Reviewer's report

Title: Virologic and Clinical Characteristics of HBV Genotypes/Subgenotypes in 487 Chinese Pediatric Patients with CHB

Version: 1 Date: 22 June 2011

Reviewer: massimo ciccozzi

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Minor Essential Revision

The authors describe the virological clinical and molecular features of HBV genotypes in pediatric patients. They collected four hundred and eighty-seven patients during the years 2007 to 2010 from 302 hospital in Beijing, determining the genetic subtypes and the resistant mutations.

The authors analyzed the relationship between HBV subgenotypes and disease progression, finding that HBV/B2 genotype had a lower incidence of inflammation and fibrosis than C2 in pediatric patients.

This finding absolutely can contribute to improve knowledge of HBV subgenotypes in pediatric patients giving a good information for the management of the diseases in this country, but I have some comments to do:

Methods

Line 2

about the enrolment the authors have to better specify if consecutive enrolment or if they have design a specific study to avoid sample bias.

In detection of serological marker…….. Section

Lines 11 and 12

the authors wrote about phylogenetic analysis please delete “evolutionary” because the software used (Mega 4.0) do not give any possibility to make a tree under an evolutionary model but it is for computing the genetic distance only.

Analysis of genotypic/subgenotypic drug mutations

Line 2 and 3

“substitution…….for analysis” have to put in results section they are not methods.

Results

Line 3

please put in bracket the normal level parameter fo alanine-aminotransferase

Line 3 to 5

“ the subgenotype distribution……. For D”. put in table 1
“among the…normal level” please put this sentences after the sentence in line 8-9 “The main characteristic……Table1”. The result section have to start with this sentence.

Please unify table 2 table 3 and table 4 in only one table

Discussion

Line 6- 7
this sentence is very confuse d, the authors wrote about genotypes , the have put in methods section the phylogenetic analysis but I do not see any trees, please show the tress built in Mega software specifying the characteristic of the analysis otherwise is not correct to write about genotyping.

In the sentence “ the difference…… to confirm the conclusion” the comparison between children and adult do not make sense with the paper and the analysis , maybe the authors have to discuss about the not statically results by the point of view of the short time of infection and therapy in pediatric cohort. Moreover I advise to analyze the sequences with phylogeny using the maximum Likelihood criteria because could be interesting to observe if the sequences are intermixed or not by the diseases status to enforce the hypothesis about the implication of C2 genotypes in disease progression also because the author have to take their affirmation with caution because larger population-based study is necessary and more appropriate genetic analysis ( i.e. genetic distance between the different genotypes involved in different disease status) are necessary.

Please check the conclusion and change the strong affirmation with probably or seems that and so on.

**Level of interest:** An article of limited interest

**Quality of written English:** Needs some language corrections before being published

**Statistical review:** No, the manuscript does not need to be seen by a statistician.