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Tatiana Dupinay, Karin Restorp, Peter Leutscher, Dominique Rousset, Isabelle Chemin, Rene Migliani, Lars O Magnus, Helene Norder

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High prevalence of hepatitis B virus genotype E in Northern Madagascar indicates a West-African lineage

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22 High prevalence of hepatitis B virus genotype E in Northern Madagascar
23 indicates a West-African lineage
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28 13 Tatiana Dupinay^{1,2,3}, Karin Restorp⁴, Peter Leutscher^{5,6}, Dominique Rousset⁷, Isabelle
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30 14 Chemin¹, Rene Migliani⁵, Lars Magnus⁴, Heléne Norder^{4*}.
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33 15
34 16
35 17 ¹ INSERM U871, 151 Cours Albert Thomas, 69003 Lyon, France;

36
37 18 ² Université Lyon 1, IFR62 Lyon Est, 69008 Lyon, France ;

38
39
40 19 ³ Ecole pratique des hautes études , 75007 Paris France
41

42 20 ⁴ Virological Department, Swedish Institute of Infectious Disease Control, Sweden
43 21

44 22 ⁵ Institute Pasteur de Madagascar, Antananarivo, Madagascar
45 23

46 24 ⁶. Department of Infectious Diseases, Aarhus University Hospital, Skejby, DK-8200 Aarhus N,
47 25 Denmark
48 26

49
50 27 ⁷ Institute de Medecine Tropicale du Service de Sante des Armées, Marseille, France.
51 28

52
53 29 * Correspondence to: Helene Norder

54 30 Department of Virology

55 31 Swedish Institute for Infectious Disease Control, SE-171 82 Solna, Sweden

56 32 e-mail : helene.norder@smi.se
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Abstract

The prevalence of hepatitis B virus (HBV) markers was investigated in 566 inhabitants aged 15 to 55 years from a sugar cane region, Sirama, and from a village, Mataipako, in Northern Madagascar. Serological markers of past or present infection were significantly higher in Sirama, 74 % versus 55 %. There was no difference in the prevalence of chronic HBsAg carriers, 8.7 versus 8.5 % between the two regions. Sequencing the S gene in 45 strains revealed a predominance of genotype E, in 53 %, followed by subgenotype A1 in 22 %, and genotype D in 18 %. Phylogenetic analyses of the genotype E strains showed homology with West African strains. All A1 isolates were similar to Malawi strains. Most genotype D strains were subgenotype D7 and related to strains from Somalia and Tunisia. One genotype D strain formed a branch between Pacific D4 and African D7 strains at neighbour-joining analysis. The precore stop mutant was found in 33 % of the genotype D strains, 17 % of E but not in any A1 strain. The high prevalence and low variability of genotype E strains in only two villages, indicates a rather recent introduction of this genotype into Madagascar from West Africa, possibly through migration or slave trade. The wider spread and genetic relationship of genotype D with East African and Austronesian strains indicate an earlier introduction of this genotype. Molecular epidemiology of HBV may thus be used to complement linguistic and genetic studies on past human migrations in Africa.

57 Introduction

58 Hepatitis B virus (HBV) is a human pathogen causing both acute and chronic hepatitis. HBV is a
59 major public health concern and approximately two billion people worldwide have serological markers
60 of past or present infection. More than 350 million people are chronically infected according to the
61 World Health Organisation (WHO). In addition, WHO estimations indicate that approximately one
62 third of all cases of cirrhosis and half of all cases of hepatocellular carcinoma can be attributed to
63 chronic HBV infection worldwide. The prevalence of chronic infection varies throughout the world
64 with South East Asia, China, Amazon Basin and Africa carrying the highest burden of disease.
65 Parenteral and sexual transmissions are globally the most common modes of transmission. In endemic
66 countries the predominant routes of transmission are perinatal transmission from mother to child
67 during birth in Asia, and horizontal transmission between children in Africa. A global hepatitis B
68 immunization program has been recommended by WHO since 1991.

69
70 Madagascar is a country with an ethnically diverse population divided into 22 tribes and a growth rate
71 of 2,8 % per year (Hewitt *et al.*, 1996; Mafrezi and Randretsa, 1985). Madagascar is classified as an
72 area of high endemicity for HBV, and about 5% of the urban population and 30 % of the rural
73 population are chronic HBsAg carriers (Boisier *et al.*, 1996; Migliani *et al.*, 2000a; Migliani *et al.*,
74 2000b; Morvan *et al.*, 1994). Hepatitis B vaccination is the most effective strategy for prevention of
75 hepatitis B. However, in Madagascar laboratory facilities are insufficient and the use of hepatitis B
76 vaccine is limited (Migliani *et al.*, 2000b).

77
78 HBV is a small, double-stranded DNA virus and the prototype of the hepadnavirus family (Ganem &
79 Varmus, 1987). HBV strains are classified into eight genotypes, designated A-H (Arauz-Ruiz *et al.*,
80 2002; Naumann *et al.*, 1993; Norder *et al.*, 1993; Okamoto *et al.*, 1987; Stuyver *et al.*, 2000). Each
81 genotype has distinct geographical distribution. Genotype A is common in North-Western Europe,
82 North America, and Africa. Genotypes B and C are predominant in East- and South East Asia, Oceania
83 and among aboriginal populations in Australia. Genotype D is found worldwide and is predominant in
84 the Mediterranean, Middle East, and India, whereas genotype E has so far been confined to
85 populations in western parts of sub-Saharan Africa apart from one report from India (Norder *et al.*,
86 2004; Singh *et al.*, 2009). Genotype G has been identified in samples from several countries, and is
87 found in patients co-infected with another HBV genotype. Genotypes F and H are found mainly in
88 Central and South America, and are the indigenous genotypes of Amerindian populations (Arauz-Ruiz
89 *et al.*, 2002; Norder *et al.*, 2004; Kumagai *et al.*, 2007; Sanchez *et al.*, 2007).

