

1 Appendix S1

2 **Parasite escape through trophic specialization in a species flock**

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6 Table S1: Numbers of host individuals with a certain parasite count.

Species	Nematoda					
	0	1	2	3	4	7
Ctho	19	1		1		
Gnpf	15	4		1		
Lida	6					
Lola	19	2				
Inlo	6					
Pefam	12					
Pefas	8	2	1			
Psba	9	2				
Pscu	6					
Sidi	56	13	1		1	
Trmo	166	12	1			1

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Species	Digenea		
	0	1	4
Ctho	21		
Gnpf	20		
Lida	6		
Lola	20	1	
Inlo	6		
Pefam	11		1
Pefas	11		
Psba	11		
Pscu	6		
Sidi	73		
Trmo	180		

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Species	cysts (intestines)		
	0	1	2
Ctho	21		
Gnpf	20		
Lida	6		
Lola	20		1
Inlo	5	1	
Pefam	12		
Pefas	11		
Psba	11		
Pscu	6		
Sidi	70	1	
Trmo	180		

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Species	<i>Gyrodactylus</i>							
	0	1	2	3	4	5	35	
Ctho	21							
Gnpf	20	1						
Lida	5	1						
Lola	18	2	1					
Inlo	6	1						
Pefam	11	1						
Pefas	10	1						
Psba	10	1						
Pscu	6							
Sidi	60	5	4	1	2	0	1	
Trmo	158	12	4	2	1	3		

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Species	Maxillipoda	
	0	1
Ctho	20	
Gnpf	21	
Lida	2	
Lola	21	
Inlo	0	
Pefam	11	
Pefas	11	
Psba	11	
Pscu	6	
Sidi	69	
Trmo	176	2

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Urogyrus

Species	0	1	2	3	4	5
Ctho	20	1				
Gnpf	17		1	1		1
Lida	6					
Lola	18	1		1	1	
Inlo	6					
Pefam	12					
Pefas	11					
Psba	10	1				
Pscu	6					
Sidi	71					
Trmo	176	2	1	1		

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Enterogyrus

Species	0	1	2
Ctho	20		1
Gnpf	20		
Lida	5	1	
Lola	21		
Inlo	6		
Pefam	11	1	
Pefas	11		
Psba	11		
Pscu	6		
Sidi	70	1	
Trmo	180		

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cysts (gills)

Species	0	1
Ctho	20	1
Gnpf	21	
Lida	2	
Lola	16	
Inlo	0	
Pefam	12	
Pefas	11	
Psba	11	
Pscu	6	
Sidi	70	
Trmo	185	

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Species	cysts (fins)			
	0	1	2	6
Ctho	20	1		
Gnpf	20			
Lida	6			
Lola	21			
Inlo	6			
Pefam	12			
Pefas	10	1		
Psba	11			
Pscu	6			
Sidi	68	2		1
Trmo	177	2	1	

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20 Table S2: Results of the generalized linear model explaining the abundance of *Acanthocephala*,
 21 *Cichlidogyrus* and *Ergasilus* for eleven host species at three sampling sites. The full model includes
 22 host species, sampling site, host standard length and host sex as explanatory variables. To assess the
 23 relative importance of each predictor, Δ Residual deviance and Δ Akaike Information Criterion (AIC)
 24 were calculated by a leave-one-out strategy.

Acanthocephala

Model	Null deviance	DF	Residual deviance	DF	AIC	Δ Residual deviance	Δ AIC
Full model	1014.81	149	602.55	134	944.14	NA	NA
- Species	1014.81	149	911.44	144	1233.00	-308.89	-288.86
- Site	1014.81	149	639.99	136	977.59	-37.44	-33.45
- SL	1014.81	149	604.09	135	943.69	-1.54	0.45
- Sex	1014.81	149	619.44	136	957.03	-16.89	-12.89

