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HBV/HIV co-infection and APOBEC3G polymorphisms in a population from Burkina Faso

Tegwinde Rebeca COMPAORE¹, Birama DIARRA¹, Maleki ASSIH¹, Dorcas Obiri-Yeboah², Serge Theophile SOUBEIGA¹, Abdoul Karim OUATTARA¹, Damehan TCHELOUGOU¹, Cyrille BISSEYE¹, Didier Romuald BAKOUAN³, Issaka Pierre COMPAORE¹, Augustine DEMBELE³, Wendkuuni Florencia DJIGMA¹, Jacques SIMPORE¹

¹ Pietro Annigoni Biomolecular Research Centre (CERBA), LABIOGENE, University Ouaga I Prof. Joseph KI-ZERBO, Ouagadougou, Burkina Faso,

² Department of Microbiology and Immunology, School of Medical Sciences, University of Cape Coast, Ghana

³ Permanent Secretary against Aids and sexually transmitted diseases, Burkina Faso

Laboratoire de Biologie Moléculaire et de Génétique (LABIOGENE), Web: www.labiogene.org

Background: Apolipoprotein B mRNA editing enzyme catalytic polypeptide-like 3G (APOBEC3G) is a potent host defense factor, which interferes with HIV-1 and HBV. Our study had three objectives, to screen a population of HIV-1 infected and uninfected patients in Burkina Faso for HBV, to screen the population for APOBEC3G variants rs6001417, rs8177832, and rs35228531 previously described, and to analyze the effect of these three variants and their haplotypes on HIV-1/HBV co-infection in Burkina Faso.

Methods: HBV detection was performed on samples from HIV-1 infected and uninfected subjects using rapid detection tests and real-time PCR. APOBEC3G genotyping was done by the TaqMan allelic discrimination method. Fisher Exact test, Odds ratio (OR), confidence intervals (CI) at 95%, Linkage disequilibrium (LD) summary statistics and haplotype frequencies were calculated.

Results: The prevalence of HBV was 56.7% among HIV-1 positive patients of our study while it was about 12.8% among HIV-1 seronegative subjects. Genotype E was the genotype of HBV present in our hepatitis B positive samples. Minor allele frequencies of rs6001417, rs8177832, and rs35228531 were higher in seronegative subjects. The T minor allele of variant rs35228531 was protective against HIV-1/HBV co-infection with OR = 0.61, 95% CI (0.42-0.90), p=0.013. There was also an association between the GGT haplotype and protection against HIV-1/HBV co-infection, OR= 0.57, 95% CI (0.33-0.99), p=0.050. The minor allele T of the rs35228531 was protective against HIV mono-infection OR=0.53, 95% CI (0.3 – 0.93), p=0.030. But there was no effect of protection against HBV mono-infection.

Conclusion: APOBEC3G through its variants rs6001417, rs8177832, and rs35228531, in this study interferes with HIV-1/HBV co-infection. The ladder could be due the HIV-1 mono-infection in a population from Burkina Faso.

