Molecular Characterization of Canine Rabies Virus, Mali, 2006–2013


We genetically characterized 32 canine rabies viruses isolated in Mali during 2006–2013 and identified 3 subgroups that belonged to the Africa 2 lineage. We also detected subgroup F rabies virus. This information should be useful for development of mass vaccination campaigns for dogs and eventual large-scale control programs in this country.

Rabies causes an estimated 70,000 human deaths annually worldwide, and >99% occur in developing countries, of which ≈43% occur in Africa, where rabies virus circulates in the dog population (1). A person bitten by a rabid dog, if not given postexposure prophylaxis, has an ≈5% (if bitten on the hand) to 70% (if bitten on the face) probability of showing development of clinical rabies (2). However, postexposure prophylaxis is often unavailable or unaffordable in many developing countries.

Numerous infectious diseases, including tuberculosis, malaria, dengue fever, and rabies, are present in Mali. The domestic dog is the major reservoir and vector of rabies in this country. Although disease surveillance is insufficient throughout Mali, the level of underreporting of rabies cases is unknown. Animal and human cases are recorded mainly in urban and suburban areas. Surveillance data reflect rabies incidence of 3.3 cases/1,000,000 persons/year despite 141 postexposure prophylaxis vaccinations/1,000,000 persons/year (4). Assuming a dog:human ratio in Bamako of 1:121, the annual incidence of rabies in dogs is≈2.24 rabid dogs/1,000 dogs during the past 13 years, which is higher than that observed in N’Djaména, Chad (6), which borders Mali.

A total of 306 (45.0%; 95% CI 38%–52%) of 680 dogs were reported as being vaccinated against rabies at least once. However only 59 (19.3%) of the 306 dogs examined had a valid vaccination certificate (4).

In Bamako, an average of 1,470 persons are bitten by animals each year, of whom 1,427 (97.1%) are bitten by dogs (3). A total of 3,544 (60.3%) of 5,870 bitten persons are young adults, including 1,920 (32.73%) children <10 years of age. Men are bitten more often than women.

Four lineages (Africa 1–4) of rabies virus and several subgroups have been detected in Africa. All lineages include classical rabies virus species and vary by geographic area, virus evolution, and reservoir species (7,8). The most comprehensive study of western and central African rabies viruses included some isolates from Mali (7). The purpose of our study was to obtain more detailed information on genetic characteristics of rabies virus circulating in Mali and to clarify the geographic distribution and transboundary spread of this virus in the canine population in Mali.

The Study

During 2002–2013, a total of 468 specimens were submitted from various regions in Mali to the CVL for rabies diagnosis (Figure 1). Samples were tested by using the
Molecular Characterization of Canine Rabies Virus

**Table 1.** Characteristics of 32 rabies virus samples from dogs, Mali, 2006–2013*

<table>
<thead>
<tr>
<th>Virus</th>
<th>GenBank accession no.</th>
<th>Sample ID no.</th>
<th>Region</th>
<th>Quantitative RT-PCR C&lt;sub&gt;t&lt;/sub&gt;</th>
<th>Subgroup of Africa 2 lineage</th>
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<td>RV01</td>
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<td>RV27</td>
<td>NA</td>
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<td>Bamako</td>
<td>29.00</td>
<td>G</td>
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</tbody>
</table>

*A fluorescent antibody test was conducted as described by Dean et al. (5). For each tested sample, test paper was impregnated with 100 µL of 10% brain suspension and subjected to molecular biological analysis. Of 100 samples tested, 32 showed positive results by this test. A conventional heminested reverse transcription PCR (RT-PCR) was performed with rabies virus primers JW12–JW6 as described (9). All samples showed positive results by this test. A quantitative RT-PCR was performed with rabies primers JW12–N165–146 (10). This PCR detected >100 RNA copies/µL. The coefficient of determination (R<sup>2</sup>) was 0.999, the Y intercept was of 36.65, and efficiency was 99%. Samples in bold (n = 15) had duplicate sequences and were not subjected to phylogenetic analysis. ID, identification; C<sub>t</sub>, cycle threshold; NA, not available.

**Figure 1.** Locations of origin for 100 specimens analyzed in this study (95 with positive results and 5 with negative results) submitted for rabies virus diagnosis, Mali, 2002–2013. Inset shows closer view of the area near the capital city of Bamako.
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fluorescent antibody test (5) and stored at –20°C for further analyses. We selected 100 samples (95 with positive results and 5 with negative results) for further testing on the basis of their geographic origin.

Supernatants (100 μL) of suspensions (10% wt/vol) of dog brains were deposited on test paper cards, which stabilize nucleic acids. Virus RNA was extracted from stabilized samples by using the Iprep PureLink Virus Kit (Invitrogen, Paris, France) and subjected to partial nucleoprotein gene amplification of a conserved sequence (positions 55–660) (9). Virus RNA was tested by using a hemi-nested reverse transcription PCR (RT-PCR) and a real-time

Figure 2. Maximum-likelihood phylogenetic tree based on a 564-nt sequence of nucleoprotein genes of 18 rabies virus sequences from Mali, 2002–2013, and representative sequences from Mali (n = 2), northern Africa (n = 6), South Africa (n = 2), West Africa (n = 32), and central Africa (n = 5). Sequences obtained in this study are identified in green, blue, and red. Green squares indicate genotype G, blue triangles indicate genotype H, and red circles indicate genotype F. The tree is rooted with 2 bat isolates used as outgroups Duvenhage virus (DUVV) (U22848) and Mokola virus (MOKV) (U22843). Bootstrap values (100 replicates) >70% are shown next to nodes. Alg, Algeria; BF, Burkina Faso; Cam, Cameroon; Gab, Gabon; Gamb, Gambia; Guin, Guinea; Maur, Mauritania; Mar, Morocco; Moz, Mozambique; Nig, Niger; Sen, Senegal; Tanz, Tanzania. Scale bar indicates nucleotide substitutions per site.
quantitative RT-PCR (10). After amplification, PCR products were sequenced in both directions by Beckman Coulter Genomics (Takeley, UK) and specific primers. A total of 32 stabilized samples showing positive results by heminested RT-PCR and real-time, quantitative RT-PCR were used for phylogenetic analyses (Table 1).