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3 90 The major HBV genotypes apart from E and H have been divided into subgenotypes based
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5 91 phylogenetic analyses and genetic divergence of complete genomes. Each subgenotype has specific
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7 92 geographical distribution. Six subgenotypes have been recognized for genotype A. A1 is prevalent in
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9 93 Africa, Asia and Indonesia (Bowyer *et al.*, 1997; Kramvis *et al.*, 2002; Banerjee *et al.*, 2006; Kramvis
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11 94 and Kew 2007; Tanaka *et al.*, 2004; Hannoun *et al.*, 2005). A2 is prevalent in North West Europe
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13 95 (McMahon 2009; Norder *et al.*, 2004; Sugauchi *et al.*, 2004; Schaefer, 2007). A3 – A6 are found in
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15 96 West and Central Africa, (Makuwa *et al.*, 2006; Kramvis and Kew 2007; Pourkarim *et al.*, 2009;
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17 97 Kurbanov *et al.*, 2005; Olinger *et al.*, 2006). There are eight subgenotypes for genotype B, and seven
18
19 98 for C. B1 and C2 are prevalent in Japan, Korea and Northern China, C2 is also found in Alaska, while
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21 99 B2 and C1 are prevalent in Southern China, Taiwan, and South East Asia (Norder *et al.*, 2004;
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23 100 Schaefer, 2007; McMahon, 2009; Wang *et al.*, 2009). B3 – B5 and B8 as well as C3 – C7 are prevalent
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25 101 in the Pacific, while B6 is found in Alaska, Northern Canada and Greenland (McMahon, 2009;
26
27 102 Mulyanto *et al.*, 2009; Cavinta *et al.*, 2009; Lusida *et al.*, 2008; Nagasaki *et al.*, 2006; Sakamoto *et al.*,
28
29 103 2006). Subgenotype B7 described from Indonesia (Nurainy *et al.*, 2008) probably represent strains of
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31 104 subgenotype B3. There are seven subgenotypes reported for genotype D. D1 is highly prevalent in the
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33 105 Middle East and in the Mediterranean countries, but also occurs in India and East Africa and (Banerjee
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35 106 *et al.*, 2006; Norder *et al.*, 2004; Schaefer 2007). D2 is prevalent in East Europe including Russia and
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37 107 the Baltic States, while D3 has a more South-Eastern distribution in Russia and is also prevalent in
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39 108 Northern India and Pakistan (Norder *et al.*, 2004; Tallo *et al.*, 2008). D3 has also a global spread
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41 109 attributed to its spread among injecting drug users. D5 is reported from Eastern India (Banerjee *et al.*,
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43 110 2006; Chandra *et al.*, 2009). D4 was defined based on complete genomes from Australia and Western
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45 111 Pacific and formed a clade with strains from North-Africa including Somalia in genetic trees based on
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47 112 the small S gene (Norder *et al.* 2004). The North-African subclade, however, is divergent sufficiently
48
49 113 to represent a new subgenotype, D7, based on analysis of strains from Tunisia (Meldal *et al.*, 2009).
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51 114 D6 reported from Papua (Lusida *et al.*, 2008) probably represents strains of subgenotype D4. The
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53 115 subgenotypes of F are found in the Americas. F1 has a Northern distribution in Alaska, Mexico, and
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55 116 Central America and has spread to Peru and Argentina, while F2 – F4 are prevalent in South America
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57 117 (McMahon, 2009; Norder *et al.*, 2004; Devesa *et al.*, 2008).

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59 118
60 119 In this study, the prevalence of HBV markers was investigated in populations in a rural area in the
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121 Northern part of Madagascar. The HBV strains from chronic carriers were characterized in order to
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123 determine the HBV genotypes and subgenotypes prevalent in this region of Madagascar.

124 **Material and Methods**

125 Materials

126 As a part of a schistosomiasis morbidity study, sera were collected from 563 inhabitants aged 15 to 55
127 years living in a rural area in Northern Madagascar (Leutscher *et al.*, 2008; Ramarakoto *et al.*, 2008).
128 Participants were from the Mataipako village and from five villages (Ambodikatakata, Ambodimanga,
129 Ankatoko, Antsaboahitra, and Tanambao) in the neighboring Sirama sugercane plantation area close to
130 the major town Ambilobe. Two-hundred-fifty-one samples (43 %) were from Mataipako and 322 from
131 the Sirama villages (Table I). Three hundred and one (54 %) were from males and 262 (46 %) from
132 females (Table II). Median age of the investigated inhabitants was 29 years for both regions, 29.8 for
133 males and 28.6 years for females. No prior HBV vaccination program or other control interventions
134 have been undertaken in the study area. Informed consent was obtained from the participants prior to
135 enrolment in accordance with the study protocol, which was approved by the committee of ethics in
136 Madagascar.

138 Serological assays

139 Sera were tested by enzyme immunoassays (EIA) with commercial kits for HBsAg detection (Sanofi
140 Diagnostics Pasteur, Marnes La Coquette, France, Murex Diagnostics, Maidenhead, England, Ortho
141 Diagnostics Systems, New Brunswick, NJ, USA, and DiaSorin, Saluggia, Italy). Samples were also
142 tested for anti-HBc (Wellcozyme, Abbott Diagnostics, Maidenhead, England, and Anti-HBc PLUS
143 BioRad, Hercules, CA, US). HBeAg and anti-HBe were determined with HBeAg-Ab Plus BioRad
144 Monolisa, and anti-HBs was detected with the EIA Anti-HBs BioRad (BioRad Laboratories AB,
145 Hercules, CA, US).

147 Extraction of HBV DNA, PCR amplification and sequencing of the S gene, the pre-core and the core 148 promoter regions.

149 HBV DNA was extracted from 50 µl serum by the standard phenol-chloroform method. Briefly, 50 µl
150 serum were incubated for 2 hours at 42°C with 250 mg/ml of proteinase K (Sigma, St Louis, MO, US),
151 1% sodium dodecylsulphate, 2,5 mM disodium EDTA (Sigma, St Louis, MO,US), 25 mM sodium
152 acetate and 0.25 µg/ml tRNA. The DNA was subsequently extracted with phenol and with a 1:1
153 mixture of phenol:chloroform. Thereafter the DNA was precipitated in absolute ethanol with 0.15 M of
154 potassium acetate and dissolved in 40 µl of milli-Q water.

