



UNIVERSITI PUTRA MALAYSIA

***EVALUATION OF POST INFANT HEPATITIS B VACCINATION AMONG
HEALTHY VACCINEES AND MOLECULAR DETECTION OF OCCULT
HEPATITIS B AMONG HEALTHY VOLUNTEERS***

HUDU ABDULLAHI SHUAIBU

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By

HUDU ABDULLAHI SHUAIBU

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirements for the Degree of Master of Science**

JANUARY 2014

DEDICATION

This thesis is dedicated to the loving memory of my late father Mallam Hudu

His Silent inspiration, encouragement and guidance still linger on.



Abstract of thesis presented to the senate of Universiti Putra Malaysia in fulfilment of the requirement for the degree of Master of Science

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January 2014

Chair: Prof. Zamberi Sekawi, MPath

Faculty: Medicine and Health Sciences

Hepatitis B virus is the commonest chronic viral pathogen affecting about 2 billion people worldwide. Of these, 378 million are chronic carriers. In Malaysia, 2.4 million people have been estimated to be hepatitis B carriers and this population continues to be a potential source of infection, to tackle these more than 100 countries adopted National policy on infant hepatitis B vaccination including Malaysia and it has been shown to effectively control the diseases even in endemic areas. The production of hepatitis B surface antibodies (anti-HBs) has been reported to confer long-term protective immunity; these antibodies are produced in response to vaccination or exposure to HBV infection. Hepatitis B core antibody (anti-HBc) on the other hand, are detected in almost all individuals that have been previously exposed to the virus. The success of childhood vaccination against hepatitis B relies mainly on persistence of immunity to adulthood, however, mutation in the surface antigen is becoming a global challenge because these mutants seldom respond to the currently available vaccine and escaped been detected by current serological screening methods. At the moment, there is lack of information regarding the assessment of HBV vaccination in Malaysia; moreover, evidences are scanty regarding occult hepatitis B infection among Blood donors and vaccinees. It is against this background that the present study was carried out with the following objectives; (i) to evaluate the persistence of immunity following childhood hepatitis B vaccination among vaccinated undergraduate Student. (ii) to investigate the prevalence of isolated hepatitis B core antibody among vaccinated undergraduate Students cohort (iii) to detect occult hepatitis B viral infection among Blood donors and undergraduate students using serological and molecular methods and (iv) to perform molecular characterization of occult hepatitis B virus using bioinformatics tools.

This study involved two population, these are undergraduate students vaccinated at infant and blood donors. Objective one and two are related to the former while objectives three and four are related to the later. Sample size was calculated using sample size formula by Daniel, 1999 for estimating minimum sample size in cross-sectional study. Minimum sample size for each of the study population was found to be 379 and 153 for undergraduate vaccines and donors respectively. However, there were 402 undergraduate students that were eligible for this study and all were included while the sample size of the blood donor was also increase to 1000 to increase the precision of the sample.

Serum samples from both vaccinated undergraduate students and the blood donors were tested for HBsAg and anti-HBc while only the undergraduate vaccines were tested for anti-HBs pre and post vaccine booster using commercially available Enzyme-linked Immunosorbent Assay (ELISA). A booster dose of 20µg recombinant hepatitis B vaccine (Euvax B, Sanofi Aventis, Malaysia) was administered to individuals with negative anti-HBs (<10 IU/L) and their anti-HBs status was evaluated one month after the booster dose. To further elucidate the genetic characteristic of hepatitis B variant, all anti-HBc positive and HBsAg negative samples from both undergraduate vaccines and blood donors were selected for hepatitis B surface mutation analysis. The DNA was extracted from all anti-HBc positive samples and Nested PCR was done using two set of primers targeting S-gene region of hepatitis B envelope proteins. Samples with positive HBV DNA were purified, sequenced and subjected to bioinformatics analyses.

The results showed that none of the samples were found to be HBsAg positive, while 5.5% were found to be anti-HBc positive. For the anti-HBs of vaccinated undergraduate student the results showed that 83.9% were anti-HBs positive (> 10 IU/L) pre booster dose, majority (67.9%) of which received three doses of the vaccine and 94% anamnestic response post booster dose with only nine non-responders and were given two doses of the vaccine to receive the third dose in six month time. All the 55 anti-HBc positive samples were found to be HBV DNA positive by nested PCR. Sequence analysis of the amplified product revealed a 99% identity to HBV with most of the local isolates having close phylogenetic relationship with HBV isolate 14 (JX869999) from Panama. This isolate belongs to genotype B, serotype *adw*² and was isolated from plasma of Chinese population living in Latin region of Panama.

