

Local host specialization, host-switching, and dispersal shape the regional distributions of avian haemosporidian parasites

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Supplementary Information, Tables *S1-S9*, Figures *S1-S4*

Table S1 All parasite lineages recovered in our study and the number of times each was sampled overall (N), the number of hosts each was found infecting, its genus, and the Genbank number(s) where the sequence can be recovered. Lineages are ordered by their abundance in our samples.

Lineage	N	Number of Hosts	Genus	Genbank Numbers
OZ 14	257	33	<i>Plasmodium</i>	AY540210, HM222474
OZ 01	253	26	<i>Plasmodium</i>	GQ395654, HQ287549, GQ395654, GQ141574
OZ 35	194	8	<i>Plasmodium</i>	HM222474-HM222480
NA 04	115	9	<i>Haemoproteus</i>	AF465562
OZ 10	80	6	<i>Haemoproteus</i>	AF465576
OZ 08	66	6	<i>Plasmodium</i>	AF540207, HM222485
LA 01	57	6	<i>Haemoproteus</i>	AF465572
OZ 03	55	15	<i>Haemoproteus</i>	AF465563
OZ 05	55	6	<i>Haemoproteus</i>	AY167241
OZ 06	52	17	<i>Plasmodium</i>	AF465554
KZ 01	50	17	<i>Plasmodium</i>	AY455663, KF359936
CHI 02PL	44	2	<i>Plasmodium</i>	KC789821
NA 15	35	6	<i>Haemoproteus</i>	GQ395665, GQ141584
CHI 08PA	28	2	<i>Haemoproteus</i>	KM280616, KM065800
OZ 02	28	10	<i>Haemoproteus</i>	AY455658
OZ 12	28	5	<i>Haemoproteus</i>	AY817748, GQ395673
OZ 45	27	11	<i>Plasmodium</i>	HM222481, HM222482
CHI 35PL	26	7	<i>Plasmodium</i>	KM280608
TI P25L	23	2	<i>Plasmodium</i>	KC680673, KC680702, KC680706
LA 22	22	3	<i>Haemoproteus</i>	HQ287537
CHI 05PL	21	5	<i>Plasmodium</i>	KC789824
CHI 20PA	20	9	<i>Haemoproteus</i>	KM065797, KM280614
CHI 09PL	18	6	<i>Plasmodium</i>	KC789828
CHI 30PA	18	2	<i>Haemoproteus</i>	KM280621, KM280624, KM280635
OZ 49	18	1	<i>Haemoproteus</i>	KJ910306, KF359931
EL 02	16	7	<i>Plasmodium</i>	KM598210
OZ 07	16	7	<i>Haemoproteus</i>	AF465580
OZ 04	15	7	<i>Plasmodium</i>	AY540197, GQ395669, GQ395657, KC680705,

