

Leptospira and Paramyxovirus Infection Dynamics in a Bat Maternity

Enlightens Pathogen Maintenance in Wildlife

Dietrich *et al.* – Supporting Information

Figure S1. Sampling site and protocol for urine collection in the *M. francoismoutoui* maternity colony. (a) Representative photo of the cave entrance. (b) Schematic map of the placement of the 16 sampling trays (T1-T16) and mean number of urine droplets, inset – representative photograph of urine droplets on a sampling tray.

(a)



(b)

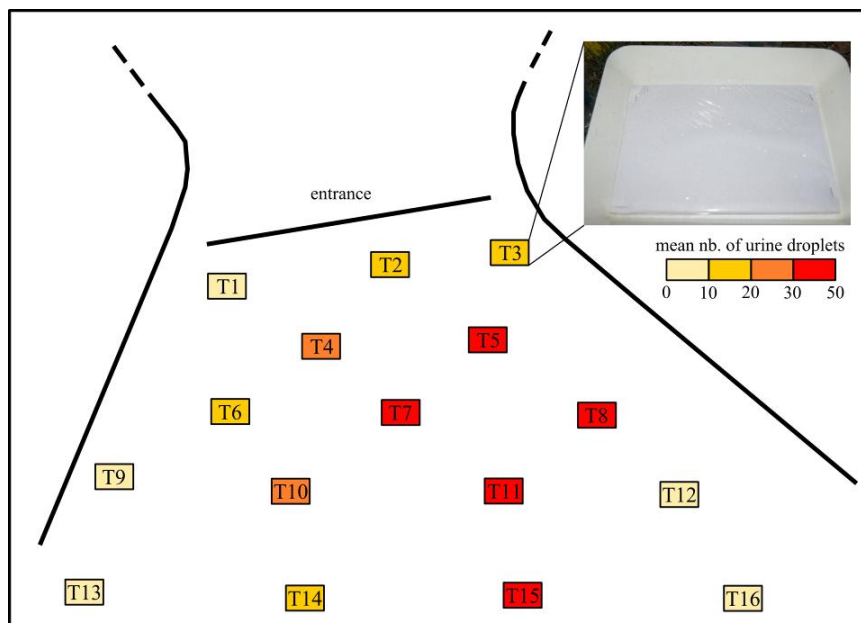
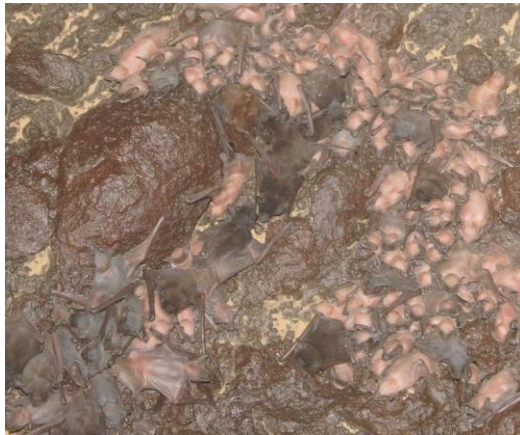


Figure S2. Photographs of the three different developmental stages observed in the *M. francoismoutoui* maternity colony. (a) Adults (brown-colored). (b) Newborns (pink). (c) Juveniles (grey).

(a)



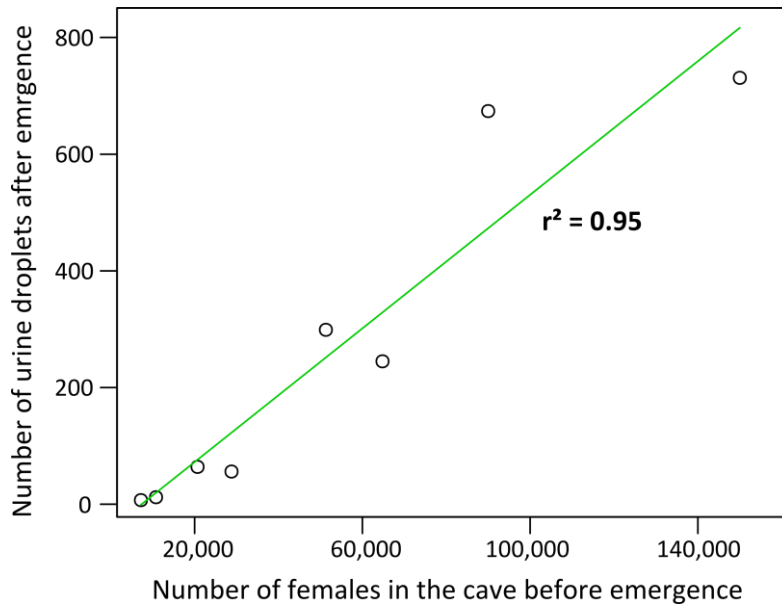
(b)



(c)



Figure S3. Correlation between the number of individuals within the colony during the first week of colony formation and the number of urine droplets shed by bats at emergence.