This study therefore, reveals the persistence of immunity for an average of 21 years post primary vaccination with recombinant hepatitis B vaccine and 67.9% of the vaccinees with protective anti-HBs (>10 IU/L) received three doses of the vaccine with a significant association between number of doses receive and persistence of immunity ($P<0.05$) which is similar to a recent finding in UK. Thus, the presence of immune memory post-infant vaccination has been confirmed in this study, as well as other related studies with anamnestic response, indicating persistence of memory beyond the duration of circulating antibodies. The rate of anti-HBc-positive subjects among the vaccinated undergraduate students was found to be 5% with isolated anti-HBc in 0.9% of the vaccinees. All the four isolated anti-HBc response to a single dose of recombinant hepatitis B vaccine which suggests primary infection with

mutant variant of HBV. Hepatitis B viral DNA was detected from all the 55 anti-HBc positive, HBsAg negative serum using nested PCR, which is in line with previous studies that demonstrated similar finding in serum, mononuclear cells and liver samples. Based on sequence and phylogenetic relationship of our HBV isolates and reference isolates from other parts of the world, we found that all our isolates belong to genotype B. Another interesting finding from this study is the occurrence of occult hepatitis in 3 % and 2 % of the blood donors and undergraduate students respectively. All hepatitis B core antibodies positive were found to be HBV DNA positive thus, indicating the reliability of hepatitis B core antibodies in screening for occult hepatitis B infection, especially in low endemic regions while nucleic acid amplification testing (NAT) is the recommended screening test in high endemic regions. Bioinformatics analysis revealed that mutation at position 16 of the amino acid is common to all the 55 isolates with substitution of Glutamine (Q) with Lysine (K) in 53 of the isolate, while the remaining 2 isolates have Arginine and stop codon respectively. A total of 105 amino acid mutations, were found in all the 55 isolates.

In conclusion, the evidence presented in this study, reveals persistence of both humoral and cellular immunity for an average of 21 years after infant vaccination and presence of isolated anti-HBc in vaccines which response to a single dose of recombinant hepatitis B vaccine suggesting primary infection with mutant variant of HBV despite the presence of cellular immunity against the none mutant hepatitis B virus. The presence of HBV DNA in all the anti-HBc positive samples may suggest the reliability of the use of hepatitis B core antibodies in screening for occult hepatitis B infection. All the 55 sequences in this study belong to genotype B and have various mutations in different regions of the S gene with the most common mutations found in this study are substitution of Glutamine at position 16 with lysine resulting in nonfunctional hepatitis B surface antigen therefore; mutation outside the α determinant region might play a role in hepatitis B surface antigen detection failure.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk ijazah master Sains

**PENILAIAN POST BAYI HEPATITIS B VACCINATION KALANGAN
VACCINEES SIHAT DAN MOLEKUL PENGESANAN GHAIB HEPATITIS
B KALANGAN SUKARELAWAN SIHAT**

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Hepatitis B virus adalah patogen utama penyakit kronik virus menjejaskan kira-kira 2 bilion orang di seluruh dunia. Daripada jumlah ini, 378 juta adalah pembawa kronik. Di Malaysia, 2.4 juta orang telah dianggarkan pembawa hepatitis B dan penduduk ini terus menjadi sumber yang berpotensi jangkitan, untuk menangani lebih 100 negara mengamalkan polisi Kebangsaan bayi vaksinasi hepatitis B termasuk Malaysia dan ia telah terbukti berkesan mengawal penyakit walaupun di kawasan endemik. Pengeluaran antibodi hepatitis B permukaan (anti -HBs) telah dilaporkan memberi imuniti perlindungan jangka panjang; antibodi ini dihasilkan sebagai tindak balas kepada suntikan atau pendedahan kepada jangkitan HBV. Hepatitis B antibodi teras (anti- HBC) di sisi lain , yang dikesan dalam hampir semua individu yang telah sebelum ini terdedah kepada kejayaan virus. The yang vaksinasi zaman kanak-kanak menentang hepatitis B bergantung terutamanya pada kegigihan imuniti kepada dewasa, bagaimanapun, mutasi dalam antigen permukaan menjadi satu cabaran global kerana mutan ini jarang bertindak balas terhadap vaksin yang sedia ada dan melarikan diri dikesan oleh kaedah pemeriksaan serologi semasa. Pada masa ini , terdapat kekurangan maklumat mengenai penilaian vaksin HBV di Malaysia; lebih-lebih lagi , bukti-bukti adalah kikir mengenai ghaib jangkitan hepatitis B di kalangan penderma darah dan vaccinees . Ia adalah bertentangan dengan latar belakang ini bahawa kajian ini telah dijalankan dengan objektif seperti berikut : (i) Menilai kegigihan imuniti berikut zaman kanak-kanak Hepatitis B vaksinasi di kalangan Pelajar ijazah pertama vaksin . (ii) Untuk menyiasat kelaziman terencil hepatitis B antibodi teras di kalangan vaksin ijazah Pelajar kohort (iii) Untuk mengesan ghaib hepatitis B jangkitan virus di kalangan penderma darah dan sarjana muda menggunakan serologi dan kaedah molekul dan (iv) Untuk melaksanakan pencirian molekul hepatitis ghaib B virus menggunakan alat bioinformatik

