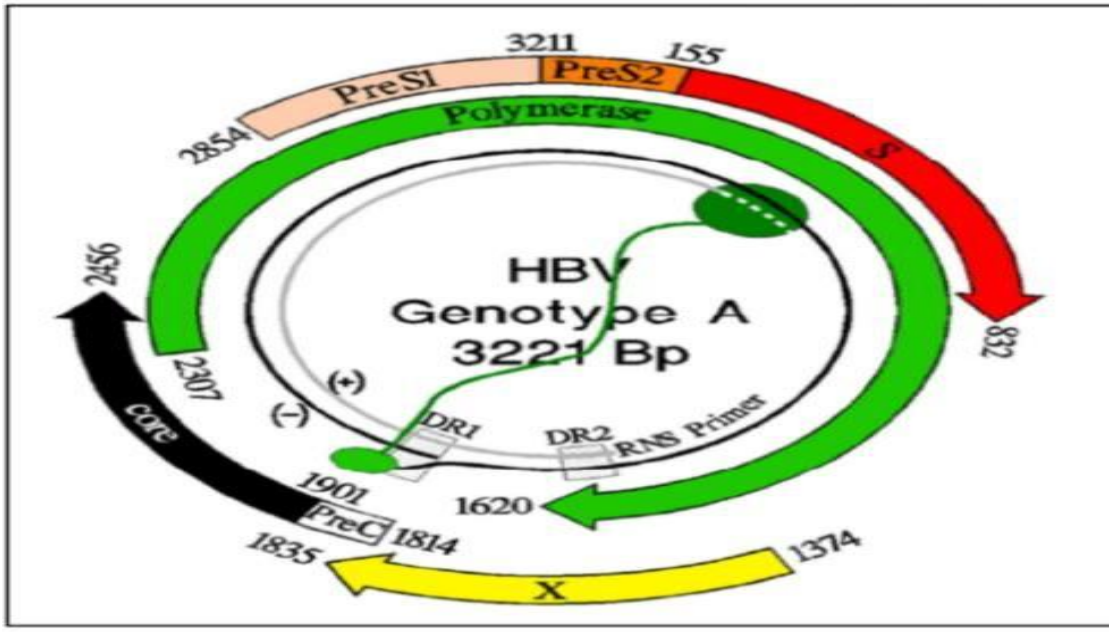
Fig 1.1. Hepatitis B virion structure shown schematically.



Transcription of proteins from the positive strand using covalently closed circular DNA (cccDNA). Seeger et al. (2007) and Bowyer and Sim's (2000) research are two examples of studies that are applicable to this discussion. The nucleocapsid surface protein is a lighter shade of blue, approaching turquoise, whereas the core protein is a deeper shade of blue. Different sized Perkins HBs were produced that year. When compared to DNA genomes, the rate of nucleotide exchange in viral genomes is 104 times greater, ranging from 0.1 to 0.7 per year (Bowyer & Sim, 2000; Zhu et al., 2010). RNA acts as a go-between in the replication process because the enzyme responsible for viral reproduction, reverse transcriptase, has a high mistake rate and poor proofreading skills.

In Figure 2, two enhancers and four promoters for viral RNA production are shown. Seeger et al. (2007) found that the length of pre-core/core mRNA was 3.5 kilobases, whereas the length of pre-S mRNA was 2.4 kilobases. S mRNA was measured to be 2.1 kilobases in length, whereas X mRNA was measured to be 0.7 kilobases.

