Analysis of a Compartmental Model for Chagas Disease Transmission in the U.S.

Harley Hanes

Tulane University
Math and Public Health

Feb 15, 2019

# Chagas Disease can Cause Fatal Conditions Years after Infection

- Caused by a blood parasite *Trypanosoma cruzi*
- Spread through feces of infected triatomines (kissing bugs).
- 30% infections have major cardiac or intestinal disorders 10-30 years after infection
- No treatment available in U.S.

Adult *T. Sanguisuga*

Chagas is Spreading into the U.S.

- Approximately 300,000 people in the U.S. are infected with *T. cruzi*
- Most US infections believed to been acquired in Latin America
- 30-60% of vectors and reservoir hosts infected in Louisiana and Texas
- Latency of disease makes case identification difficult
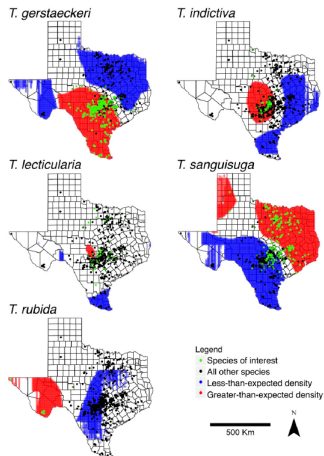
Curtis-Robles R., Bionomics and Spatial Distribution of Triatomine Vectors

Research Questions

We seek to,

- Quantify the current Chagas disease risk in Louisiana and its susceptibility to change
- Identify reservoir hosts that contribute most to high prevalence of infected triatomines near homes
- Determine the most effective control strategies to reduce human risk in Louisiana

Housing Conditions Determine Risk

- Majority of *T. cruzi* infections occur in high risk homes

Risk Factors for triatomine invasion

- Poor sealing of home
- Lack of air conditioning
- Dog kennels or chicken coops near the home
- Proximity to forested areas

U.S. Homes can be High Risk

- Hurricanes can create structural openings sealing of home
- Air conditioning is not universal
- Common to keep animals around homes in parts of Louisana
- Many communities are adjacent to swamps or forests

A home in Concordia Parish, LA
- Vox Media

# U.S. Acquired Cases are Likely Underestimated

- Blood donor surveillance in Texas suggests a much higher prevalence of locally acquired Chagas disease than previously thought.

Case Estimate	Confrimed	Moderate	High
U.S. Acquired Cases	34	1235	4760
Cases per year	-	24	94
Incidence (per 1,000,000)	-	.81	3.07

Figure: Risk estimation for Louisiana and Texas

**Lack of U.S. risk surveillance studies is a major barrier to risk estimation**
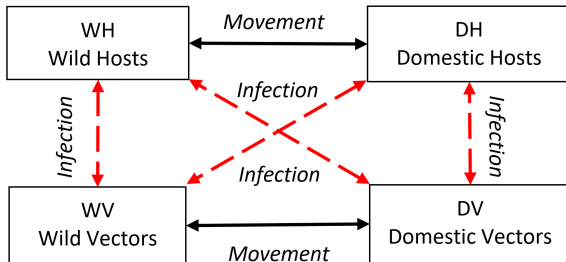
- Model divided into hosts and vectors in either wild or domestic environments
- Each compartment is an SI model with life-long infection and constant population
- Both species can move between wild and domestic areas

Biological Interpretation of R_0

$R_0 < 1$ is a stability condition for the disease-free equilibrium and is the average number of infections produced by a single infected individual
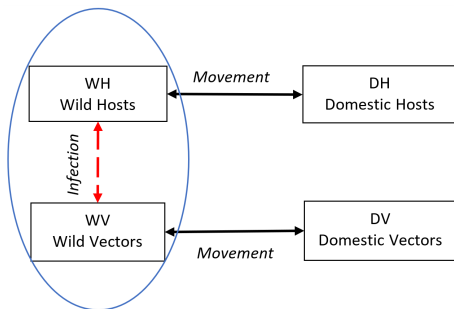
$$R_0 = \sqrt[4]{R_{WV,WH} * R_{DV,DH} * R_{WV,DH} * R_{DV,WH}}$$

$$R_{WV,WH} = \sqrt{r_{WV} * r_{WH}}$$

r_{WH} is the number of wild vectors infected by a single wild host

Movement Creates Geometric Series in R_0

$$r_{WH} = \alpha_{WV}^{WH} * \frac{(\gamma_{DH} + \lambda_H)}{(\gamma_{DH}\gamma_{WH} + \gamma_{DH}\lambda_H + \gamma_{WH}\lambda_H)}$$

- Lifespan of wild host
  $\frac{(\gamma_{DH} + \lambda_H)}{(\gamma_{DH}\gamma_{WH} + \gamma_{DH}\lambda_H + \gamma_{WH}\lambda_H)}$
  $= \sum\limits_{i=0}^{\infty} L^i$ where

- $L = \frac{\lambda_M}{\gamma_{DH} + \lambda_M} * \frac{\lambda_M}{\gamma_{WH} + \lambda_M}$

- $\frac{\lambda_M}{\gamma_{DH} + \lambda_M}$ is the time before leaving domestic area for wild area

