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HBV genetic diversity: Implication in pathology, therapy and evolution of infection

epatitis B virus (HBV) is responsible of chronic HBV genotypes and to detect the presence of viral infection in 350 million people worldwide and represents a major factor for liver cirrhosis and hepatocellular carcinoma. There are eight main HBV genotypes with particular geographic distribution. Mutations appear as a response to external pressure and host's conditions. Assays are available to determine

mutants, including those that confer drug resistance. Vaccine escape mutants are also studied. The genetic diversity of HBV plays an important role in the evolution of HBV infections and has been associated with clinical outcome and response to antiviral therapy.

Biography

Lia Monica Junie is an MD, PhD and the professor at the Microbiology Department of Iuliu Hatieganu University of Medicine and Pharmacy, Cluj Napoca, Romania. She is leadership PhD doctor's thesis in Medicine field. She is a board member of European professional Societies ESCMID (ESGCP Study Groups), Society of Chemotherapy, Scientia Parasitologica Pro Vita and is reviewer of international reviews, Member of International organizations, director/coordinator in research projects. She has more than 65 papers published in full in international journals and is an editorial board member of national reviews. She is an organizer/president, keynote, invited speaker and Chair of International and National Congresses.

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