in all. Basal determinations of HBV-DNA (RT-PCR, Cobas TaqMan VHB) and quantitative HBsAg (Architect HBsAg; Abbott), with lower limit of detection of 0.05 IU/ml, were performed. Patients were prospectively followed annually or biannually, with a mean follow-up of 52±28 months.
Results: 57/297 (19%) were initially HBV-DNA negative. Mean HBsAg level was 8.852±17.700 IU/ml. During the follow-up, 49 patients (16.5%) became HBsAg-negative. In univariate analysis (Kaplan–Meier), HBsAg negativization was not associated with sex ($p = 0.18$), ALT normal or high values ($p = 0.8$), liver elastography < or ≥6.2 kPa ($p = 0.45$), or race ($p = 0.96$). The probability of HBsAg negativization was significantly higher in patients >30 years ($p = 0.02$), HBV-DNA-negative ($p < 0.001$) and with initial HBsAg <1000 UI ($p < 0.001$). In multivariate analysis, initial HBV-DNA absence (HR 2.37 [95% CI 1.34–4.19], $p = 0.03$) and basal HBsAg <1000 IU/ml (HR 49.4 [95% CI 6.76–361.02], $p < 0.001$) were independently associated with the probability of HBsAg clearance. The presence or absence of these factors allowed to establish three groups of patients with a significant different probability of HBsAg negativization at 5 years: In those without any favorable factor ($n = 151$) such probability was 0%, in those with one factor ($n = 101$) 27.2%, and in patients with both of them ($n = 45$) 53.5% ($p < 0.001$). Isolated use of HBsAg was also useful to distinguish three groups of patients with different probability of HBsAg negativization at 5 years: 0% in those with HBsAg >1000 UI/ml, 15.2% if HBsAg was between 100 and 1000 IU/ml and 53% when it was <100 IU/ml. However, area under the ROC curve was greater in the model using HBsAg and HBV-DNA (0.88 [0.83–0.92]) than in the one based only in HBsAg (0.84 [0.78–0.89]).
Conclusions: In a series of HBV-IC, mainly Caucasians, the combination of HBsAg cuantification and the presence or absence of HBV-DNA is useful to predict the probability of infection resolution at 5 years.

P0594
CAN SERUM LEVEL OF HEPATITIS B SURFACE ANTIGEN (HBsAg) DIFFERENTIATE HBsAg INACTIVE CARRIER STATE FROM CHRONIC HEPATITIS B?

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Background and Aims: HBeAg-negative hepatitis B virus (HBV) infection exerts both inactive carrier (IC) state and chronic hepatitis B (CHB) which are sometimes difficult to be differentiated. Recently, serum HBsAg level has been introduced to evaluate treatment response to interferon and probably help in diagnosis of hepatitis B clinical stages. We aimed to assess the role of HBsAg level in differentiation of IC and CHB among a group of chronic HBeAg-negative HBV-infected patients.
Methods: A total of 251 HBeAg-negative HBV-infected patients were enrolled. Serum alanine transaminase (ALT), HBV DNA and HBsAg levels were determined for each patient. Liver histology was evaluated by liver biopsy using Knodell scoring system. HBV DNA and HBsAg levels were assessed using COBAS TaqMan HBV test and HBsAg II quant assay, respectively.
Results: A total of 243 HBeAg-negative HBV-infected patients including 139 ICs and 104 CHB patients were evaluated. All HBV isolates were identified as genotype D. HBV DNA and HBsAg levels were significantly higher in CHB patients than in ICs. HBV DNA quantification with cutoff value 2,000 IU/mL for diagnosis of CHB had 99.0% sensitivity and 74.1% specificity. A cutoff value of HBsAg level at 1,000 IU/mL was more reliable for diagnosis of CHB with 82.7% sensitivity and 66.2% specificity than other HBsAg level cutoffs. Combination of HBV DNA and HBsAg levels did not increase diagnostic performance of HBV DNA level for differentiation of IC and CHB stages. There was a positive correlation between HBV DNA and HBsAg levels in both IC ($r = 0.43$, $P < 0.001$) and CHB ($r = 0.42$, $P < 0.001$) groups.
Conclusions: Single point HBsAg quantification did not have enough sensitivity and specificity for diagnosis of HBV clinical stages.

