

Abstracts

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Comparative entomological study on ecology and behaviour of malaria vectors in Badar-Abbas district, southern of Iran

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INTRODUCTION In areas in which malaria has been eliminated, disease transmission and vector are still the major challenges.

AIM Highland area of Bandar Abbas County located in southern Iran more recently became free of malaria transmission and to measure potential of malaria transmission, entomological study was conducted in the area.

METHODS Adult and larvae mosquitoes were collected monthly during 2014 using different collection methods. In addition, ELISA test was also used to measure the human blood index (HBI) of mosquitoes.

CONCLUSION Four species of malaria vectors including *Anopheles stephensi*, *An. culicifacies* s.l., *An. dthali*, *An. fluviatilis* s.l., were collected in the study area. Among total of 2330 female anopheles and 5881 larvae *An. stephensi* was the dominant species was captured in indoor places while *An. dthali*, *An. fluviatilis* s.l., were observed more in outdoor shelters. Although, all species were captured during landing catch collection, *An. fluviatilis* was the most abundant mosquito. In addition, the abdominal condition (gravid/semi gravid ratio) of female mosquitoes indicated that *An. stephensi* had more propensities to rest indoor places. Human blood index was calculated as 20.7% for *An. stephensi* 19% for *An. culicifacies* s.l. and 27% *An. fluviatilis* s.l.

Malaria vector control is always a big challenge in any eliminated area. The north of Badar-Abbas is a potent area for malaria transmission because three main vectors are present. Therefore the routine entomological survey for malaria free area such as north of Bandar-Abass is so essential.

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Lassa virus distribution and phylogeny in rodent populations in Bo district, Sierra Leone

METHODS Six villages in the district of Bo were investigated in 2014–2016. Each 3 months, a standardized trapping session was performed in different habitats: houses, surrounding fields, and cultivated forest. The rodents were first morphologically identified using taxonomic keys and their necessary organs obtained for molecular identification and further analyses. Blood was spotted on filter papers and other organs stored in appropriate containers. Blood samples were tested by two RT-PCRs targeted on the small and large LASV segments. To access the phylogeny, a bayesian analysis was performed on the LASV sequences using the software BEAST.

RESULTS A total of 1490 rodents dispatched in 16 rodent species (510 molecular identifications) and 1 shrew genera were captured in the six villages. The most abundant species was *M. natalensis* (356, 24%), followed by *Praomys rostratus* (345, 23%) and *Rattus rattus* (260, 17%). *M. natalensis* and *R. rattus* were sharing the house habitat whereas *P. rostratus* was living outside. About 15 rodents samples have been tested positive for LASV. The LASV positive rodents were distributed in 4 of the 6 villages. There are too few positive animals per village to show a viral dynamics per season. First phylogenetic analysis showed these sequences different from many others obtained in Kenema.

CONCLUSION Our results shows that LASV is present in rodents in Bo district, and belongs to a Sierra Leonean sub-lineage within lineage IV.

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Manipulation of sandfly distribution within the peridomestic environment, and implications for the control of vector-borne disease

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INTRODUCTION A crucial component of vector-borne disease control is to reduce contact between vectors and infectious or susceptible hosts. In Brazil, sandflies are responsible for transmission of zoonotic visceral leishmaniasis (ZVL) between dogs and to humans. The principal vector, female *Lutzomyia*