# Article information:

Molecular evaluation of hepatitis B virus infection and predominant mutations of pre-core, basal core promoter and S regions in an Iranian population with type 2 diabetes mellitus: a case-control study - PubMed
<https://pubmed.ncbi.nlm.nih.gov/35715756/>

# Article summary:

1. A case-control study was conducted to evaluate the prevalence, genotypic patterns, and predominant mutations of hepatitis B virus (HBV) infection among diabetic patients in Iran.

2. Of 733 diabetic patients, 12.82% were positive for HBcAb, 3.82% were positive for HBsAg, and 2.59% had HBV-DNA with genotype D, sub-genotype D1/D3 and subtype ayw2.

3. P120T/G145R, G1896A/G1899A, and A1762T/G1764T were the most frequent point substitution mutations detected in the S, pre-core, and BCP regions of the HBV genome respectively.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

This article is a case-control study that evaluates the prevalence, genotypic patterns, and predominant mutations of hepatitis B virus (HBV) infection among diabetic patients in Iran. The authors used nested PCR targeting S and pre-core regions of the HBV genome followed by sequencing to determine HBV genotypes and predominant mutations in the S, basal core promoter (BCP), and pre-core regions of the HBV genome. The results showed that 12.82% of 733 diabetic patients were positive for HBcAb, 3.82% were positive for HBsAg, and 2.59% had HBV-DNA with genotype D, sub-genotype D1/D3 and subtype ayw2. P120T/G145R, G1896A/G1899A, and A1762T/G1764T were the most frequent point substitution mutations detected in the S, pre-core, and BCP regions of the HBV genome respectively.

The article is generally reliable as it provides detailed information on its methods used to collect data as well as its results from testing samples from both diabetic patients and non-diabetic controls which allows readers to draw their own conclusions about its findings without bias or partiality from the authors’ side. Furthermore, it also mentions potential risks associated with screening for hepatitis B virus infection such as false positives or false negatives due to low sensitivity or specificity of tests used which shows that possible risks are noted by authors when conducting this study which adds to its trustworthiness even more so than if these risks are not mentioned at all in this article.

However there are some points that could be improved upon such as providing more details on how exactly samples were collected from both groups (diabetic patients vs non-diabetic controls). Additionally there could be more discussion on other factors that may have contributed to higher prevalence rates of hepatitis B virus infection among diabetic patients such as lifestyle choices or environmental factors which could provide further insights into why this population is more susceptible to this type of infection compared to non-diabetics controls who have lower prevalence rates according to this study’s findings.

# Topics for further research:

* Hepatitis B virus infection prevalence
* Diabetes and hepatitis B virus infection
* Nested PCR for HBV genotyping
* Point substitution mutations in HBV genome
* Risk factors for HBV infection in diabetics
* False positives and false negatives in HBV testing

# Report location:

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