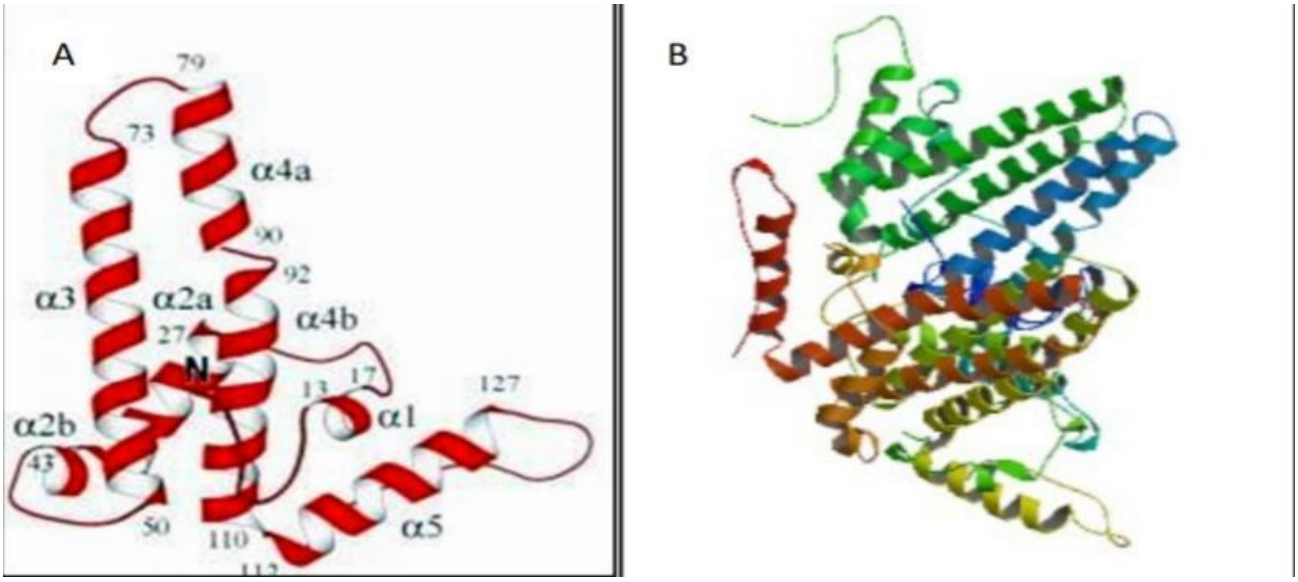
Primer design and genomic sequence interpretation are also affected by the sequencing strand, mostly because of differences in strain mapping. Valenzuela et al.'s stranded reference sequence, which they submitted using ECORI codes, is a match for genebank accession X02763.



The nucleotide values of the EcoR1 site for the proteins of the four overlapping reading frames inside the HBV genome are shown in Figure 1.2.

HBc

In question is a pure form of protein that hasn't been tampered with in any way. Since the virus was first discovered, researchers have used the virus's core protein's antigenicity to identify and track infections (Seeger et al., 2007). HBcAg's main antigen is made up of 183 different amino acids. The synthesis of dimeric capsid proteins requires the enzymatic degradation of the quantity of amino acids at N-terminal position 149. Each of the two parts of the HBa Ag dimer consists of four bundles of alpha helices. There are 90–120 triangular dimers in the capsid's quaternary structure, and four of these dimers come together to form a spike. Additionally, the dimers are covalently bonded to neighboring alpha-helices.



Monomeric HBV Core protein has a ribbon-like conformation (A) in its tertiary structure (Wynne et al., 1999). The core protein has been shown to be dimeric using X-ray crystallography and the Protein Data Bank entry 1QG.

HBE

The solvent protein pre C releases a smaller protein called e-antigen (HBeAg), which regulates the host immune response during HBV infection (Seeger et al., 2007). There are distinctions between HBcAg and HBeAg antigens (Watt et al., 2010). Antigenic specificity, solvency, features of data collecting, occupational exposure energy, and other examples fall within this category.DNA polymerase protein is abbreviated p-protein.The nucleotide sequence 2307-1620 provides the genetic coding for the pol quality of the viral DNA polymerase. Upstream reverse transcriptase, upstream RNAseH, and a DNA strand introduction for the less abundant strand are the three functional components of the item.