Kajian ini melibatkan dua penduduk , ini adalah pelajar ijazah pertama vaksin pada bayi dan darah penderma. Satu matlamat dan dua berkaitan dengan bekas manakala objektif tiga dan empat berkaitan dengan kemudian. Saiz sampel dikira menggunakan saiz sampel formula oleh Daniel , 1999 untuk menganggarkan saiz sampel minimum dalam kajian keratan rentas. Saiz sampel minimum bagi setiap penduduk kajian didapati 379 dan 153 untuk vaksin ijazah dan penderma masing-masing . Walau bagaimanapun , terdapat 402 pelajar ijazah yang layak untuk kajian ini dan telah dimasukkan semasa saiz sampel penderma darah juga meningkat kepada 1000 untuk meningkatkan ketepatan sampel.

Serum dari kedua-dua pelajar ijazah pertama vaksin dan penderma darah telah diuji untuk HBsAg dan anti- HBC manakala hanya vaksin ijazah sarjana muda telah diuji untuk anti -HBs pra dan vaksin pasca penggalak menggunakan boleh didapati secara komersial Enzim berkaitan imunoserapan assay (ELISA). Satu dos booster 20µg rekombinan vaksin hepatitis B (Euvax B, Sanofi Aventis, Malaysia) telah diberikan kepada individu yang negatif anti -HBs (<10 IU / L) dan status anti -HBs mereka telah dinilai satu bulan selepas dos penggalak . Untuk menjelaskan lagi ciri genetik hepatitis B varian , semua anti- HBC sampel negatif positif dan HBsAg dari kedua-dua vaksin ijazah dan penderma darah telah dipilih untuk analisis hepatitis B permukaan mutasi. DNA tersebut telah diekstrak daripada semua anti- HBC sampel positif dan Bersarang PCR telah dilakukan dengan menggunakan dua set primer mensasarkan kawasan S - gen hepatitis B protein sampul surat. Sampel dengan positif HBV DNA telah disucikan , urutan dan tertakluk kepada bioinformatik analisis.

Hasil kajian menunjukkan bahawa tidak ada sampel telah didapati HBsAg positif , manakala 5.5 % telah didapati anti- HBC positif. Bagi anti -HBs daripada pelajar sarjana muda vaksin keputusan menunjukkan bahawa 83.9 % adalah anti -HBs positif (> 10 IU / L) pra dos booster, majoriti (67.9 %) di mana menerima tiga dos vaksin dan 94% anamnestic post tindak balas booster dos dengan hanya sembilan bukan balas dan telah diberi dua dos vaksin untuk menerima dos ketiga dalam enam masa bulan. Semua 55 anti- HBC sampel positif didapati HBV DNA positif oleh bersarang PCR. Analisis urutan produk dikuatkan mendedahkan identiti 99% kepada virus hepatitis B dengan kebanyakan pencilan tempatan yang mempunyai hubungan rapat dengan filogenetik HBV mengasingkan 14 (JX869999) dari Panama. Isolat ini kepunyaan genotip B, serotype adw2 dan telah diasingkan daripada plasma daripada penduduk Cina yang tinggal di kawasan Latin Panama.