We constructed a maximum-likelihood phylogenetic tree (Figure 2) that excluded 15 duplicate sequences (Table 2) by using MEGA version 6 software (11). We also constructed a maximum-parsimony haplotype network by using TCS version 1.21 software (12).

We analyzed phylogenetic relationships between 18 partial nucleoprotein gene sequences and 31 representative sequences of Africa lineages of rabies virus. This analysis (online Technical Appendix Figure 1, http://wwwnc.cdc.gov/EID/article/22/5/15-0470-Techapp1.pdf) showed that all samples that belonged to the Africa 2 lineage were widely distributed in western and central Africa (7), including Mali and neighboring countries (Mauritania, Guinea, Senegal, Niger, Nigeria, Côte d’Ivoire, and Burkina Faso).

We found <2.1% divergence between all isolate sequences. For 17 haplotypes, 10 sequences were identified as belonging to subgroup G; this subgroup also included 3 sequences from Mali, Mauritania, and Senegal. Seven sequences (forming 6 haplotypes; RV88 was identical to RV90) belonged to subgroup H, which contained representative sequences from Côte d’Ivoire, Mauritania and Mali. One sequence from Mali (isolate RV57) belonged to subgroup F, which was similar to sequences from neighboring countries (Niger and Burkina Faso). Our data indicate that subgroup H might contain 2 distinct groups (online Technical Appendix Figure 2).

Analysis of the nucleoprotein gene identified canine rabies subgroups G and H in Mali, as reported (7), and subgroup F, which was found throughout Burkina Faso and Niger (8). Subgroup G circulates in Mauritania, Burkina Faso, and Senegal. Subgroup H contains viruses from Mauritania, Mali, Burkina Faso, and Côte d’Ivoire. The RV57 isolate included in subgroup F was isolated from a rabid dog at the border with Niger in 2010. Strong nucleotide identity (99.6%) was shown between RV57 and the strain isolated in Niger in 2010 (Genbank accession no. EU853646).

**Conclusions**

We identified 3 subgroups of the Africa 2 lineage of rabies virus in Mali. The presence of subgroup F could be explained by the movement of rabid animals across country borders. Previous studies reported rabies virus transmission by human-mediated animal movements (13,14). The information we obtained in this study should be useful for development of mass vaccination campaigns for dogs and eventual large-scale control programs in this country.

This study was supported by the European Union Seventh Framework Program (grant no. 221948, Integrated Control of Neglected Zoonoses) and the French Agency for Food, Environmental, and Occupational Health and Safety.

Dr. Abdallah Traoré is a research scientist at the Central Veterinary Laboratory, Bamako, Mali. His primary research interest is diagnosis of viral diseases in livestock and poultry.

**Table 2. Characteristics of representative nucleoprotein gene sequences for rabies virus isolates, Mali, 2006–2013**

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Haplotype</th>
<th>Identical sequences (–546 nt of the N gene)</th>
<th>Phylogroup</th>
</tr>
</thead>
<tbody>
<tr>
<td>RV09</td>
<td>2</td>
<td>RV50, RV56, RV51, RV19, RV79</td>
<td>G (Africa 2)</td>
</tr>
<tr>
<td>RV96</td>
<td>6</td>
<td>RV84, RV95</td>
<td>G (Africa 2)</td>
</tr>
<tr>
<td>RV90</td>
<td>11</td>
<td>RV67, RV60, RV68, RV88, RV89, RV22</td>
<td>H (Africa 2)</td>
</tr>
<tr>
<td>RV87</td>
<td>14</td>
<td>RV14, RV27</td>
<td>H (Africa 2)</td>
</tr>
</tbody>
</table>

*All identical sequences have 100% nucleoprotein (N) gene identity on the basis of 546 nt (positions 71–618) compared with the reference isolate. RV, rabies virus.

**References**

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Health and Safety, Agricultural and Veterinary Technopole Pixérécourt,
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    in Pet Birds, Chickens, and Mammals, Bangladesh
  • Pyrethroid and DDT Resistance and Organophosphate
    Susceptibility among Anopheles spp. Mosquitoes,
    Western Kenya
  • Hendra Virus Infection in Dog, Australia, 2013
  • Kinetics of Serologic Responses to MERS Coronavirus
    Infection in Humans, South Korea
  • No Evidence of Gouléako and Herbert Virus Infections
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Technical Appendix

Technical Appendix Figure. A) Locations and phylogenetic clades for 32 rabies virus isolates obtained in Mali during 2006–2013. Clades were identified on the basis of results of gene phylogenetic analysis of nucleoprotein gene sequences. B) Maximum-parsimony haplotype network of 32 rabies virus isolates based on 564-nt nucleoprotein gene sequences. Numbers 1–17 indicate haplotype ID, dot size indicates number of samples per haplotype. Each line indicates 1 mutation, empty dots indicate haplotypes not sampled, Sequence codes in red and italics (Table 1 in main text) indicate samples not from the Bamako region.