Comparing risk factors for hepatitis B infection between indigenous and non-indigenous population in Pahang based on a 5-year database

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ABSTRACT

Introduction: Despite substantial progress in reducing hepatitis B prevalence in the general population, the indigenous population in Malaysia continues to face a significant burden of infection, with high seroprevalence rates. It is hypothesised that transmission patterns differ between the indigenous and non-indigenous populations. This study aimed to compare key risk factors for hepatitis B transmission in indigenous and non-indigenous cases.

Materials and Methods: This is a comparative cross-sectional study using secondary data from the eNotifikasi system and hepatitis B case investigation forms between 2018 and 2022 from four district health offices in Pahang, Malaysia. Demographic data, hepatitis B vaccination status and risk factors were assessed. Data analysis employed independent chi-squared tests, t-tests and binary logistic regression.

Results: The study included 285 cases (141 indigenous and 145 non-indigenous). Among the indigenous cases, 72.3% were unvaccinated and 59.6% reported a history of infected mother, followed by percutaneous exposure, multiple sexual partners, and sharing syringe. The odds for those with a history of an infected mother being indigenous group is 2.5 times (95% CI: 1.4–4.4) compared to those with a history of an infected mother being non-indigenous group.

Conclusion: Significant difference exists in hepatitis B risk factors between indigenous and non-indigenous populations. The main risk factor for indigenous community is history of infected mother. Thus, the necessity of incorporating hepatitis B screening into the current practice of antenatal HIV screening, specifically targeting the indigenous community, should be given consideration.

KEYWORDS:

Hepatitis B, indigenous peoples, risk factors

INTRODUCTION

Hepatitis B infection poses a major global public health challenge, leading to the development of chronic liver diseases such as cirrhosis and hepatocellular carcinoma, resulting in an estimated 820,000 deaths each year. Despite its highly infectious nature, this disease is preventable through vaccination, screening and the implementation of harm reduction programmes. The transmission of hepatitis B occurs through four main routes, namely perinatal, percutaneous, sexual and close person-to-person contact, often facilitated via open cuts and sores. In areas with a high prevalence of infection, vertical transmission is believed to be the primary mode of transmission.

Over the years, Malaysia has made outstanding progress in reducing the prevalence of hepatitis B infection within its general population. From an intermediate seroprevalence rate of 5.2% in the 1990s, the country has achieved a remarkable decline, with current rates ranging between 1.1% and 1.7%. Despite this, the indigenous population in Malaysia continues to face a considerable burden of hepatitis B infection, with high seroprevalence rates of 8.7% and 10.3%.

The higher prevalence of hepatitis B among indigenous populations compared to the general population is a well-known phenomenon. Similar trends have been observed in other countries as well. For instance, in Australia, the seroprevalence of hepatitis B virus among indigenous Australians is reported to be 6.1%, significantly higher than the rate of 1.6% among non-indigenous Australians. Likewise, high endemicity of hepatitis B infection has been found among certain indigenous communities in Mexico and Venezuela in Latin American countries.

In the general population, hepatitis B cases predominantly occur among Malay males aged between 20 and 40 years, with intravenous drug abuse being the main transmission route. However, there is a scarcity of research exploring the risk factors for hepatitis B transmission, specifically within the indigenous community in Malaysia. A study conducted by Sahlan et al. shed some light on this issue, revealing that among the indigenous community, hepatitis B cases mostly involve males above 35 years of age, and potential modes of transmission include perinatal exposure, tattooing and body piercing. However, it is important to note that this study had a small sample size and focused solely on the Negrito tribes.

Indigenous people in the Peninsular Malaysia are classified into three main groups: Negrito, Senoi and Proto-Malay.
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Among them, a notable proportion, accounting for 37.9%, reside in the state of Pahang. As a result, Pahang is noteworthy for having the highest number of indigenous communities compared to other states in the Peninsular Malaysia. The indigenous population in Pahang is estimated to be approximately 80,924 individuals, constituting approximately 5% of the state’s total population.

