Carezza Botto-Mahan, Antonella Bacigalupo, Juana P. Correa, Francisco E. Fontúrbel, Pedro E. Cattan and Aldo Solari. Prevalence, infected density or individual probability of infection? Assessing vector infection risk in the wild transmission of Chagas disease. Proceedings of the Royal Society of London. DOI: 10.1098/rspb.2019.3018.

ELECTRONIC SUPPLEMENTARY MATERIAL

Figure S1. Graphical overlapping procedure. Black circle corresponds to the 12.13 m-buffer around each vector colony (462 m$^2$ of area) (only one vector colony depicted). Green and red circles correspond to the buffer around every trapping location of each small mammal, using the maximum recapture distances considering species, grid and year. Green circles represent rodents inside the vector colony influence area; therefore, potential hosts for that specific colony; in this case, *Octodon degus* (top) and *Phyllotis darwini* (bottom) are intersecting. The red circle represents a non-intersecting rodent, which in this case is *Abrothrix olivaceus*. Circle diameters are not scaled (only referential).

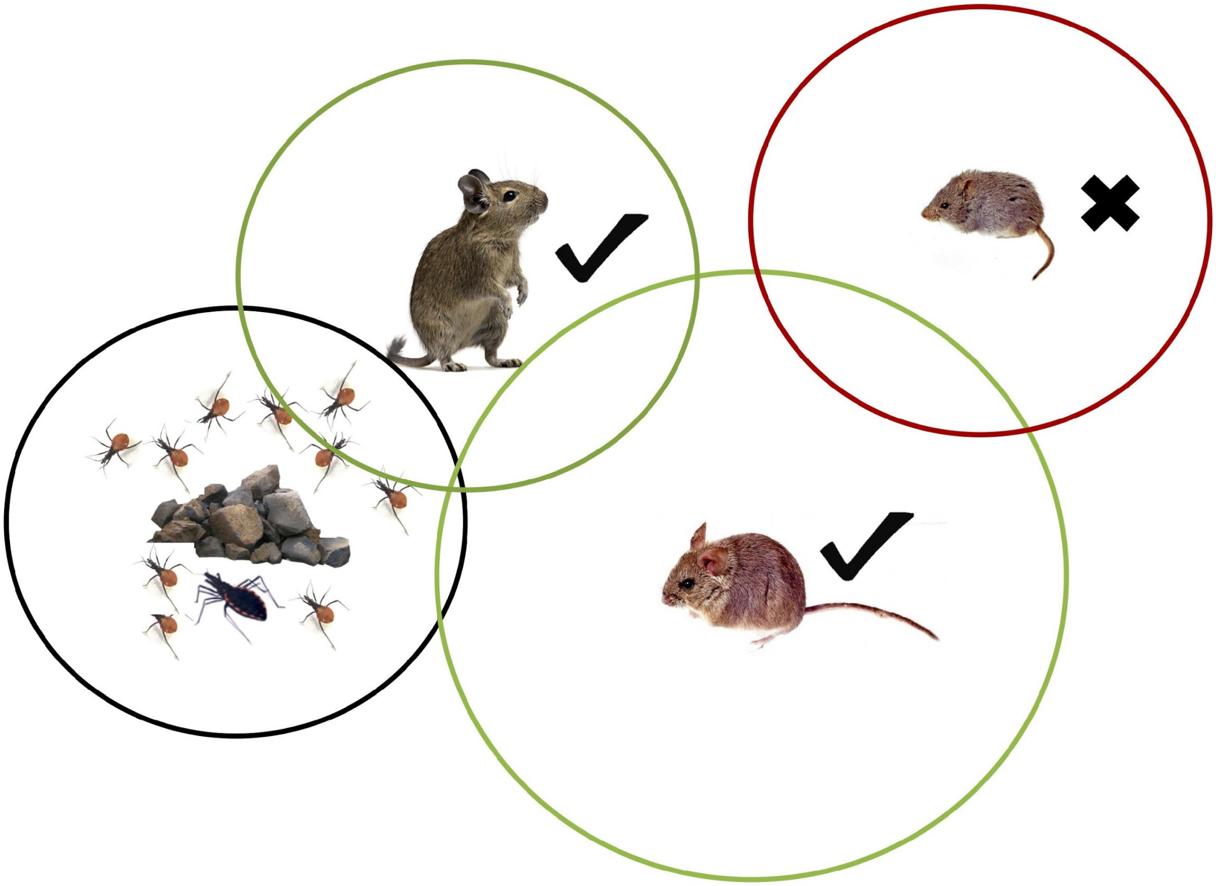


Table S1. Candidate models contrasted for (a) infection prevalence, (b) infection density, and (c) vector infection probability. Abbreviations: propinfv = proportion of infected vectors, H = Shannon-Wiener diversity index (all species captured included), inf_rod = overall number of infected rodents (three species combined), TotalPd = *Phyllotis darwini* individuals (infected and non-infected), TotalOd = *Octodon degus* individuals (infected and non-infected), TotalAo = *Abrothrix olivaceus* individuals (infected and non-infected), RF = random factors (year for models (a) and (b); year and colony identification for models (c)), totalinfv = overall number of infected vectors, status = non-infected vector (0) or infected vector (1). AIC: Akaike Information Criterion.

| **Models** | **AIC** | **deltaAIC** |
|---|---|---|
| **(a) Infection prevalence** | | |
| propinfv~H+inf_rod+TotalPd+TotalOd+TotalAo+RF | -1.82 | 0.00 |
| propinfv~colony_size+H+inf_rod+TotalPd+TotalOd+TotalAo+RF | 0.17 | 1.99 |
| **(b) Infection density** | | |