				KC680692, KC680679
OZ 26	15	2	<i>Haemoproteus</i>	AY540212
OZ 16	14	9	<i>Haemoproteus</i>	AY817750
JA 01	12	4	<i>Plasmodium</i>	KM598212
OZ 17	11	3	<i>Haemoproteus</i>	GQ395632, AY817751, AY167244
CHI 23PA	10	2	<i>Haemoproteus</i>	KM280611
NA 01	9	7	<i>Plasmodium</i>	AF465547
OZ 13	9	1	<i>Haemoproteus</i>	AY540209, AY540209, GQ395674, GU252006
OZ 09	8	3	<i>Plasmodium</i>	AY540208, KC680672
OZ 25	8	4	<i>Plasmodium</i>	AY540211, GQ395679, GQ141593
IN 01	7	1	<i>Haemoproteus</i>	KM598226
NA 05	6	1	<i>Haemoproteus</i>	AF465564
OZ 38	6	4	<i>Plasmodium</i>	AF465559, HQ287545
CHI 16PL	5	3	<i>Plasmodium</i>	KC680714
MI 02	5	1	<i>Plasmodium</i>	KM598221
NA 14	5	1	<i>Haemoproteus</i>	AY540205
OZ 54	5	3	<i>Plasmodium</i>	KF359933
OZ 58	5	1	<i>Haemoproteus</i>	KM598223
PR 03	5	4	<i>Haemoproteus</i>	AY455659
OZ 36	4	1	<i>Plasmodium</i>	AY540220, AY167248
YU 01	4	3	<i>Plasmodium</i>	DQ838997, DQ659549, HQ287539, GQ395688, GQ141598
GAM 06	3	3	<i>Plasmodium</i>	KP771715
KZ 02	3	3	<i>Plasmodium</i>	AY540195
NA 16	3	2	<i>Haemoproteus</i>	HM222472, GQ395666, GU252003
OZ 19	3	3	<i>Plasmodium</i>	AY455661
OZ 21	3	3	<i>Haemoproteus</i>	AY167242, HQ287540
OZ 28	3	1	<i>Haemoproteus</i>	AY817753
OZ 53	3	2	<i>Haemoproteus</i>	KJ91307, KM065799
OZ 55	3	1	<i>Plasmodium</i>	KF359934
TI P10	3	3	<i>Plasmodium</i>	KC680707
CHI 26PA	2	2	<i>Haemoproteus</i>	KM280632
IN 04	2	1	<i>Haemoproteus</i>	KP771716
MI 01	2	1	<i>Plasmodium</i>	KM598218
NA 11	2	2	<i>Plasmodium</i>	AF465549
OZ 27	2	2	<i>Haemoproteus</i>	AY817752
CE hapH	1	1	<i>Haemoproteus</i>	JX501902
CHI 17PL	1	1	<i>Plasmodium</i>	JN792148, EU627845
CHI 19PA	1	1	<i>Haemoproteus</i>	KM280617
CHI 27PA	1	1	<i>Haemoproteus</i>	KM280631
CHI 28PA	1	1	<i>Haemoproteus</i>	KM280633
DR 07	1	1	<i>Haemoproteus</i>	HM222464

IN 02	1	1	<i>Plasmodium</i>	KM598227
IN 05	1	1	<i>Plasmodium</i>	KP771717
JA 04	1	1	<i>Plasmodium</i>	KM598213
LA 07	1	1	<i>Haemoproteus</i>	GQ395658, GU252000
LSW 01	1	1	<i>Plasmodium</i>	KP771718
MI 03	1	1	<i>Haemoproteus</i>	KM598220
MI 04	1	1	<i>Haemoproteus</i>	KM598219
MI 05	1	1	<i>Plasmodium</i>	KM598228
NA 10	1	1	<i>Haemoproteus</i>	AY540202
OZ 29	1	1	<i>Haemoproteus</i>	AY817754
OZ 31	1	1	<i>Haemoproteus</i>	AF465582
OZ 32	1	1	<i>Haemoproteus</i>	AY540214
OZ 34	1	1	<i>Haemoproteus</i>	AY540216, GQ395682, GQ141596
OZ 43	1	1	<i>Haemoproteus</i>	AY817755
OZ 51	1	1	<i>Plasmodium</i>	KJ910311, KF359932
OZ 57	1	1	<i>Haemoproteus</i>	GU252022
OZ 60	1	1	<i>Plasmodium</i>	KP771719
TN 24	1	1	<i>Haemoproteus</i>	KM065796
YU 03	1	1	<i>Haemoproteus</i>	GQ395690, GU252009

Table S2 Information on each sampling location, including the total number of samples collected (N).

