Comparative Analysis of the Virological and Clinical Spectrum of HBeAg-Negative and HBeAg-Positive Chronic Hepatitis B Infections

Authors:
Athalye S[1], Banerjee A[1], Khargekar N[1], Panale P[1], Shinde S[1], Pujari V[1], Swamidurai G[1], Chavan S[1]

[1] ICMR-National Institute for Research on Blood and Immune Disorders, Mumbai, India

Background: *HBeAg plays a key role in the virus-host interaction and the development of chronic infection. HBeAg-negative chronic hepatitis B (CHB) has emerged as a major form of HBV-related liver disease worldwide and is associated with progressive liver damage despite the absence of detectable HBeAg. HBeAg-negative CHB can progress to cirrhosis, with annual progression rates of 3% to 10%, while spontaneous remissions are rare (under 2%). This study compared the clinical, biochemical, and molecular characteristics of HBeAg-negative and HBeAg-positive CHB patients.*

Methods: *Sixty CHB patients (30 HBeAg-positive and 30 HBeAg-negative) were enrolled. HBeAg and anti-HBe were detected by ELISA. HBV DNA was extracted and the surface (S), precore/core (preC/C), and polymerase (P) genes were amplified by nested PCR and sequenced. Mutations and genotypes were identified using Chromas, Geno2Pheno, and NCBI genotyping tools.*

Results: *HBeAg-positive patients demonstrated higher HBV DNA levels (6.95 vs. 3.46 $\log_{10}$ IU/mL) and elevated liver enzymes compared with HBeAg-negative patients. Among HBeAg-negative cases, 93.3% were anti-HBe positive and 16.7% were inactive carriers. The S, P, and preC/C genes were detected in 85.0%, 86.7%, and 76.7% of samples, respectively. Genotype D predominated in both groups. Surface gene mutations T118V, T127P, and A128V were observed in 17.39% of HBeAg negative cases, while T118V and A128V appeared in 23.07% of HBeAg positives. T127P was found in 7.69% of HBeAg positives (p=0.4002). No samples showed the G1896A precore mutation, indicating HBeAg negativity was not due to spontaneous mutations. Core start-codon mutations were identified in 30.0% of HBeAg-negative and 73.1% of HBeAg-positive cases.*

Conclusion: *Distinct molecular and clinical profiles were observed between HBeAg-negative and HBeAg-positive CHB patients. Viral mutations may influence immune escape, viral persistence, and disease progression. Molecular characterization of HBV remains important for understanding pathogenesis and guiding diagnostic and management strategies.*

Disclosure of Interest Statement: The authors declare no competing interests. No commercial funding or industry support was received for this study. The study was conducted as part of institutional research activities.