Chagas disease is a human parasitic disease in the Western Hemisphere that is caused by Trypanosoma cruzi, and transmitted by blood-sucking insects of the subfamily Triatominae (Hemiptera: Reduviidae). The taxon is transmitted by blood-sucking insects of the subfamily Triatominae and is frequently found in corrals of domestic animals, on stony hills, and in rock crevices of arid and semiarid zones of central Chile. Mepraia gajardoi is a genetically related triatomine described as a separate species from M. spinolai. It has similar feeding behavior and is distributed along the northern coast of Chile between 18°S and 21°S. Blood meal analyses from an insular population of M. spinolai from the southern Pacific Ocean coast of Chile (26°S) showed that coastal populations feed on seabirds, marine mammals, and reptiles.

The purpose of this study was to determine T. cruzi genotypes in M. gajardoi from wild ecotopes of northern Chile. To meet this objective, we quantified infection on M. gajardoi from two wild ecotopes in northern Chile by detection of minicircle DNA by polymerase chain reaction. The wild capture sites were classified into two ecotopes: a fully wild ecotope (ecotope 1) and a wild ecotope near human dwellings (ecotope 2). Infection rates varied between 11% and 27%. Minicircle hybridization assays showed that T. cruzi lineages Tc II and Tc VI were commonly detected in ecotope 1 and ecotope 2, respectively. These results are discussed in the context of insect proximity to human dwellings, the alimentary profile of Mepraia sp., and T. cruzi lineages detected in the past in the same disease-endemic area circulating in humans, and Triatoma infestans.
Results from genotyping indicated that *M. gajardoi* is mainly infected with Tc II (n = 26), in ecotope 1, followed by Tc I (n = 6), Tc V (n = 5), Tc VI (n = 1), and unknown lineages (n = 3). In contrast, Tc VI (n = 13) was the most prevalent lineage in ecotope 2, followed by Tc I (n = 4), Tc V (n = 4), and Tc II (n = 3).

Statistical analyses indicated that Tc II is significantly more frequent in ecotope 1 than in ecotope 2 (P < 0.001), and Tc VI is more frequent in ecotope 2 than ecotope 1 (P < 0.001). The geo-reference of each triatomine locality and detailed genotyping results is shown in Table 1. Specifically, in locality-based analyses, results indicated that TcII is more common in Vitor than in Rio Seco (P < 0.001) and San Marcos (P < 0.01). The TcVI lineage is less common in Vitor than in Rio Seco (P < 0.001) and San Marcos (P < 0.001). Representative results of *T. cruzi* lineages of triatomine samples from ecotope 1 are shown in Figure 2. Some triatomine samples (3, 5, and 7) corresponded to mixed infections with two and up to three lineages. Other triatomine samples (2 and 9) are infected with unknown *T. cruzi* lineages.

We showed that *M. gajardoi* in Chile is naturally infected with *T. cruzi*. Overall, the percentage of *M. gajardoi* nymphs infected was low (14%). There were few cases of mixed infections compared with those in *M. spinolai*, in which *T. cruzi* infection can reach up to 46.2% in some areas of central Chile, with up to half of the insects containing mixed infections.\(^{17}\) Our results indicate that infection would not be widely spread in the ecotopes studied. One explanation could be that blood donor vertebrates inhabiting coastal areas may be refractory or dead-end hosts for maintaining and propagating *T. cruzi*. Birds have an immune system with a potent complement system and are naturally resistant to *T. cruzi* infection.\(^{18,19}\) In all study localities, reptiles and marine birds are among the most frequent vertebrates found.

### Table 1

<table>
<thead>
<tr>
<th>Location</th>
<th>Coordinates</th>
<th>Distance to human dwellings (km)</th>
<th>Tc I</th>
<th>Tc II</th>
<th>Tc V</th>
<th>Tc VI</th>
<th>ND</th>
<th>No. infected vectors</th>
<th>No. vectors analyzed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vitor</td>
<td>18°28′47″S, 70°19′27″W</td>
<td>0.080–0.100</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>8</td>
<td>77</td>
</tr>
<tr>
<td>Rio Seco</td>
<td>18°45′45″S, 70°20′34″W</td>
<td>45</td>
<td>2</td>
<td>19</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>19</td>
<td>151</td>
</tr>
<tr>
<td>San Marcos</td>
<td>19°12′16″S, 70°16′08″W</td>
<td>0.050–0.070</td>
<td>2</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>3</td>
<td>9</td>
<td>95</td>
</tr>
</tbody>
</table>

*ND = not determined.*

In our study, we found higher infection rates in insects from ecotope 2, which is a wild area but near human dwellings compared with the ecotope 1, which is a fully wild area. This observation could be explained by the different feeding source of insects in ecotope 2, which probably includes more mammals (humans, domestic animals, and/or synanthropic rodents) than in ecotope 1. The potential importance of *M. gajardoi* and *M. spinolai* in transmitting *T. cruzi* as secondary vector cannot be overlooked because the domestic and wild transmission cycles may overlap, as occurs in other disease-endemic areas.\(^{20}\) *Mepraia* sp. has a patchy distribution,\(^{21}\) a home range of 47 meters\(^2\), and a maximum mobility distance of 12 meters.\(^{7}\) This information is relevant to ascertain overlapping between insect focus points and human dwellings.

Although the southern Pacific Ocean coast of Chile has been considered an area without active transmission of Chagas disease,\(^{10}\) our results indicate that some coastal populations of *M. gajardoi* are infected with *T. cruzi* and represent a threat for humans, such as fisherman and algae collectors, living in those areas. Lineages of *T. cruzi* found in *M. gajardoi* in Rio Seco and San Marcos differ substantially from those found in Corazones, Camarones, and Vitor. A high prevalence of Tc VI is found in ecotope 2, which is an identical lineage to the *T. cruzi* clone V195 isolated in this area and used as probe,\(^{22}\) and other *T. cruzi* stocks circulating in the highlands of San Pedro de Atacama at 23°S as described.\(^{23,24}\) Previous studies of *T. cruzi* lineages in northern Chile showed that Tc V was found in humans, whereas Tc I and Tc VI were found in *T. infestans*.\(^{25}\) The finding of Tc VI in ecotope 2 is similar to findings in northern Argentina, where this lineage is frequently found in humans, *T. infestans*, and dogs.\(^{20,26}\) In contrast, Tc I is the most prevalent lineage found in *M. spinolai* at 31°S.\(^{17}\) A high prevalence of Tc II was found in ecotope 1, which is the same lineage detected in *Mepraia* sp., in a coastal locality at 24°S.\(^{27}\)

![Figure 1](image-url)  
**Figure 1.** A. Map of northern Chile showing triatomine collection localities. B. Caleta Vitor (locality in ecotope 1). Note the presence of abundant stony areas and the absence of sand. C. San Marcos (locality in ecotope 2). Note the abundant stony area. Several fishermen’s dwellings are seen.
A 330-basepair (bp) product indicates a positive result. 

Different vertebrate hosts maintaining vector populations could explain the dissimilar geographic distribution of *T. cruzi* lineages in the two study ecotopes. These different host species in two types of ecotopes studied could transmit different *T. cruzi* lineages. Nevertheless, geographic distances between our sampling sites (ecotopes 1 and 2) may also explain the observed dissimilarity.

REFERENCES