Location	Abbreviation	Longitude (°W)	Latitude (°N)	Sample Years	N	Sample Type
Alabama	ALA	87.84833	31.13	2001	108	Community-level
Champaign	CHAMP	88.54445	40.3126	2014	37	Restricted to several species
Chicago	CHI	87.7607	41.74647	2006, 2007	2023	Community-level
western Chicago	CHI2	88.78047	41.83926	2014	13	Restricted to several species
Connecticut	CT	73.25889	41.145	2002, 2003	301	Community-level
Indiana	IN	86.75176	39.06639	2012, 2013	500	Community-level
Louisiana	LA	89.71083	30.4025	2013	157	Community-level
Michigan	MI	85.34944	42.32667	2012	381	Community-level
Mississippi	MS	88.812	33.474	2013	39	Restricted to one species, <i>Cardinalis cardinalis</i>
Ozarks	OZ	91.0374	37.12555	1999, 2000, 2001, 2002, 2005, 2007, 2011	1438	Community-level
Pennsylvania	PA	75.88861	41.24472	2012, 2013	204	the 2012 sample was restricted to several species, the 2013 sample was community-level
St. Louis	STL	90.5625	38.52472	2008, 2009	338	Community-level
Tennessee	TN	84.48111	35.87361	2013	328	Community-level

Table S3 Simple Mantel correlations for the connections in Fig 2. All associated *P* values are lower than 0.05.

	Birds	Parasites	Climate
Parasites	0.446		
Climate	0.815	0.424	
Space	0.572	0.326	0.595

Table S4 Results of a principal components analysis (PCA) of 19 bioclim variables downloaded from <http://www.worldclim.org/> for each of our community sampling locations. We report the proportion of variance and cumulative variance explained by each axis up to eight axes, although we only used five in our analysis.

	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Proportion of variance	0.7435	0.1312	0.08014	0.02375	0.01187	0.00695	0.00211	0.00038
Cumulative variance	0.7435	0.8747	0.95481	0.97856	0.99043	0.99738	0.99949	0.99988

Table S5 Results of partial Mantel tests comparing hypothesized relationships between space (i.e., geographic distance between sites), the environment (i.e., climatic differences between sites), birds (i.e., host community dissimilarity between sites), and parasites separated by genus (i.e., parasite community dissimilarity between sites). Relationships between birds and the environment and space (not including parasites) can be found in Table 1.

Parasite Genus	Relationship between		Controlling for	r_p	P
<i>Haemoproteus</i>	Birds	Environment	Parasites	0.80	< 0.001
	Birds	Space	Parasites	0.53	0.006
	Parasites	Environment	Birds	0.10	0.292
	Parasites	Space	Birds	0.14	0.226
	Parasites	Environment	Space	0.17	0.163
	Parasites	Space	Environment	0.13	0.237
	Birds	Parasites	Environment	0.10	0.291
	Birds	Parasites	Space	0.17	0.135
<i>Plasmodium</i>	Birds	Environment	Parasites	0.78	< 0.001
	Birds	Space	Parasites	0.51	0.010
	Parasites	Environment	Birds	0.24	0.113
	Parasites	Space	Birds	0.18	0.216
	Parasites	Environment	Space	0.30	0.086
	Parasites	Space	Environment	0.13	0.257
	Birds	Parasites	Environment	0.04	0.395
	Birds	Parasites	Space	0.22	0.108

Table S6 We also analyzed the relationships between distance matrices presented in Figure 2 using multiple regression on distance matrices (MRM), and we present those results here. MRM analysis involves unfolding the upper elements of a distance matrix (above the diagonal) into a vector and using this vector in a multiple regression analysis, where significance of model coefficients and the model R^2 value are determined by permutation of the response variable (1). Here we calculate a “whole model” where the response variable is derived from the distance matrix of bird distributions (“Hosts”) or the distance matrix of parasite distributions (“Parasites”), and all of the remaining distance matrices from Figure 2 are included as explanatory variables after being converted to vectors (“Geography” refers to the matrix of geographic distances between sampling locations). These models were constructed using all parasites together and each parasite genus separately. We report an R^2 and corresponding P value in parentheses for each whole model, and the model coefficients for each explanatory variable (i.e., distance matrix) and their corresponding P values. Following Krasnov et al. (2), we removed each explanatory variable from the whole model and re-calculated the R^2 and corresponding P value for the model without that explanatory variable (“ R^2 Without”). “ R^2 Pure” is the whole model R^2 minus “ R^2 Without”, and represents a measure of the variance explained by the explanatory variable that was removed. Finally, we calculated the percentage of the model variance explained by each explanatory variable by dividing “ R^2 Pure” by the whole model R^2 and multiplying by 100 (“% Variance explained due to “Pure” effect”). MRM analysis was conducted using the R package ecodist (3). These results are largely consistent with the results of the partial Mantel tests (Table 1).

