

Ecología de la transmisión de *Trypanosoma cruzi*

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La enfermedad de Chagas

Nova tripanozomiaze humana.

Estudos sobre a morfologia e o ciclo evolutivo do *Schizotrypanum cruzi* n. gen., n. sp.,
agente etiologico de nova entidade morbida do homem

pelo

Dr. Carlos Chagas,

Assistente.

(Estampas 9 a 13 e 10 figuras no texto)

Ueber eine neue Trypanosomiasis des Menschen.

Studien über Morphologie und Entwicklungszyklus des *Schizotrypanum cruzi* n. gen., n. sp.,
Erreger einer neuen Krankheit des Menschen

von

Dr. Carlos Chagas,

Assistenten.

(Mit Tafeln 9—13 und 10 Textfiguren)

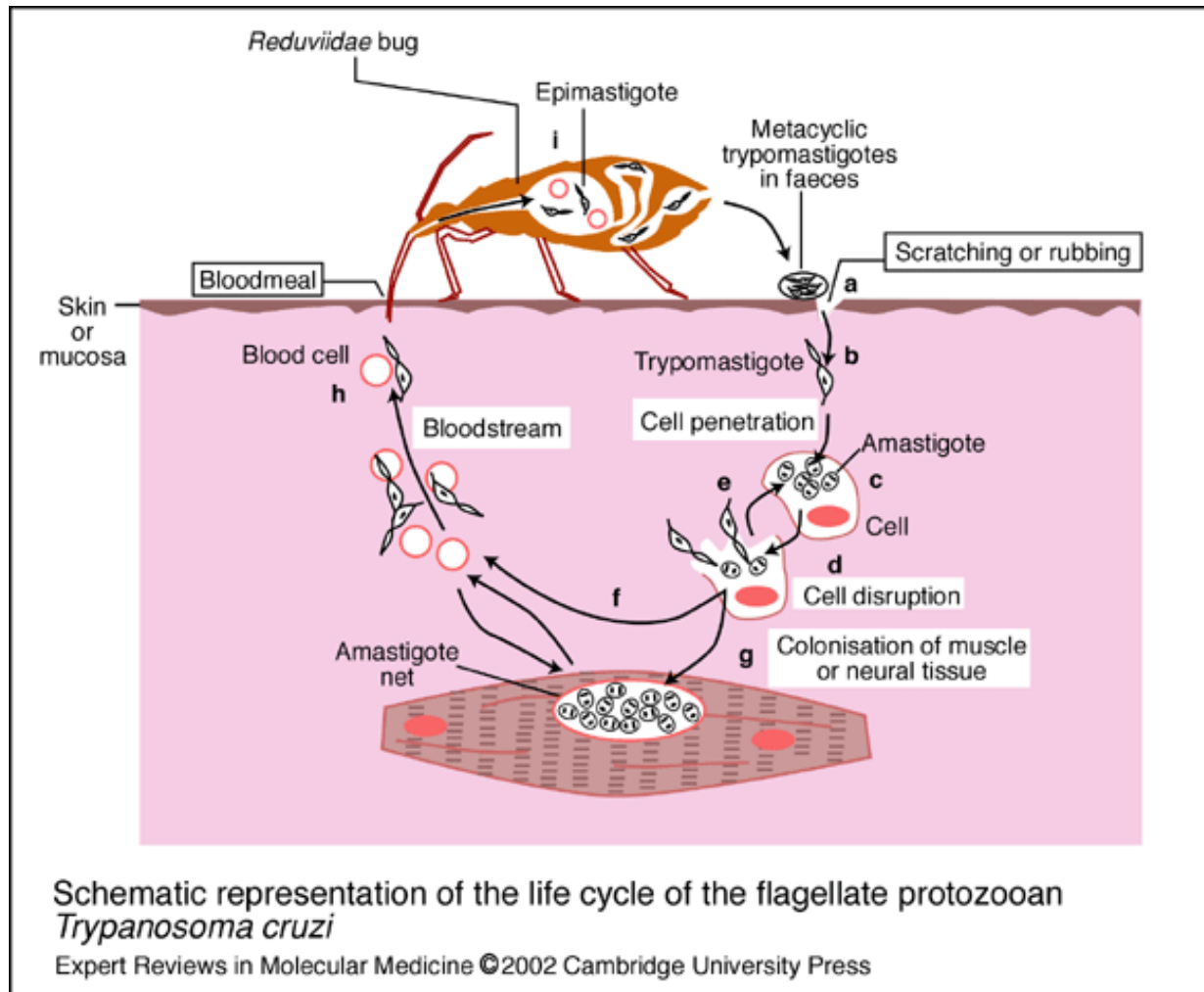
Introdução.

Em 1907 fomos incumbido pelo diretor
Dr. OSWALDO GONÇALVES CRUZ, de executar
a campanha anti-paludica nos serviços de cons-

Einleitung.

Im Jahre 1907 wurde ich von Dr. OSWALDO
GONÇALVES CRUZ, Leiter des Institutes von
Manguinhos beauftragt, die Bekämpfung der

Mecanismo de transmisión vectorial de *T. cruzi*



100 años después



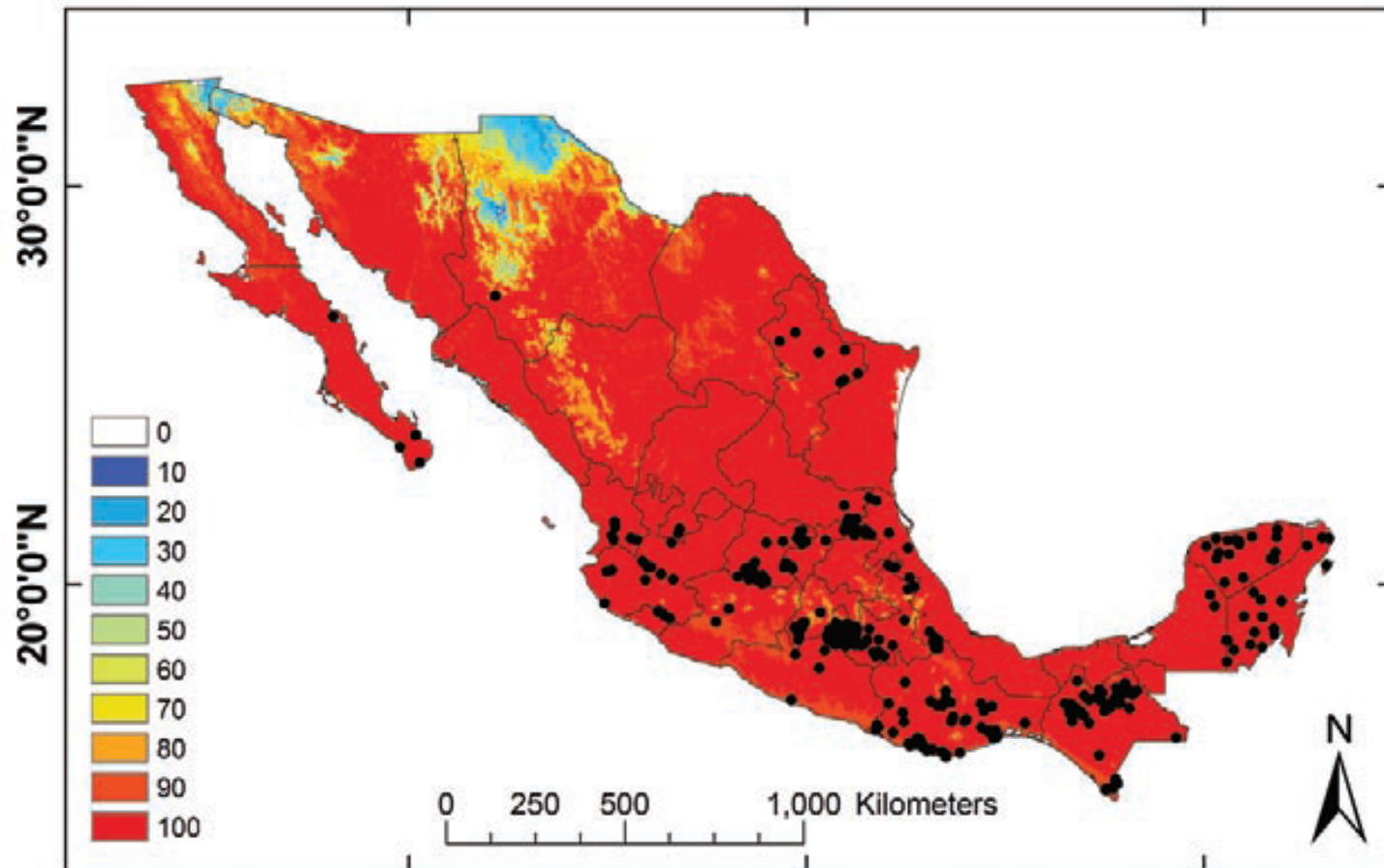
Nature: Outlook: Chagas Disease. Vol. 465, No. 7301 suppl. ppS3-S22. Who, how, what and where?. Nature. 465, S8—S9 (24 June 2010)