| totalinfv~colony_size+H+inf_rod+TotalPd+TotalOd+TotalAo+RF | 120.04 | 0.00 |
| totalinfv~H+inf_rod+TotalPd+TotalOd+TotalAo+RF | 121.95 | 1.91 |
| **(c) Vector infection probability** | | |
| status~H+inf_rod+ TotalPd+TotalOd+TotalAo+RFs | 9427.27 | 0.00 |
| status~colony_size+H+inf_rod+TotalPd+TotalOd+TotalAo+RFs | 9429.43 | 2.16 |

Table S2. Descriptive data for *Mepraia spinolai* colonies and small mammals at Las Chinchillas National Reserve (Chile) shown as mean (±1 SD) by year. For *M. spinolai*: mean number corresponds to the total number of vectors captured in all evaluated colonies during one hour by one-person, divided by the number of colonies, and mean infected number corresponds to those vectors positive for *Trypanosoma cruzi*. For host species: mean number corresponds to the total number of the most abundant rodent species interacting with the vector colonies, divided by the number of colonies, and mean infected number corresponds to those rodents positive for *T. cruzi*. For all the colonies we used the same area unit (462 $m^2$), corresponding to the maximum area of action of a vector colony, as previously described [16].

| | 2010 | 2011 | 2012 | 2013 |
|---|---|---|---|---|
| *Mepraia spinolai* | | | | |
| Number of colonies | 9 | 12 | 12 | 12 |
| Mean number/colony | 47.0 ±18.6 | 49.6 ± 11.9 | 28.8 ± 11.8 | 51.0 ± 15.1 |
| Mean infected number/colony | 24.8 ± 15.2 | 7.3 ± 7.2 | 12.3 ± 4.8 | 11.3 ± 11.2 |
| *Phyllotis darwini* | | | | |
| Mean number/colony | 27.9 ± 3.4 | 44.8 ± 31.3 | 18.1 ± 6.0 | 18.3 ± 6.1 |
| Mean infected number/colony | 16.0 ± 4.2 | 3.7 ± 2.2 | 2.6 ± 2.4 | 2.7 ± 2.3 |
| *Octodon degus* | | | | |
| Mean number/colony | 17.0 ± 12.9 | 9.7 ± 5.6 | 24.3 ± 8.4 | 8.6 ± 4.7 |
| Mean infected number/colony | 11.6 ± 9.6 | 2.2 ± 0.7 | 5.9 ± 1.6 | 5.1 ± 3.4 |
| *Abrothrix olivaceus* | | | | |
| Mean number/colony | 2.4 ± 2.1 | 3.4 ± 0.8 | 1.5 ± 1.5 | 2.6 ± 0.5 |
| Mean infected number/colony | 1.4 ± 1.2 | 0.3 ± 0.5 | 0.1 ± 0.3 | 1.5 ± 1.2 |

Figure S2. Mean number (± 1 SE) of *Mepraia spinolai* individuals per colony by developmental stage and sampling year. I, II, III, IV and V correspond to the five nymphal stages, and A corresponds to adults.