Response matrix	Explanatory matrices	R^2	Coefficient	R^2 Without	R^2 Pure	% Variance explained due to "Pure" effect
Hosts	Whole model	0.686 ($P < 0.001$)				
	Parasites (all)		0.111 ($P = 0.321$)	0.676 ($P < 0.001$)	0.010	1.46
	Geography		0.121 ($P = 0.303$)	0.677 ($P < 0.001$)	0.009	1.31
	Environment		0.696 ($P < 0.001$)	0.402 ($P = 0.002$)	0.284	41.40
Hosts	Whole model	0.676 ($P < 0.001$)				
	Parasites (<i>Plasmodium</i>)		0.009 ($P = 0.935$)	0.676 ($P < 0.001$)	0.000	0.00
	Geography		0.132 ($P = 0.282$)	0.665 ($P < 0.001$)	0.011	1.63
	Environment		0.732 ($P < 0.001$)	0.36 ($P = 0.005$)	0.316	46.75
Hosts	Whole model	0.678 ($P < 0.001$)				
	Parasites (<i>Haemoproteus</i>)		0.045 ($P = 0.657$)	0.676 ($P < 0.001$)	0.002	0.29
	Geography		0.127 ($P = 0.286$)	0.668 ($P < 0.001$)	0.010	1.47
	Environment		0.727 ($P < 0.001$)	0.347 ($P = 0.004$)	0.331	48.82
Parasites (all)	Whole model	0.214 ($P = 0.120$)				
	Hosts		0.279 ($P = 0.384$)	0.188 ($P = 0.056$)	0.026	12.15

	Geography	0.076 (<i>P</i> = 0.776)	0.210 (<i>P</i> = 0.054)	0.004	1.87
	Environment	0.152 (<i>P</i> = 0.628)	0.206 (<i>P</i> = 0.047)	0.008	3.74
Parasites (<i>Plasmodium</i>)	Whole model	0.203 (<i>P</i> = 0.162)			
	Hosts	0.022 (<i>P</i> = 0.948)	0.203 (<i>P</i> = 0.068)	0.000	0.00
	Geography	0.145 (<i>P</i> = 0.612)	0.190 (<i>P</i> = 0.083)	0.013	6.40
	Environment	0.330 (<i>P</i> = 0.341)	0.169 (<i>P</i> = 0.117)	0.034	16.75
Parasites (<i>Haemoproteus</i>)	Whole model	0.107 (<i>P</i> = 0.262)			
	Hosts	0.123 (<i>P</i> = 0.669)	0.102 (<i>P</i> = 0.130)	0.005	4.67
	Geography	0.140 (<i>P</i> = 0.536)	0.095 (<i>P</i> = 0.155)	0.012	11.21
	Environment	0.111 (<i>P</i> = 0.702)	0.104 (<i>P</i> = 0.140)	0.003	2.80

1. Lichstein JW (2007) Multiple regression on distance matrices: a multivariate spatial analysis tool. *Plant Ecol* 188(2):117–131.
2. Krasnov BR, et al. (2010) Similarity in ectoparasite faunas of Palaearctic rodents as a function of host phylogenetic, geographic or environmental distances: Which matters the most? *Int J Parasitol* 40(7):807–817.
3. Goslee SC, Urban DL (2007) The ecodist package for dissimilarity-based analysis of ecological data. *J Stat Softw* 22(7):1–19.

Table S7 Mantel correlation coefficients (r) and P values from comparisons of host phylogenetic distances and host Bray-Curtis dissimilarities based on parasite sharing for each “community” sampling location. Only parasite lineages sampled at least 10 times in each location were included in the analysis. N.Host and N.Parasite represent the number of host species and parasite lineages, respectively, considered in each analysis. Alabama, Connecticut, Pennsylvania, and Louisiana were left out of the analysis due to low sample sizes.