HBx

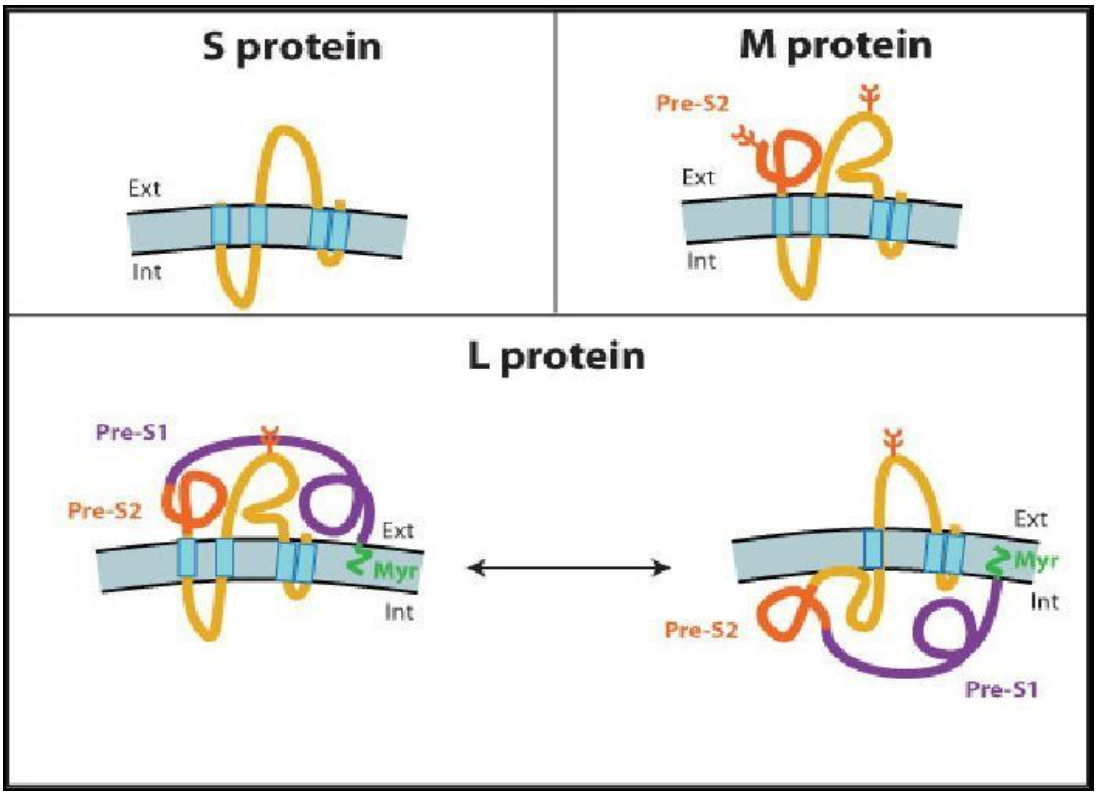
Hepatitis B X antigen (HBxAg), also called X protein, is located deep inside the virus's nucleus and is thought to have a connection to the cytoskeleton. This feature is sometimes seen in hepadnaviruses from animals. Toh et

al. (2013) and Seeger et al. (2007) report that HBx interacts with NF-kB, AP 12, cEBP, ATFCREB, and NFAT limiting sites, all of which are cellular transcription factors. The possibility for hepatocarcinogenesis has been linked to these relationships.

HBs

Pre-SS (2854-832) refers to the three transmembrane glycoproteins present in viral membranes. Proteins with myristolated L-forms are made by the S open reading frame, pre-S1, pre-S2, and S regions (PDB 1KCR). The protein specifically binds to viral receptors on hepatocytes. M-protein, whose translation begins at a start codon inside the protein's secondary structure, displays recognition of a structure larger than HBsAg but smaller than L-protein.

The first 55 amino acids of the M-protein are particularly reactive and interact with the pre-S2 region. Since the protein has no detectable effect on virion assembly, its exact functional capabilities are unknown. The smallest form of the S-protein, HBsAg, contains the crucial antigenic markers used to identify HBV. These markers are employed in the diagnosis of active infections and in the development of HBV vaccines (Seeger et al., 2007).



The following image depicts the two different L HB conformations described in the 2011 paper Viral Zone. Before DNA sequencing HBV strains based on large differences in the amino acid sequence of its structural components. ADW2, ADWRQ+, ADWRQ-, acid sequence (124-147) by Locarnini and Yuen (2010) places the start of the antigenic loops at positions 137 and 138. Locarnini and

became commonplace, serologists used HBsAg to categorize

and ADWR are the most common serotypes. The predicted amino

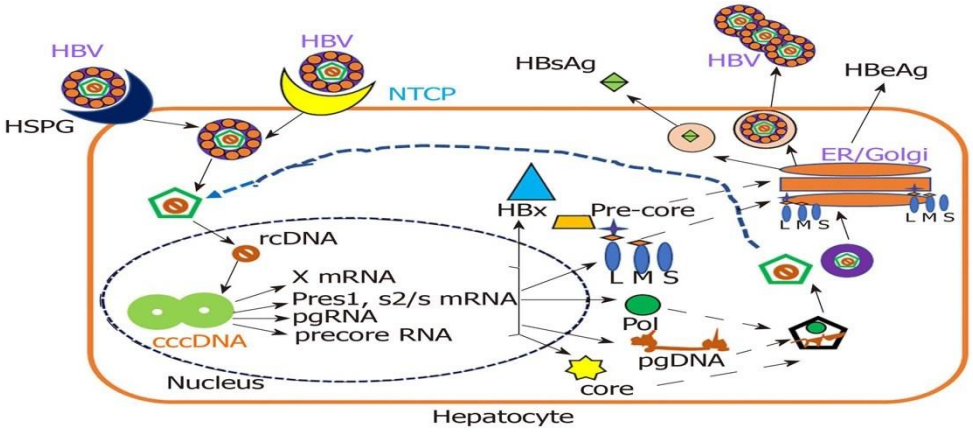
Yuen (2010) found that all serotypes of HBsAg have a

common antigenic determinant that is exceptionally well preserved. The substitution of arginine for lysine at either position 122 or 160 in the protein is thought to be responsible for the occurrence of Yd

and wr variants. The differences between w12 and w3, w4 and thr, and w4 and leu are encoded at position 127. Most strains express the q determinant, which is made up

of amino acid residues 177 and 178 (Norder et al., 2004). In Figure 1.5, HBsAg may be