Atlas of Mexican Triatominae (Reduviidae: Hemiptera) and vector transmission of Chagas disease

Janine M Ramsey¹, A Townsend Peterson², Oscar Carmona-Castro¹,
David A Moo-Llanes¹, Yoshinori Nakazawa², Morgan Butrick², Ezequiel Tun-Ku¹,
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Trypanosoma cruzi

Transmision silvestre de *T. cruzi*

















Colecta de chinches



Por ejemplo, *Triatoma longipennis*



Busqueda de reservorios



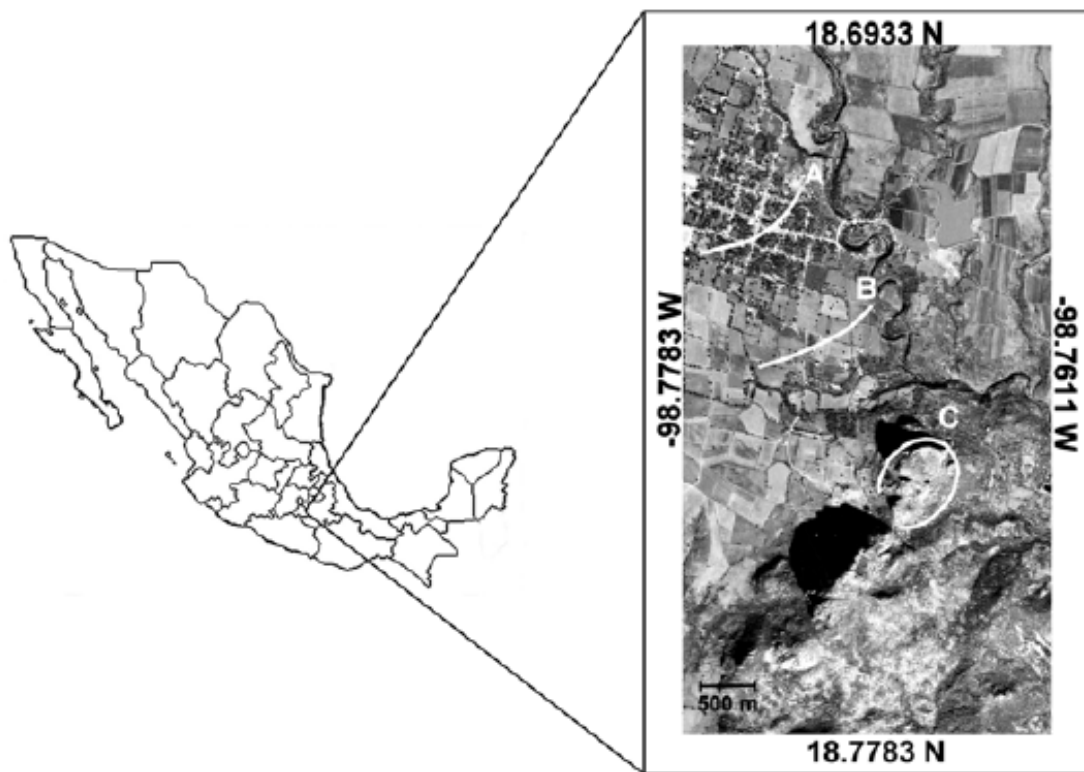
Procesamiento de reservorios potenciales



Ecological Connectivity of *Trypanosoma cruzi* Reservoirs and *Triatoma pallidipennis* Hosts in an Anthropogenic Landscape with Endemic Chagas Disease

Janine M. Ramsey¹, Ana E. Gutiérrez-Cabrera¹, Liliana Salgado-Ramírez¹, A. Townsend Peterson², Victor Sánchez-Cordero³, Carlos N. Ibarra-Cerdeña^{1,3*}

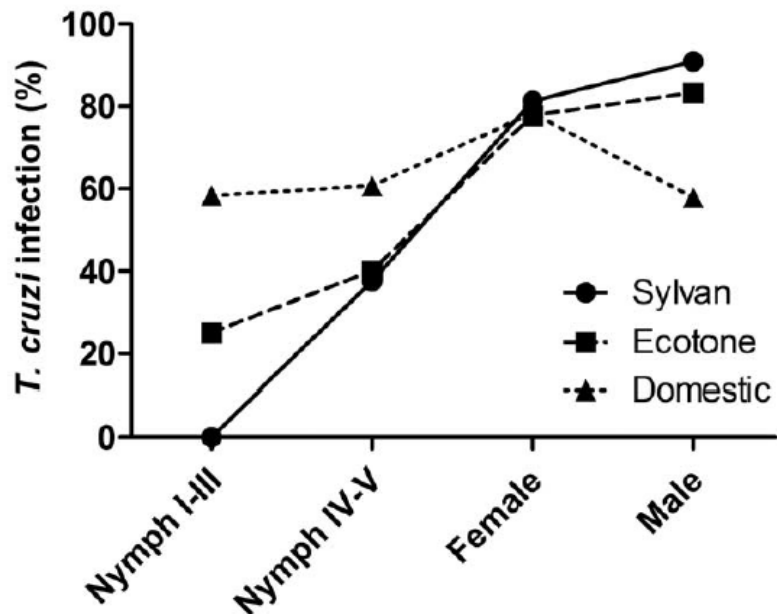
¹ Centro Regional de Investigación en Salud Pública, Instituto Nacional de Salud Pública, Tapachula, Chiapas, México, ² Biodiversity Institute, The University of Kansas, Lawrence, Kansas, United States of America, ³ Instituto de Biología, Universidad Nacional Autónoma de México, Ciudad Universitaria, Distrito Federal, México



Ecological Connectivity of *Trypanosoma cruzi* Reservoirs and *Triatoma pallidipennis* Hosts in an Anthropogenic Landscape with Endemic Chagas Disease

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Species	RI * RA	PBM	PMBM	CRI	Rank
<i>Mus musculus</i>	0.13	0.36	0.57	1.06	1
<i>Sigmodon hispidus</i>	0.14	0.2	0.14	0.48	2
<i>Didelphis virginiana</i>	0.02	0.16	0.14	0.32	3
<i>Liomys irroratus</i>	0.28	0	0	0.28	4
<i>Canis familiaris</i>	0.02	0.16	0	0.18	5
<i>Felis catus</i>	0.01	0.16	0	0.17	6
<i>Neotoma mexicana</i>	0.16	0	0	0.16	7
<i>Gallus gallus</i> *	0	0.04	0	0.04	8
<i>Baiomys musculus</i>	0.04	0	0	0.04	9
<i>Peromyscus levipes</i>	0.03	0	0	0.03	10
<i>Rattus rattus</i>	0.01	0	0	0.01	11

**T. pallidipennis* host but not a *T. cruzi* host.



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Landscape ecology of *Trypanosoma cruzi* in the southern Yucatan Peninsula