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156 PCR amplification of the S- region was performed by using primers hep75 and 73b in the first PCR
157 and hep3/hep33 and hep4/hep34 for nesting (Norder *et al.*, 1992). The pre-core region was amplified

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3 158 with primer promC and hep68 (Sendi *et al.*, 2005), and nested with primers hep67 and hep68 (Arauz-
4 159 Ruiz *et al.*, 1997). For amplification of the core promoter region, primers hep64 and hep70 were used
5 160 in the first round of PCR and hep64 and hep54 in the nested PCR (Sendi *et al.*, 2005).
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9 162 Purified products were used as templates in the sequencing reaction using the dideoxy-nucleotide
10 163 chain-termination method with an ABI PRISM BigDye terminator cycle-sequencing reaction kit
11 164 (version 3; Applied Biosystems, Foster City, CA, US). The primers used in the PCR were used as
12 165 sequencing primers. All amplification products were sequenced bi-directionally.
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14 166 An ABI PRISM 3100 genetic analyser (Applied Biosystems) was used for electrophoresis and data
15 167 collection.
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18 169 Phylogenetic analysis

19 170 Sequences obtained were edited manually using the SeqMan program in the LASERGENE package
20 171 (DNASTAR, Inc, Madison, WI). The sequences were thereafter aligned with the corresponding region
21 172 in sequences retrieved from GenBank.
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24 174 Phylogenetic analysis was carried out with the PHYLIP program package version 3.53 (Felstenstein,
25 175 1993). Evolutionary distances were estimated with the DNADIST program using the F81 model.
26 176 Phylogenetic trees were constructed using UPGMA and neighbour-joining (N-J) algorithm in the
27 177 PHYLIP package. Genotypes and subgenotypes were determined by phylogenetic analysis of the
28 178 amplified fragments of the S gene with sequence from previously genotyped and subgenotyped strains
29 179 (Norder *et al.*, 2004). The deduced amino acid sequence of the S gene region was used to determine
30 180 the subtype, which was assessed from the substitutions at codons 122, 127, and 160 (Norder *et al.*,
31 181 1992; Okamoto *et al.*, 1987).
32
33 182

34 183 **Results**

35 184 *Seroprevalence of hepatitis B markers*

36 185 There was an overall high prevalence of HBV markers (66 %). It was significantly higher in the
37 186 Sirama villages, 74 % versus Mataipako, 55 %, ($p < 0.0001$; Fisher's exact test; Table I), whereas there
38 187 was no major difference between males and females (69% versus 65%, $p = 0.34$). In all, 370 inhabitants
39 188 had HBV markers, 322 (57 %) were negative for HBsAg but had anti-HBc and/or anti-HBs as markers
40 189 of past infection, while 48 (8.5 %) individuals were positive for HBsAg (Table I). Anti-HBs as only
41 190 serological marker was found in nine (1.6 %) inhabitants (Table I). There was a significantly higher
42 191 rate of HBV markers among males in the Sirama villages compared to Mataipako village, 70% versus

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192 54%, ($p < 0.0001$; Fisher's exact test). There was no correlation between age and prevalence of HBV markers (Table I).

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195 Among the 48 HBsAg positive patients, 20 (42 %) were HBeAg positive, another 26 (54 %) were anti-HBe positive, while two patients were negative for both these markers (Table II). There was no significant difference in HBeAg or anti-HBe prevalence between regions or sexes.

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199 *Genotype distribution*

200 Three HBV genotypes A, D, and E, were identified in 45 samples by sequencing and analyzing the S-gene region (Table III). Most strains belonged to genotype E, 24/45 (53 %), followed by genotype D, 11/45 (24 %) and A, 10/45 (22 %). One individual was infected dually with one genotype A strain expressing *ayw1* and one genotype D strain expressing *ayw2*. The HBV genotype could not be determined for two individuals due to low level HBV DNA.

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206 Most of the 24 genotype E strains originated from inhabitants in two villages, 12 from Mataipako, and 10 from one village in the Sirama region (Table III). Seven of the genotype A strains were from inhabitants in two villages in the Sirama region, and three were from inhabitants in Mataipako. The genotype D strains originated from inhabitants in all villages with HBsAg positive individuals (Table III).

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212 *Phylogenetic analysis*

213 Phylogenetic analysis of the small S gene revealed that all genotype A isolates belonged to subgenotype A1 and specified subtype *ayw1*. In the phylogenetic tree, these isolate segregated into one clade and being most similar to strains from Malawi (Fig 1a). This clade was also supported by N-J analysis (data not shown). Five strains from inhabitants in two villages in the Sirama region, Ambodimanga and Ambodikatakata, had identical S gene sequences and differed by only one nucleotide from two other strains from Mataipako (Fig 1a). Another three strains were more divergent, although they were found in the same major cluster as the other genotype A strains from Madagascar.

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221 All but two genotype D strains could be classified into two subgenotypes, D2 (one strain) and D7 (8 strains) in the phylogenetic analyses. The D7 strains, specifying *ayw2*, were found in one cluster and shared similarity with strains from Somalia and Tunisia in both the UPGMA and N-J analyses (Figs 1b; 1c). These D7 isolates originated from inhabitants in three villages, two in the Sirama region (Ambodikatakata, and Tanambao), and Mataipako. The D2 strain specifying *ayw3* was from a male

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3 226 from Ankatoko in the Sirama region, and was similar to strains from East Europe (Figs 1b; 1c). The
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5 227 D2 and D7 strains formed separate clades also in the N-J analysis, although in this analysis the D1 and
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7 228 D3 strains were split into two and three clades, respectively (fig. 1c). The D4 and D7 strains formed
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9 229 the first split in the N-j tree, although this was not the case in the UPGMA tree. Six D1 and two D2
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11 230 strains classified based on complete genomes, could not be classified into a subgenotype by UPGMA
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13 231 but belonged to their respective subgenotypes in the N-J analysis (figs 1b; 1c). On the other hand there
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15 232 were five D1 strains based on complete genomes that were classified as D1 in the UPGMA tree but
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17 233 could not be classified into a subgenotype by N-J (figs 1b; 1c). Two genotype D strains from
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19 234 Madagascar were not classifiable with any of the analyses. One, 1500-02, from a female from
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21 235 Mataipako encoding *ayw4*, was found between genotype D and E strains in the N-J tree (fig 1c). The
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23 236 other strain, 600-02, from a male from Ambodimanga specified *ayw2*. This strain was similar to a
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25 237 strain from aboriginal populations in Australia in the UPGMA tree and formed a separate branch
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27 238 between the Asian D4 and the African D7 strains in the N-J tree (figs 1b; 1c).