Location	r	P	N.Host	N.Parasite
Chicago	0.303	0.035	19	13
Indiana	0.473	0.008	11	5
Michigan	0.229	0.210	7	2
Ozarks	0.147	0.099	22	10
St. Louis	0.293	0.016	17	4
Tennessee	0.100	0.096	19	4

Table S8 Pairwise Spearman correlations coefficients (ρ) were calculated between parasite relative abundances (separated by genus) and host species abundances across the region. We report the mean observed ρ and its SE, and whether either statistic differed from a randomized distribution of the statistics derived by row-shuffling the parasite relative abundance matrix and recalculating them 9999 times.

Parasite Genus	Mean observed ρ	P (mean ρ)	SE	P (SE)
<i>Plasmodium</i>	0.006	0.868	0.012	0.086
<i>Haemoproteus</i>	-0.026	0.355	0.010	0.565

Table S9 Host species codes corresponding to three letter host species codes in Dataset S1. “N” refers to sample size, “AOU species code” is a four letter code for host species commonly used by bird banders. The “Genus” and “Species” columns reflect the taxonomy used at <http://birdtree.org/>. The “Current” column represents current taxonomy (when different) based on the American Ornithological Union’s Checklist of North American Birds (<http://checklist.aou.org/>).

Host species code	N	AOU species code	Genus	Species	Current	Common Name
PDO	565	HOSP	<i>Passer</i>	<i>domesticus</i>		House Sparrow
TMI	491	AMRO	<i>Turdus</i>	<i>migratorius</i>		American Robin
CCA	353	NOCA	<i>Cardinalis</i>	<i>cardinalis</i>		Northern Cardinal
DCA	348	GRCA	<i>Dumetella</i>	<i>carolinensis</i>		Gray Catbird
VOL	284	REVI	<i>Vireo</i>	<i>olivaceus</i>		Red-eyed Vireo
PCY	231	INBU	<i>Passerina</i>	<i>cyanea</i>		Indigo Bunting
VGR	220	WEVI	<i>Vireo</i>	<i>griseus</i>		White-eyed Vireo
MME	219	SOSP	<i>Melospiza</i>	<i>melodia</i>		Song Sparrow
IVI	210	YBCH	<i>Icteria</i>	<i>virens</i>		Yellow-breasted Chat
CTR	209	AMGO	<i>Carduelis</i>	<i>tristis</i>	<i>Spinus tristis</i>	American Goldfinch
WCI	142	HOWA	<i>Wilsonia</i>	<i>citrina</i>	<i>Setophaga citrina</i>	Hooded Warbler
HMU	136	WOTH	<i>Hylocichla</i>	<i>mustelina</i>		Wood Thrush
OFO	130	KEWA	<i>Oporornis</i>	<i>formosus</i>	<i>Geothlypis formosa</i>	Kentucky Warbler
MVA	128	BAWW	<i>Mniotilta</i>	<i>varia</i>		Black-and-White Warbler
EVI	127	ACFL	<i>Empidonax</i>	<i>virescens</i>		Acadian Flycatcher
GTR	110	COYE	<i>Geothlypis</i>	<i>trichas</i>		Common Yellowthroat
HVE	108	WEWA	<i>Helmitheros</i>	<i>vermivorum</i>		Worm-eating Warbler
SAU	106	OVEN	<i>Seiurus</i>	<i>aurocapilla</i>		Ovenbird
CME	101	HOFI	<i>Carpodacus</i>	<i>mexicanus</i>	<i>Haemorhous mexicanus</i>	House Finch
TLU	91	CAWR	<i>Thryothorus</i>	<i>ludovicianus</i>		Carolina Wren
PPU	82	DOWO	<i>Picoides</i>	<i>pubescens</i>		Downy Woodpecker
BBI	71	TUTI	<i>Baeolophus</i>	<i>bicolor</i>		Tufted Titmouse
SVU	69	EUST	<i>Sturnus</i>	<i>vulgaris</i>		European Starling
QQU	68	COGR	<i>Quiscalus</i>	<i>quiscula</i>		Common Grackle
APH	60	RWBL	<i>Agelaius</i>	<i>phoeniceus</i>		Red-winged Blackbird
PAM	59	NOPA	<i>Parula</i>	<i>americana</i>		Northern Parula