Figure 1.5 is a schematic illustration of the principal antigenic determinant (a-



observed.

determinant) of the

HBV surface antigen and its accompanying major and minor loops. Mutations in the Overlapping

polymerase gene have been linked to resistance to antiviral drugs, as seen by the darkened regions, as reported by Locarnini and Yuen (2010).

THE SPREADING AND MULTIPLYING PROCESSES

In the first stage, viruses bind to host cells. In a duck HBV model, we found that the N-terminal S-domain (amino acids 1-23) and the pre-S2 domain translocation motifs (TLM) peptide interact with carboxypeptidase D (CPD). Individuals are the focus of Schadler and Hildt's (2009) research.

Schadler and Hildt (2009) found that HBV has persisted in spreading while facing challenges such connection breakdown and cloaking. This discovery raises the possibility that HBV is spread either automatically or after an intentional period of covertexchange. Figure 1.6 from (Schuktz et al., 2004). Relaxed circular DNA from the genome is converted into complementary circular DNA (cccDNA) in step four, and thiscccDNA then acts as a transcription templatein step five. Seeger et al. (2007) and Schadler and Hildt (2009) conducted the research. Sub-genomic and pre-genomic RNA molecules are transported from the nucleus tothe cytoplasm with the help of post-transcriptional regulatory mechanisms, as established by Seeger et al. (2007).

Four sub-genomic mRNA ORFs code for functional proteins: HBcAg, HBsAg, HBe Ag, HBx, and p. The signal is a stem-circular structure seen in pre-genomic RNA; it is called the kramvis and kew (2002) signal. It helps the chaperone and the p protein interact during the detection of stage 8 encapsidation sites. Protein dimers develop at the nucleation sites of pgRNA-p, which then polymerize to produce frame polymers. Seeger et al. (2007), Schultz et al. (2004), andSchadler and Hildt (2009) have all conducted considerable research on the embryonic RNAnucleocapsid.

A full nucleocapsid is formed once the e signal detects replication has begun and RNA begins the laborious process of transcribing record stage 9 into DNA in the cytoplasm. The endoplasmic reticulum, golgi complex, and pre-S and post-S sections of the large surface protein all play a role in preparing the nucleocapsid for transportation to the core during stage 10 (Schultz et al., 2004; Schadler and Hildt, 2009), which in turn allows the replication cycle to continue.

Hepatitis B virus (HBV) replication might be sped up by the presence of other disorders

(Capobianchi, 2013; Bowyer & Sim, 2000; Simmods& Midgley, 2005). Beerenwinkel, Gunthard, et al. (2012) did research on the importance of protecting genetic diversity in highly fragmented communities at risk of contracting contagious illnesses. Theresearch also investigates the factors that encourage the creation of viral quasispecies.

About 240 million people are chronically infected with hepatitis B virus (HBV) across the globe (Seeger et al., 2007; globe Health Organization, 2013), making it a major public health problem.

DIAGNOSIS USING LABORATORY TESTING

Testing for relevant antigen antibodies, such HBcAb, is a part of the diagnostic procedure. Core antibody subtyping has the potential to distinguish between acute (IgM class) and chronic (IgG class) HBV infection. The detection of hepatitis B virus (HBV) DNA is often employed as an additional indicator of the severity of HBV infection.

In order to determine the prevalence of infections between 1985 and 1992 for each of the eight (23) possible combinations (presence or absence) of the three primary serological markers, the South African National Institute of Virology (NIV), now known as the National Institute of Communicable Diseases (NICD), used data mining techniques. In order to automate the interpretation of laboratory results, the research team compiled a large database of diagnoses and accompanying notes (see table 1.1). Measurements of ALT and HBV DNA may be useful in establishing disease progression. Two of the eight possible combinations of tests (stage II and stage II) still lack enough data to be considered reliable, however.Over time, HBsAg titres decline.