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29 240 The 24 genotype E isolates were found intermixed with strains from West Africa in the phylogenetic
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31 241 tree (Fig. 1d). Fourteen of the Madagascar strains were found in two clades. In the major clade, 11 of
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33 242 the Madagascar strains were intermixed with strains from Cameroon, Nigeria, Ivory Coast, and Mali
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35 243 (Fig. 1d). Eight of these strains were from Mataipako, and four from two villages in the Sirama region,
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37 244 Tanambao and Ankatoko. In the second cluster 4 isolates from Tanambao were intermixed with strains
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39 245 from Congo (Fig 1d).

40 246 41 247 *Pre-core and core promoter region*

42 248 The pre-core region was sequenced in 36 strains. A premature stop codon related to the G1896A
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44 249 mutation was observed in six sequences (16.6%). This pre-core mutant was found in three of seven
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46 250 investigated genotype D7 strains and in three of 18 genotype E strains. It was not found in any of nine
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48 251 genotype A strains investigated. All strains with the pre-core stop mutant were from patients with anti-
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50 252 HBe. Another pre-core mutation, G1896T, converting Trp¹⁸⁹⁶ to Leu¹⁸⁹⁶, was found in two genotype D
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52 253 strains and in one genotype E strain. This variant was found in two patients with anti-HBe and in one
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54 254 patient lacking HBe markers.

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57 256 The core promoter region was amplified and sequenced in 16 strains, three were genotype A, another
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59 257 three were genotype D, and 10 were genotype E strains. All genotype D and E strains expressed A¹⁷⁵⁷,
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61 258 and the genotype A strains expressed G¹⁷⁵⁷. One genotype A strain had C1766T and T1768A

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3 259 mutations in the core promoter region, and one genotype E strain had a triple mutation, A1762C,
4 260 G1764T and C1766G. All other strains had wild type promoter sequence.
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7 261 8 9 262 **Discussion**

10 263 The prevalence of hepatitis B markers in the rural populations from the Northern region of Madagascar
11 264 was high, although not as high as the prevalence described in other rural population in the centre of
12 265 Madagascar; where up to 18 % were HBsAg positive (Boisier *et al.*, 1996; Migliani *et al.*, 2000a;
13 266 Morvan *et al.*, 1994). Only 1.6 % of the inhabitants from this study had anti-HBs only which strongly
14 267 suggest that implementation of control programs for hepatitis B in these areas is warranted. The
15 268 present findings on the epidemiological features of persons infected with hepatitis B such as age, sex,
16 269 and origin showed that the prevalence of infection appears to be higher among males from rural
17 270 villages.
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26 272 In this study, there was a high frequency of HBeAg positive HBsAg carriers (42 %), mainly among
27 273 those infected with genotypes A1 and E. This prevalence of HBeAg was higher than that from other
28 274 parts of East and Central Africa as Zimbabwe, Cameroon, Ethiopia, Benin and the Central African
29 275 Republic (Tswana *et al.*, 1996; Rapicetta *et al.*, 1991; Abebe *et al.*, 2003; Fujiwara *et al.*, 2005;
30 276 Pawlowsky *et al.*, 1995; Abiodun *et al.*, 1994). In addition, there was a low prevalence of strains with
31 277 mutations in the pre-core and core promoter despite the relatively high presence of A1 and D strains.
32 278 In Mediterranean countries, genotype D has been shown to present in high frequency in negative
33 279 chronic HBV infection without HBeAg, associated with HBV mutants in the pre-core region (Brunetto
34 280 *et al.*, 1993). The most common precore mutation, G1896A, which creates a stop codon, has been
35 281 associated previously with the subgenotypes found in this study (Chu *et al.*, 2002; Kramvis *et al.*,
36 282 1997; Lok *et al.*, 1994; Olinger *et al.*, 2006). This mutant was only found in 38 % of the genotype D
37 283 strains and in none of the A1 strains. There were also only two strains, one genotype A and one
38 284 genotype E, with core promoter mutations. The high HBeAg prevalence and low frequency of precore
39 285 and core promoter may be due to the prevalent HBV genotypes if genotypes A1 and E have prolonged
40 286 replicative phase with HBeAg expression, as is described for genotypes B and C in Asia (Kao, 2002;
41 287 Orito *et al.*, 2001). It is not known if chronic carriers infected with A1 and E have a higher prevalence
42 288 of HBeAg positivity than those infected with genotype D also in other parts of Africa, or if it is
43 289 specific for this studied population.
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60 291 The Malagasy population has a widespread origin from Asiatic to sub-Saharan African descendants
292 and a mixture of the two (Hurles *et al.*, 2005; Singer *et al.*, 1957). Although both African and