Sury Antonio López-Cancino^a, Ezequiel Tun-Ku^a, Himmler Keynes De la Cruz-Felix^a, Carlos Napoleón Ibarra-Cerdeña^b, Amaia Izeta-Alberdi^a, Angélica Pech-May^{a,c}, Carlos Jesús Mazariegos-Hidalgo^a, Alba Valdez-Tah^d, Janine M. Ramsey^{a,*}

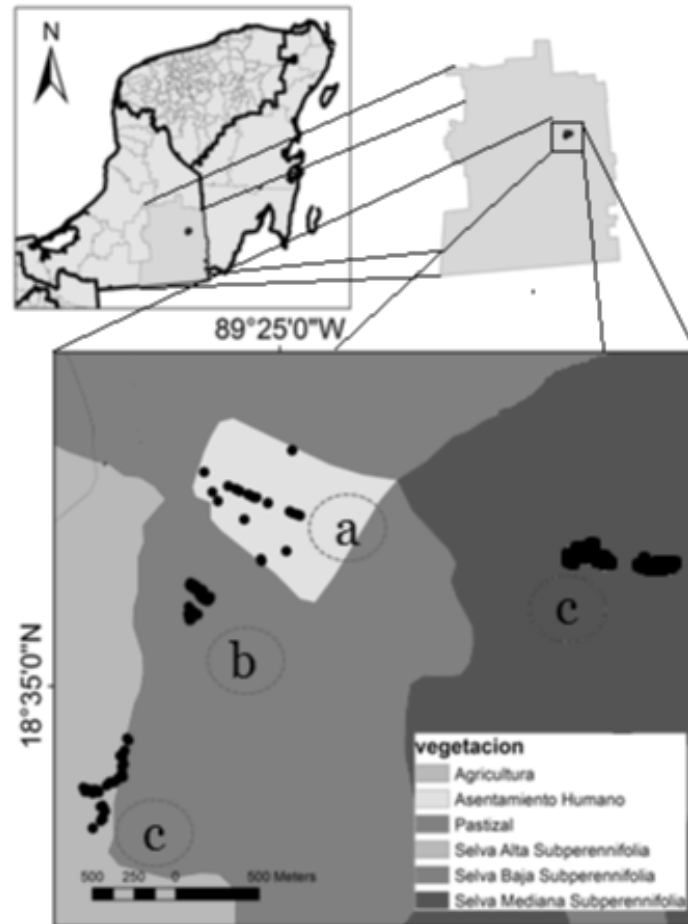
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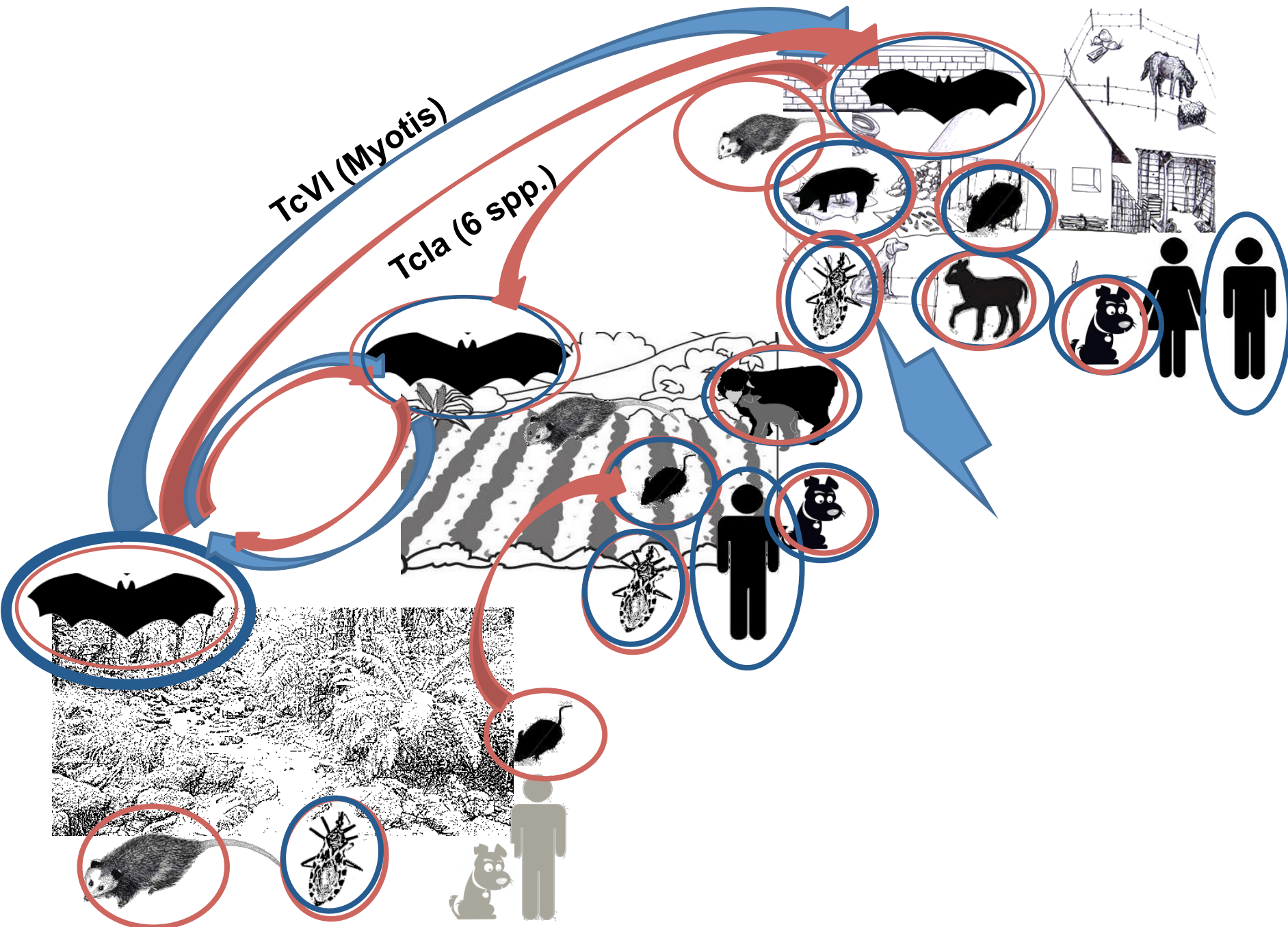
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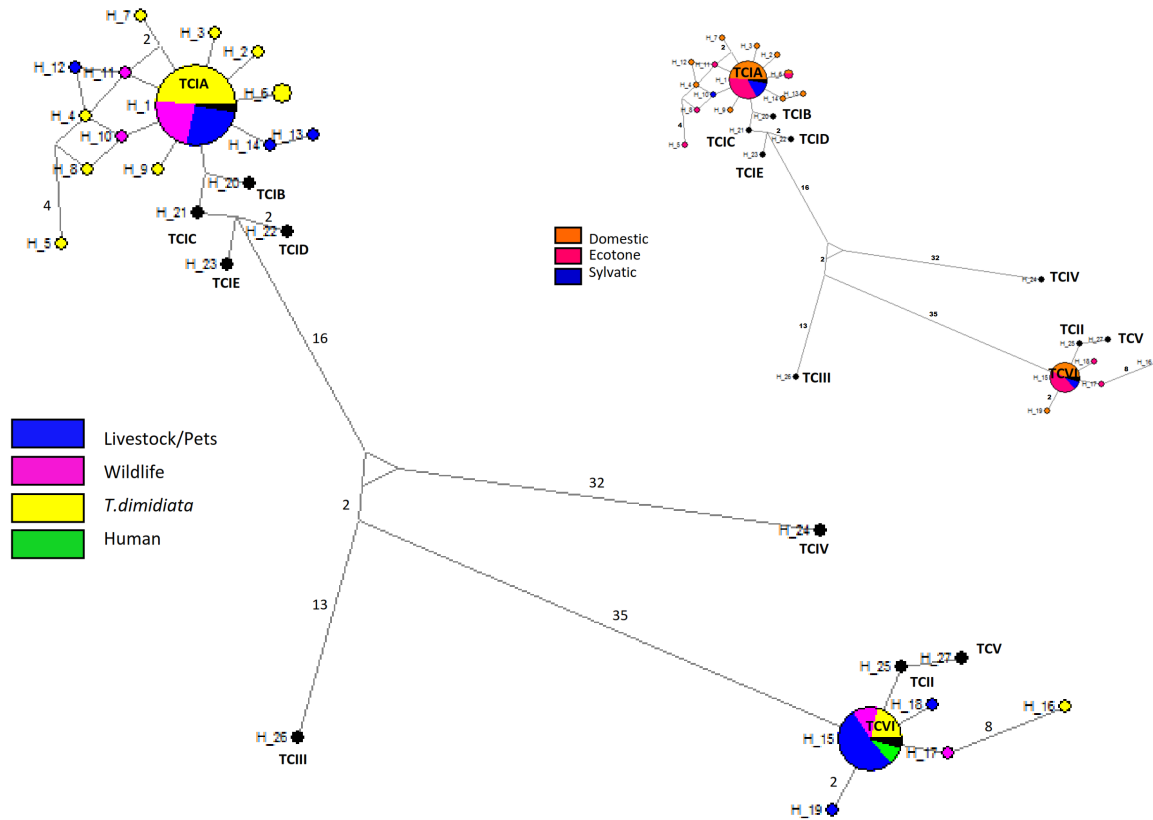
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Ecologia de Trypanosoma cruzi en Calakmul