Methodology: During the first five weeks of colony formation in October 2014, we monitored the number of females within the cave and the number of urine droplets shed by bats. We used the method previously used by Héré et al. (2009) to estimate the number of bats: this consists in estimating the surface of the cave covered by bats just before dusk, and multiplying it by the maximum density of bats (900 individuals/m² for adults of this bat species). It is important to note that during the first weeks of colony formation, all bats exit the cave at dusk, thus the number of bats within the cave just before dusk is representative of the number of bats exiting the cave at dusk. Using plastic trays placed at specific positions in front of the cave entrance, we were able to count the number of urine droplets shed by bats after emergence at dusk. Statistical analysis of the correlation between the number of bats in the cave and the number of urine droplets was performed using a Pearson's correlation test in the R software. The line on the graph corresponds to the least-squared line and the correlation coefficient is indicated on the graph. There was a strong and significant correlation between the two parameters measured ($p < 0.001$) allowing us to validate that the number of urine droplets is correlated to the number of bats exiting the cave.

Figure S4. Phylogenetic relationship of *Leptospira* circulating in the colony of *M. francoismoutoui* based on the *16S rRNA* gene fragment analysis. Samples from this study are represented in green and are coded with sample ID and date (month-day-year). Reference sequence labels refer to the host species and geographic location. Genbank accession numbers are indicated in parentheses. Bootstrap values higher than 80% are represented by a dark circle.

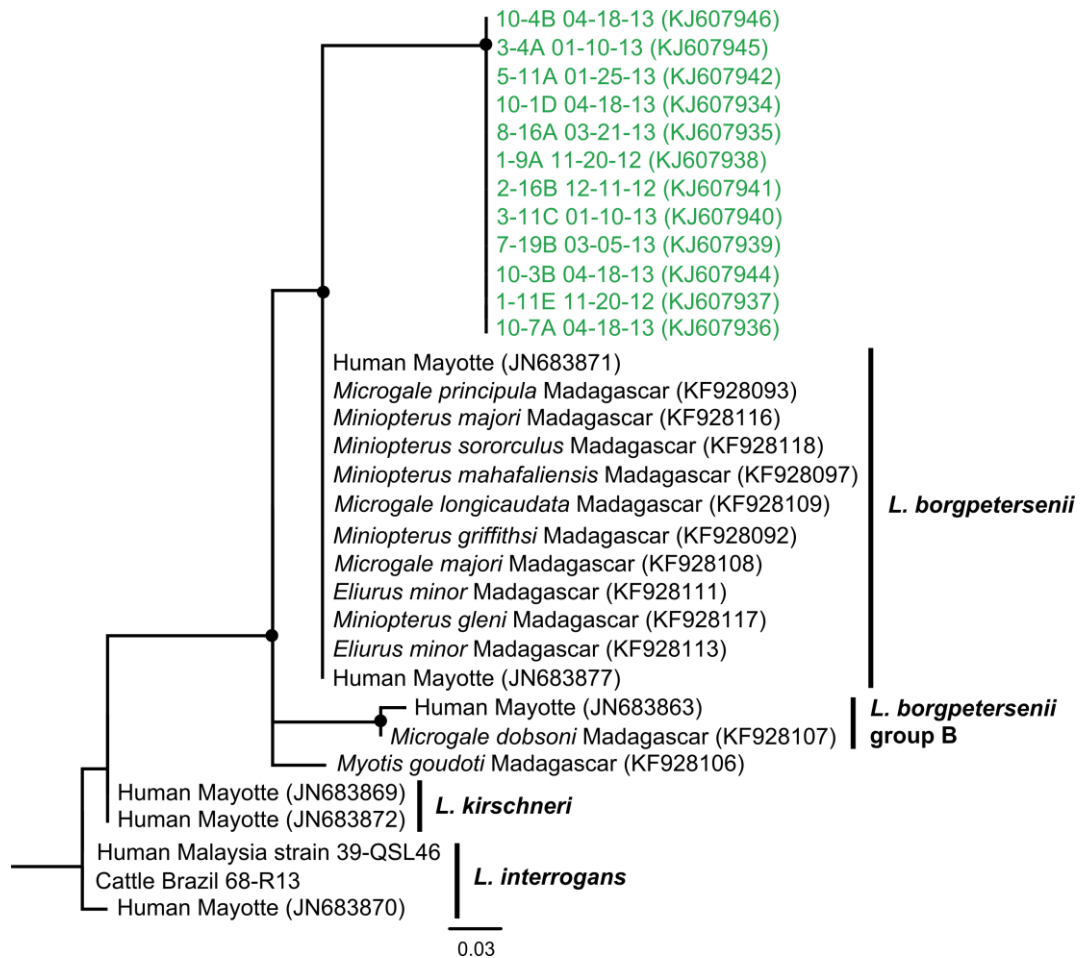


Table S1. Details of the reference sequences used in the maximum likelihood phylogeny of *Leptospira*. NA = not available.