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3 293 Southeast Asian populations have contributed to Madagascar's gene pool, those of Asian origin are
4 294 most predominant in the central highlands, while the coastal populations often are of African origin
5 295 (Chow *et al.*, 2005; Regueiro *et al.*, 2008; Hurles *et al.*, 2005).
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9 297 The origin of the population may also be reflected by the prevalent HBV genotypes. The subgenotype
10 298 A1 strains were similar and mainly found in two villages. This subgenotype dominates in all East
11 299 African countries including South Africa, Malawi, Tanzania, Uganda, and Somalia (Kramvis & Kew,
12 300 2007). The isolates from Madagascar were similar to Malawi isolates, suggesting that this subgenotype
13 301 was introduced into Madagascar from East Africa. Geographically Malawi is close to the North
14 302 Western part of Madagascar and historically, in the nineteenth century, the trade route from Malawi to
15 303 the western coast of Madagascar became exploited increasingly for slave trading.
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17
18 305 The genotype E strains in this study showed high sequence similarity to West African strains, where
19 306 this genotype is confined. Previous studies have shown a low genetic diversity of genotype E strains
20 307 isolated from a large geographical area in West Africa (Kramvis *et al.*, 2005; Quintero *et al.*, 2002).
21 308 Several studies have proposed that this low genetic divergence together with few findings of genotype
22 309 E in the Americas indicates a recent introduction of genotype E into the human population (Mulders *et*
23 310 *al.*, 2004; Odemuyiwa *et al.*, 2001; Suzuki *et al.*, 2003). The genotype E strains in this study were
24 311 mainly from inhabitants in two villages, which may indicate a recent introduction, and that sufficient
25 312 time has not yet passed for its subsequent spread into the rest of the country. The inhabitants in the
26 313 two villages were working in the rice fields, and they may be slave descendant with origin from
27 314 mainland Africa. West African origin of some Malagasy populations is supported by genetic studies on
28 315 Y-chromosomal polymorphism and mitochondrial sequence diversities and on β -globulin haplotypes
29 316 (Hurles *et al.*, 2005; Hewitt *et al.*, 1996). In addition, hepatitis C virus genotype 2 strains, common in
30 317 West Africa, have been isolated from Malagasy populations, further supporting previous human
31 318 migrations from West Africa to Madagascar (Markov *et al.*, 2009).
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34 320 Interestingly, 24 % of the strains in this study were genotype D, and found in all five villages with
35 321 HBsAg positive individuals. The majority were subgenotype D7, which are also found in Somalia and
36 322 Tunisia. This is consistent with the subdivision of the previous classified D4 strains into two
37 323 subgenotypes, D4 represented by strains from the Australia and Western Pacific, and D7 with North
38 324 African strains (Meldal *et al.* 2009; Schaefer *et al.*, 2009). The D4 and D7 strains formed the first split
39 325 in the genotype D phylogenetic tree, when N-J algorithm was used, as they do when complete
40 326 genomes are analysed (Meldal *et al.*, 2009; Norder *et al.*, 2004; Tallo *et al.*, 2008). N-J analyses of

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3 327 genotype D S –genes thus seems better to mirror the tree obtained from complete genomes than
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5 328 UPGMA. The split of genotype D strains into two main branches, one with D4 and D7 and one with
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7 329 the other D subgenotypes, with D5 as first split, might support that genotype D has followed two waves
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9 330 of two human migrations out of Africa. The D4 subgenotype being linked to the early settlement of
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11 331 Papua-Australia-Melanesia followed by a later wave of settlement reaching India supported by India,
12 332 being populated before Europe, and D5 being the first split in this branch.
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16 334 There were in this study five different D7 strains, all showing close relationship with strains from
17
18 335 Somalia. It has been proposed that there has been a migration wave into Madagascar from central East
19 336 Africa based on human genetic and linguistic studies (Dahl, 1988; Hewitt *et al.*, 1996; Hurles *et al.*,
20
21 337 2005). Interestingly, there was one genotype D strain similar showing a distant genetic relationship to
22
23 338 a strain from Australia, and formed a separate branch between the African D7 and the Asian D4
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25 339 strains, suggesting also Asian import of genotype D into Madagascar. This is in agreement with
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27 340 genetic studies showing a South East Asian and Pacific origin of some Malagasy populations (Hurles
28 341 *et al.*, 2005; Migot *et al.*, 1995; Soodyall *et al.*, 1995). The dissemination of genotype D in the
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30 342 majority of the villages and its higher genetic variability compared to genotype A and E, indicate an
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32 343 earlier introduction of genotype D into the Malagasy populations than the other two identified
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34 344 genotypes.
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37 346 It is well known that the prevalence of the different HBV genotypes and subgenotypes vary in
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39 347 geographical areas and correlate strongly with ethnicity. Studying the genetic variability of the HBV
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41 348 strains in endemic regions may thus be helpful when studying migration patterns of populations of
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43 349 different origins. This study showed that molecular epidemiology of HBV in the North-western part of
44 350 Madagascar confirms linguistic and human genetic studies on human migrations in Africa.
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53 356 are deposited in GenBank with accession numbers xxx- yyy.
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Table I. Age, sex and hepatitis B serological markers of investigated inhabitants in villages with mainly farmers (Sirama) and non-farmers (Mataipako) in Northern Madagascar. Figures in parenthesis are number of individuals with anti-HBs as the only marker.

Age	<i>Males</i>				<i>Females</i>				<i>TOTAL</i>			
	N	HBsAg pos	HBsAg neg anti-HBc and/or anti-HBs	% with total markers	N	HBsAg pos	HBsAg neg anti-HBc and/or anti-HBs	% with total markers	N	HBsAg pos	HBsAg neg anti-HBc and/or anti-HBs	% with total markers
Sirama												
15-19	27	3	19	81%	37	1	22 (1)	62%	64	4	41 (1)	70%
20-24	28	3	21	86%	20	0	13 (1)	65%	48	3	34 (1)	71%
25-29	35	5	22 (1)	77%	26	3	16	73%	61	8	38 (1)	62%
30-34	20	2	14	80%	32	3	16	59%	52	5	30	67%
35-39	20	2	11 (1)	65%	21	1	11	57%	41	3	22 (1)	54%
40-44	17	1	13	82%	15	1	12	87%	32	2	25	78%
45-	18	2	15 (1)	94%	6	1	5	100%	24	3	20 (1)	96%
Sub-total	165	18	115 (3)	81%	157	10	95 (2)	67%	322	28	210 (5)	74%
		10.9%	70%			6.4%	60%			8.7%	65%	
Mataipako												
15-19	21	1	4	24%	18	1	8 (1)	50%	39	2	12 (1)	36%
20-24	35	6	16 (1)	63%	26	2	15	65%	61	8	31 (1)	64%
25-29	19	1	11	63%	17	2	7	53%	36	3	18	58%
30-34	14	1	6	50%	15	1	10	73%	29	2	16	62%
35-39	22	1	12	59%	14	1	6	50%	36	2	18	55%
40-44	16	2	8 (1)	62%	7	1	1	29%	23	3	9 (1)	52%
45-	9	0	4 (1)	44%	8	0	4	50%	17	0	8 (1)	47%
Sub-total	136	12	61 (3)	54%	105	8	51 (1)	56%	241	20	112 (4)	55%
		8.8%	45%			7.6%				8.3%	46%	
TOTAL												
15-19	48	4	23	56%	55	2	30 (2)	58%	103	6	53 (2)	57%
20-24	63	9	37 (1)	73%	46	2	28 (1)	65%	109	11	65 (2)	70%
25-29	54	6	33 (1)	72%	43	5	23	65%	97	11	56 (1)	69%
30-34	34	3	20	68%	47	4	26	64%	81	7	46	65%
35-39	42	3	23 (1)	62%	35	2	17	54%	77	5	40 (1)	58%
40-44	33	3	21 (1)	73%	22	2	13	68%	55	5	34 (1)	71%
45-	27	2	19 (2)	78%	14	1	9	71%	41	3	28 (2)	76%
TOTAL	301	30	176 (6)	68%	262	18	146 (3)	62%	563	48	322 (9)	66%
		10%				6.7%				8.5%		