Decreases in levels of pollution in the air. Hepatitis B surface antigen (HBsAg) levels dropping below the detection threshold, which might indicate the success of the treatment, are very unusual. The fact that HBV DNA may still be found in the circulation is, however, evidence that total eradication has not been accomplished. The medical community is at a loss to explain these illnesses. Liver tissue, serum, peripheral blood mononuclear cells, and other lymphoid tissues may harbor trace amounts of hepatitis B virus (HBV) DNA that can be detected with whole genome PCR amplification tests in cases of chronic infections (Gunther et al., 1995). The Pre-S1/S2 and S regions have been modified as a

consequence of A-D recombination. Allain et al. (2009) found that among South African blood donors, the detection of HBsAg had a false negative rate of around 1 in 4067. In this discussion, we'll look into serology and how it applies to a wide range of diseases.

In order to make educated judgments and lessen the impact of any unfavorable results, it is crucial to weigh the risks associated with a certain activity or scenario.

The prevalence of viral hepatitis among medical professionals is high.Hepatitis virus infections are more common in certain population subsets and geographic areas. If a caregiver gets hepatitis through touching infected blood, they might potentially spread it to a patient.Users of intravenous drugs (IDUs) pose a threat to public health because they may transmit communicable infections. Transfusions may expose this group to the danger of contracting viral hepatitis. Transmission of infectious diseases from mother to child may result from a lack of attention to hygienic procedures and a lack of medical understanding during labor and delivery.

The transmission of diseases inside families was also studied by the researchers. The spread of hepatitis might be facilitated by the lack of adequate hygienic procedures in barbershops. Blood donation and transfusion are the principal vectors for the spread of bloodborne diseases. It's crucial to remember that untested blood might transmit harmful blood cells. Human contact is a key factor in the spread of hepatitis viruses. The fast spread of the virus has been linked to high-risk sexual activity, such as having intercourse with several people. This is a common mode of transmission for viruses. Blood contamination and needle stick occurrences are much more common as a result of the rising number of people getting dental work done.

A complete analysis requires collecting and reviewing data over a certain time frame, which is referred to as the analysis period. It is aBilal Hospital's blood bank in Rawalpindi collected its data from the beginning of 2020 to the end of the following year, on October 31, 2021.

LEARNING ENVIRONMENTS

Bilal Hospital, the only publicly funded hospital in Pakistan with a blood bank, was the site of the study. The donation of blood is a typical way for people to help others in need. Most of the 35,000 people who get blood transfusions each year are men. In

October of 2021, researchers analyzed a group of 966 blood donors for the presence of anti-HBc and other hepatitis B virus (HBV) antigens. Donations were not accepted from anyone who had recently been diagnosed with jaundice, had hemoglobin levels below 13 g/dL, had BMIs below 50, or who had fevers on the day of donation. The median prevalence of HBsAg, Hostile to HCV, anti-HIV, intestinal disease, and syphilis indicators in blood samples was determined by analyzing data from screenings performed between January 1, 2020, and October 31, 2021. Analytical sampling is the practice of selecting and collecting samples that are meant to be representative of a broader population for the purpose of analysis.

Each donor's blood was drawn using a syringe and needle measuring 5 cubic centimeters in total capacity. The blood samples were then centrifuged in an A vacutainer at a rate of 1500 revolutions per minute for 3 minutes to aid the separation of serum. The Guangzhou Wondfo Biotech Co. is a Chinese biotech firm with headquarters in the city of Guangzhou. Ltd. The HBsAg test kit with the one-step cassette format accurately detected a concentration of less than 1 ng/ml. Discrete test strips were used to examine each serum sample. After 10 seconds, the strips were removed and dried for 15 minutes on a nonabsorbent surface before being analyzed.

Methods for Detecting Human Papillomavirus (HPV) Using PCR and Serology

Donor blood samples were tested for HBsAg, anti-HCV, and anti-HIV using commercial compound immunoassays (EIAs; AxSYM, Abbott Labs, Abbott Park, IL). Between January 2020 and October 2021, a total of 94,177 participants were surveyed. The Treponema pallidum hemagglutination assay (TPHA) from Crumlin, UK-based Randox was used to diagnose syphilis, while the presence of malaria was confirmed by analyzing thick blood films dyed with ethyl-Enediaminetetraacetate. Antibody testing for HBc (Center) (AxSYM, Abbott Labs) was performed in October 2021 on 966 blood donors. A secondary aggressive anti-HBc EIA (DiaSorin, Saluggia, Italy) was used to evaluate the reactions. Supplier-provided absorbance measurements were put to the test by choosing a value that was somewhat off from the calibrators' average. If the tests didn't achieve both goals, then they couldn't be trusted.