Red genética de *Trypanosoma cruzi*



RESEARCH

Open Access



Geographical, landscape and host associations of *Trypanosoma cruzi* DTUs and lineages

Amaia Izeta-Alberdi¹, Carlos N. Ibarra-Cerdeña², David A. Moo-Llanes³ and Janine M. Ramsey^{3*}

Abstract

Background: The evolutionary history and ecological associations of *Trypanosoma cruzi*, the need to identify genetic markers that can distinguish parasite subpopulations, and understanding the parasite's evolutionary and selective processes have been the subject of a significant number of publications since 1998, the year when the first DNA sequence analysis for the species was published.

Methods: The current analysis systematizes and re-analyzes this original research, focusing on critical methodological and analytical variables and results that have given rise to interpretations of putative patterns of genetic diversity and diversification of *T. cruzi* lineages, discrete typing units (DTUs), and populations, and their associations with hosts, vectors, and geographical distribution that have been interpreted as evidence for parasite subpopulation specificities.

Results: Few studies use hypothesis-driven or quantitative analysis for *T. cruzi* phylogeny (16/58 studies) or phylogeography (10/13). Among these, only one phylogenetic and five phylogeographic studies analyzed molecular markers directly from tissues (i.e. not from isolates). Analysis of *T. cruzi* DTU or lineage niche and its geographical projection demonstrate extensive sympatry among all clades across the continent and no significant niche differences among DTUs. DTU beta-diversity was high, indicating diverse host assemblages across regions, while host dissimilarity was principally due to host species turnover and to a much lesser degree to nestedness. DTU-host order specificities appear related to trophic or microenvironmental interactions.

Conclusions: More rigorous study designs and analyses will be required to discern evolutionary processes and the impact of landscape modification on population dynamics and risk for *T. cruzi* transmission to humans.

Keywords: *Trypanosoma cruzi*, Discrete Type Unit, Host specificity, Niche identity, Ecological niche modeling, Chagas disease

Trypanosoma cruzi classification

	DTU						L1		L2		
	I	II	III	IV	V	VI	I	II	I	II	III
Mammal order											
Artiodactyla	nr	nr	nr	nr	nr	nr	nr	nr	nr	nr	nr
Carnivora	More than expected	nr	Less than expected	More than expected	nr	More than expected	More than expected	More than expected	nr	nr	More than expected
Carnivora without pets	More than expected	nr	nr	More than expected	nr	nr	More than expected	More than expected	More than expected	nr	More than expected
Chiroptera	nr	More than expected	nr	nr	nr	nr	nr	nr	nr	nr	nr
Cingulata	More than expected	nr	More than expected	Less than expected	nr	nr	More than expected	More than expected	More than expected	nr	More than expected
Didelphimorphia	More than expected	nr	nr	nr	nr	nr	More than expected	Less than expected	More than expected	Less than expected	More than expected
Primates	More than expected	nr	Less than expected	nr	More than expected	Less than expected	More than expected	Less than expected	nr	nr	Less than expected
Primates without humans	nr	More than expected	nr	More than expected	nr	nr	nr	nr	nr	More than expected	nr
Rodentia	More than expected	nr	nr	nr	nr	nr	More than expected	Less than expected	More than expected	nr	Less than expected
Vector genus											
<i>Panstrongylus</i>	nr	nr	nr	nr	nr	nr	nr	Less than expected	nr	nr	nr
<i>Rhodnius</i>	More than expected	nr	nr	nr	nr	nr	More than expected	Less than expected	nr	nr	Less than expected
<i>Triatoma</i>	Less than expected	More than expected	More than expected	nr	More than expected	More than expected	Less than expected	More than expected	nr	More than expected	More than expected

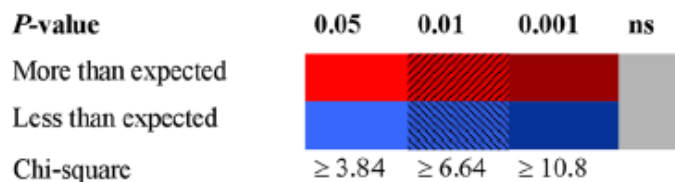


Fig 1 Frequency significance for *Trypanosoma cruzi* DTUs and lineages in mammal orders and three primary vector genera. Abbreviations: L1, Lineage L1 [14]; L2, Lineage L2 [18]. Abbreviations: nr, not reported; ns, not significant