Table II. HBeAg and anti-HBe in sera from 48 HBsAg positive inhabitants in the Sirama region and Mataipako

	HBsAg positive		HBeAg positive Anti-HBe negative		HBeAg negative Anti-HBe positive		HBeAg negative Anti-HBe negative	
	Male	Female	Male	Female	Male	Female	Male	Female
Ambodikatakata	3	1	2	0	1	1	0	0
Ambodimanga*	6	2	4	0	2	2	0	0
Ankatoko	2	1	1	0	1	1	0	0
Tanambao	7	6	3	4	3	2	1	0
Sirama subtotal	18	10	10	4	7	6	1	0
Mataipako	12	8	5	1	7	6	0	1
Total	30	18	15	5	14	12	1	1
Total both sexes	48		20		26		2	

Table III. The infecting HBV genotypes in strains from 45 HBsAg positive inhabitants in five villages in Northern Madagascar

	HBsAg +	Genotype Male/ Female						Total
		A/ayw1 A1	D/ayw2 D7	D/ayw3 D2	D/ayw4	D/ayw2	E/ayw4	
Ambodikatakata	3/1	2/0	1/1	0/0	0/0	0/0	0/0	3/1
Subtotal	4	2	2	0	0	0	0	4
Ambodimanga	6/2	3/2	0/0	0/0	0/0	1/0	1/0	5/2
Subtotal	8	5	0	0	0	1	1	7
Tanambao	7/6	0/0	1/2	0/0	0/0	0/0	6/4	7/6
Subtotal	13	0	3	0	0	0	10	13
Ankatoko	2/1	0/0	0/0	1/0	0/0	0/0	0/1	1/1
Subtotal	3	0	0	1	0	0	1	2
Subtotal	18/10	5/2	2/3	1/0	0/0	1/0	7/5	16/10
Sirama regioion	28	7	5	1	0	1	12	26
Mataipako	12/8	3/0	1/2	0/0	0/1	0/0	8/4	12/7
Subtotal	20	3	3	0	1	0	12	19
Total M/F	30/18	8/2	3/5	1/0	0/1	1/0	15/9	28/17
Total	48*	10	8	1	1	1	24	45

* Two HBV strains could not be genotyped due to low amount of HBV DNA. One individual was double infected with two strains of genotypes A and D.

FIGURE LEGEND

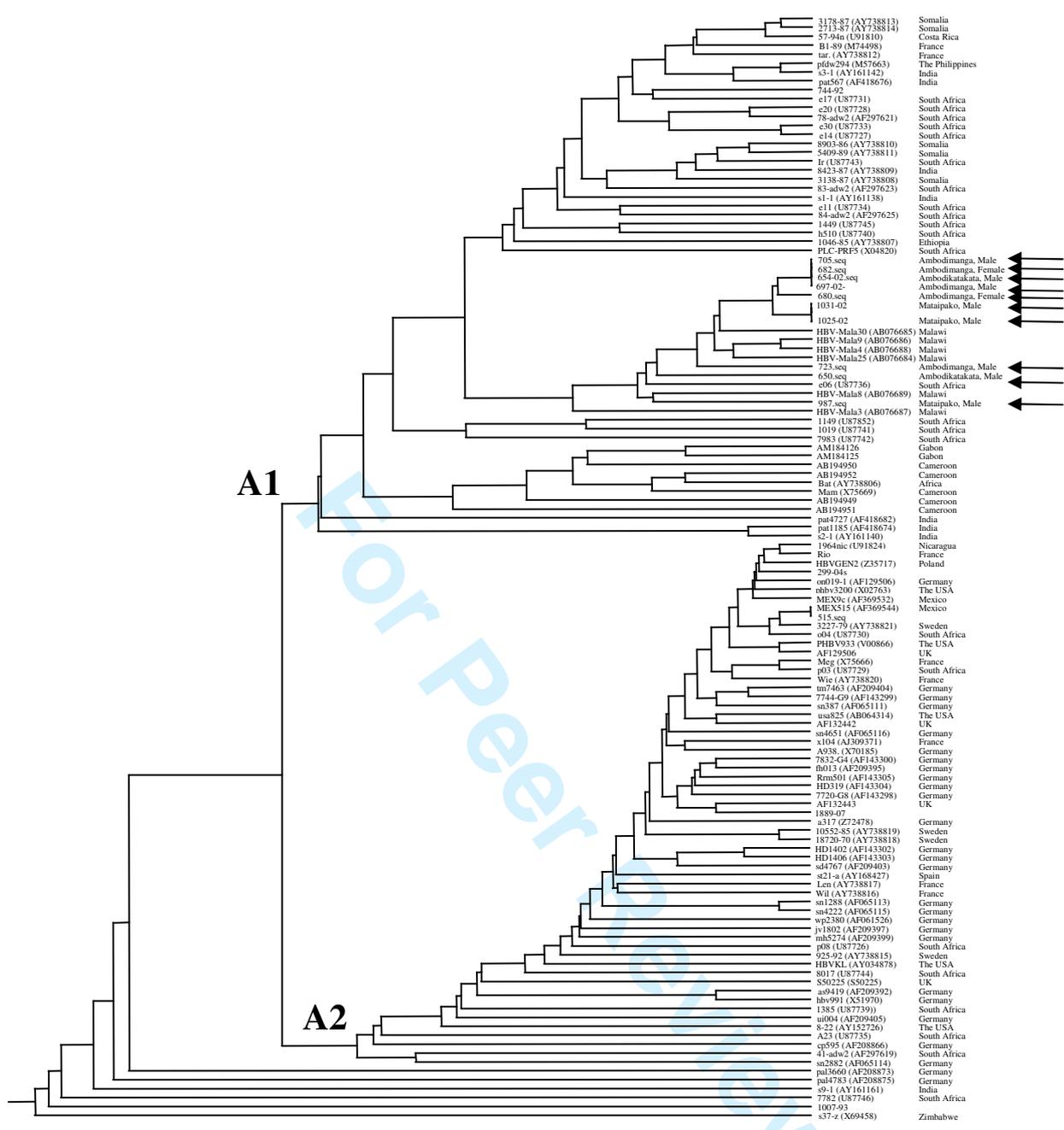
Figure 1

Dendrograms based on phylogenetic analysis of 681 nucleotides of the S gene in

a) UPGMA tree with 10 genotype A strains from Madagascar; b) UPGMA tree with 11 genotype D strain from Madagascar; c) Neighbor-Joining tree with 11 genotype D strains from Madagascar and d) UPGMA tree with 24 genotype E strains from Madagascar together with sequences of the corresponding region obtained from GenBank. Sequences from GenBank are indicated with accession numbers. The designation and origin of each strain are indicated at the nodes of the branches. The strains from Madagascar are indicated by arrows.