Kajian ini oleh itu , mendedahkan kegigihan imuniti selama purata 21 tahun vaksinasi jawatan utama dengan vaksin hepatitis B rekombinan serupa dengan apa yang dilaporkan di Thailand. Kajian kami mendapati bahawa 67.9 % daripada vaksin dengan perlindungan anti -HBs (> 10 IU / L) menerima tiga dos vaksin dengan persatuan yang signifikan antara bilangan dos menerima dan kegigihan imuniti ($P < 0.05$) yang serupa dengan penemuan baru-baru ini di UK yang dilaporkan oleh Yates et al. , 2013. Oleh itu , kehadiran memori imun vaksin selepas bayi telah disahkan dalam kajian ini, serta lain-lain kajian yang berkaitan dengan sambutan anamnestic , menunjukkan kegigihan memori di luar tempoh antibodi . Kadar subjek anti- HBC - positif di kalangan pelajar ijazah pertama vaksin didapati 5% dengan

terpencil anti- HBC dalam 0.9 % daripada vaccinees . Semua empat terpencil anti- HBC tindak balas kepada dos tunggal rekombinan vaksin hepatitis B yang mencadangkan jangkitan utama dengan varian mutan HBV dengan kehilangan anti - HBs liar, yang berbeza dengan kajian yang dijalankan sebelum pengenalan vaksin HBV negara di Taiwan, di mana kebanyakan terpencil anti- HBC tidak menunjukkan sebarang tindak balas terhadap vaksin hepatitis B dos booster . Hepatitis B DNA virus dikesan dari semua 55 anti- HBC positif , serum negatif HBsAg menggunakan bersarang PCR , yang adalah selaras dengan kajian sebelum ini yang menunjukkan dapatan yang sama dalam serum , sel-sel mononuklear dan sampel hati. Berdasarkan turutan dan hubungan filogenetik diasingkan HBV dan rujukan diasingkan dari bahagian-bahagian lain di dunia , kami mendapati bahawa semua pencilan kami milik genotip B. Satu lagi penemuan menarik daripada kajian ini ialah berlakunya hepatitis ghaib dalam 3 % dan 2 % daripada penderma darah dan sarjana muda masing-masing . Semua antibodi teras hepatitis B positif didapati HBV DNA positif dengan itu , menunjukkan kebolehpercayaan antibodi teras hepatitis B dalam pemeriksaan untuk ghaib jangkitan hepatitis B, terutama di kawasan-kawasan endemik rendah manakala asid nukleik penguatan ujian (NAT) adalah ujian pemeriksaan yang dicadangkan di dalam kawasan endemik yang tinggi. Analisis bioinformatik mendedahkan bahawa mutasi pada kedudukan 16 asid amino adalah perkara biasa kepada semua 55 mengasingkan dengan penggantian Glutamin (Q) dengan Lysine (K) dalam 53 isolat , manakala baki 2 pencilan mempunyai Arginine dan berhenti codon masing-masing . Seramai 105 mutasi asid amino, terdapat dalam kesemua 55 pencilan .

Kesimpulannya, keterangan yang dikemukakan dalam kajian ini , mendedahkan kegigihan kedua-dua imuniti tindakbalas humoral dan sel untuk purata 21 tahun selepas suntikan bayi dan kehadiran terpencil anti- HBC dalam vaksin yang tindak balas kepada dos tunggal rekombinan vaksin hepatitis B mencadangkan jangkitan utama dengan varian mutan HBV walaupun kehadiran sel imuniti terhadap mutan tiada virus hepatitis B . Kehadiran HBV DNA dalam semua anti- HBC sampel positif mungkin mencadangkan kebolehpercayaan penggunaan antibodi teras hepatitis B dalam pemeriksaan untuk ghaib jangkitan hepatitis B . Semua 55 urutan dalam kajian ini milik genotip B dan mempunyai pelbagai mutasi di rantau yang berbeza gen S dengan mutasi yang paling biasa ditemui dalam kajian ini adalah penggantian Glutamin di kedudukan 16 dengan lisin menyebabkan nonfunctional hepatitis B antigen permukaan oleh itu, mutasi di luar rantau penentu mungkin memainkan peranan dalam hepatitis B permukaan kegagalan pengesanan antigen.

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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Masters of Science. The members of the Supervisory Committee were as follows:

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LIST OF ABBREVIATIONS

AIDS	Acquired Immunodeficiency Syndrome
Anti-HBc	Hepatitis B Core Antibodies
Anti-HBe	Hepatitis B e antigen
Anti-HBs	Hepatitis B Surface Antibodies
cccDNA	Covalently Closed Circular DNA
CD4 ⁺	Cluster of differentiation 4
CD8 ⁺	Cluster of differentiation 8
CDC	Centers for Disease Control
COV	Cut off value
°C	Degree Celsius
HBsAg	Hepatitis B Surface Antigen
HBV	Hepatitis B Virus
HCC	Hepatocellular Carcinoma
HIV	Human Immunodeficiency Virus
HLA	Human Leukocyte Antigen
HRP	Anti-Horseradish Peroxidase
IgG	Immunoglobulin G
IgM	Immunoglobulin M
IMR	Institute for Medical Research
IU	International Unit
Kb	Kilo base
L	Litre
mg	Mili gram
MHR	Major Hydrophilic Region
ML	Maximum Likelihood
ml	Mili litre
µg	Micro gram
NAT	Nucleic Acid Amplification Test
NCBI	National Center for Biotechnology Information
NTC	No Template Control
NTCP	Sodium Taurocholate Co Transporting Polypeptide
OHBI	Occult hepatitis B infection
OD	Optical Density
ORF	Open Reading Frame
P value	Probability
PC	Positive Control
PCR	Polymerase Chain Reaction
pegINF	Pegylated Interferon
RNA	Ribo Nucleic Acid
RT	Room Temperature
SC	Sub cutaneous
SD	Standard Deviation
STIs	Sexual Transmitted Infections

TAE
UK
UPM
USA
WHO

Tris-Acetate EDTA
United Kingdom
Universiti Putra Malaysia
United State of America
World Health Organisation



CHAPTER 1

INTRODUCTION

The history of hepatitis B virus (HBV) dates back to 1967 when an unidentified antigen was recognized to be linked with hepatitis B viral infection in Australia, which was later referred to as hepatitis B surface antigen (Blumberg, 1967). Since then, hepatitis B surface antigen (HBsAg) has functioned as a significant diagnostic marker of hepatitis B viral infection qualitatively. Although, remarkable improvements in the development of quantitative HBsAg assays have been made, which allowed viral replication monitoring (Ahn, 2011). Hepatitis B virus has been classified as Hepatotropic virus, in the genus Orthohepadnavirus, belonging to the family of Hepadnaviridae. It is a DNA virus composing of; an envelope, core, viral polymerase, and DNA genome. It is a partially double-stranded circular DNA with about 3200 nucleotides (Kann and Gerlich, 2007; Scaglioni, 1996). Hepatitis B virion is spherical in shape and measured 42-45 nm in diameter (intact hepatitis B viral particle), and can be visualized using electron microscope. It has a shell which has two layers; the outer shell is called the envelope protein and also referred to as hepatitis B surface protein, the inner shell is known as the core protein. The hepatitis B surface protein is further divided into S, M and L (small, middle and large) proteins respectively (Kann and Gerlich, 2007).

Hepatitis B surface antigen is an essential marker in screening and diagnostic assay as well as the principal serological marker of HBV infection. The detection limit for HBsAg, is directly proportional to diagnostic ability and inversely proportional to the amount of HBsAg, this implies that; the lower the detection limit for HBsAg, the smaller the diagnostic ability in early infection, most especially within the 'window phase' (Nick and Scheiblaue, 2007; Scheiblaue et al., 2006) and the higher the capability to detect the smallest amounts of HBsAg in chronic carriers and asymptomatic patients (Carman et al., 1997). HBsAg contains a region that is common to all hepatitis B subtypes called the *a* determinant (Howard and Allison, 1995). The *a* determinant region (codon 124–147) which is a two loop structure located in the major hydrophilic region of the surface antigen is the key target for the neutralizing antibody produced following vaccination or through hepatitis B natural infection (Waters, 1987). The emergence of mutation in this region (*a* determinant), may lead to evading neutralization by antibody produced against hepatitis B (anti-HBs) and escaped detection by current diagnostic assay, this leads to potential threat to vaccine efficacy and increases the risk of unsafe blood transfusion. The most effective preventive measure against hepatitis B is implementing early childhood hepatitis B vaccination.

Published data, reveals that; 95% of vaccines produced protective antibody to hepatitis B surface antigen (anti-HBs) providing long lasting immunity against hepatitis B infection in immunocompetent individuals (Gabbuti et al., 2007; Hammitt et al., 2007). However, the extent of the anti-HBs response is essentially influenced by vaccine regimen, site, route of administration, age immunocompetency and body mass (Zuckerman, 1996). Incorporating infant hepatitis B vaccine into universal immunisation strategy may lead to sustained decreased in HBV prevalence and related death as observed in countries that have successfully eliminate it most especially countries that were classified previously as high endemic area, but now classified as low endemic (Zanetti, 2008). In Thailand, prevalence of HBV drops drastically to 0.7% 12 years after implementing universal hepatitis B vaccination for children between 6 months and 18 years of age (Chongsrisawat et al., 2006). Similarly, in Taiwan up to 87% decline in HBV seroprevalence was achieved 20 years post routine infant vaccination with 68% decreased in rate of fulminant hepatitis as well as 75% drop in hepatocellular carcinoma (HCC) (Chien, 2006). Likewise, in Malaysia the prevalence of HBV among children decreases to 0.4% from 3.0% prior to introduction universal infant hepatitis B vaccination (Ng et al., 2005). However, the prevalence in general population ranges from 1.5 to 9.8% but reported to be lower (0.4%) among repeated blood donors (Yousuf et al., 2007).