Cichlidogyrus

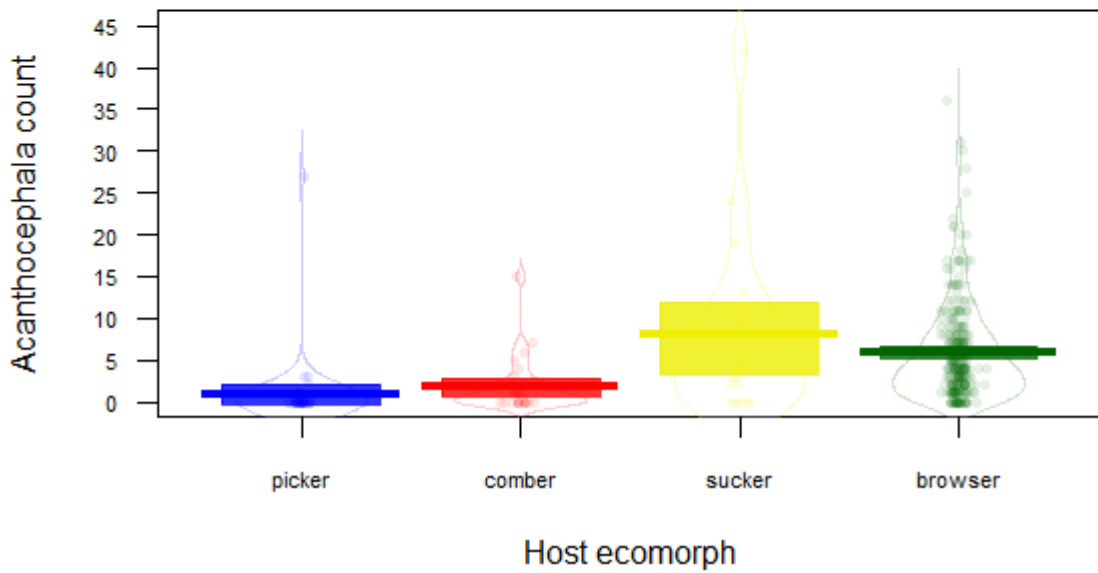
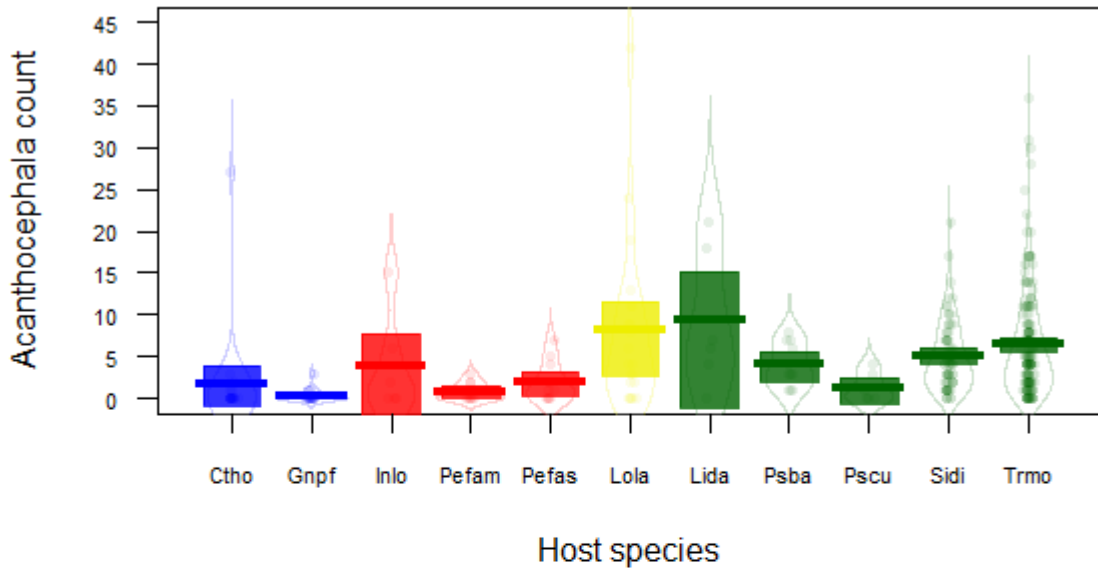
Model	Null deviance	DF	Residual deviance	DF	AIC	Δ Residual deviance	Δ AIC
Full model	5841.7	149	2198	134	2779.6	NA	NA
- Species	5841.7	149	3632.50	144	4193.7	-1434.5	-1414.1
- Site	5841.7	149	2593.4	136	3170.5	-395.4	-390.9
- SL	5841.7	149	3142.9	135	3722.1	-944.9	-942.5
- Sex	5841.7	149	2265.5	136	2842.6	-67.5	-63.0

Ergasilus

Model	Null deviance	DF	Residual deviance	DF	AIC	Δ Residual deviance	Δ AIC
Full model	1413.92	148	409.31	133	829.65	NA	NA
- Species	1413.92	148	1081.60	143	1421.9	-672.29	-592.25
- Site	1413.92	148	578.02	135	934.36	-168.71	-104.71
- SL	1413.92	148	633.33	134	991.67	-224.02	-162.02
- Sex	1413.92	148	471.51	136	827.85	-62.2	1.8

