
Rodent-Borne Diseases

Review of hosts of Lassa virus in west Africa

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Lassa virus (LASV) causes a deadly haemorrhagic fever in humans, killing several thousand people in West Africa annually. For more than 40 years, the Natal multimammate mouse, *Mastomys natalensis*, has been assumed to be the sole host of LASV. But three other species have been found LASV positive recently: the African wood mouse, *Hylomyscus pamfi*, the Guinean multimammate mouse, *Mastomys erythroleucus* and the pygmy mouse *Mus baoulei*. This presentation is a review gathering these recent findings in Nigeria, Guinea, Benin and Ghana. There is no specific *Mastomys* host per lineage since *Mastomys natalensis* is host to lineages II and IV, and *Mastomys erythroleucus* is host to lineages III and IV. Only *Hylomyscus pamfi* and *Mus baoulei* seem specific to new LASV lineages. A time-calibrated phylogeny of the partial glycoprotein sequences suggests a recent host-switching (40-60 years) between *Mastomys natalensis* and humans in Sierra Leone and Nigeria, but an older one (150-200 years) in Guinea and Mali. Analyse suggests a very old host-switching (500-600 years) between *Hylomyscus pamfi*, or *Mus baoulei* and humans, or may be between *Hylomyscus pamfi* or *Mus baoulei* and commensal rodents such as *Mastomys natalensis* and *Mastomys erythroleucus*. A general model of transmission between rodents and humans is proposed as part of the eco-pathosystem.

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Phylogenetic analysis and prevalence of Lassa virus in multimammate mice within the highly endemic Edo-Ondo hotspot for Lassa fever, Nigeria

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Lassa fever is a rodent-borne viral hemorrhagic fever that kills thousands of humans yearly in Nigeria and certain other west African countries. Recently, multiple host species of the Lassa virus (LASV) were recorded in preliminary surveys of small mammal populations around Nigeria. LASV lineage II was detected in the multimammate mouse *Mastomys natalensis* in southwestern Nigeria while lineage III was discovered in *Mastomys erythroleucus* to the east. This calls for more site-specific investigations to further understand the virus-rodent distribution and prevalence of LASV per endemic area. In this study we focus on 6 localities spanning the Lassa fever hotspot that runs through Edo and Ondo States within southwestern Nigeria, where LASV lineage II was previously discovered in *Mastomys natalensis*. During 2014-2016 1,038 small mammal specimens, representing at least 13 species, were captured. Whole blood from these specimens was screened for LASV by RT-PCRs targeted on S and L segments. Out of these *Mastomys natalensis* was LASV-positive in 5 localities while *Mastomys erythroleucus* also tested positive in one of the 5 localities. Phylogenetic analysis of virus sequences obtained from PCR-positive rodents show they all belong to LASV lineage II, the first time this lineage has been found in *Mastomys erythroleucus*. This demonstrates it is probably easier than previously thought for LASV to jump between *Mastomys* hosts. LASV phylogenetic clades clustered according to geographical location only to a certain extent. Our findings also show that LASV prevalence in rodents, even within this heavily endemic zone, is quite varied; ranging from 0% to 78% for *Mastomys natalensis*, for example. Our results provide increased insight concerning the risk of rodent-to-human transmission of LASV in the Edo-Ondo area, especially as concerns the identity and distribution of natural rodent reservoirs. In addition, our findings point out high-prevalence localities where disease-control efforts can be focused.

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Manifold implications of host species diversity on parasite occurrence: a community perspective

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Host species diversity is expected to have dramatic effects on parasite occurrence via multiple, sometimes contrasting, mechanisms. We employed a natural gradient of rodent species diversity and explored the bacterial community in the wild rodents' blood. In exploring the entire bacterial community, we have shown that it becomes more diverse with greater host diversity. However, the two dominant bacterial species responded differently to the diversity gradient; *Mycoplasma* bacterium was diluted with increased host diversity, whereas the *Bartonella* bacterium reached its peak of occurrence at medium host diversity levels. Laboratory experiments suggest that this difference in bacterial response is the result of their distinct transmission mechanisms and the level of specificity to the rodent species. Taken together, our results highlight the contribution of a community approach for understanding host diversity-parasite occurrence relationships and suggest that although these relationships may be complex in nature, they are somewhat predictable.

