

Leishmaniasis are neglected vector-borne tropical diseases caused by more than twenty parasite species belonging to the *Leishmania* genus (Kinetoplastida: Trypanosomatidae) and transmitted to humans by the bite of Phlebotominae (Diptera: Psychodidae) sand flies [1]. In this study, an epidemiological investigation of leishmaniasis was conducted in a new hypoendemic focus of HL, located in the province of Tipaza, northern Algeria. In Algeria, epidemiological surveillance of leishmaniasis infections was generally based on serological assays for human and canine leishmaniasis, while vector incrimination was carried out by dissecting freshly caught or cryopreserved specimens for isolation and isoenzymatic characterization of *Leishmania* strains present in their midguts [10,11,23,24]. Epidemiological investigations and entomological surveys have always been crucial to better understand endemicity of leishmaniasis foci as well as determining the relationship between the vector species and the reservoirs involved in the wild transmission cycle of *Leishmania* [21,22]. *Leishmania* parasites have a digenetic life cycle, alternating between mammalian hosts, including humans, and female sand fly vectors belonging to the *Phlebotomus* genus in the Old World and the *Lutzomyia* genus in the New World [2]. It is noteworthy that *Leishmania* species reported in this region are the causes of two forms of leishmaniasis: sporadic cutaneous leishmaniasis, due to *L. infantum* MON-24 and visceral leishmaniasis (VL) due to *L. infantum* MON-1, with an average incidence of 200 and 150 cases per year, respectively [10–14]. Recently, many PCR-based molecular approaches with a high degree of sensitivity and specificity have proven to be useful in species detection and identification of *Leishmania* parasites in sand fly vectors. Regarding this species, the suspected reservoir host is *Mus musculus*, a rodent close to the *Ctenodactylus gundii* that has been found naturally infected with *L. killicki* in Tunisia [20]. Algeria is considered to be one of the ten most affected countries with a higher prevalence of cutaneous (CL) than visceral leishmaniasis (VL) [5]. The wild rodents, *Psammomys obesus* and *Meriones shawi* are the main reservoir hosts of this species [6]. *L. killicki* has recently been reported in several parts of Algeria (Ghardaia, Annaba, Tipaza) and is generally sympatric with *L. major* [15–19]. Indeed, such studies enable the identification of the potential mammalian reservoirs and vector feeding preferences [22] and identify their blood meal sources.