Given the notably higher prevalence of hepatitis B infection within the indigenous community compared to the general population, it is postulated that there may exist distinct patterns of transmission in contrast to the non-indigenous population. Therefore, this study aimed to compare the risk factors for hepatitis B transmission between the indigenous and non-indigenous cases.

MATERIALS AND METHODS
Study Design
This is a comparative cross-sectional study using secondary data obtained from eNotifikasi (online infectious disease notification system for Ministry of Health Malaysia) and hepatitis B case investigation forms (HepB/1x/1-2008 form) that were available at the district health offices. These forms were employed by the district health inspectors during field investigations for each notified hepatitis B case in the eNotifikasi system.

Locations and Study Population
The study was conducted in four district health offices, namely Rompin, Pekan, Kuala Lipis and Temerloh. These districts were selected because they have the highest number of indigenous population within the state. Data collection for the study was carried out in June 2023. The study population comprised individuals diagnosed and reported with hepatitis B infection in the state of Pahang, while the sampling frame consisted of hepatitis B infection cases reported in the eNotifikasi system within the four selected districts from the year 2018 to 2022.

Data Collection and Sampling Strategy
The inclusion criteria were individuals in the four selected districts who were registered as having hepatitis B based on eNotifikasi (online infectious disease notification system between the year 2018 and 2022 with positive hepatitis B surface antigen (HbsAg)). This was based on the Ministry of Health’s Case Definitions for Infectious Diseases in Malaysia, which defined a confirmed chronic hepatitis B case as the presence of HbsAg in the patient’s blood for a duration of more than 6 months. However, considering the challenges in accurately determining the exact duration of positive HbsAg, the criterion for chronic illness was simplified to include individuals who tested positive for HbsAg alone, as suggested by Terrault et al.

Exclusion criteria encompassed non-Malaysian individuals, cases lacking an investigation form and cases with incomplete data specifically pertaining to hepatitis B vaccination status and risk factors.

The relevant information, such as hepatitis B immunisation status and risk factors for hepatitis B infection, was extracted from the investigation forms. In cases where multiple risk factors were reported, all of these factors were included in the analysis.

Initially, this study intended to classify the cases into two groups: indigenous and non-indigenous, followed by random sampling method. However, during the data collection phase, it became apparent that a significant number of randomly selected subjects did not meet the inclusion and exclusion criteria, particularly concerning the availability of investigation forms. As a result, the cases were still categorised into two groups, but the sampling strategy subsequently shifted to universal sampling, involving the examination of all hepatitis B investigation forms available at the district health offices.

Sample Size
The sample size for this study was determined using OpenEpi software version 3.01. The calculation took into account the prevalence rates of hepatitis B infection in both the general population and the indigenous population in Pahang. The prevalence of hepatitis B infection in the general population (1.7%) was derived from the National Health and Morbidity Survey (NHMS) 2020, while the prevalence among the indigenous population in Pahang (10.3%) was obtained from the study by Mohd Firdaus et al.

To achieve a statistical power of 80% and a significance level (alpha) of 0.05, a sample size of 240 was initially calculated. Considering a potential 20% rate of missing data, the minimum required sample size for this study was adjusted to 288 (144 for each group).

Data Analysis
The collected data was entered into SPSS software version 28.0 for analysis. The investigation forms identified multiple risk factors for hepatitis B infection, which were regrouped in this study to facilitate analysis. The final classification of the risk factors for the transmission is as follows:

i) Infected mother—refers to cases where the mother has a reported history of hepatitis B infection

ii) Infected spouse/partner—refers to cases where the spouse/partner has a reported history of hepatitis B infection

iii) History of medical procedures—any history of healthcare procedure, such as surgery, dental treatment, blood transfusion and haemodialysis

iv) History of percutaneous exposure—any history of process that involves puncturing through the skin, such as acupuncture, tattooing and body piercing

v) Sharing syringes—refers to a history of sharing syringes and/or needles while intravenously administering illegal substances

vi) Multiple sexual partners—refers to a history of engaging in high-risk sexual practices involving multiple partners

