Malaria parasitaemia in children aged 1-5 years in Aba, South Eastern Nigeria

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**Background:** Malaria has become a threat to health in the tropical and other developing countries. No wonder this has become one of the components of the Millennium Development Goals (MDGs). Malaria accounts for one in five of all childhood deaths in Africa. Yet much of the impact of this disease on the world’s children could be prevented with currently available interventions.

**Methods & Materials:** This study was carried out in Aba, Abia State, Nigeria between the months of July and October, 2012. Three hundred patients were tested using thick film method for the presence of malaria parasites. A pre-tested structural questionnaire was used to obtain the demographic data and home management practices from parents of the children.

**Results:** Out of 300 children sampled, 195 (65.0%) were infected with malaria parasites. Ninety seven (62.2%) of those infected were males, while 98 (68.1%) were females. However, the prevalence rate of infection among the males and females were statistically insignificant (P-value < 0.05). Children of age five had the highest prevalence of 73.8%, followed by the children of age two with prevalence rate of 68.0%. Children living in homes where preventive measures were adopted recorded lower rate of infection. Those using insecticide treated nets (ITNs) had the lowest rate of infection (23.1%). This is followed by those using combined window/door net plus insecticide sprays (45.5%), while the homes where no control measures were adopted recorded 92.7% rate of infection.

**Conclusion:** The difference in prevalence rates among homes using different control measures were statistically significant (P-value < 0.05). Children of age five had the highest prevalence of 73.8%, followed by the children of age two with prevalence rate of 68.0%. Children living in homes where preventive measures were adopted recorded lower rate of infection. Those using insecticide treated nets (ITNs) had the lowest rate of infection (23.1%). This is followed by those using combined window/door net plus insecticide sprays (45.5%), while the homes where no control measures were adopted recorded 92.7% rate of infection.

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Controversial role of leishmania RNA virus as a determinant of pathogenicity in human leishmaniasis


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**Background:** American tegumentary leishmaniasis (ATL) is a neglected disease of South America where metastatic mucosal lesions (ML) can be seen in up to 5-20% of Leishmania Viannia complex infections. The *Leishmania* RNA virus-1 (LRV1) has been recently implicated as a possible pathogenic agent in ATL since disseminated disease (DisL) was induced by high LRV1-expressing amastigotes in an animal model, and human cases of DisL have been reportedly infected with LRV1-containing *Leishmania* parasites. None of these studies clearly supported its role in human disease.

**Methods & Materials:** Fifty-six subjects with parasitologically confirmed ATL were clinically and parasitologically assessed. Lesion biopsy specimens were processed for detection and quantification of *Leishmania* (Viannia) DNA by a quantitative real-time PCR (qPCR) assay targeting kinetoplast DNA (kDNA) minicircles. *Leishmania* (Viannia) species were identified by PCR targeting the mpi gene and PCR-RFLP assays targeting *cpb* and *hsp70* genes. LRV1 RNA detection was performed using reverse transcription (RT)-qPCR targeting conserved viral sequences.

**Results:** Subjects were clinically classified as follows: a) Localized cutaneous leishmaniasis (LCL, 42.9%), b) ML (n = 28, 50%), and c) DisL (n = 4, 7.1%). Strain identification by clinical category was: a) LCL: *L. (V.) braziliensis* (56%) and *L. (V.) guyanensis* (31.3%), b) ML: *L. (V.) braziliensis* (60%) and *L. (V.) peruviana* (40%), and c) DisL: *L. (V.) guyanensis*. Rate of LRV1 detection was 7.1% in ML (2/28), 8.3% in LCL (2/24) and 50% in DisL (2/4). Considering DisL and ML as metastatic disease (MD) and LCL as non-metastatic disease (nMD), the rate of LRV1 detection was 8.3% in nMD and 12.5% in MD (p = 1.0). Even though detection of LRV1 was higher in DisL, an important co-morbidity was detected in those patients: HIV infection, subclinical TB infection, and disseminated mycobacterial disease. Parasite load in MD and nMD was comparable (37.8 vs. 86.4 parasites per 10^6 human cells, p = 0.52). There were no clinical or parasitological differences between parasite infected and non-infected by LRV1.

**Conclusion:** Our findings do not resemble those reported in animal models. LRV1 may be a conditional contributor to metastatic...