SRU	57	AMRE	<i>Setophaga</i>	<i>ruticilla</i>		American Redstart
VPI	50	BWWA	<i>Vermivora</i>	<i>pinus</i>	<i>Vermivora cyanoptera</i>	Blue-winged Warbler
SNO	46	NOWA	<i>Seiurus</i>	<i>noveboracensis</i>	<i>Parkesia noveboracensis</i>	Northern Waterthrush
SPU	45	FISP	<i>Spizella</i>	<i>pusilla</i>		Field Sparrow
PCA	43	CACH	<i>Parus</i>	<i>carolinensis</i>	<i>Poecile carolinensis</i>	Carolina Chickadee
ZAL	43	WTSP	<i>Zonotrichia</i>	<i>albicollis</i>		White-throated Sparrow
POL	41	SCTA	<i>Piranga</i>	<i>olivacea</i>		Scarlet Tanager
DPE	38	YEWA	<i>Dendroica</i>	<i>petechia</i>	<i>Setophaga petechia</i>	Yellow Warbler
MAT	37	BHCO	<i>Molothrus</i>	<i>ater</i>		Brown-headed Cowbird
ZMA	36	MOD0	<i>Zenaida</i>	<i>macroura</i>		Mourning Dove
CFU	30	VEER	<i>Catharus</i>	<i>fuscescens</i>		Veery
DMA	30	MAWA	<i>Dendroica</i>	<i>magnolia</i>	<i>Setophaga magnolia</i>	Magnolia Warbler
BCE	29	CEDW	<i>Bombycilla</i>	<i>cedrorum</i>		Cedar Waxwing
PCE	29	BGGN	<i>Polioptila</i>	<i>caerulea</i>		Blue-gray Gnatcatcher
PER	29	EATO	<i>Pipilo</i>	<i>erythrophthalmus</i>		Eastern Towhee
SPA	29	CHSP	<i>Spizella</i>	<i>passerina</i>		Chipping Sparrow
DDI	26	PRAW	<i>Dendroica</i>	<i>discolor</i>	<i>Setophaga discolor</i>	Prairie Warbler
LSW	26	SWWA	<i>Limnothlypis</i>	<i>swainsonii</i>		Swainson's Warbler
CVI	25	EAWP	<i>Contopus</i>	<i>virens</i>		Eastern Wood-Pewee
TRU	25	BRTN	<i>Toxostoma</i>	<i>rufum</i>		Brown Thrasher
ETR	23	WIFL	<i>Empidonax</i>	<i>traillii</i>		Willow Flycatcher
SCR	23	WBNU	<i>Sitta</i>	<i>carolinensis</i>		White-breasted Nuthatch
DCN	21	CAWA	<i>Wilsonia</i>	<i>canadensis</i>	<i>Cardellina canadensis</i>	Canada Warbler
IGA	19	BAOR	<i>Icterus</i>	<i>galbula</i>		Baltimore Oriole
PAT	19	BCCH	<i>Parus</i>	<i>atricapillus</i>	<i>Poecile atricapillus</i>	Black-capped Chickadee
SMO	19	LOWA	<i>Seiurus</i>	<i>motacilla</i>	<i>Parkesia motacilla</i>	Louisiana Waterthrush
SPH	18	EAPH	<i>Sayornis</i>	<i>phoebe</i>		Eastern Phoebe
TAE	17	HOWR	<i>Troglodytes</i>	<i>aedon</i>		House Wren
CCR	16	BLJA	<i>Cyanocitta</i>	<i>cristata</i>		Blue Jay
DCO	16	YRWA	<i>Dendroica</i>	<i>coronata</i>	<i>Setophaga coronata</i>	Yellow-rumped/Myrtle