A comparison of socio-demographic characteristics and risk factors for hepatitis B infection between the two groups was conducted using independent chi-squared tests and t-tests. Subsequently, binary logistic regression was performed to compare the risk factors for hepatitis B infection between indigenous and non-indigenous cases, while adjusting for age at diagnosis and hepatitis B vaccination status, which
Comparing risk factors for hepatitis B infection between indigenous and non-indigenous population

Table I: Comparing the socio-demographic characteristics for hepatitis B transmission between the indigenous and non-indigenous cases in four districts in Pahang, 2018–2022 (n = 285)

<table>
<thead>
<tr>
<th>Risk factor</th>
<th>Indigenous (n = 141)</th>
<th>Non-indigenous (n = 144)</th>
<th>Total (n = 285)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sex</td>
<td>Male</td>
<td>65 (46.1)</td>
<td>81 (56.3)</td>
<td>146 (51.2)</td>
</tr>
<tr>
<td></td>
<td>Female</td>
<td>76 (53.9)</td>
<td>63 (43.8)</td>
<td>139 (48.8)</td>
</tr>
<tr>
<td>Age at diagnosis (years)</td>
<td></td>
<td>34.4 (16.5)</td>
<td>47.5 (16.5)</td>
<td>41.0 (17.6)</td>
</tr>
<tr>
<td>Area of residence</td>
<td>Urban</td>
<td>1 (0.7)</td>
<td>42 (29.2)</td>
<td>43 (15.1)</td>
</tr>
<tr>
<td></td>
<td>Rural</td>
<td>140 (99.3)</td>
<td>102 (70.8)</td>
<td>242 (84.9)</td>
</tr>
<tr>
<td>Districts</td>
<td>Rompin</td>
<td>86 (61.0)</td>
<td>62 (43.1)</td>
<td>148 (51.9)</td>
</tr>
<tr>
<td></td>
<td>Kuala Lipis</td>
<td>48 (34.0)</td>
<td>38 (26.4)</td>
<td>86 (30.2)</td>
</tr>
<tr>
<td></td>
<td>Pekan</td>
<td>7 (5.0)</td>
<td>16 (11.1)</td>
<td>23 (8.1)</td>
</tr>
<tr>
<td></td>
<td>Temerloh</td>
<td>0 (0.0)</td>
<td>28 (19.4)</td>
<td>28 (9.8)</td>
</tr>
<tr>
<td>No hepatitis B vaccination</td>
<td></td>
<td>102 (72.3)</td>
<td>125 (86.8)</td>
<td>227 (79.6)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>ß</th>
<th>S.E.</th>
<th>Wald</th>
<th>df</th>
<th>p value</th>
<th>Adjusted OR</th>
<th>95% CI OR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infected mother</td>
<td>0.89</td>
<td>0.30</td>
<td>8.87</td>
<td>1</td>
<td>0.030</td>
<td>2.45</td>
</tr>
<tr>
<td>History of percutaneous exposure</td>
<td>0.57</td>
<td>0.46</td>
<td>1.52</td>
<td>1</td>
<td>0.218</td>
<td>1.77</td>
</tr>
<tr>
<td>Multiple sexual partners</td>
<td>−0.17</td>
<td>0.50</td>
<td>0.12</td>
<td>1</td>
<td>0.727</td>
<td>0.84</td>
</tr>
<tr>
<td>Infected spouse/partner</td>
<td>1.06</td>
<td>0.59</td>
<td>3.28</td>
<td>1</td>
<td>0.070</td>
<td>2.90</td>
</tr>
<tr>
<td>Sharing syringes</td>
<td>−1.19</td>
<td>0.69</td>
<td>2.96</td>
<td>1</td>
<td>0.085</td>
<td>0.31</td>
</tr>
<tr>
<td>History of medical procedures</td>
<td>−1.02</td>
<td>0.82</td>
<td>1.54</td>
<td>1</td>
<td>0.215</td>
<td>0.36</td>
</tr>
</tbody>
</table>

*Within the indigenous or non-indigenous group.  
1Within total sample.