Commercial kits (AxSYM, Abbott Research Centers) were able to identify HBeAg, anti-

HBe, and HBsAg in HBc-negative samples after they were stored in aliquots at 30 degrees Celsius. Polymerase chain reaction (PCR) was used to identify HBV DNA, and a commercially available kit (BioSewoom; Seoul, Korea) and piece of machinery (GeneAmp 5700; Applied Bio-Frameworks; Foster City, California) were used to do so. After amplification, the DNA sample was run through an agarose gel UV transilluminator (UVItec; Cambridge, UK) set to 150 V for analysis. Two independent checks confirmed the reliability of the HBV DNA results. The manufacturer predicts a detection limit of 50 DNA copies per milliliter in serum.

Authentication

AccuBioTech Co.'s products and services were utilized in this research. Rapid testing made possible via the use of multi-use cassette devices. Two drops of the sample and one drop of the kit were applied to the instrument for in vitro testing, and the instrument was incubated for five minutes before a result was recorded.

Establishing and using the same file formats, data structures, and definitions across an organization is what we call "data standardization."

SPSS, Adaptation 10.0 (SPSS Inc., Chicago, IL) was used on a personal computer to analyze the data. The chi-square test and Fisher's exact test were used to analyze data from frequency and rate surveys in this research. For a t-test comparison between anti-HBc positive and negative groups, the mean and standard deviation of blood donor time are provided. P values less than 0.05 were considered significant in this study.

In this research, we look at survey data and try to make sense of it.Over the last 15 to 20 years, the prevalence of HBsAg among healthy people in Pakistan has decreased significantly, from 813 to 10 to 15%. Rawalpindi and Islamabad have a high Hepatitis B Virus (HBV) prevalence, according to the World Health Organization (WHO). If hepatitis B were to be added to Pakistan's existing newborn vaccination schedule, coverage among infants would likely increase to 65.5% by 2019. The observed decline in hepatitis B virus (HBV) positive cases may be attributable to the improved reliability of HBsAg EIA testing.

Over the previous decade, the vaccination rate for healthcare workers against hepatitis B at Bilal Emergency Clinic has increased significantly, from 86% to 98%

(unpublished perspective 16). However, several regional practices have not seen comparable changes (5). These include the reusing of disposable and glass needles, the use of potentially contaminated razors by hairstylists, and the prevalence of unlicensed dentistry clinics. The prevalence of Hepatitis C Virus (HCV) is predicted to remain unchanged at 2.4% in 2019 and 4.16% at now, despite the availability of effective antiviral medication. The prevalence of HBsAg positive among blood donors is comparable to that seen in India, falling somewhere between 1.7% and 2.2%. This framework has the potential to improve blood donors' knowledge of illness prevention, treatment, and prognosis. Twenty-two percent of the 966 people who tested positive for HBsAg also tested positive for the presence of a particular factor, according to this study. Additionally, the percentage of Indian replacement blood donors that tested negative for HCV was much lower, falling between 0.25 and 0.918% and 0.21 percent. In addition, just 0.50% of Indian donors tested HIV-negative.

About nine percent (9%) of the total sample size of 966 blood donors tested positive for Hepatitis B Virus (HBV) when tested for the presence of Hepatitis B core antigen (HBc). Nine percent (9.6%) of the whole sample size showed immunity to HBc by testing negative for HBsAg; this included 167 people. The viral signature is independent of environmental conditions. Researchers found that 14.95 percent of Greek blood donors and 10.82 percent of Indian blood donors were HBsAg-negative and HBc-resistant. These results point to the growing adoption of routine disease screening and immunization regimens. Donors who test positive for HBc produce more anti-HCV antibodies than those who test negative for HBsAg. Anti-HBc sentiment is characteristic of the HCV transporter area. At the moment, Anti-HBc can only be used to detect people who are HBV carriers in their last stages of infection. However, a threefold increased risk of non-A, non-B hepatitis was seen among receivers of blood that tested positive for Anti-HBc compared to those who received blood that tested negative for Anti-HBc. Concerns have been raised about the quality of Pakistan's blood supply after HBV DNA was found in five serum samples that were negative for HBsAg but positive for Anti-HBc. as Shown. It is possible to classify the donors into three groups: those who are anti-HBc positive only (3), those who are anti-HBc positive in addition to being anti-