Label	Geographic origin	Host species	Reference	Genbank nbs (<i>secY</i> / <i>rrs2</i>)
<i>Leptospira interrogans</i>				
68-R13	Brazil	Cattle	Ahmed <i>et al.</i> (2006)	NA
39-QSL46	Malaysia	Human	Ahmed <i>et al.</i> (2006)	NA
st. 200901482	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683938/JN683870
<i>Leptospira kirschneri</i>				
st. 200902933	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683940/JN683872
st. 200901480	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683937/JN683869
<i>Leptospira borgpetersenii</i>				
272	Madagascar	<i>Myotis goudoti</i>	Dietrich <i>et al.</i> (2014)	KF928134/KF928106
122	Madagascar	<i>Miniopterus mahafaliensis</i>	Dietrich <i>et al.</i> (2014)	KF928125/KF928092
635	Madagascar	<i>Miniopterus majori</i>	Dietrich <i>et al.</i> (2014)	KF928144/KF928116
685	Madagascar	<i>Miniopterus gleni</i>	Dietrich <i>et al.</i> (2014)	KF928145/KF928118
136	Madagascar	<i>Miniopterus griffithsi</i>	Dietrich <i>et al.</i> (2014)	KF928120/KF928097
653	Madagascar	<i>Miniopterus sororculus</i>	Dietrich <i>et al.</i> (2014)	KF928146/KF928117
1309	Madagascar	<i>Microgale principula</i>	Dietrich <i>et al.</i> (2014)	KF928121/KF928093
588	Madagascar	<i>Microgale majori</i>	Dietrich <i>et al.</i> (2014)	KF928136/KF928108
590	Madagascar	<i>Microgale longicaudata</i>	Dietrich <i>et al.</i> (2014)	KF928137/KF928109
625	Madagascar	<i>Eliurus minor</i>	Dietrich <i>et al.</i> (2014)	KF928141/KF928113
620	Madagascar	<i>Eliurus minor</i>	Dietrich <i>et al.</i> (2014)	KF928139/KF928111
st. 201003760	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683945/JN683877
st. 200901483	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683939/JN683871
<i>Leptospira borgpetersenii</i> group B				
575	Madagascar	<i>Microgale dobsoni</i>	Dietrich <i>et al.</i> (2014)	KF928135/KF928107
st. 200901122	Mayotte	Human	Bourhy <i>et al.</i> (2012)	JN683931/JN683863

Table S2. Details of the reference sequences used in the maximum likelihood phylogeny of paramyxovirus.