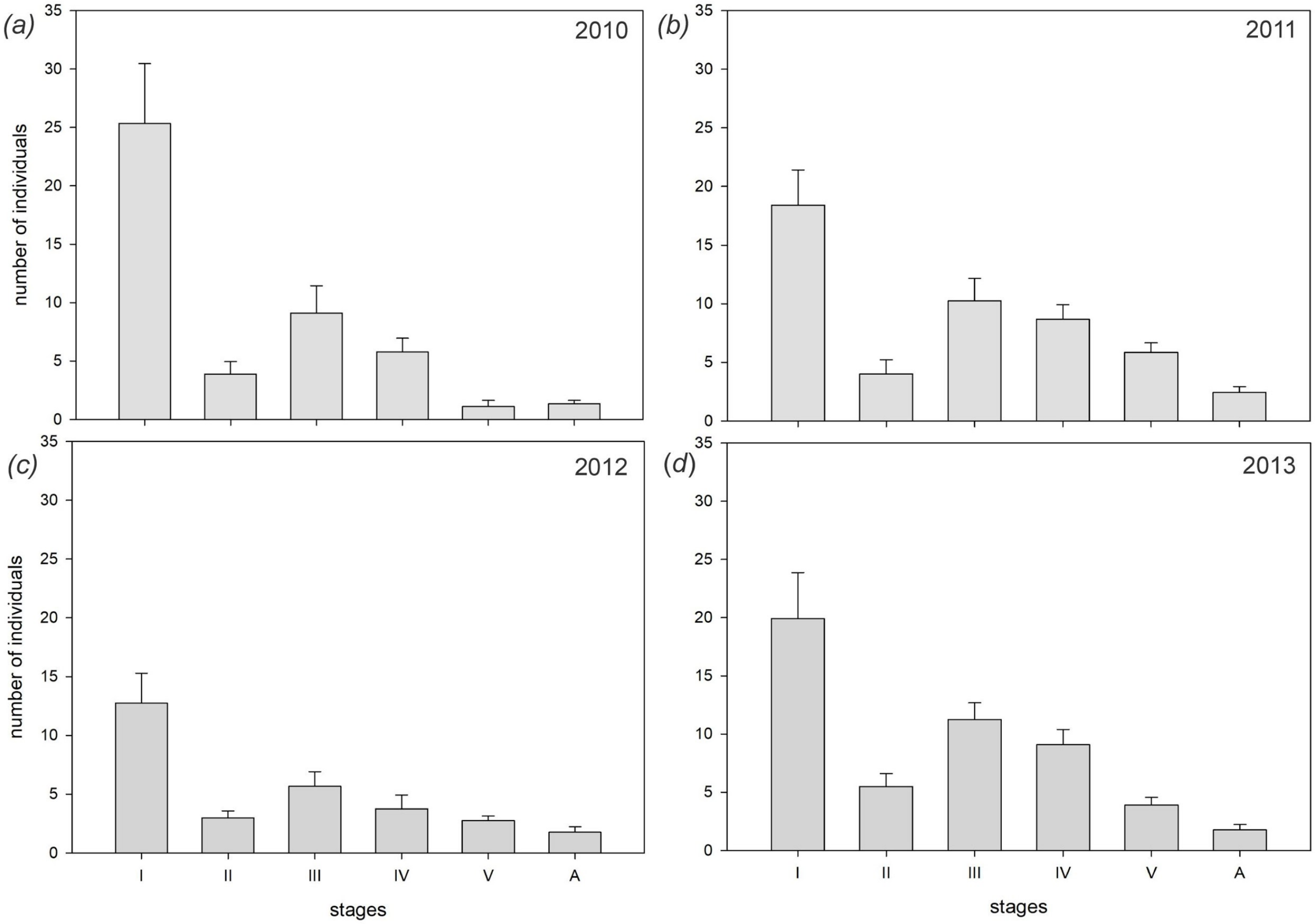
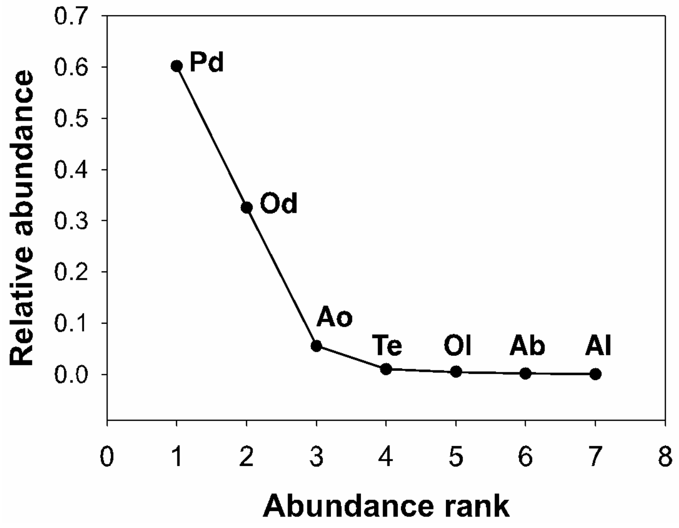