The predominant mode of transmission in Asia Pacific is perinatal, and the disease is transmitted vertically during early childhood from mother to the infant (Dwivedi et al., 2011; Shao et al., 2011), however, both horizontal and vertical transmission have been reported in the Sub Saharan Africa (Botha et al., 1984). In Southeast Asia, about 100 million people are chronic carriers of HBV, with estimated annual mortality of 300,000 mainly due to hepatocellular carcinoma (HCC) and liver cirrhosis. Therefore, all countries in the Asia Pacific Region view hepatitis B as a serious public health issue and maintain policies, goals and plans, targeting at prevention and control of hepatitis B, but in most countries, implementation is not sufficient, sometimes following a series of uncoordinated programmes rather than a consistent strategic approach (WHO 2011).

Hepatitis B viral infection affects more than 2 billion people globally, with at least 378 million chronic infections, which stand at risk of developing fulminant hepatitis, HCC and death (WHO, 2009). In the United States, nearly 78,000 people are infected with HBV in 2001 with the highest infection rate in young adults and annual mortality of about 5,000 people (www.cdc.gov/mmwr/preview/mmwrhtml/mm5251a3.htm). While in Malaysia, hepatitis B carriers were estimated to be 2.4 million people, constituting a potential source of infection (Malaysian Liver Foundation, 2005). In 1997, 5.24% of healthy volunteers, screened for HBsAg were found to be positive (Merican et al., 2000).

Since 1989, it has been a policy in Malaysia to vaccinate newborn, against HBV, thus HBsAg seroprevalence is expected to decline over time. However, persistence of immunity into adolescence and adulthood is the key marker for a successful infant vaccination. Mutations in the HBsAg, also called S-gene mutations have several clinical effects, including; (i) reduced sensitivity to available diagnostic tests, (ii) lack of immunity following vaccination with non-mutant HBV variant (vaccine escaped mutant) and (iii) failure of passive immunization with hepatitis B specific immunoglobulin (El Chaar, 2010). Failure of diagnostic assay may be a major threat in recipients of blood transfusion or organ transplant (Levicnik-Stezinar, 2004; Thakur et al., 2005). Hepatitis B surface mutants are stable and can be spread through either vertical, or horizontally transmission (Hunt et al., 2000).

WHO has set up year 2012 as target to achieve less than 2% seroprevalence of HBV for all countries of the world (WHO 2008), in order to actualize this goal, Malaysia embarked on childhood vaccination against HBV from 1989 to date, however, there is lack of information regarding the assessment of HBV vaccination as well as the seroprevalence of surface antigen mutation status of Malaysian population. Moreover, HBV surface mutation is becoming a worldwide problem and the mutants seldom respond to the currently available screening and diagnostic assays. Therefore the study of persistence of immunity post hepatitis B vaccination as well as vaccine and diagnostic escaped hepatitis B infection is essential, hence, the objectives of this study.

General Objective

To study the persistence of immunity post hepatitis B vaccination as well as occult hepatitis B infection among healthy volunteers.

Specific Objectives

1. To evaluate the persistence of immunity following childhood hepatitis B vaccination among vaccinated undergraduate student.
2. To investigate the prevalence of isolated hepatitis B core antibody and its response to vaccine booster among vaccinated undergraduate Students.
3. To detect occult hepatitis B viral infection among blood donors and undergraduate students using serological and molecular methods.
4. To perform molecular characterization of occult hepatitis B virus using bioinformatics tools.

Hypothesis

H_{A1}: There is persistence Immunity following childhood hepatitis B vaccination among undergraduate student.

H_{A2}: Isolated anti-HBc is prevalent among vaccinated undergraduate student and it response to hepatitis B vaccine booster

H_{A3}: HBsAg mutation is prevalent among among blood donors and undergraduate student in Malaysia.

H_{A4}: There is significant genetic diversity among hepatitis B surface antigen mutant detected in blood donors and undergraduate students.



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