For Peer Review

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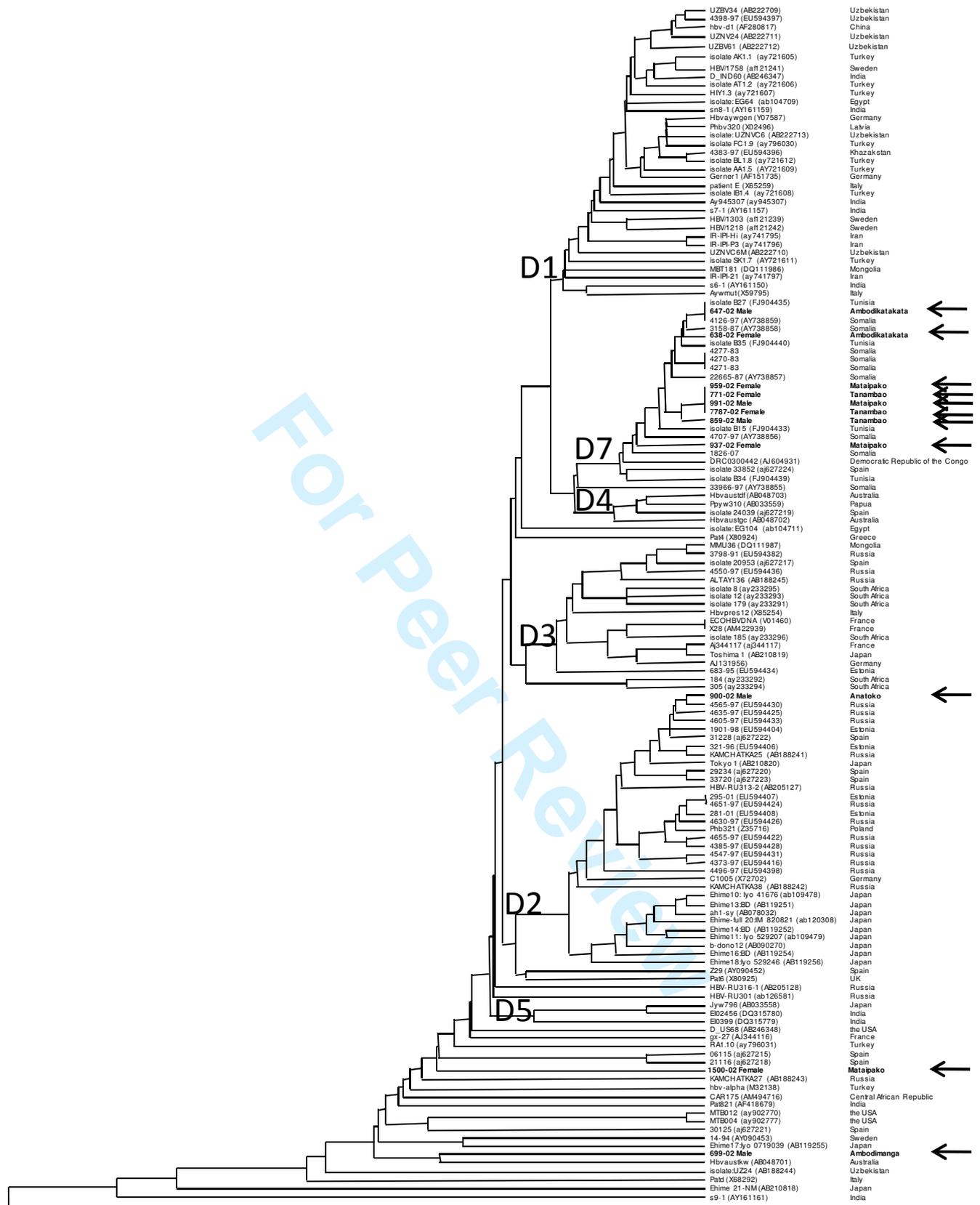