P0595
HIGH FREQUENCY OF ACTIVE HCV INFECTION AMONG SEROPOSITIVES IN WEST AFRICA AND EVIDENCE FOR MULTIPLE TRANSMISSION PATHWAYS

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Background and Aims: Sub-Saharan Africa (SSA) has among the highest global Hepatitis C Virus (HCV) sero-prevalence estimates. However, reports suggesting high rates of serologic false positives and low levels of detectable viremia has led to uncertainty regarding the burden of active HCV infection in this region. Additionally, little is known about the predominant transmission risk factors and mechanisms in this region. The aims of this study were to determine the frequency of active infection among persons who screened positive for HCV infection and identify risk factors for HCV infection.
Methods: Between May 2013 and January 2014 we recalled 363 blood donors [180 rapid screen assay (RSA) (Accu-Tell HCV) positive and 183 RSA negative at time of donation] to identify the level of active infection and risk factors at Komfo Anokye Teaching Hospital in Kumasi, Ghana. Participants had blood drawn for serologic and virologic testing (HBVsAg Abbott Architect CIA, HIV 4th generation Ab/Ag test, the HCV Advia Centaur HCV CIA, and Abbott RealTime PCR assay for HCV RNA quantitative levels). HCV genotypes were determined by the generated NS5b sequences (SuperScript® VILO™ cDNA Synthesis Kit). A questionnaire on demographics and risk factors was administered.
Results: The frequency of active infection varied based on serologic testing results, but was overall high. In subjects with a positive CIA Serologic Antibody Assay [Signal to Cut-off ratio (S/C) >1], the rate of active viremia was 74.4%, and increased to 88% among the individuals with a CIA S/C ≥11. Individuals were predominantly infected with genotype 2, and the median viral load among actively infected individuals was 5.75 log cp/ml. Blood donors from the northern and upper regions of Ghana had substantially higher risks of infection compared to those from the middle belt. Individual level Odds ratio statistical significant risk factors included: traditional circumcision (3.8), home birth (2.0), tribal scarring (2.2) and HBV co-infection (2.7). See Table 1.
Conclusions: Among serologically confirmed cases, active infection rates were high. Appropriate testing algorithms should be widely implemented to define the true HCV burden in SSA. These data also suggest that several transmission modes, particularly

those associated with cultural skin-piercing practices, are likely contributing to the current HCV epidemic in Ghana, and the distribution of these practices may result in regional variation in prevalence.

Table 1. Multivariable logistic regression model for HCV seropositivity

Variable	OR (95% CI)	*p*-value
Region of Origin		<0.001
Northern vs. Ashanti	6.64 (2.44–18.23)	<0.001
Other vs. Ashanti	1.15 (0.33–3.93)	0.83
Upper vs. Ashanti	18.69 (8.27–42.22)	<0.001
Education level		0.01
Nil/Primary vs. Tertiary	0.42 (0.16–1.11)	0.08
JHS/MSLC/SHS/Tech vs. Tertiary	0.29 (0.12–0.66)	0.003
Marital status	2.31 (0.80–6.70)	0.06
Married vs Single	0.93 (0.45–1.92)	0.83
Other vs. Single	8.04 (1.28–50.35)	0.03
HBsAg positive	3.82 (1.08–13.53)	0.04
Circumcision		0.01
None vs. Hospital	3.46 (1.31–9.12)	0.01
Traditional vs. Hospital	3.26 (1.47–7.21)	0.004

OR, covariate-adjusted odds ratio. CI, confidence interval for estimate.