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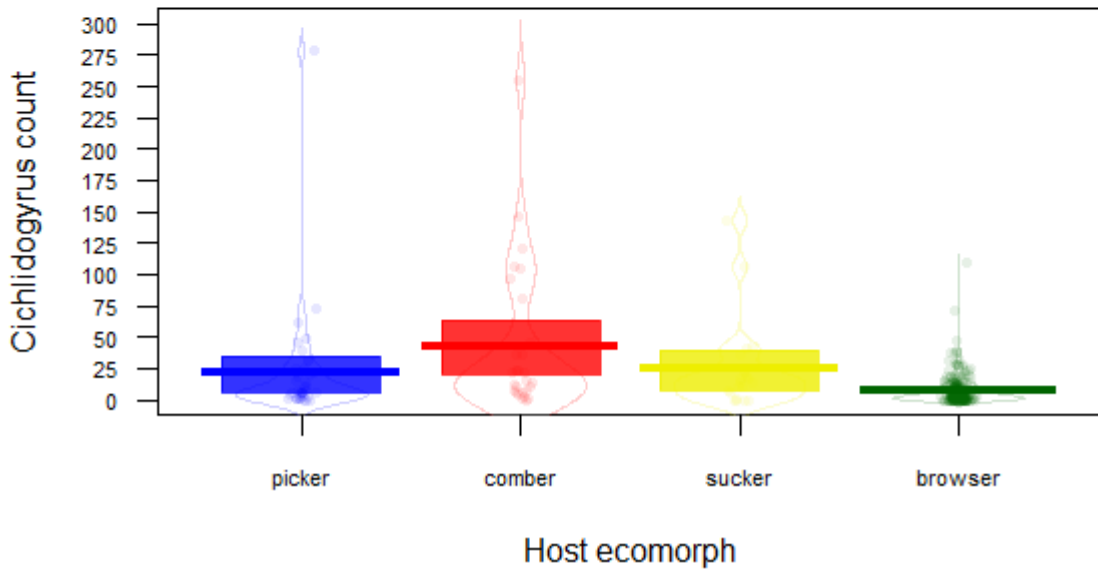
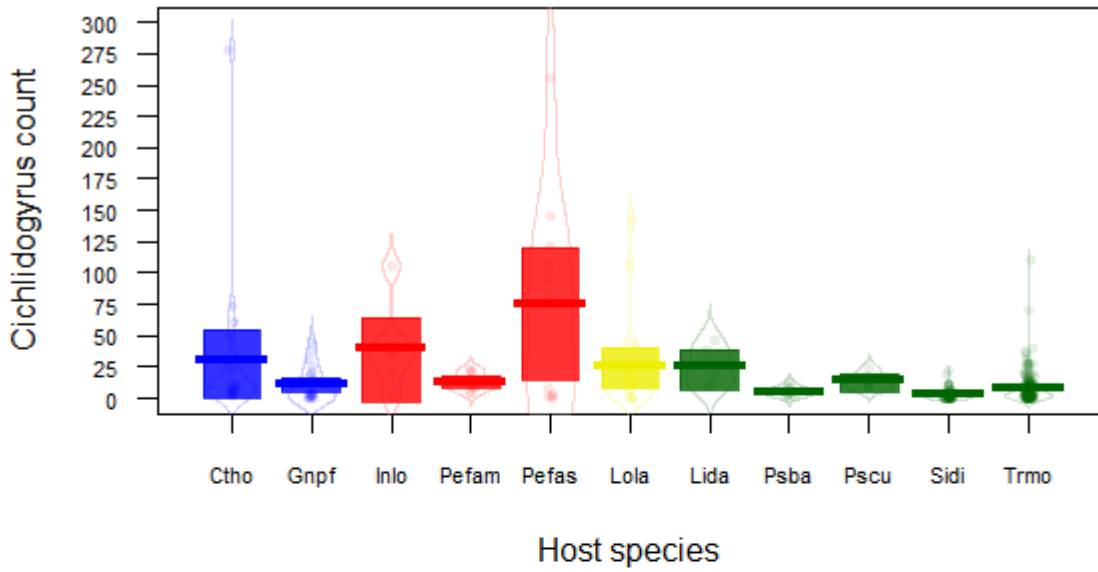


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28 Fig. S1: Raw Acanthocephala counts in eleven Tropheini species (upper panel) and the four trophic
 29 ecomorphs (lower panel). Colours refer to different ecomorphs. Plots are drawn in R using the
 30 *pirateplot* function of the *yarr* package (Phillips, 2016). Points are raw data, beans illustrate density
 31 of points, bars depict mean counts and boxes represent 95 % Bayesian Highest Density Intervals.