Table S3. Summary of the Generalized Linear Models (with Poisson error distribution) fitted to assess interannual variation (2010-2013) for the total number and *Trypanosoma cruzi* infected number of *Mepraia spinolai*, *Phyllotis darwini*, *Octodon degus* and *Abrothrix olivaceus* individuals in vector colonies. SE = standard error. Statistically significant *p*-values in bold.

| | Total | | | | Infected | | | |
|---|---|---|---|---|---|---|---|---|
| Species / Year | Estimate | SE | z value | *p*-value | Estimate | SE | z value | *p*-value |
| *M. spinolai* | | | | | | | | |
| 2010 | 3.850 | 0.049 | 79.186 | **<0.001** | 3.210 | 0.067 | 47.935 | **<0.001** |
| 2011 | 0.054 | 0.064 | 0.841 | 0.400 | -1.229 | 0.126 | -9.722 | **<0.001** |
| 2012 | -0.489 | 0.073 | -6.741 | **<0.001** | -0.704 | 0.106 | -6.630 | **<0.001** |
| 2013 | 0.082 | 0.063 | 1.292 | 0.196 | -0.782 | 0.109 | -7.189 | **<0.001** |
| *O. degus* | | | | | | | | |
| 2010 | 2.833 | 0.081 | 35.045 | **<0.001** | 2.447 | 0.098 | 24.956 | **<0.001** |
| 2011 | -0.565 | 0.123 | -4.585 | **<0.001** | -1.674 | 0.098 | -7.635 | **<0.001** |
| 2012 | 0.355 | 0.100 | 3.557 | **<0.001** | -0.669 | 0.154 | -4.348 | **<0.001** |
| 2013 | -0.683 | 0.128 | -5.362 | **<0.001** | -0.821 | 0.161 | -5.092 | **<0.001** |
| *P. darwini* | | | | | | | | |
| 2010 | 3.328 | 0.063 | 52.729 | **<0.001** | 2.773 | 0.083 | 33.271 | **<0.001** |
| 2011 | 0.473 | 0.077 | 6.184 | **<0.001** | -1.473 | 0.172 | -8.553 | **<0.001** |
| 2012 | -0.433 | 0.093 | -4.674 | **<0.001** | -1.824 | 0.198 | -9.210 | **<0.001** |
| 2013 | -0.420 | 0.093 | -4.542 | **<0.001** | -1.792 | 0.195 | -9.168 | **<0.001** |
| *A. olivaceus* | | | | | | | | |
| 2010 | 0.894 | 0.213 | 4.192 | **<0.001** | 0.368 | 0.277 | 1.326 | 0.185 |
| 2011 | 0.335 | 0.264 | 1.267 | 0.205 | -1.754 | 0.641 | -2.739 | **<0.010** |
| 2012 | -0.488 | 0.318 | -1.537 | 0.124 | -2.853 | 1.038 | -2.750 | **<0.010** |
| 2013 | 0.055 | 0.279 | 0.198 | 0.843 | 0.038 | 0.364 | 0.104 | 0.917 |

Figure S3. Rank-abundance plot. Only small mammal individuals related to vector colonies were considered. Top panel: Pd: *Phyllotis darwini*, Od: *Octodon degus*, Ao: *Abrothrix olivaceus*, Te: *Thylamys elegans*, Ol: *Oligoryzomys longicaudatus*, Ab: *Abrocoma bennetti*, Al: *Abrothrix longipilis*. Bottom panel: BDG analyses plot showing log-normal distribution in relation to increasing N. S: Species richness, E: Shannon-Wiener evenness index, H: Shannon-Wiener diversity index.