P0596
ASSOCIATION OF HEPATITIS E VIRUS AND CRYOGLOBULINEMIA

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Background and Aims: Several extrahepatic manifestations have been observed in the context of acute or chronic hepatitis E virus infections. Recently a case indicated an association between HEV infection and cryoglobulinemia (Pischke et al. Lancet Inf. Dis. 2014), but this observation still needs to be confirmed and clarified.
Methods: Stored serum samples of 68 German patients with cryogluobulinemia were retrospectively tested for anti HEV IgG (Wantai assay). Seroprevalence rates were compared in patients with essential cryoglobulinemia (n = 33) and in patients with cryoglobulinemia secondary to various underlying conditions (n = 35) using chi square test.
Results: Within the group of patients with essential cryoglobulinemia 46% (n = 15) tested positive for anti HEV IgG, while in the group of patients with different underlying conditions 23% (n = 8) tested positive (p = 0.043).
Conclusions: Patients with essential cryoglobulinemia tested positive more frequently for anti HEV than patients with secondary cryoglobulinemia due to well defined causes. This indicates that development of cryoglobulinemia of unknown origin is a relevant extrahepatic manifestation of hepatitis E.

Table 1. Characteristics of patients

	Essential cryoglobulinemia (n = 33)	Cryoglobulinemia of defined origin (n = 35)	p-value
Anti HEV IgG positive	15 (46%)	8 (23%)	0.043
Male	12 (36%)	14 (40%)	ns
Age in years, range (mean±SD)	37–83 (61.7±13.2)	36–76 (57.4±10.8)	ns
OD value of anti HEV IgG	0.004–3.239 (0.686±1.035)	0.000–3.205 (0.326±0.758)	ns

P0597
THE ROLE OF GENOTYPE, PRE-CORE, BASAL CORE PROMOTER AND PRE-S MUTATIONS OF HBV IN PATIENTS OF HEPATOCELLULAR CARCINOMA WITH HEPATITIS C AND OCCULT HEPATITIS B

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Background and Aims: HBV coinfected with chronic hepatitis C subjects were found to increase the risk to develop advanced liver disease later in their life. In chronic HBV patients, some virological factors such as genotype C, preS deletion and core promoter/precore mutations are found to increase the risk of HCC. However, little was known about the role of the virological risk factors of HBV in chronic HCV patients with occult HBV.
Methods: One hundred and eighty-one HBsAg-negative, HCV-Ab positive HCC patients (group A), 153 HBsAg-negative, HCV-Ab positive chronic hepatitis patients (group B), and 20 HCC subjects with both positive HBsAg and HCV-Ab (group C) were enrolled. The preS, core promoter/precore region and S gene were amplified by nested PCR and direct-sequenced. Viral phylogenetic analysis was also performed.
Results: The occult HBV infection was found for 20.4% (37/181) in the group A, and 34.0% (52/153) in group B. In addition, the genotype C (P = 0.019), BCP mutations (P = 0.004) and 1858 mutation (P < 0.001), 1896 mutation (P = 0.032) were more common in chronic HCV patients with HCC. PreS1 deletion (P = 0.033), BCP (P = 0.014) and precore 1896 mutation (P = 0.008) were more common in chronic HCV patients with overt than occult HBV.
Conclusions: In patients with chronic HCV and occult HBV infection, HBV genotype C, BCP, 1858 and 1896 mutations seemed to be associated with the development of HCC.

P0598
NATURAL HISTORY OF CHRONIC HEPATITIS B INFECTION IN THE GAMBIA, WEST AFRICA: A LONGITUDINAL POPULATION-BASED STUDY

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Background and Aims: The natural history of chronic hepatitis B (CHB) infection in sub-Saharan Africa is poorly documented. This study describes the natural history of CHB in The Gambia, West Africa.
Methods: An open community cohort of treatment-naïve CHB carriers was recruited from rural villages in the West Kiang district, The Gambia between 1974 and 2008. The cohort was used to estimate the rates of hepatitis B e (HBeAg) and surface antigen (HBsAg) clearance and incidence of hepatocellular carcinoma (HCC). In 2012–2013 we invited members of the cohort for a comprehensive liver assessment to estimate the prevalence of chronic liver disease as part of the PROLIFICA study.
Results: 405 chronic carriers were identified in 10 sero-surveys, and the median length of follow up was 28.4 years. Annually, 7.4% (95% CI: 6.3–8.8) and 1.0% (95% CI: 0.8–1.2) of the carriers cleared HBeAg and HBsAg, respectively (Figure). The incidence