HBe positive (2), indicating that they are in the recovery phase of HBV infection, as evidenced by the presence of anti-HBs and a decrease in HBsAg below detectable limits, and those who are chronic carriers with HBsAg below detectable limits (2). It is important to note that even if a patient's clinical state improves, leading to the disappearance of HBsAg, the generation of anti-HBs, and the restoration of normal liver function, there is still a possibility of detecting low quantities of HBV DNA in the bloodstream. This was observed in Pakistan, where 0.53% of blood donors who were found to be negative for HBsAg also tested positive for HBV DNA. There may be trace levels of HBV DNA in serum, and studies have shown that cytotoxic white blood cells may eliminate the virus without damaging hepatocytes. Transmission of HBV from donors who test negative for HBsAg is a real risk in Pakistani blood bonding facilities due to the absence of antiHBc screening. Transfusions acquired from donors that test positive for anti-Hepatitis B core antibody (antiHBc) are preferred by patients with compromised immune systems because they are devoid of Hepatitis B Virus (HBV) DNA. Blood donors who tested positive for HBs antigen exhibited an immunological response of more than 100 mIU/mL in 87 (67%) of the cases. In contrast, more than 30 mIU of neutralizers were present in 86% of those who tested negative for HBs antigen.

First-time contributor involvement would reduce by 17% if ideas inspired by HBc were disregarded. Most Pakistani bonding facilities lack the resources to do HBV DNA screening on all HBc-positive blood donations, despite the obvious advantages of doing so. Due to their positive status for different illnesses such HBsAg, HCV, HIV, TPHA, and malaria antigen, around 7% of potential donors are excluded from participation.

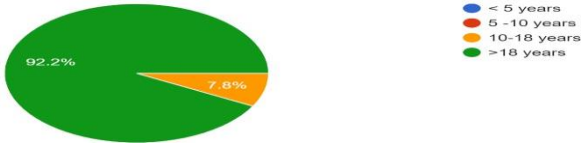
Many blood banks lack both trained staff and enough funding to purchase necessary equipment. In the context of the transfusion-based system, it is crucial to stress that screening donors for HBc, with or without HBV DNA, remains a difficulty even in rich socioeconomic situations or well-equipped blood donation facilities. Nucleic acid testing is challenging with current techniques since most blood donation facilities cannot screen for EIA viruses. Proactive recruiting of volunteer blood donors by transfusion centers may improve the efficacy and cost-efficiency of Anti-HBc screening. Blood banks need to

aggressively seek for a large pool of donors who routinely test negative for HBsAg and anti-HBc in order to keep up with the demand. These givers need encouragement and help. This group will be tested for HBsAg, anti-HCV, and anti-HIV during future visits to the blood transfusion facility. Blood transfusion clinics should emphasize selecting healthy young donors aged 18-25 due to the reduced risk of Hepatitis B virus (HBV) transmission due to the existence of antibodies against Hepatitis B core antigen (HBc) in traditional screening procedures. The people who are immune to HBc and who test negative for HBsAg should be drawn to the bonding facilities. Encourage regular blood donations within this population. It is advised that these donors be tested for HBsAg, HCV, and HIV at the blood transfusion clinic. People between the ages of 18 and 25 have a lower chance of getting Hepatitis B Virus (HBV), making them an ideal population to target for scheduled blood drives. Therefore, due to limited resources, anti-HBc testing may be limited to first-time blood donors exclusively. Those with anti-HBs levels of 100 mIU per mL or more and a negative HBV DNA test result are considered suitable blood donors. This method may allow for more efficient use of funding provided by benefactors. After updating its federal and provincial blood transfusion systems, Pakistan may decide to adopt this strategy. Volunteer blood donor recruitment is a problem for many hospitals, as is keeping blood and blood products in stock. This means that people all around the country have access to these centers' full blood transfusion services. In its current form, the evaluation ignores regional differences in prevalence rates. As a result, a major effort from the public or private sector, together with substantial investments in infrastructure, trained employees, and equipment, are required to develop voluntary blood donation programs and improve blood safety. Therefore, there is a chance that prevalence studies are inaccurate.

