High endemicity and low molecular diversity of hepatitis B virus infections in pregnant women in a rural district of North Cameroon

Submitted by Françoise Lunel... on Fri, 06/19/2015 - 13:55

Titre
High endemicity and low molecular diversity of hepatitis B virus infections in pregnant women in a rural district of North Cameroon

Type de publication
Article de revue

Auteur
Ducancelle, Alexandra [1], Abgueguen, Pierre [2], Birguel, Jacques [3], Mansour, Wael [4], Pivert, Adeline [5], Le Guillou-Guillemette, Hélène [6], Sobnangou, Jean-Jacques [7], Rameau, Amélie [8], Huraux, Jean-Marie [9], Lunel-Fabiani, Françoise [10]

Pays
Etats-Unis

Editeur
Public Library of Science

Ville
San Francisco

Type
Article scientifique dans une revue à comité de lecture

Année
2013

Langue
Anglais

Date
12/11/2013

Numéro
11

Pagination
e80346

Volume
8

Titre de la revue
PLoS One

ISSN
1932-6203

Mots-clés
Adolescent [11], Adult [12], Cameroon [13], Female [14], Genetic Variation [15], Genotype [16], Hepatitis B [17], Hepatitis B e Antigens [18], Hepatitis B Surface Antigens [19], hepatitis B virus [20], Humans [21], Middle Aged [22], Mutation [23], Phenotype [24], Pregnancy [25], Prevalence [26], Rural Population [27], Serotyping [28], Viral Load [29], Young Adult [30]
BACKGROUND: A program, supported by the GEMHEP (Groupe d'étude Moléculaire des Hépatites), was established in 2007 in the sanitary district of Tokombéré, to prevent perinatal transmission of hepatitis B virus (HBV). It comprises screening for HBV surface antigen (HBsAg) in all pregnant women and vaccinating the newborn if tests are positive.

METHODS/PRINCIPAL FINDINGS: 1276 women were enrolled in the study after providing informed consent. Demographic data and blood samples were available for 1267 of the enrolled patients. HBsAg was determined locally using a rapid test (Vikia HBsAg, Biomerieux). Tests for HBV and HDV virological markers (HBeAg, anti-HDV antibodies (Ab), HBV-DNA, HDV-RNA, HBV and HDV genotypes) were performed on the confirmed HBsAg-positive samples in the virology unit of the Angers University Hospital (France). HBsAg was found in 259 of the 1267 pregnant women (20.4%) between January 2009 and April 2010, of whom 59 were HBeAg-positive (22.7%) with high levels of HBV-DNA. Anti-HDV Ab were found in 19 (7.3%) of the HBsAg-positive women. The prevalence rates of HBsAg and HDV were not age-dependent whereas HBeAg carriers were statistically younger than non carriers. Basal core promoter (BCP) and precore (PC) mutations and genotypes were determined by sequencing. Of 120 amplified sequences, 119 belonged to HBV genotype E (HBV/E) and the 9 HDV strains belonged to HDV clade 1. In the PC region, 83/228 patients (36.4%) harbored a G1896A mutant or mixed phenotype virus. In the BCP region, the double mutation A1762T/G1764A and the G1757A substitution were detected respectively in 26/228 patients (11.4%) and 189/228 patients (82.8%).

CONCLUSIONS: Our results confirm the high prevalence and low molecular diversity of HBV in Far Northern Cameroon; more than 20% of the infected women were highly viremic, suggesting a high rate of HBV perinatal transmission and supporting the WHO recommendation to vaccinate at birth against hepatitis B.