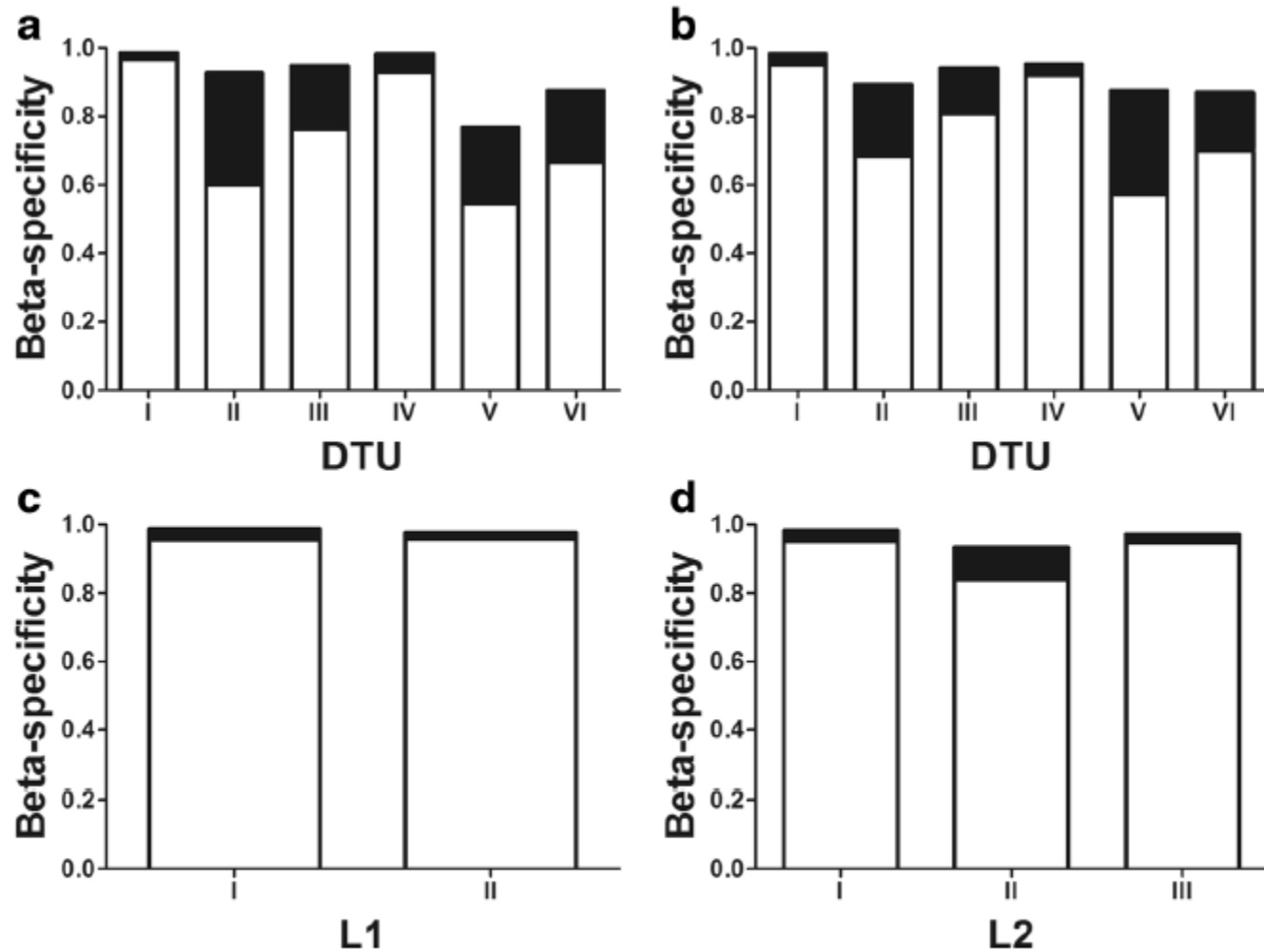
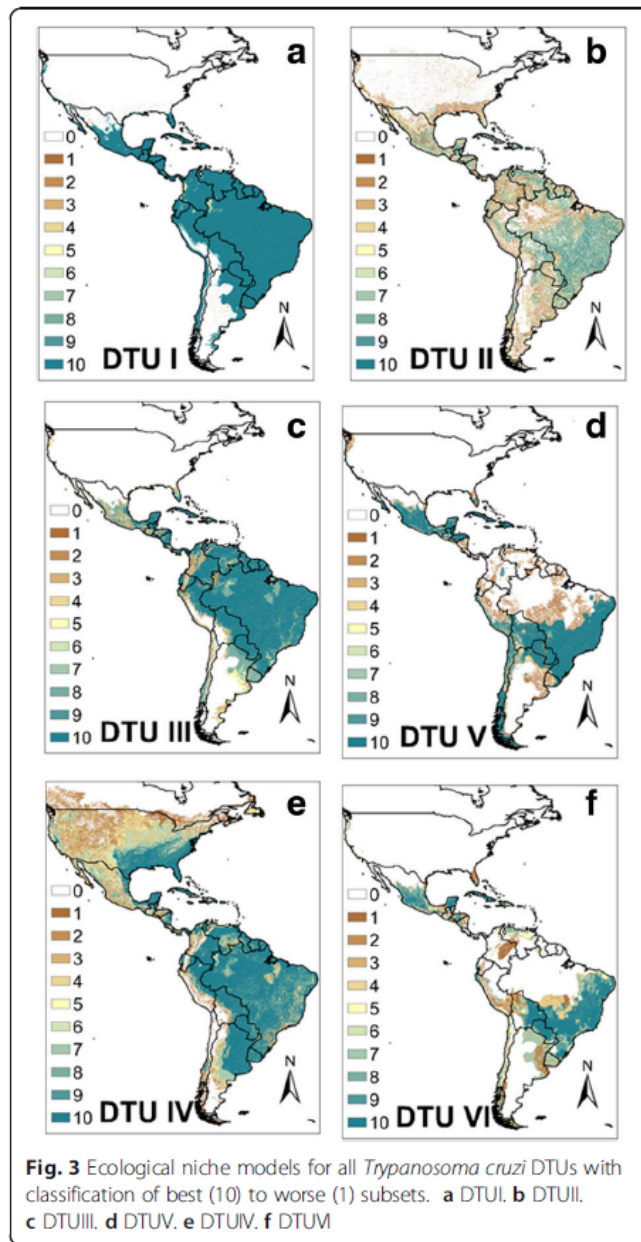


Fig. 2 Host beta-specificity for *Trypanosoma cruzi* DTUs (a) for the three primary vector genera and (b) for mammal orders. Beta specificity for mammals according to major lineage schemes (c) L1 and (d) L2. Bars in white are beta dissimilarity due to host species turnover and in black due to nestedness. The range is between 0 (absence of species interchange across multiple regions) and 1 (complete species interchange across regions)



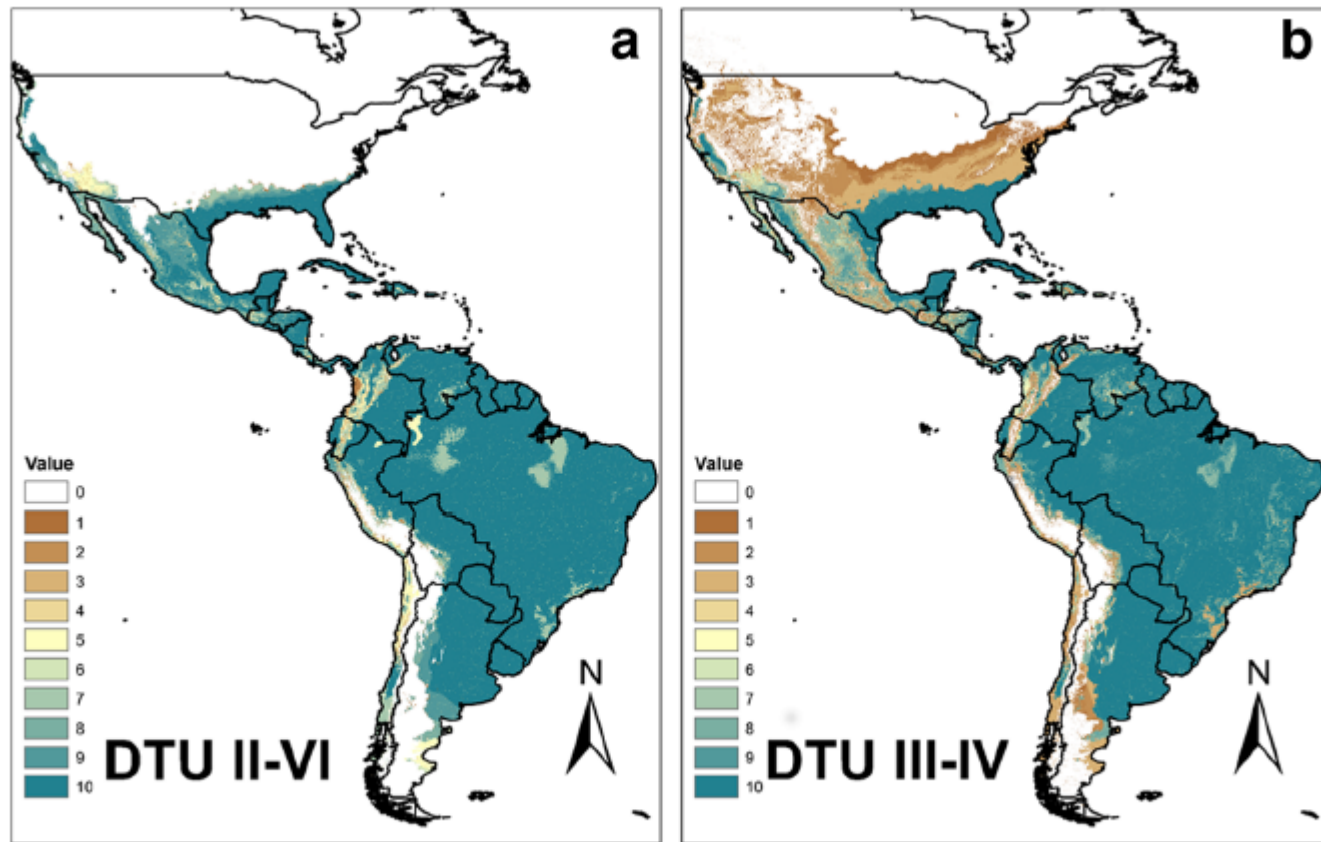


Fig. 4 Ecological niche models for lineages from both principal schemes. Ecological niche models for *Trypanosoma cruzi* lineage I of L1 (a) and lineage III of L2 (b) with classification of best (10) to worse (1) subsets