- $\frac{\lambda_M}{\gamma_{WH} + \lambda_M}$ is the time before leaving wild area for domestic area

| Parameter	Meaning
α_{WV}^{WH}	Rate of infection for wild vectors from wild hosts
γ_{DH}	Death rate for domestic hosts
γ_{WH}	Death rate for wild hosts
λ_H	Rate hosts move between wild and domestic areas
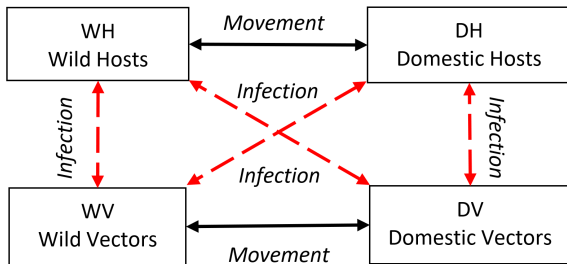
- Host and vector species can vary greatly between areas
- Need to identify key host species to identify areas to focus observation and control
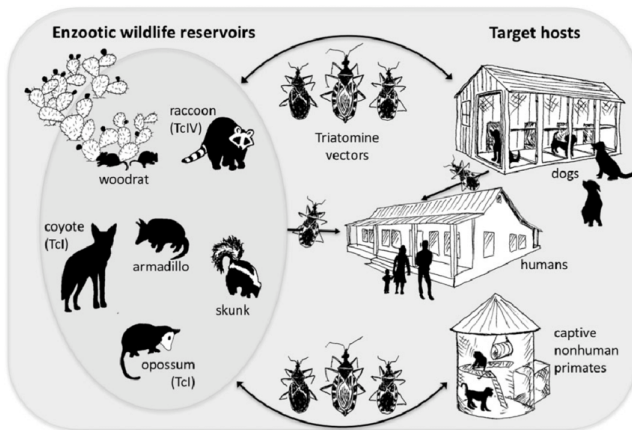
Species Diversity Complicates Modeling

- Over 11 of species of vector and 150 of hosts
- Humans do not contribute to infection cycle
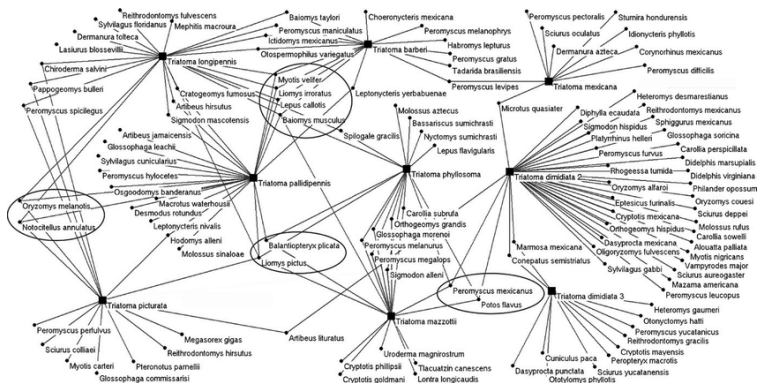
-Rengifo Correa L., Understanding transmissibility patterns of Chagas

Species Diversity Complicates Modeling

- Over 11 of species of vector and 150 species of hosts
- Humans do not contribute to infection cycle

-Hodo C., Toward an Ecological Framework for Assessing Reservoirs

Sensitivity Analysis Can Identify Where To Focus Research Efforts

- Relative sensitivity analysis indicates infected vectors near homes is most dependent on domestic hosts infecting domestic vectors
- Model insensitive to movement rate between wild and domestic populations or cross-spatial infection

	θ_{WH}^{WT}	θ_{WT}^{WH}	θ_{WT}^{DT}	θ_{DH}^{WH}	θ_{DH}^{WH}	θ_{DT}^{DH}
Final Infected DV	0.024	0.13	0.026	0.0048	0.049	0.25
Infected DV at t=2	0.16	0.22	0.044	0.045	0.1	0.51
R_0	0.13	0.13	0.13	0.13	0.13	0.13

- We add rats as a reservoir host as they live almost primarily domestically to further investigate domestic transmission to triatomines.
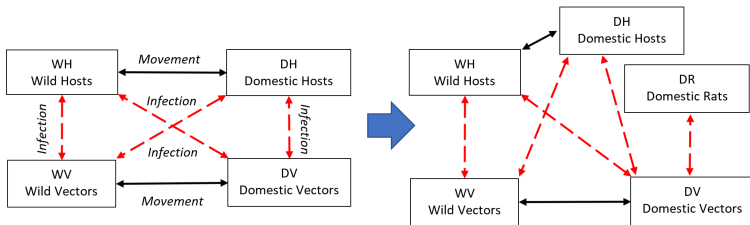
- We will iterate this method to identify host species to match to data and to focus data collection

Future Work

- Use vector blood-meal analysis to determine risk caused by an infected vector near homes
- Continue using sensitivity analysis to build most accurate model of *T. cruzi* transmission
- Use transmission model to complete risk analysis for Louisiana

Acknowledgments