Table II: Comparing the risk factors for hepatitis B transmission between the indigenous and non-indigenous cases in four districts in Pahang, 2018–2022 (n = 285)

<table>
<thead>
<tr>
<th>Risk factors</th>
<th>Indigenous (n = 141)</th>
<th>Non-indigenous (n = 144)</th>
<th>Total (n = 285)</th>
<th>p value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infected mother</td>
<td>84 (59.6)</td>
<td>45 (31.3)</td>
<td>129 (45.3)</td>
<td>0.002</td>
</tr>
<tr>
<td>History of percutaneous exposure</td>
<td>17 (12.1)</td>
<td>11 (7.6)</td>
<td>28 (9.8)</td>
<td>0.210</td>
</tr>
<tr>
<td>Multiple sexual partners</td>
<td>9 (6.4)</td>
<td>15 (10.4)</td>
<td>24 (8.4)</td>
<td>0.220</td>
</tr>
<tr>
<td>Infected spouse/partner</td>
<td>11 (7.8)</td>
<td>5 (3.5)</td>
<td>16 (5.6)</td>
<td>0.112</td>
</tr>
<tr>
<td>Sharing syringes</td>
<td>3 (2.1)</td>
<td>13 (9.0)</td>
<td>16 (5.6)</td>
<td>0.011</td>
</tr>
<tr>
<td>History of medical procedures</td>
<td>2 (1.4)</td>
<td>10 (6.9)</td>
<td>12 (4.2)</td>
<td>0.020</td>
</tr>
<tr>
<td>Undetermined</td>
<td>28 (19.9)</td>
<td>53 (36.8)</td>
<td>81 (28.4)</td>
<td>0.002</td>
</tr>
</tbody>
</table>

*Within the indigenous or non-indigenous group.  
1Within total sample.

Table III: Comparing the risk factors for hepatitis B infection between the indigenous and non-indigenous cases, adjusted for age at diagnosis and hepatitis B vaccination status, in four districts in Pahang, 2018–2022 (n = 285)

<table>
<thead>
<tr>
<th>Mode of transmission</th>
<th>ß</th>
<th>S.E.</th>
<th>Wald</th>
<th>df</th>
<th>p value</th>
<th>Adjusted OR</th>
<th>95% CI OR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Infected mother</td>
<td>0.89</td>
<td>0.30</td>
<td>8.87</td>
<td>1</td>
<td>0.030</td>
<td>2.45</td>
<td>1.36, 4.40</td>
</tr>
<tr>
<td>History of percutaneous exposure</td>
<td>0.57</td>
<td>0.46</td>
<td>1.52</td>
<td>1</td>
<td>0.218</td>
<td>1.77</td>
<td>0.72, 4.37</td>
</tr>
<tr>
<td>Multiple sexual partners</td>
<td>−0.17</td>
<td>0.50</td>
<td>0.12</td>
<td>1</td>
<td>0.727</td>
<td>0.84</td>
<td>0.32, 2.23</td>
</tr>
<tr>
<td>Infected spouse/partner</td>
<td>1.06</td>
<td>0.59</td>
<td>3.28</td>
<td>1</td>
<td>0.070</td>
<td>2.90</td>
<td>0.92, 9.17</td>
</tr>
<tr>
<td>Sharing syringes</td>
<td>−1.19</td>
<td>0.69</td>
<td>2.96</td>
<td>1</td>
<td>0.085</td>
<td>0.31</td>
<td>0.08, 1.18</td>
</tr>
<tr>
<td>History of medical procedures</td>
<td>−1.02</td>
<td>0.82</td>
<td>1.54</td>
<td>1</td>
<td>0.215</td>
<td>0.36</td>
<td>0.07, 1.81</td>
</tr>
</tbody>
</table>

OR = odds ratio.  
Adjusted for age at diagnosis and hepatitis B vaccination status.
RESULTS
Between 2018 and 2022, a total of 655 hepatitis B cases were registered in the four districts of Pahang. Among these cases, 566 were identified as Malaysians. After applying other exclusion criteria (a lack of an investigation form or incomplete data on the investigation form), 285 cases (141 indigenous and 144 non-indigenous cases) remained and were therefore included in the final analysis of this study (Fig. 1).