Interacciones (macro)ecológicas vector-reservorio

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 PLOS one

Using Biotic Interaction Networks for Prediction in Biodiversity and Emerging Diseases

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RESEARCH ARTICLE

Leishmania (L.) mexicana Infected Bats in Mexico: Novel Potential Reservoirs

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Abstract


Leishmania (Leishmania) mexicana causes cutaneous leishmaniasis, an endemic zoonosis affecting a growing number of patients in the southeastern states of Mexico. Some foci are found in shade-grown cocoa and coffee plantations, or near perennial forests that provide rich breeding grounds for the sand fly vectors, but also harbor a variety of bat species that live off the abundant fruits provided by these shade-giving trees. The close proximity be-

RESEARCH ARTICLE

Can You Judge a Disease Host by the Company It Keeps? Predicting Disease Hosts and Their Relative Importance: A Case Study for Leishmaniasis

Christopher R. Stephens^{1,2*}, Constantino González-Salazar^{2*}, Víctor Sánchez-Cordero³, Ingeborg Becker⁴, Eduardo Rebollar-Tellez⁵, Ángel Rodríguez-Moreno³, Miriam Berzunza-Cruz⁴, Cristina Domingo Balcells⁴, Gabriel Gutiérrez-Granados⁶, Mircea Hidalgo-Mihart⁷, Carlos N. Ibarra-Cerdeña⁸, Martha Pilar Ibarra López⁹, Luis Ignacio Iñiguez Dávalos⁹, María Magdalena Ramírez Martínez¹⁰



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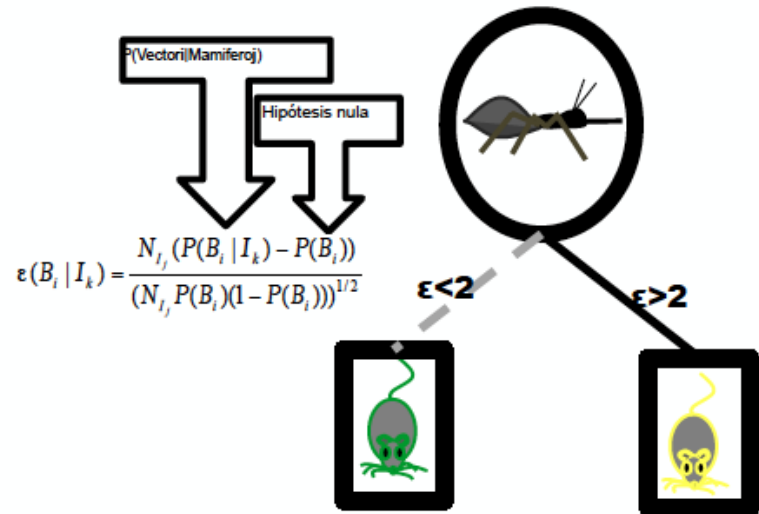
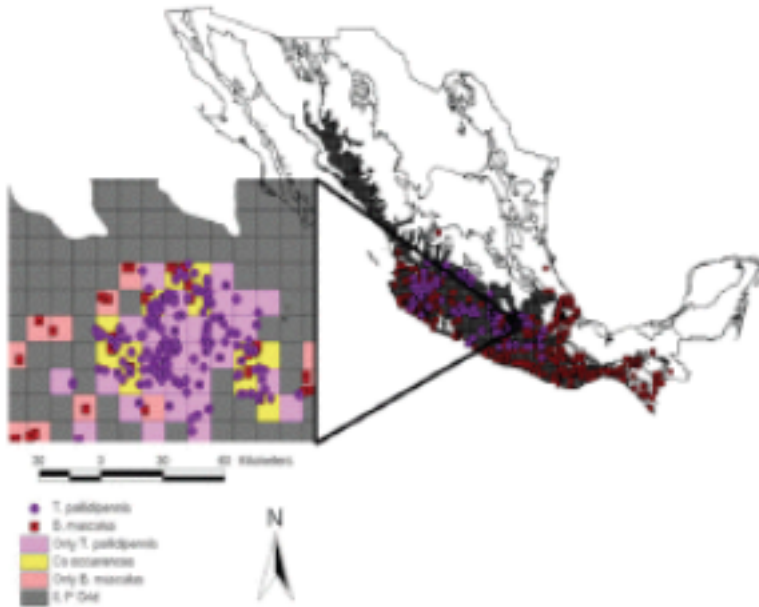
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Abstract

Zoonoses are an important class of infectious diseases. An important element determining the impact of a zoonosis on domestic animal and human health is host range. Although for

Interacciones (macro)ecológicas vector-reservorio



Trypanosoma cruzi reservoir - triatomine vector co-occurrence networks reveal meta-community effects by synanthropic mammals on geographic dispersal

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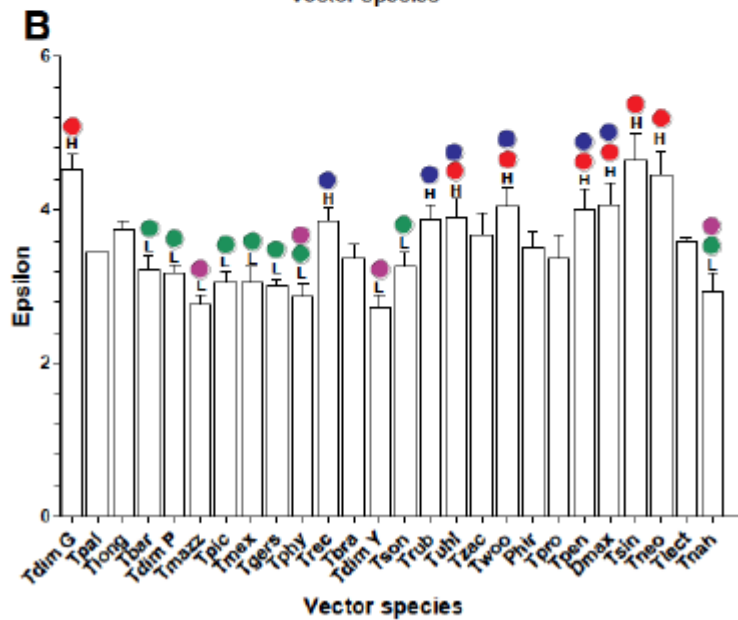
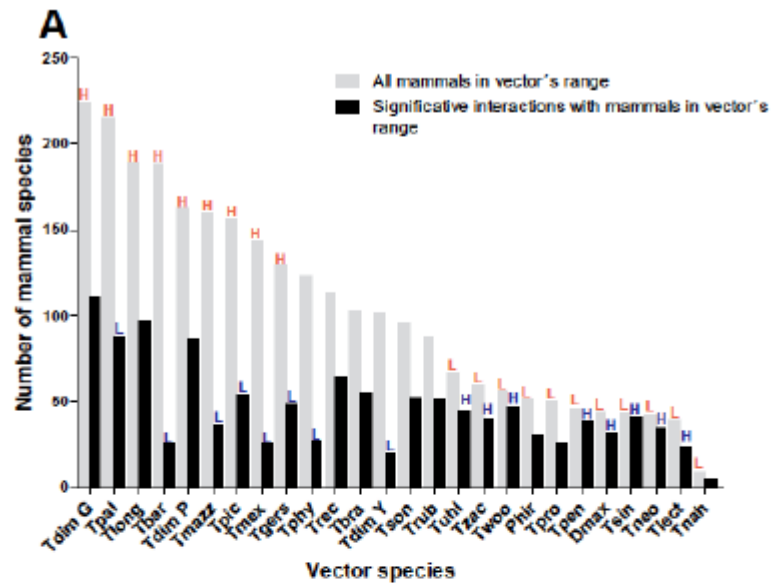
⁶ Centro Regional de Investigaciones en Salud Pública, Instituto Nacional de Salud Pública, Tapachula, Chiapas, México

