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## Novel Detection of *Leishmania* RNA Virus-1 in Clinical Isolates of *Leishmania Viannia* panamensis

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## Abstract:

American tegumentary leishmaniasis (ATL) comprises a discrete set of clinical presentations of leishmaniasis endemic to Central and South America. Leishmania RNA virus-1 (LRV-1) is a double stranded RNA virus identified in 20-25% of Leishmania Viannia braziliensis and L. V. guyanensis, and is believed to be a predictive biomarker of severe ATL. To date, LRV-1 has been reported in other members of the Viannia complex including L. V. peruviana and L. V. lainsoni, however not in L. V. panamensis. We describe the novel detection of LRV-1 in L. V. panamensis and its associations with clinical phenotypes of ATL. Clinical isolates identified as L. V. panamensis by PCR, RFLP analysis, and Sanger sequencing at our institutions between 2012 and 2018 were screened for LRV-1 by real-time PCR. Isolates were stratified according to clinical phenotype: localized cutaneous leishmaniasis (LCL) was defined as "non-severe" ATL, whereas "severe ATL" was defined as mucosal or mucocutaneous leishmaniasis (ML/MCL); erythematous, purulent, or painful ulcers and/or lymphatic involvement (inflammatory ulcers); or multifocal/disseminated ulcers ( $\geq 4$  in  $\geq 2$  anatomic sites). Of 22 isolates of L. V. panamensis, represented countries of acquisition were Peru (n=9, 41%), Costa Rica (n=7, 32%), Ecuador (n=5, 23%), and Panama (n=1, 0.5%). The severe phenotype occurred in 9 (41%) of infections, and non-severe in 13 (59%). Of 9 severe cases, 3 (33%) were due to LRV-1-positive isolates of *L. V. panamensis* while 4 (31%) of 13 non-severe cases were LRV-1 positive (p=0.90). Median age of patients did not differ by clinical phenotype (45.8 years in severe ATL vs. 31.9 years in non- severe ATL, p=0.09), or LRV-1 status (34.1 years in LRV-1 positive cases vs. 38.3 years in LRV-1 negative cases, p=0.64). Differences in sex were not observed with either clinical phenotype (p=0.60) or LRV-1 status (p=0.52). We describe the novel detection of LRV-1 in isolates of L. V. panamensis from both Central and South America. Although LRV-1 is postulated to influence disease severity in L. V. braziliensis and L. V. guyanensis infections, we failed to demonstrate such an association in this small sample of *L. V. panamensis* isolates. The role of LRV-1 in clinical phenotypes of *L. V. panamensis* requires further exploration.