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Bacterial parasite communities of the fossorial water vole *Arvicola terrestris* during a period of high abundance: richness and similarity in a dynamic world

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The fossorial water vole *Arvicola terrestris* is a grassland rodent and significant agricultural pest in the eastern French region of Franche-Comté. This species exhibits population outbreaks with a mean period of 6 years and a high abundance phase of 1-3 years. Little is known about the bacterial parasites found in this species or how bacterial parasite communities may change during the peak phase. We used high-throughput sequencing to sequence the V4 region of the 16s rRNA gene of bacterial DNA extracted from spleens, livers, lungs, hearts, and kidneys of *Arvicola terrestris* individuals collected during autumn 2014, spring and autumn 2015 and spring 2016 from 5 sites in Franche-Comté to determine if bacterial parasite communities in this host vary spatially and temporally during the host high abundance phase. 32 bacterial operational taxonomic units (OTUs) corresponding to 12 parasitic bacterial genera were detected, including *Bartonella* sp., *Mycoplasma* sp., *Leptospira* sp., *Mycobacterium* sp., and *Bordetella* sp. Generalized linear modelling was used to identify significant predictors of OTU richness at the host individual (infracommunity) and host population (component community) scale; infracommunity richness ranged from 0 to 9 OTUs/animal and was best predicted by sampling site and date, with spring richness significantly lower than autumn richness. Bootstrapped component community richness ranged from 6.9 to 17.7 OTUs/population and was best predicted by local host abundance, with high-abundance populations hosting richer communities than low-abundance populations. Communities from autumn 2014 were significantly richer than spring communities despite low local host abundance at one site. Mantel tests using Jaccard and geographic distance indicate that infracommunity similarity, but not component community similarity, decay (weakly) with geographic distance. Characterization of infra- and component community richness and similarity at high abundance provides us with a foundation from which changes in bacterial parasite communities during the decline and low-abundance phase can be explored.

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Parasites of urban rodents representing sanitary risk in La Plata city, Argentina: an example of the Latin American situation

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Argentina, as the rest of Latin America, is characterized by an important social fragmentation. There are numerous areas, mostly around big cities, where people live in conditions that represent a constant risk for their health. These conditions are represented mostly by environmental and structural factors (as accumulated garbage, polluted water bodies, absence of sewage networks, etc.). This context generates a suitable scenario for the presence of urban rodents, which are represented by the Norway rat (*Rattus norvegicus*), the black rat (*Rattus rattus*) and the house mouse (*Mus musculus*). These synanthropic species are related to a high number of pathogens that directly affect to human health. The aim of this study was to register parasites of urban rodents that represent sanitary risk in different areas of La Plata city and to analyze factors that could be favouring their presence. Seasonal samplings were carried out in seven areas of Gran La Plata, Buenos Aires province, Argentina: six shantytowns and peripheral neighbourhoods and one area of the inner city of La Plata. A total of thirteen species of parasites were found: *Acantocephala* spp., *Capillaria hepatica*, *Eimeria* spp., *Heterakis spumosa*, *Hymenolepis diminuta*, *Neospora caninum*, *Nippostrongylus brasiliensis*, *Rodentolepis nana*, *Strobilocercus fasciolaris*, *Strongyloides ratti*, *Syphacia muris*, *Toxoplasma gondii* and *Trichuris muris*; and one genus bacteria: *Leptospira* spp. Six of these taxa represent a potential sanitary risk for human and domestic animals: *Strobilocercus fasciolaris*, *Hymenolepis diminuta*, *Hymenolepis nana*, *Capillaria hepatica* (helminths); *Toxoplasma gondii* (Protozoa) and *Leptospira* spp. (bacteria). The highest number of zoonotic species was observed in the areas with water bodies passing through and accumulation of garbage. This study shows urban rodents as sentinels of zoonotic diseases, alerting about the necessity of implementing actions tending to decrease their presence, with the final aim of avoiding risks to human and animal health.