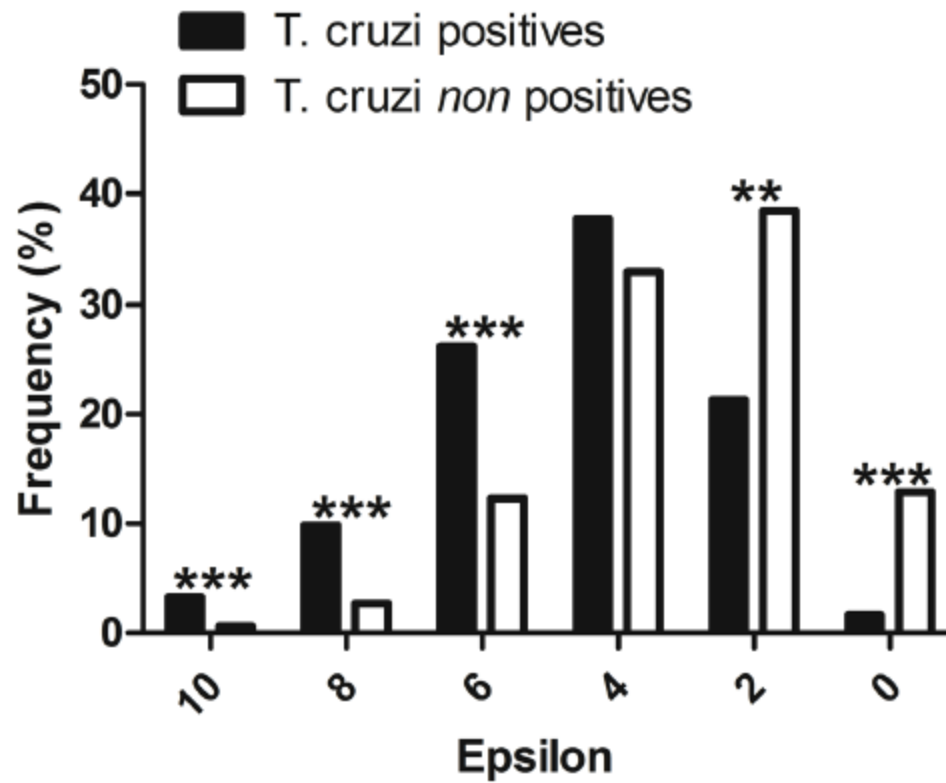
Corresponding Authors: Carlos N. Ibarra-Cerdeña, Janine M. Ramsey

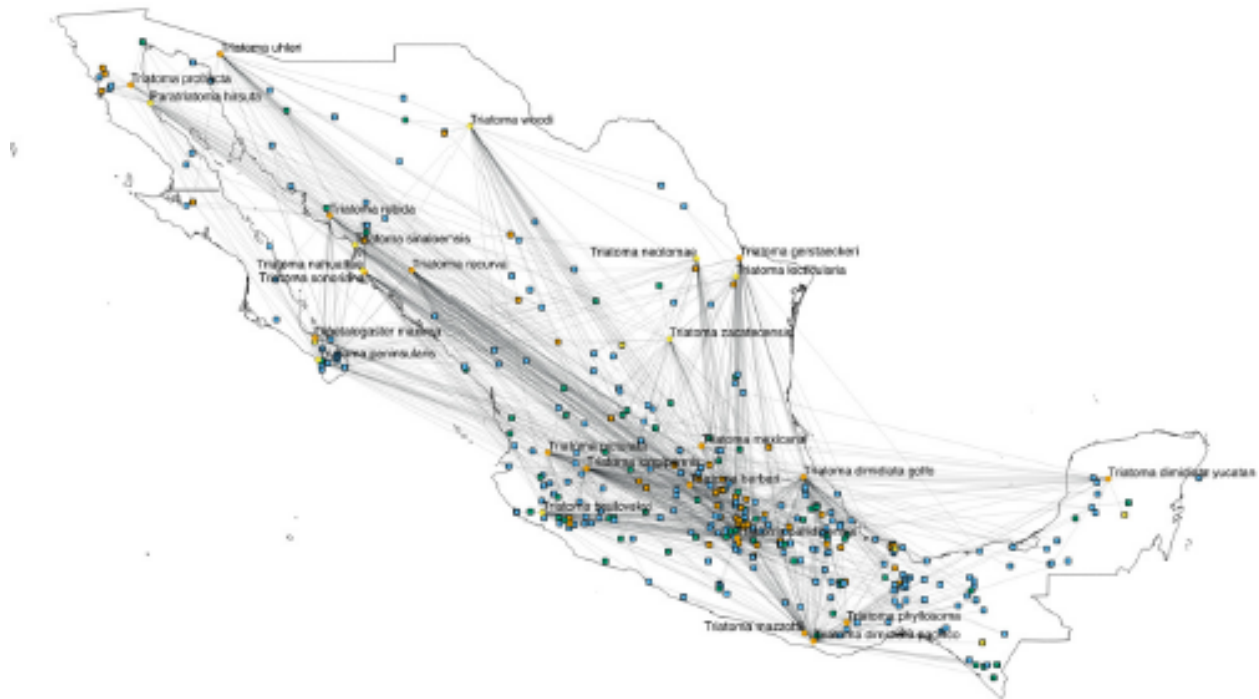
Email address: ibarra.cerdena@gmail.com, jramsey@insp.mx

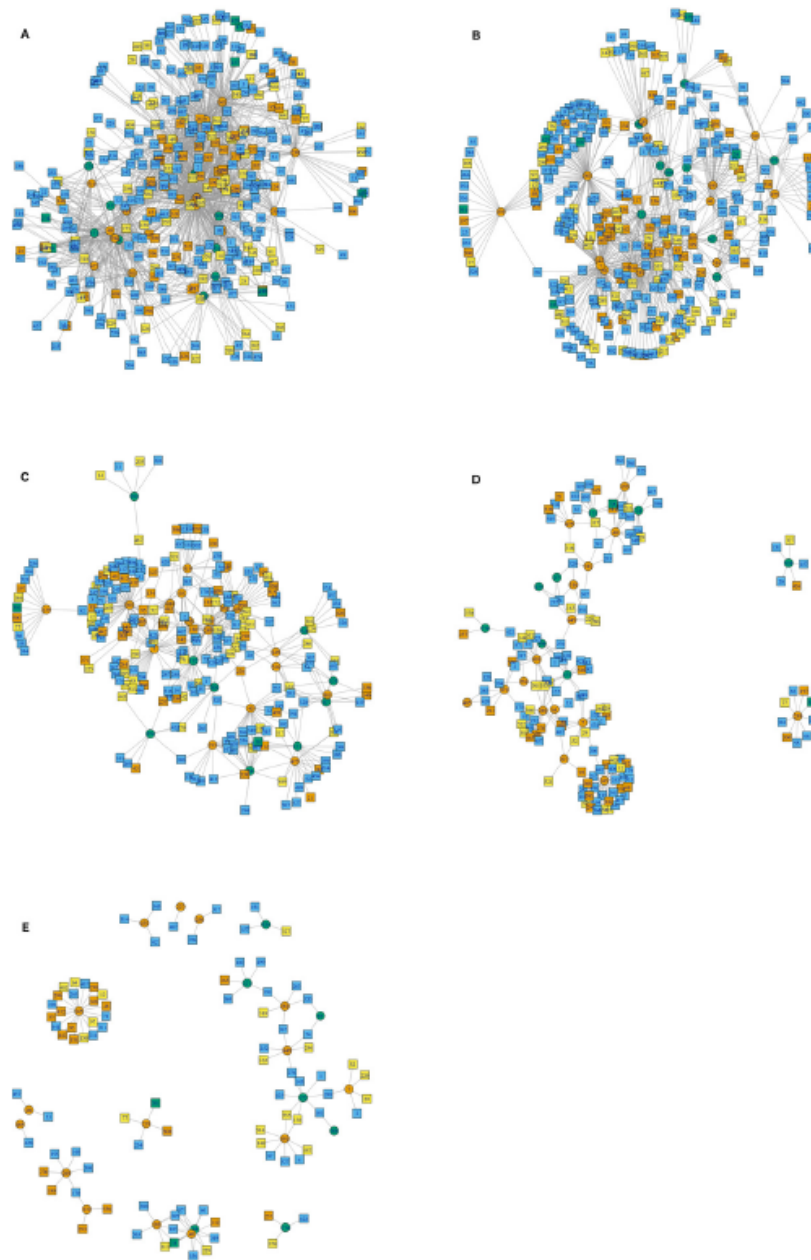
Table 1. Summary of mammals attributes related with their relationships with vector co-occurrences and with *Trypanosoma cruzi* reports.