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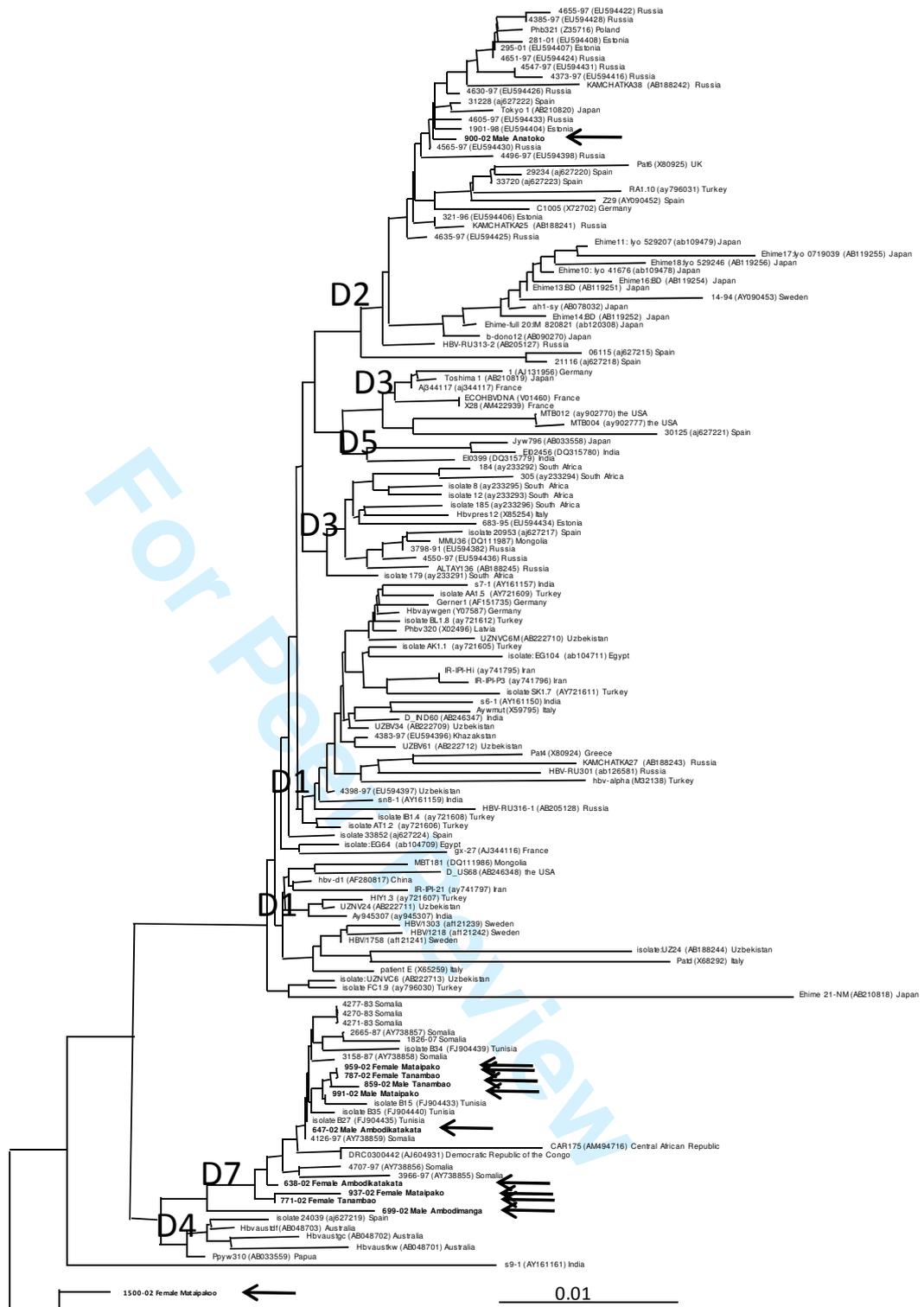
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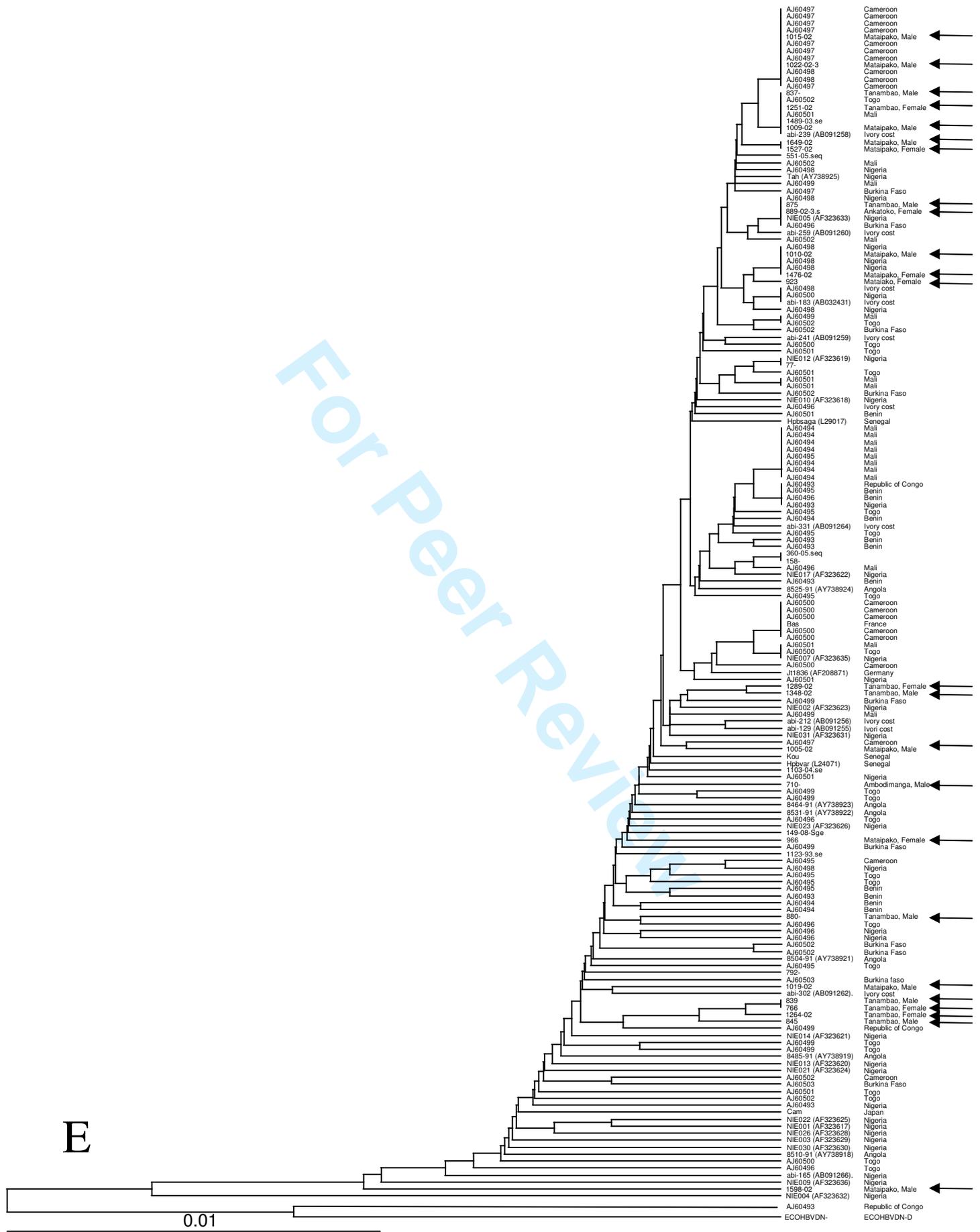
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