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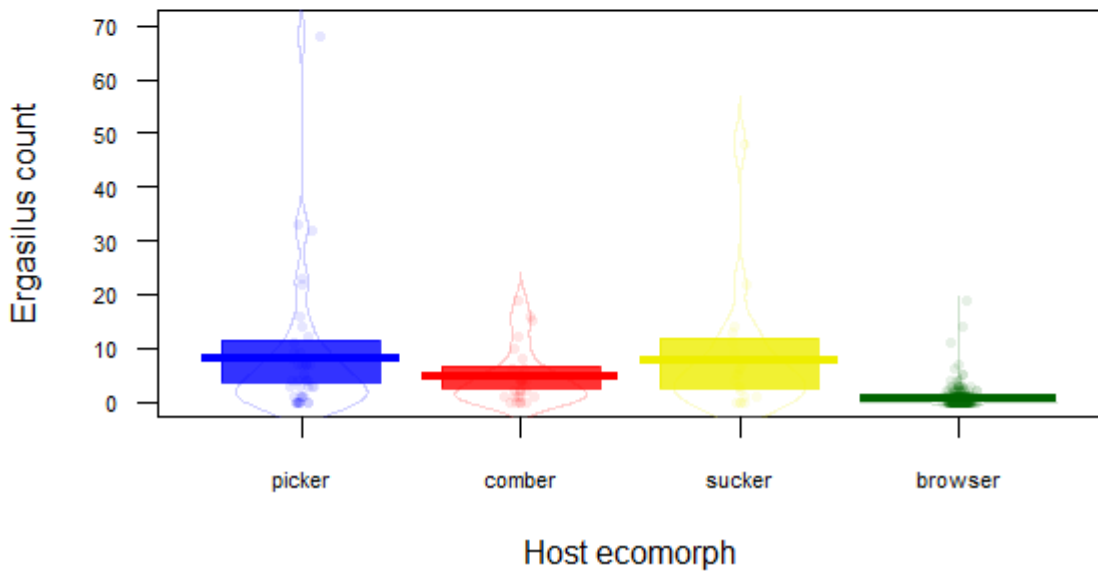
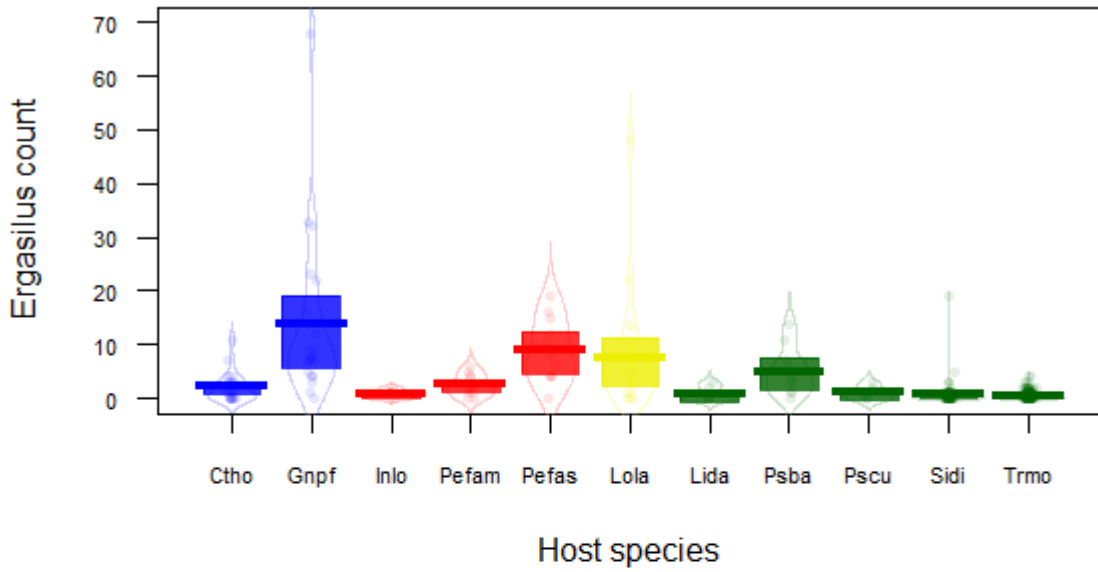
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35 Fig. S2: Raw *Cichlidogyrus* counts in ten Tropheini species (upper panel) and the four trophic
 36 ecomorphs (lower panel). Colours refer to different ecomorphs. Plots are drawn in R using the
 37 *pirateplot* function of the *yarr* package (Phillips, 2016). Points are raw data, beans illustrate density
 38 of points, bars depict mean counts and boxes represent 95 % Bayesian Highest Density Intervals.

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41 Fig. S3: Raw *Ergasilus* counts in ten Tropheini species (upper panel) and the four trophic ecomorphs
 42 (lower panel). Colours refer to different ecomorphs. Plots are drawn in R using the *pirateplot*
 43 function of the *yarr* package (Phillips, 2016). Points are raw data, beans illustrate density of points,
 44 bars depict mean counts and boxes represent 95 % Bayesian Highest Density Intervals.

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46 Supplementary references

47 Phillips N (2016) Package 'yarr' v0.1.2: A Companion to the e-Book "YaRrr!: The Pirate's Guide to R".

48 <https://cran.r-project.org/web/packages/yarr/index.html>