Data Article

Data on Gabonese rodents and their Plasmodium

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A B S T R A C T

In this paper present data on the description of rodent species living around human dwelling in some villages of Gabon and their malaria parasites. Rodents are known to colonize various environments, such as forest; domestic or peridomestic environment. They are known to be the hosts of many parasites. Data presented here the circulation of malaria parasites in Gabonese rodents was shown; the estimation of pairwise genetic distances (p-distance) between rodents malaria parasites. We also provide data on rodent species diversity in Gabon. Three hundred and forty-five samples from rodents conserved in biobank of International Center of Medical Researches of Franceville (CIRMF) were used for the study. These samples were collected in six villages of southeastern of Gabon between 2009 and 2016 for routine monitoring of infectious disease. Such data can be used to describe and understanding the evolution and systematics of malaria parasite. This data set support the main findings presented in the research article [1].

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1. Data

The dataset presented here describes methods of identification of the rodent diversity and Plasmodium species infecting the rodents dwelling peri-domestic environment. Fig. 1 describes different steps of characterization of malaria parasites using whole blood or organs (liver/spleen). Fig. 2 described phylogenetic relationships between the rodents captured in Gabon and other from other countries from Genbank using a portion of mitochondrial gene (Cyt-b). Table 1 describes the diversity and percentage each parasite obtained according to the material used and the infected host species. Table 2 presents results of molecular characterization of the species of the rodents. Table 3 presents results of estimation of the pairwise genetic distance (p-distances) between cytochrome b of Plasmodium lineages obtained and others lineages indexed in Genbank and Table 4 S1 presents complete data base of captured rodents.

2. Experimental design, materials, and methods

All rodents were captured using Tomahawk and Shermann traps in peri-domestic habitats (up to 250 m from the houses). The traps being set inside and around human dwellings, in each city. For each individual, species or genus identification of the rodent was based on morphological characters and the parameters like sex, age, weight or morphometric limbs (foot and arm) were taken (Table S1). After the euthanasia, samples of different organs were collected (liver, spleen, kidney, lung, heart, intestine and brain), frozen and transported to the Centre International de Recherches Médicales de Franceville. Finally, the collected samples were stored at –80 °C until needed for molecular analyses.

Total DNA, for each selected animal was extracted from approximately 100 mg of organ tissue (spleen or liver) mixed with 500 µl of PBS solution or 200µl of blood according to the procedures
described by Boundenga et al. [2,3]. We ground the samples on an automaton set at 2000 rpm for 5 minutes, then we used 200 µl from each sample for DNA extraction (Fig. 1). Total DNA was extracted from with the DNeasy Blood and Tissue Kit (Qiagen, Courtaboeuf, France) and used as template for the detection of Plasmodium parasites of rodents according to a previously described protocol [3]. For amplification of malaria parasites, a nested PCR was performed on each sample targeting a ~930bp fragment of the Plasmodium cytochrome b (cyt-b) gene is based on a nested PCR with 2 sets of primers such as described in Ref. [4].

The first was developed by Perkins and Schall (2002) (DW2 5’-TAATGCCTAGACGGTTTCTGATTATCCAG-3’ and DW4 5’-GTGTTGGAGCTGTATAAATGTC-3’). For this first round, we used 2 µl of DNA template in a 20 µl reaction volume, containing: 4 µl of 5 x Reaction Buffer, 1.5 mM MgCl2, 200 µM of each dNTP, 20 pmol of each primer (DW2 and DW4), and 2.5 U Taq DNA Polymerase (Promega). Cycling conditions for the first round were as follows: 3 min at 94 ºC; 20 sec at 94 ºC; 20 sec at 60 ºC; 1 min 30 sec at 72 ºC (repeated for 35 cycles); 10 min at 72 ºC. For the second round of Cyt b gene amplification, we used the primers from Schwöbel et al. (2003) (Cytb1 5’-CTCTATATTGAATAGCACA-3’ and Cytb2 5’-ACAGAATAATCTCTAGCACC-3’) and we used 1 µl of 1st PCR template in a 25 µl reaction volume, containing: 5 µl of 5 x buffer, 1.25 mM MgCl2, 250 µM of each dNTP, 37.5 pmol of each primer (Cytb1 and Cytb2), and 0.5 U Taq DNA Polymerase (Invitrogen). Cycling conditions for the second round were as follows: 5 min at 95 ºC; 30 sec at 94 ºC; 30 sec at 45 ºC; 1 min 30 sec at 72 ºC (repeated for 35 cycles); 10 min at 72 ºC. This combination of primers can amplify the cyt-b from other haemosporidian parasites infecting a diverse range of hosts (see Prugnolle et al., 2010, 2011; Boundenga et al., 2016; Makanga et al., 2016). All amplified products (10µl) were run on 1.5% agarose gels in Tris-acetate-EDTA (TAE) buffer. After analyze, the PCR-amplified products were used as templates for sequencing. DNA sequencing was performed Sanger method. All Plasmodium species identified in our study were mentioned in Table 1. Table 2 show the summary of the pairwise genetic distance estimate. This analyze was done to compare the divergence between sequence de cytochrome-b obtained in our study and sequences listed in Genbank.

