Life-histories as determinants of infection prevalence for trypanosomatids: A meta-analysis

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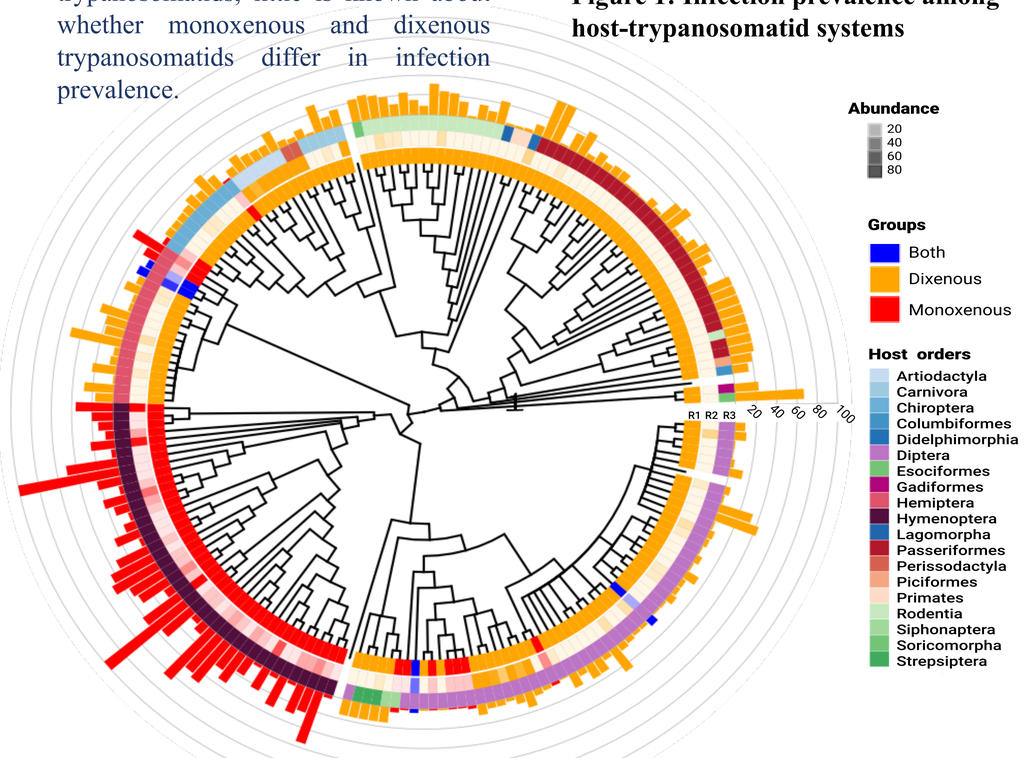
Introduction

- Trypanosomatids are a diverse family of protozoan parasites, some of which cause devastating human and livestock diseases.
- There are two distinct infection life-cycles in trypanosomatids; some species complete their entire life-cycle in a single host (monoxenous) and others infect two hosts (dixenous).
- While infection prevalence has been described for subsets of hosts and trypanosomatids, little is known about whether monoxenous and dixenous trypanosomatids differ in infection prevalence.

Methods

- We synthesised all published evidence of trypanosomatid infection prevalence for the last 20 years using semi-automated screening protocol, with machine learning and natural language processing resulting in 569 qualitatively included and 261 quantitatively included citations.
- We used meta-regression models with nested random design to examine how prevalence relates to parasite life history.

Figure 1: Infection prevalence among host-trypanosomatid systems



Results

- Monoxenous species are more than three-fold more prevalent in insects (20.9%) than dixenous species (6.61%).
- We find striking difference in infection prevalence with monoxenous species having twice the infection prevalence (19.8%) than dixenous species (8.68%) when combining insect and non-insect hosts (Fig 2).
- No significant difference between insects and non-insects without accounting for life-history traits.
- Trypanosomatids are less prevalent in insects than their definitive hosts across dixenous genera (Table 1).
- Monoxenous trypanosomatids have the highest prevalence in bees, which does not vary between wild and managed bees.
- Microscopic diagnostics revealed higher infection prevalence in insects whereas molecular assays report higher infection prevalence in non-insects

Figure 2: Infections are more prevalent in monoxenous species across all hosts

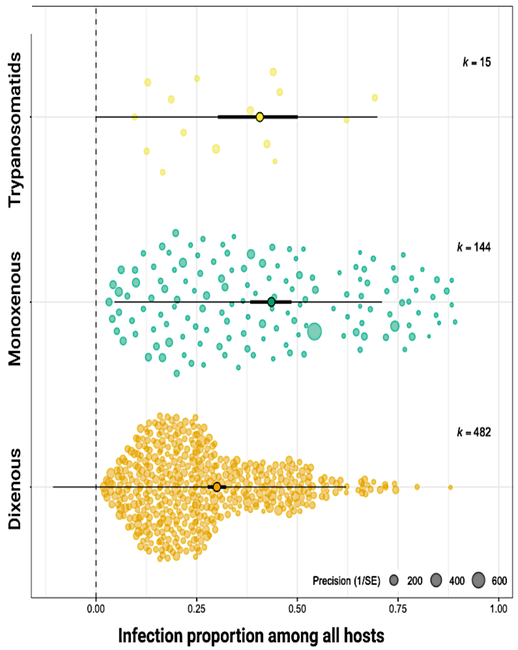


Table1: Pooled prevalence across groups

Hosts	K	Dixenous	Monoxenous	*P-value*
Insects	313	6·61	20·9	<·001
Flies	155	4·80	2·45	0·44
Truebugs	33	11·5	11·6	0·99
Parasites	**K**	**Insects**	**Non-insects**	***P-value***
Dixenous spp	390	5·51	9·38	<·001
Leishmania spp·	125	2·02	14·5	<·001
Trypanosoma spp·[1]	226	4·09	5·85	<·001
Trypanosoma cruzi	39	14·51	8·17	0·17
Bees	**K**	**Wild**	**Managed**	***P-value***
All	123	26·8	22·2	0·75
Honeybee	17	34·2	20·1	0·50
Bumblebee	106	24·4	24·2	0·99

Discussion

- We present three non exclusive arguments that could explain differences in infection prevalence associated with trypanosomatid life-history:

- Monoxenous parasites have more opportunity to approach their evolutionary optima while dixenous parasites may be forced to trade-off infection relevant traits in one host for traits in the second host

- The same hypothetical number of infectious units are simply shared among more host species in dixenous parasites, thus diluting the infection prevalence in any one host species - to approximately half.

- Different host characteristics such as lifespan, recruitment rate, sociality, and physiology may explain some of the variation in infection prevalence.

- Our results implies that efforts to suppress trypanosomatid infection in insects may have outsized effects on overall infection burden as insects represent potential "weak-links" in infection chain.

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