The mean age for all cases was 41.0 (17.8) years. The indigenous group had a younger age profile, with individuals averaging 34.4 (16.5) years, while the non-indigenous group had an older mean age of 47.5 (16.5) years. The majority of the cases (84.9%) resided in rural areas, with the indigenous group almost exclusively located in rural areas (99.3%). In contrast, only 70.8% of non-indigenous cases resided in rural areas (Table I).

A notable proportion (79.6%) has not received prior hepatitis B vaccination. Specifically, 72.3% of indigenous cases and 86.8% of non-indigenous cases reported no history of hepatitis B vaccination. Of these cases, 45.3% reported a history of their mother being infected with hepatitis B, while 9.8% reported a history of percutaneous exposure. Other factors reported included multiple sexual partners (8.4%) and sharing syringes or having infected partners (both 5.6%) (Table II).

Table III presents the odds ratios and corresponding 95% confidence intervals, adjusted for age at diagnosis and vaccination status, of the risk factors for hepatitis B infection. The odds for those with a history of an infected mother being indigenous group is 2.5 times (95% CI: 1.4–4.4) compared to the odds of those with a history of an infected mother being non-indigenous group.

DISCUSSION
In the socio-demographic findings of this study, a remarkable 13-year gap emerged between the two groups, indicating that indigenous cases were diagnosed at an earlier age. This difference could be linked to the pilot implementation of universal hepatitis B screening among pregnant women in Pahang since 2019, as part of the National Strategic Plan For Hepatitis B And C 2019–2023. This initiative likely led to intensified contact tracing and screening efforts, especially among the younger family members, such as husbands and children. Given the presumption that vertical transmission is more prevalent in the indigenous people, it is possible that the detection of positive cases among their younger generation is higher. Nevertheless, the statistical analysis for this study has been appropriately adjusted for age.

Moreover, almost all indigenous individuals in this study were found to reside in the rural areas. This pattern is likely a reflection of cultural ties, consistent with findings from a study among indigenous people in Australia, which
Comparing risk factors for hepatitis B infection between indigenous and non-indigenous population

demonstrated a stronger cultural attachment among those living in the remote areas. Similar observations were noted in Malaysia, where the unique customs and taboos of some indigenous groups were found to be significantly influenced by the remoteness of their settlements. Since the 1980s, resettlement programmes have been implemented in Malaysia to facilitate the provision of public utilities and amenities, as well as to improve the socio-economic profile of the indigenous people, but the locations of these resettlements have been concentrated in the rural areas. However, in more recent times, the impact of modernisation has emerged as a factor contributing to the erosion of cultural beliefs among these communities, potentially signalling a shift in this residential trend in the future.

Our study found that a substantial proportion (79.6%) of hepatitis B cases were found to have no history of prior hepatitis B vaccination. Other notable risk factors for the infection included having an infected mother (45.3%), percutaneous exposure (9.8%), having multiple sexual partners, sharing syringes and having infected spouses or partners. Most of these findings differ from the NHMS 2020, which indicated a higher prevalence of histories of medical procedures (dental and surgical procedures) associated with hepatitis B infection among the general population. It is also noteworthy to highlight that in NHMS 2020, zero respondent reported any history of unsafe sexual practices or injectable substance use. The only common similarity observed between NHMS 2020 and this study is the presence of a family history of hepatitis B and percutaneous exposure as the risk factors for hepatitis B infection.

These variations can be attributed to differences in methodology. The NHMS 2020 utilised multistage random sampling from the general population, specifically adult populations aged 15 and above, encompassing both healthy participants and those with hepatitis B. In contrast, our study’s sample population specifically concentrated on individuals diagnosed with hepatitis B infection. Additionally, the NHMS 2020 employed self-administered questionnaires to assess participants’ risk factors, whereas our study relied on investigation forms completed by health inspectors who performed face-to-face interviews with the patients. Moreover, as the NHMS 2020 was conducted nationally, unlike our study which focused solely on one East Coast state in the Peninsular Malaysia, it is likely that there are disparities in demographic characteristics, socio-economic conditions and healthcare infrastructures among these diverse populations.