Label	Geographic origin	Host species	Reference	Genbank nb
SMG16723	Comoros	<i>Miniopterus griveaudi</i>	Wilkinson <i>et al.</i> 2012	JQ886100
SMG16753	Comoros	<i>Miniopterus griveaudi</i>	Wilkinson <i>et al.</i> 2012	JQ886102
SMG17000	Mauritius	<i>Mormopterus acetabulosus</i>	Wilkinson <i>et al.</i> 2012	JQ886105
SMG16797	Madagascar	<i>Miniopterus sororculus</i>	Wilkinson <i>et al.</i> 2012	JQ886104
SMG16468	Madagascar	<i>Miniopterus gleni</i>	Wilkinson <i>et al.</i> 2012	JQ886097
SMG17568	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928254
SMG17957	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928265
SMG17572	Madagascar	<i>Vespertilionidae</i> sp.	Wilkinson <i>et al.</i> 2014	KF928255
SMG17144	Madagascar	<i>Mormopterus jugularis</i>	Wilkinson <i>et al.</i> 2014	KF928225
SMG17799	Madagascar	<i>Miniopterus griveaudi</i>	Wilkinson <i>et al.</i> 2014	KF928258
SMG17589	Madagascar	<i>Chaerephon leucogaster</i>	Wilkinson <i>et al.</i> 2014	KF928256
SMG17773	Madagascar	<i>Miniopterus griveaudi</i>	Wilkinson <i>et al.</i> 2014	KF928257
SMG17802	Madagascar	<i>Miniopterus griveaudi</i>	Wilkinson <i>et al.</i> 2014	KF928260
SMG17544	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928249
SMG17156	Madagascar	<i>Mormopterus jugularis</i>	Wilkinson <i>et al.</i> 2014	KF928226
SMG17559	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928252
SMG17165	Madagascar	<i>Myotis goudoti</i>	Wilkinson <i>et al.</i> 2014	KF928227
SMG17557	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928250
SMG17558	Madagascar	<i>Mops leucostigma</i>	Wilkinson <i>et al.</i> 2014	KF928251
GLM058	Reunion	<i>Rattus rattus</i>	Wilkinson <i>et al.</i> 2014	KF245949
GLM007	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF408257
GLM008	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF408258
GLM009	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF408259
GLM014	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245943
GLM010	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245939
GLM062	Reunion	<i>Rattus rattus</i>	Wilkinson <i>et al.</i> 2014	KF245950
GLM011	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245940
GLM013	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245942
GLM015	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245944
GLM042	Reunion	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245948
MDI005	Mayotte	<i>Rattus rattus</i>	Wilkinson <i>et al.</i> 2014	KF245957
MDI007	Mayotte	<i>Rattus rattus</i>	Wilkinson <i>et al.</i> 2014	KF245958
GR062	Seychelles	<i>Rattus norvegicus</i>	Wilkinson <i>et al.</i> 2014	KF245955
Beilong virus	China	<i>Rattus norvegicus</i>	Li <i>et al.</i> 2006	DQ100461
Tailam virus TL8K	China	<i>Rattus andamanensis</i>	Woo <i>et al.</i> 2011	JN689227
J-virus	Australia	<i>Mus musculus</i>	Jack <i>et al.</i> 2005	NC007454
Mossman virus	Australia	<i>Rattus rattus</i>	Miller <i>et al.</i> 2003	AY286409

Table S3. Description of statistical models used to analyse bat population and infection dynamics over the breeding season of *M. francoismoutoui*. N gives the number of observations included in each analysis. "Maximal model" gives the complete set of explanatory variables tested (and their interactions) included in the model. "Minimal model" gives the model containing only the significant variables and their interactions. The "*" and "+" symbols refer to interaction and no interaction between variables, respectively.

Variable of interest	Model nb.	N	Maximal model	Minimal model
Nb. of urine droplets	1	72	tray*date	tray*date
<i>Leptospira</i> infection	2	420	date*paramyxovirus	date+paramyxovirus
Paramyxovirus infection	3	420	date*leptospira	date+leptospira
<i>Leptospira</i> intensity	4	112	tray*date*paramyxovirus	date
Co-infection	5	420	date	date

Table S4. Details of the number of urine samples tested (n_{tested}), positive samples (n_{pos}) and detection rates for *Leptospira* and paramyxovirus in the *M. francoismoutoui* maternity colony.

Sampling date	n_{tested}	<i>Leptospira</i>		Paramyxovirus	
		n_{pos}	Detection rate (95%CI)	n_{pos}	Detection rate (95%CI)
<i>2012-2013 season</i>					
November 20, 2012	52	21	40.38% (+/-13.34%)	22	42.31% (13.43%)
December 11, 2012	71	32	45.07% (11.57%)	43	60.56% (11.37%)
January 10, 2013	41	10	24.39% (13.15%)	17	41.46% (15.08%)
January 25, 2013	52	4	7.69% (7.24%)	2	3.85% (5.23%)
February 8, 2013	52	3	5.77% (5.77%)	4	7.69% (7.24%)
March 5, 2013	50	11	22.00% (11.48%)	6	12.00% (9.01%)
March 21, 2013	54	21	38.89% (13.00%)	19	35.19% (12.74%)
April 18, 2013	48	10	20.83% (11.49%)	15	31.25% (13.11%)
<i>Total</i>	<i>420</i>	<i>112</i>	<i>26.67% (4.23%)</i>	<i>128</i>	<i>30.48% (4.40%)</i>
<i>2013-2014 season</i>					
October 17, 2013	29	8	27.59% (16.34%)	6	20.69% (16.36%)
October 21, 2013	29	10	34.48% (17.36%)	10	34.48% (17.36%)
October 24, 2013	54	23	42.59% (13.20%)	21	38.89% (13.01%)
October 28, 2013	29	18	62.07% (17.67%)	15	51.72% (18.19%)
<i>Total</i>	<i>141</i>	<i>59</i>	<i>41.84% (8.13%)</i>	<i>52</i>	<i>36.88% (7.96%)</i>

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