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## Hepatitis B Virus envelope variability of genotype A strains correlated with HBsAg persistence in patients with acute or chronic hepatitis B and in HBV/HIV co-infected patients.

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Around 240 million people are chronically infected by Hepatitis B virus (HBV) worldwide. The clearance of HBV surface Antigen (HBsAg) correlated with a good clinical prognosis is rarely achieved, even on anti-HBV treatments. HBV envelope proteins play a crucial role in virus cellular entry and in immune recognition. Our hypothesis is that the variability of HBV envelope proteins could influence HBsAg clearance or persistence, as suggested in our previous study on HBV genotype D (Velay et al., JVH, 2016). This study was extended to HBV genotype A infected patients with different clinical profiles: acute (n=4) or chronic hepatitis B (n=6) and HBV/HIV coinfection under treatment (n=6). In each group, patients with HBsAg clearance (Resolvers-R) were compared to Non-Resolvers (NR). For this purpose, HBV S and preS sequences were studied by bulk genotyping and ultra-deep sequencing (UDS). Amino acid sequences were analyzed with bioinformatics for predicted antigenicity. More frequent major mutations were observed in S gene than in preS region (p=0.02 in acute HBV infection). Among mutations found exclusively in NR, nine were observed several times (W4stop, T173K/A in preS; R79H, T118A, F134Y, Y161F, E164D, V209L in S). The mutation sY161F, found in four NR, led to a decrease in predicted antigenicity (22.6%). In the pol gene overlapping the S gene, the number of mutations tended to be higher in treated than in untreated patients (7.7 vs 3 mutations/patient). These results argue in favor of an influence of HBV envelope variability on the evolution of Hepatitis B in various clinical contexts.

### Biography

Marine ESCHLIMANN is a PhD student, currently the second year of her thesis. After a license in Cell Biology and Animal Physiology at the Faculty of Sciences, Reims, France, she focused on Microbiology in the Master BioMANE at the Faculty of Sciences, Nancy, France. After a study on bacterial biofilms, she was involved in a research program in Virology, in the University of Medicine, Nancy, France, with Pr E. Schvoerer *et al.* Thus she contributed to several investigations on the variability of HBV envelope proteins with the support of a ministerial scholarship.

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