Our study found that the risk factors of hepatitis B transmission between the indigenous and non-indigenous population are different. Among the indigenous population, mother-to-child transmission is a significant risk factor as compared to non-indigenous population. This is consistent with previous research conducted in Malaysia and Australia, which also identified vertical transmission as a primary mode of hepatitis B transmission among aboriginal communities. The high prevalence of hepatitis B among the indigenous population likely contributes to the heightened risk of vertical transmission. Additionally, limited access to preventive interventions might exacerbate this issue. A systematic review by Akter et al. suggested that the indigenous women in lower- and middle-income countries face challenges in accessing maternal healthcare services due to culturally insensitive intervention programmes, along with financial and logistical barriers. Similar phenomenon has also been observed in Malaysia, where the indigenous community experiences unequal accessibility to healthcare services.

Contrary to Sahlan et al., this study discovered that percutaneous exposure, such as tattooing or body piercing, is not a significant risk factor for hepatitis B infection among indigenous population as compared to non-indigenous population. This discrepancy may be attributed to variations in the indigenous populations studied. Sahlan et al. focused on the Negrito tribe (Bateq and Mendriq), whereas this study primarily involved the Proto-Malay tribe (Jakun) in Rompin and Pekan districts and the Senoi tribe (Semai) in Kuala Lipis district, with only a small proportion of the Negrito tribe (Bateq) in Kuala Lipis. Further research is required to comprehend the prevailing trends of tattooing or body piercing within the indigenous population, particularly among the younger generation.

In addition, a cross-sectional study on indigenous populations in Peru highlighted sexual contact as a significant risk factor for hepatitis B infection, which was not observed in this study. This disparity may stem from the differences in the study design. While our study sample population focused exclusively on individuals diagnosed with hepatitis B, the Peru study included both healthy participants and those with hepatitis B. Furthermore, substantial variations in socio-economic conditions, healthcare infrastructures, and cultural practices likely exist between Peru and Malaysia, potentially influencing the observed differences in risk factors across these populations.

Recognising the distinct pattern of risk factors for hepatitis B infection among the indigenous population, it is important to adopt targeted strategies in an effort to address this issue. This is in line with WHO’s recommendation that indigenous people need tailored approaches in the prevention, care and treatment of hepatitis B infection. Therefore, it is recommended to implement perinatal hepatitis B screening programme specifically targeting the indigenous community. Additionally, once a hepatitis B infection is diagnosed, appropriate interventions and treatments for both the mothers and their children should be promptly administered, such as immunophylaxis with hepatitis B immunoglobulin and antiviral treatment.

**Strengths and Limitations**

This is the first study comparing the risk factors for hepatitis B transmission between the indigenous and non-indigenous groups in Malaysia. This study’s strength lies in the more reliable data on the risk factors for hepatitis B transmission since the investigations were conducted by health inspectors, who were presumed to possess a deep understanding of the local culture and norms, through face-to-face interviews with the cases. Furthermore, the risk factors analysed in this study were adjusted for age and hepatitis B vaccination status, thus accounting for potential confounding variables to provide a more accurate understanding of the situation.
One limitation of this study is the reliance on secondary data, which consisted of readily available information only. This constraint restricts the study’s ability to address additional questions that may be of interest to the researchers. Regarding data collection, it is important to acknowledge that the quality of the data depended heavily on the competence and experience of the health inspectors performing the investigations. Without proper systematic pre-data collection training similar to other research utilising primary data, the standardisation of the interview process could not be guaranteed, increasing the risk of interviewer bias.

Another aspect contributing to the study’s limitations is the exclusion of cases, specifically, 38.7% of indigenous cases and 52% of non-indigenous cases were not included due to missing investigation forms or incomplete data, which may potentially give rise to selection bias. As a result, universal sampling method was employed to mitigate selection bias and enhance the validity of this study.

CONCLUSION
Significant differences exist in hepatitis B risk factors between indigenous and non-indigenous populations. The main risk factor for indigenous community is the history of infected mother. Therefore, the necessity of incorporating hepatitis B screening into the current practice of antenatal HIV screening, specifically targeting the indigenous community, should be given consideration. In addition, it is essential to maximise the coverage of hepatitis B vaccination to effectively address the transmission risk within these communities.

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