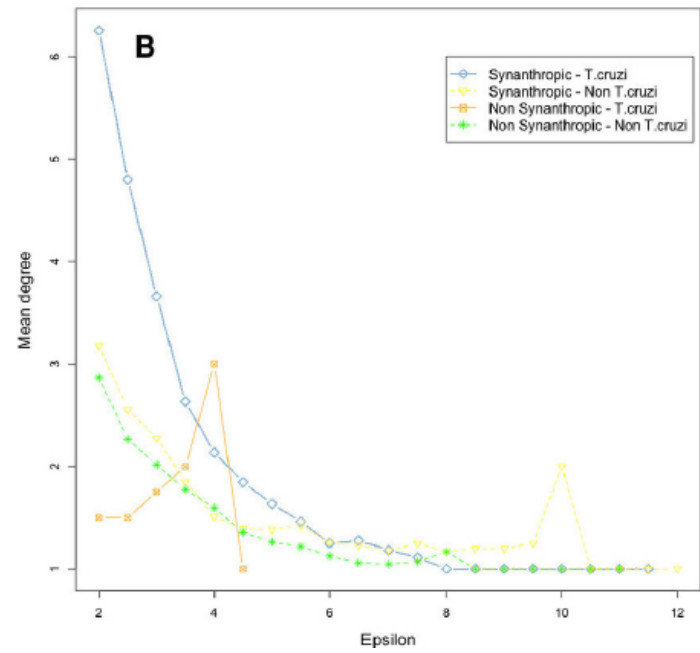
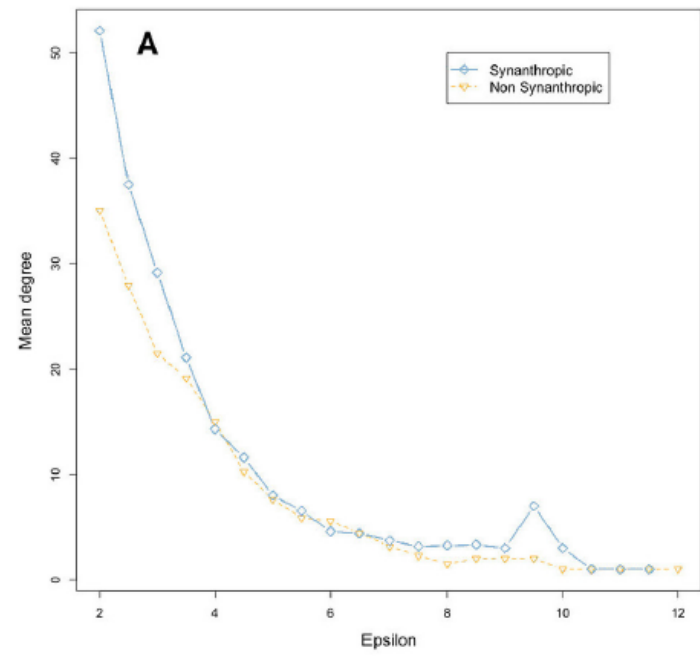
Mammal order	Species	Synanthropic species	Reservoir species	Links per species	Epsilon		
	N	N	N		Mean	SE	Max
Artiodactyla	7	0	0	2.6	3.4	0.29	6.06
Carnivora	29	11	9	4.9	3.95	0.15	13.65
Chiroptera	131	18	16	4.77	4.59	0.1	17.79
Cingulata	1	1	1	8	2.86	0.25	4.31
Didelphimorphia	6	4	4	5.3	4.91	0.63	19.42
Lagomorpha	8	0	0	5.5	4.84	0.4	13.48
Pilosa	2	0	0	4.5	4.02	0.84	10.25
Primates	3	0	0	4.5	6.4	1.48	10.83
Rodentia	170	94	34	3.82	5.78	0.13	24.84
Soricomorpha	15	0	0	2.73	4.91	0.44	12.96

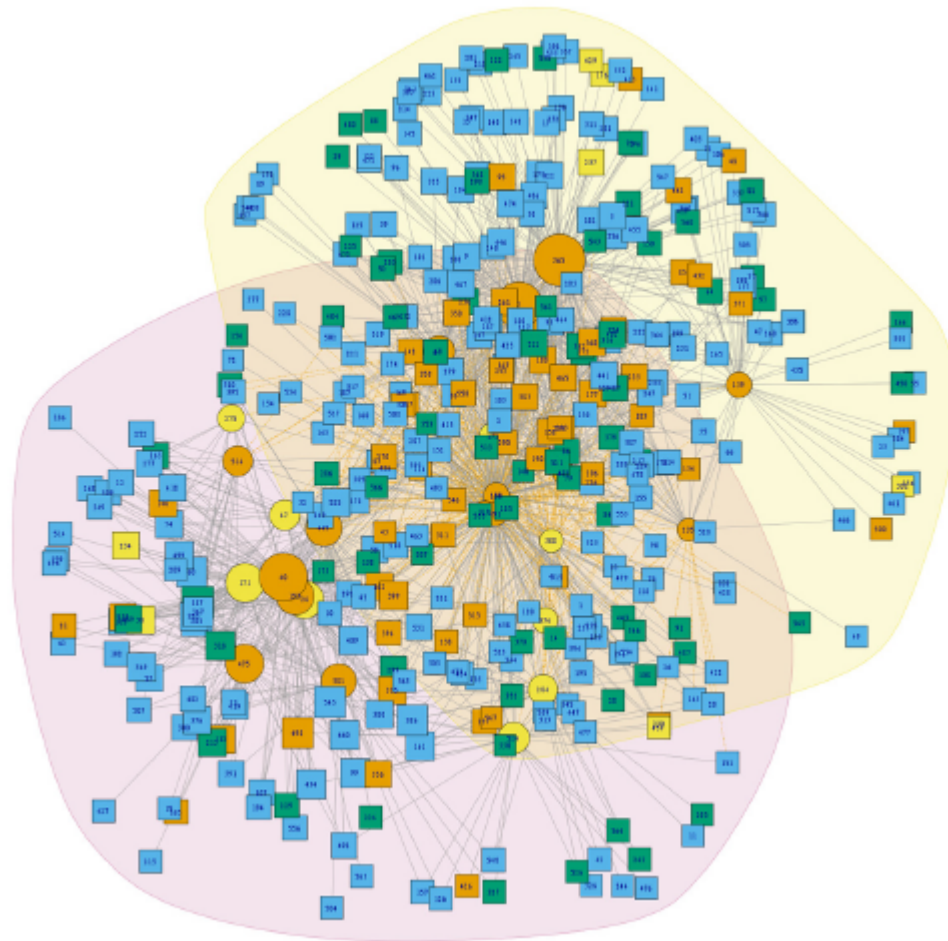












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