To confirm host species, we performed molecular analyses to amplify cyt-b gene of rodents such as described in Refs. [5,6]. Thus, for amplification of cyt-b gene we used S330 (5′-CCAATGACATGAAATCATTG) and S331 (5′-GGGATAGTCTTCTTCATTG). PCR conditions for an initial denature period of 94 ºC for 2 min, followed by 35–40 cycles of 94 ºC for 30–45 seconds, 55 ºC for 45 seconds, and 72 ºC for 1.5 minutes, and the reaction was terminated with a single cycle of 72 ºC for 7 minutes. The phylogenetic tree was built with cyt-b sequences of rodent obtained and others rodent sequence known so far indexed in Genbank. All results are contained in Table 3, Table 4 S1 and Fig. 2.

Fig. 1. Illustration of the different steps of Plasmodium diagnostic in mammals used whole blood or organs (liver/spleen) for DNA extraction. This methods was more explained in our previous studies [2,3] where we used firstly this protocol to identification of malaria parasites in wildlife.
Fig. 2. Phylogenetic relationships between the Cyt-b sequences of rodents obtained in our study (bold) and the others sequences from existing databases. The tree was built based on partial sequences of Cyt-b (750 bp-long) using PhyML (freely available at the ATGC bioinformatics platform http://www.atgc-montpellier.fr/) using NNI (Nearest Neighbor Interchange) + SPR (Subtree Pruning Regrafting) branch swapping and 100 bootstrap replicates. The names of our isolates (for instance, n14GB-Ron48_Mus musculus-DJM) include: 1) the year and country of collection (n14GB: n14: 2014 and GB: Gabon); 2) the sample number (Ron48: Rodent number 48); 3) the rodent species and 4) the abbreviation of the sample site (FCV: Franceville; MIM: Mimongo, LEK: Lekoni, DJM: Djoumou; MKK: Makokou; KLM: Koulamoutou).
Table 1
Describes of the diversity and percentage of *Plasmodium* species identified.

| *Plasmodium* species | Biological materials | Rodent species infected | Percentage (%)       | Accession number of the *Plasmodium* detected |
|----------------------|----------------------|-------------------------|----------------------|----------------------------------------------|
|                      | Whole blood (N = 60) | Liver and spleen (N = 285) |                      |                                              |
| *Plasmodium vinckei* | 3/60                 | 5/285                    | - *Mastomy natalensis* | 2.31 (8/345) MK519275; MK519276; MK519274; MK519273 |
|                      |                      |                         | - *Mus musculus*      |                                              |
|                      |                      |                         | - *Praomys* sp.       |                                              |
|                      |                      |                         | - *Lemniscomys striatus* |                                              |
|                      |                      |                         | - *Grammomys poensis* |                                              |
|                      |                      |                         | - *Praomys* sp.       |                                              |
|                      |                      |                         | - *Lemniscomys striatus* |                                              |
| *Plasmodium yoelii*  | 1/6                  | 2/285                    | - *Praomys* sp.       | 0.86 (3/345) MK519270; MK519272 |
|                      |                      |                         | - *Lemniscomys striatus* |                                              |
| *P. sp. GAB*         | 1/285                | 1/285                    | - *Mus musculus*      | 0.57 (2/345) MK519279; MK519278 |
|                      |                      |                         |                      |                                              |
Table 2
Results of molecular characterization of the species of the rodents. This table consider inly the positive individual of our study. The species were identified using the methods described in [5,6]. Thus our data show the presence of these species in the peri-domestic environment of Gabon.

| Identifier   | Year of collection | Localization | Species identification | Genbank number | Gene analyzed |
|--------------|--------------------|--------------|------------------------|-----------------|---------------|
| 14GB-Ron7    | 2014               | Franceville  | Lemniscomys striatus   | MK519268        | Cytochrome b  |
| 14GB-Ron23   | 2014               | Franceville  | Lemniscomys striatus   | MK519269        | Cytochrome b  |
| 13GB-Ron301  | 2013               | Franceville  | Proamys sp.            | MK519270        | Cytochrome b  |
| 13GB-Ron259  | 2013               | Lekoni       | Proamys sp.            | MK519271        | Cytochrome b  |
| 14GB-Ron152  | 2011               | Lekoni       | Proamys sp.            | MK519272        | Cytochrome b  |
| 14GB-Ron10   | 2014               | Koulamoutou  | Mastomys natalensis    | MK519273        | Cytochrome b  |
| 14GB-Ron35   | 2013               | Lekoni       | Mastomys natalensis    | MK519274        | Cytochrome b  |
| 15GB-Ron180  | 2015               | Makokou      | Mastomys natalensis    | MK519275        | Cytochrome b  |
| 14GB-Ron205  | 2014               | Makokou      | Mastomys natalensis    | MK519276        | Cytochrome b  |
| 14GB-Ron215  | 2014               | Makokou      | Grammomys poensis      | MK519277        | Cytochrome b  |
| 14GB-Ron11   | 2014               | Djoumou      | Mus musculus           | MK519278        | Cytochrome b  |
| 14GB-Ron63   | 2014               | Mimongo      | Mus musculus           | MK519279        | Cytochrome b  |
| 14GB-Ron48   | 2014               | Djoumou      | Mus musculus           | MK519280        | Cytochrome b  |
Table 3
The pairwise genetic distance ($p$-distances) between cytochrome b of *Plasmodium* lineages obtained in rodents samples shown in Table 1. This estimation was made using Kimura two-parameter model of substitutions.