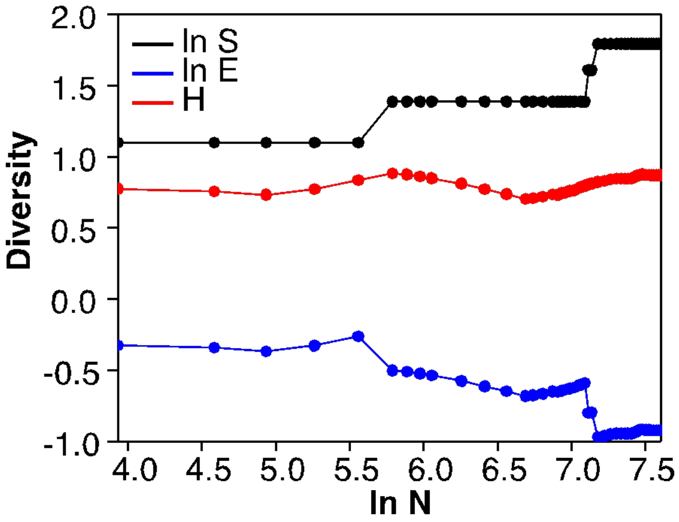


Table S4. Mean abundances (mean ± SE) of the most abundant rodent species in the study area and their mean probability of capture (p-hat), during four sampling years (2010-2013). Estimations were obtained using a robust model for closed captures implemented in MARK software (version 1995).

| | 2010 | | 2011 | | 2012 | | 2013 | |
|---|---|---|---|---|---|---|---|---|
| Species | N | p-hat | N | p-hat | N | p-hat | N | p-hat |
| *P. darwini* | 117 ± 2.29 | 0.24 | 74 ± 1.79 | 0.37 | 56 ± 1.56 | 0.22 | 37 ± 0.84 | 0.28 |
| *O. degus* | 92 ± 1.88 | 0.27 | 63 ± 1.66 | 0.27 | 119 ± 2.55 | 0.30 | 33 ± 2.53 | 0.21 |
| *A. olivaceus* | 23 ± 0.99 | 0.27 | 11 ± 0.42 | 0.39 | 5 ± 0.38 | 0.37 | 12 ± 1.32 | 0.33 |

Table S5. Mixed-Effects Generalized Linear Model (with Gaussian error distribution and identity link function) fitted to assess vector infection prevalence (population level). SE = standard error. Random effect standard deviation: year = 0.105. Statistically significant *p*-values in bold.

| Variable | Estimate | SE | z value | *p*-value |
|---|---|---|---|---|
| Intercept | 0.695 | 0.243 | 2.858 | **0.007** |
| Host species diversity | -0.438 | 0.253 | -1.727 | 0.092 |
| Density of *P. darwini* | -0.006 | 0.003 | -2.224 | **0.032** |
| Density of *O. degus* | 0.001 | 0.004 | 0.171 | 0.865 |
| Density of *A. olivaceus* | 0.038 | 0.027 | 1.367 | 0.179 |
| Density of infected rodents | 0.004 | 0.005 | 0.824 | 0.415 |

Table S6. Mixed-Effects Generalized Linear Model (with a negative binomial error distribution) fitted to assess vector infection density (population level). SE = standard error. Random effect standard deviation: year = 2.027e-05. Statistically significant *p*-values in bold.

| Variable | Estimate | SE | z value | *p*-value |
|---|---|---|---|---|
| Intercept | 4.036 | 0.942 | 4.283 | **<0.001** |
| Host species diversity | -1.203 | 1.026 | -1.173 | 0.248 |
| Density of *P. darwini* | -0.038 | 0.011 | -2.621 | **0.012** |
| Density of *O. degus* | -0.008 | 0.014 | -0.580 | 0.565 |
| Density of *A. olivaceus* | -0.027 | 0.110 | -0.250 | 0.804 |
| Density of infected rodents | 0.031 | 0.011 | 2.286 | **0.028** |

Table S7. Mixed-Effects Generalized Linear Model (with a binomial error distribution) fitted to assess vector infection probability (individual level). SE = standard error. Random effects standard deviations: year = 0.311, colony = 1.083. Statistically significant *p*-values in bold.

| Variable | Estimate | SE | t value | *p*-value |
|---|---|---|---|---|
| Intercept | 1.605 | 1.374 | 1.168 | 0.243 |
| Host species diversity | -2.823 | 1.477 | -1.911 | 0.056 |
| Density of *P. darwini* | -0.049 | 0.016 | -2.990 | **0.003** |
| Density of *O. degus* | 0.022 | 0.022 | 1.018 | 0.309 |
| Density of *A. olivaceus* | 0.066 | 0.159 | 0.418 | 0.676 |
| Density of infected rodents | 0.037 | 0.022 | 1.653 | 0.103 |

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