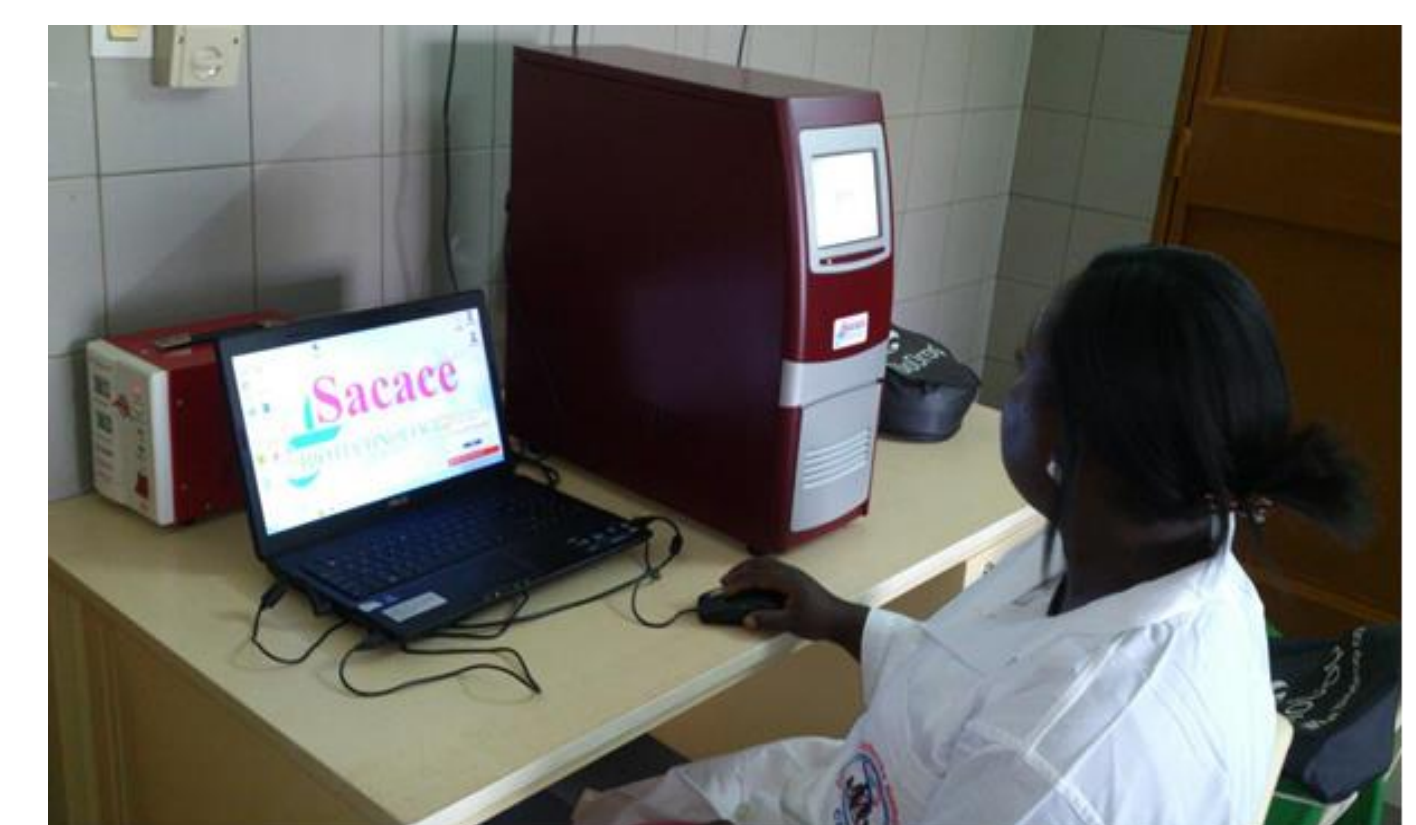
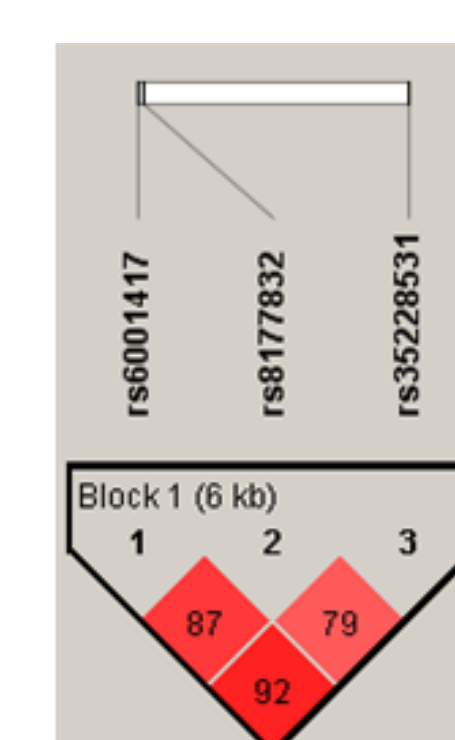


Fig 1. SaCycler-96 Real-time PCR (Sacace Biotechnologies, Italy)

Table I : Study participants' baselines data

	HIV(+)/HBV(+)	HIV(+)	HBV(+)	HIV(-)/HBV(-)
	n=85	(n=35)	(n=65)	n=239
Detectable HBV Viral Load	35	-	20	-
Mean HIV-1 Viral Loads	65,963.68 +/- 20,2480	6,758.13 +/- 30368.61	-	-
Mean CD4 counts	423.45 +/- 300.33	375.12 +/- 277.20	N/A	N/A
HBV genotypes E n (%)	100	-	100	-

a. VHB+/VIH+



b. Control

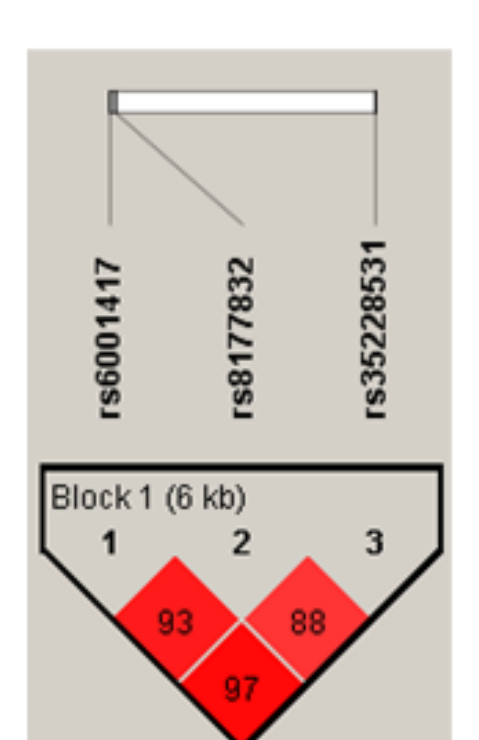


Fig 2. Linkage disequilibrium of 3 variants of APOBEC3G of cases and control

Table II: Haplotypes of HIV/HBV+ cases and controls

	HIV(+)/HBV(+)	HIV(-)/HBV(-)	OR	CI	p-Value
CAC	0.54	0.51	1.27	0.77 - 2.1	0.38
GGC	0.11	0.11	1.45	0.62 - 3.73	0.37
GGT	0.27	0.31	0.57	0.33 - 0.99	0.05
CGC	0.04	0.02	2.15	0.47 - 9.81	0.40
GAT	0.02	0.02	1.41	0.25 - 7.87	0.65
GAC	0.01	0.01	0.94	0.1 - 9.1	1