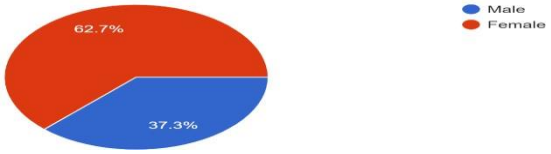
RESULTS AND DISCUSSION

Questionnaires Response

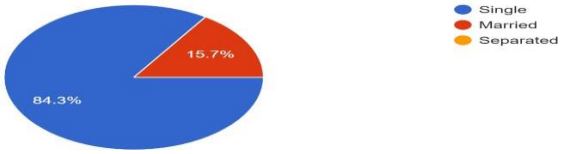
Age
51 responses



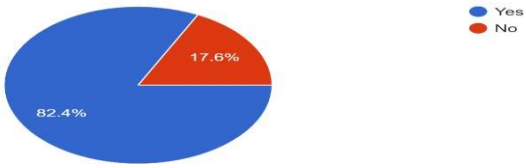
Gender
51 responses



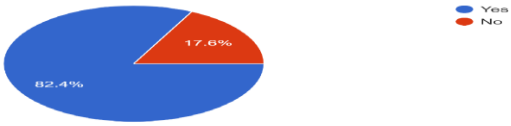
Martial Status
51 responses



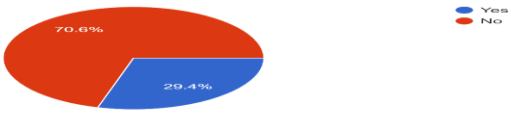
Do you know about Hepatitis B
51 responses



Do you know about Hepatitis B
51 responses

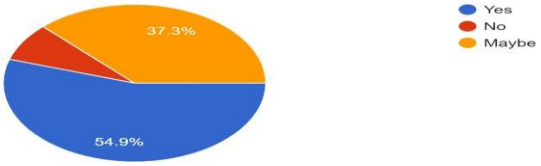


Do you have family history of Hepatitis B
51 responses

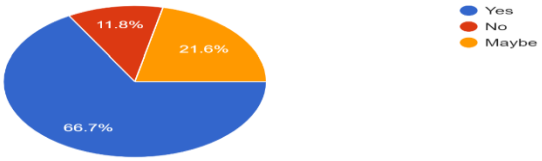


Hepatitis B can be transmitted through sexual contact
51 responses

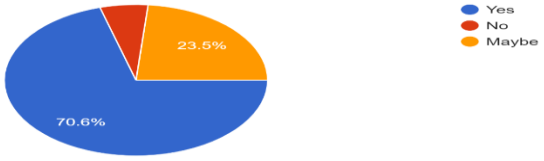
Hepatitis B can be transmitted from mother to child at birth
51 responses



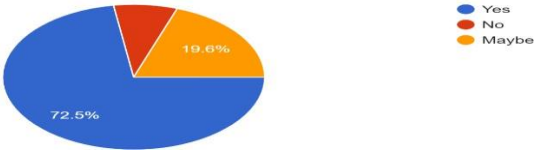
Hepatitis B can cause liver disease
51 responses

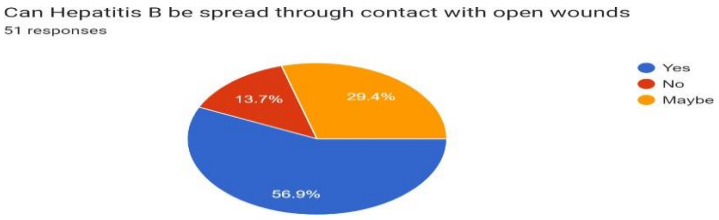


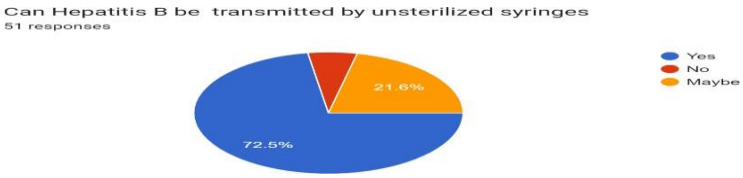
Hepatitis B can be cured?
51 responses

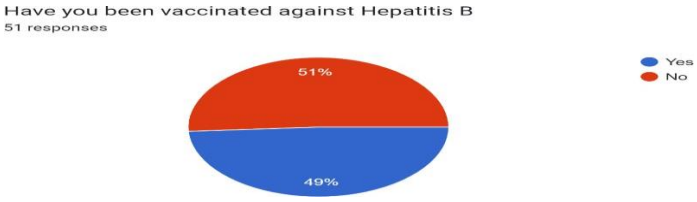


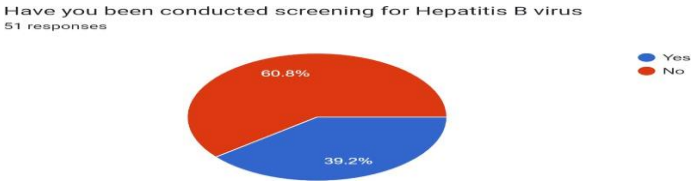
Can vaccine used to prevent Hepatitis B
51 responses











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