| Parasite species          | 1  | 2  | 3  | 4  | 5  | 6  | 7  | 8  | 9  | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 |
|--------------------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
| (1) 14GB-Ron152_M.muscullus | 0.06 | | | | | | | | | | | | | | | | | | | | | | |
| (2) 14GB-Ron7_L.striatus    | 0.06 | | | | | | | | | | | | | | | | | | | | | | |
| (3) 14GB-Ron63_M.muscullus  | 0.03 | 0.08 | | | | | | | | | | | | | | | | | | | | | |
| (4) 14GB-Ron11_M.muscullus  | 0.03 | 0.08 | 0.00 | | | | | | | | | | | | | | | | | | | | |
| (5) 14GB-Ron23_L.striatus   | 0.00 | 0.06 | 0.03 | 0.03 | | | | | | | | | | | | | | | | | | | | |
| (6) 14GB-Ron48_M.muscullus  | 0.06 | 0.01 | 0.08 | 0.08 | 0.07 | | | | | | | | | | | | | | | | | | | | |
| (7) 14GB-Ron10_M.natalensis | 0.06 | 0.00 | 0.08 | 0.08 | 0.06 | 0.01 | | | | | | | | | | | | | | | | | | | |
| (8) 14GB-Ron35_M.natalensis | 0.06 | 0.00 | 0.08 | 0.08 | 0.06 | 0.01 | 0.00 | | | | | | | | | | | | | | | | | |
| (9) 15GB-Ron180_M.natalensis| 0.06 | 0.00 | 0.07 | 0.07 | 0.06 | 0.01 | 0.00 | 0.00 | | | | | | | | | | | | | | | | |
| (10) 14GB-Ron205_M.natalensis| 0.06 | 0.00 | 0.08 | 0.08 | 0.06 | 0.01 | 0.00 | 0.00 | 0.00 | 0.01 | | | | | | | | | | | | | |
| (11) DQ414654-P.v._lentum    | 0.06 | 0.01 | 0.08 | 0.08 | 0.07 | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | | | | | | | | | | |
| (12) DQ414653-P.v._lentum    | 0.06 | 0.01 | 0.08 | 0.08 | 0.07 | 0.02 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | | | | | | | | | |
| (13) DQ414655-P.v._petteri   | 0.06 | 0.03 | 0.08 | 0.08 | 0.06 | 0.04 | 0.03 | 0.03 | 0.03 | 0.03 | 0.04 | 0.04 | 0.04 | | | | | | | | | |
| (14) DQ414656-P.v._petteri   | 0.06 | 0.03 | 0.08 | 0.08 | 0.06 | 0.04 | 0.03 | 0.03 | 0.03 | 0.03 | 0.04 | 0.04 | 0.04 | 0.00 | | | | | | | | | |
| (15) DQ414650-P.v._vinckei   | 0.06 | 0.03 | 0.08 | 0.08 | 0.06 | 0.04 | 0.03 | 0.03 | 0.03 | 0.03 | 0.04 | 0.04 | 0.04 | 0.00 | 0.00 | | | | | | | | |
| (16) DQ414652-P.v._vinckei   | 0.06 | 0.05 | 0.08 | 0.08 | 0.06 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 |
| (17) DQ414651-P.v._vinckei   | 0.06 | 0.05 | 0.07 | 0.07 | 0.07 | 0.06 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 | 0.05 |
| (18) DQ414659-P.y._nigeriensis| 0.00 | 0.06 | 0.03 | 0.03 | 0.00 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 |
| (19) DQ414660-P.y._yoelii    | 0.00 | 0.06 | 0.03 | 0.03 | 0.00 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 |
| (20) AY099051-P.yoelii      | 0.00 | 0.06 | 0.03 | 0.03 | 0.00 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 |
| (21) DQ414658-P.y._killicki  | 0.01 | 0.06 | 0.03 | 0.03 | 0.01 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.07 | 0.07 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 | 0.06 |
| (22) DQ414657-P.yoelii-EL   | 0.00 | 0.06 | 0.03 | 0.03 | 0.00 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.07 | 0.07 | 0.07 | 0.06 | 0.06 | 0.06 | 0.06 | 0.07 | 0.00 | 0.00 | 0.00 | 0.01 |
| (23) AY099054-P.atheruri    | 0.06 | 0.03 | 0.08 | 0.08 | 0.06 | 0.04 | 0.03 | 0.03 | 0.03 | 0.04 | 0.04 | 0.04 | 0.04 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.06 | 0.06 | 0.06 |
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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.dib.2019.104646.

Conflict of Interest

The authors declare that they have no competing interests.

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