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Helminth communities in synanthropic rodents of Buenos Aires (Argentina)

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The murine rodents *Mus musculus*, *Rattus rattus* and *Rattus norvegicus* are considered among the best urban adapted mammal species around the world and are host of different human pathogens, including zoonotic helminth species. As their presence in cities is related to poor hygienic and environmental conditions, rodents represent good biological models for pathogen transmission studies in urban environments. In this study, rodents were captured in the City of Buenos Aires (Argentina) for parasitological screening in 3 representative environments: residential neighborhoods (where the dominant species *Rattus rattus* is); shantytowns (the dominant species are *Rattus norvegicus* and *Mus musculus*) and parks (*Rattus norvegicus* and *Mus musculus* are the dominant species, accompanied by the native *Oligoryzomys flavescens*). Seventy-five percent of the rodents were parasitized with at least one of the 12 identified helminth species (1 acanthocephala, 3 cestodes and 8 nematodes), including species like *Hymenolepis nana* and *Hymenolepi diminuta*, recognized worldwide from a zoonotic aspect. Our results showed that helminth communities of urban rodents could be grouped according to composition and relative abundances and responded to the structure of host community. Each rodent species presented its own characteristics in terms of richness, diversity and helminth composition, keeping these characteristics still occupying more than one landscape unit. Several mechanisms contribute to complexity of the structure of parasite communities, where parasites itself, definitive and intermediate hosts and environmental and anthropogenic factors all play a role in the dynamics of parasitological communities. Inhabitants of shantytowns would be the most exposed to zoonotic diseases transmitted by rodents. As shantytowns they are not included in urban planning programs, it is essential to focus efforts on individual and community actions in improve environmental quality to reduce exposure to rodent-borne diseases.

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Towards understanding the role of small mammals in the transmission of Lyme disease in Virginia, USA

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Larvae and nymphs of many species of ticks select small mammals, reptiles, and birds as hosts. Since 2011, we have examined more than 1,000 small mammals of 10 species and collected a small tissue sample as well as all visible ticks; rates of infestation range from 18% in harvest mice to 53% in meadow voles. Identification of immature ticks is challenging and requires molecular or genetic methods beyond classification as being from the genus *Ixodes* or another genus. *Ixodes* ticks include *Ixodes scapularis*, the species that transmits the Lyme disease-causing bacterium *Borrelia burgdorferi* to humans. Of the approximately 2,300 ticks collected from small mammals, 491 were identified as *Ixodes* spp. ticks.

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Connecting the dots: linking *Yersinia pestis* seroprevalence in rodents and shepherd dogs to flea abundance in western China

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The People's Republic of China still suffers from many outbreaks of plague (caused by *Yersinia pestis*), since plague was firstly recorded around 1353 in the northeastern Hebei province. In order to understand its epidemiological dynamics for controlling reasons, in this study, the distribution and prevalence dynamics of *Yersinia pestis* in Sichuan Province (China) was investigated during the period 1997-2013. Rodents and fleas from captured rodents' fur and their burrows were collected from 2001-2012. Moreover, this information was analyzed combining with the seroprevalence in shepherd dogs screened from 1997 to 2013. 6,101 (43%) of the 14,202 investigated rodents carried infected fleas. However, the % of rodents carrying infected fleas and the flea index varied over the different years. Temperature, air humidity and precipitation can predict the incidence *Yersinia pestis* in Qinghai voles. The average number of fleas in the burrows varied over the years and between the different months of the year. Generally, flea numbers are still low in the period May-June, but peak in August and September. The average number of fleas per burrow and the % of infected dogs were strongly correlated, $r(7) = 0.89$, $p < 0.01$. The seroprevalence in shepherd dogs was 9.7% (78/801). The results indicated that the risk for pathogen transmission is likely to be most eminent in the time of year that the average number of fleas per burrow is the largest. The shepherd dogs are the most possible vectors that transfer the pathogen among its owners and rodents.