						Warbler
DPN	16	CSWA	<i>Dendroica</i>	<i>pensylvanica</i>	<i>Setophaga pensylvanica</i>	Chestnut-sided Warbler
VGI	16	WAVI	<i>Vireo</i>	<i>gilvus</i>		Warbling Vireo
TBC	14	TRSW	<i>Tachycineta</i>	<i>bicolor</i>		Tree Swallow
MGR	13	SWSP	<i>Melospiza</i>	<i>georgiana</i>		Swamp Sparrow
CAM	12	YBCU	<i>Coccyzus</i>	<i>americanus</i>		Yellow-billed Cuckoo
PRU	12	SUTA	<i>Piranga</i>	<i>rubra</i>		Summer Tanager
VRU	11	NAWA	<i>Vermivora</i>	<i>ruficapilla</i>	<i>Leiothlypis ruficapilla</i>	Nashville Warbler
DCR	10	BTBW	<i>Dendroica</i>	<i>caerulescens</i>	<i>Setophaga caerulescens</i>	Black-throated Blue Warbler
DDO	10	YTWA	<i>Dendroica</i>	<i>dominica</i>	<i>Setophaga dominicana</i>	Yellow-throated Warbler
PCI	10	PROW	<i>Protonotaria</i>	<i>citrea</i>		Prothonotary Warbler
SSI	10	EABL	<i>Sialia</i>	<i>sialis</i>		Eastern Bluebird
MPO	9	NOMO	<i>Mimus</i>	<i>polyglottos</i>		Northern Mockingbird
ISP	8	OROR	<i>Icterus</i>	<i>spurius</i>		Orchard Oriole
MCA	8	RBWO	<i>Melanerpes</i>	<i>carolinus</i>		Red-bellied Woodpecker
RCA	8	RCKI	<i>Regulus</i>	<i>calendula</i>		Ruby-crowned Kinglet
VFL	7	YTVI	<i>Vireo</i>	<i>flavifrons</i>		Yellow-throated Vireo
CAU	6	NOFL	<i>Colaptes</i>	<i>auratus</i>		Northern Flicker
CMN	6	GCTH	<i>Catharus</i>	<i>minimus</i>		Gray-cheeked Thrush
MCR	6	GCFL	<i>Myiarchus</i>	<i>crinitus</i>		Great Crested Flycatcher
VPE	6	TEWA	<i>Vermivora</i>	<i>peregrina</i>	<i>Oreothlypis peregrina</i>	Tennessee Warbler
PVI	5	HAWO	<i>Picoides</i>	<i>villosus</i>		Hairy Woodpecker
CVR	4	BOBW	<i>Colinus</i>	<i>virginianus</i>		Northern Bobwhite
EFV	4	YBFL	<i>Empidonax</i>	<i>flaviventris</i>		Yellow-bellied Flycatcher
DFU	3	BLBW	<i>Dendroica</i>	<i>fusca</i>	<i>Setophaga fusca</i>	Blackburnian Warbler
DVI	3	BTNW	<i>Dendroica</i>	<i>virens</i>	<i>Setophaga virens</i>	Black-throated Green Warbler
GCA	3	BLGR	<i>Passerina</i>	<i>caerulea</i>		Blue Grosbeak
OPH	3	MOWA	<i>Oporornis</i>	<i>philadelphia</i>	<i>Geothlypis philadelphia</i>	Mourning Warbler
CER	2	BBCU	<i>Coccyzus</i>	<i>erythrophthalmus</i>		Black-billed Cuckoo
CGU	2	HETH	<i>Catharus</i>	<i>guttatus</i>		Hermit Thrush

EAL	2	ALFL	<i>Empidonax</i>	<i>alnorum</i>		Alder Flycatcher
HRS	2	BASW	<i>Hirundo</i>	<i>rustica</i>		Barn Swallow
PMN	2	ETSP	<i>Passer</i>	<i>montanus</i>		Eurasian Tree Sparrow
CCN	1	NOHA	<i>Circus</i>	<i>cyaneus</i>		Northern Harrier
CFM	1	BRCR	<i>Certhia</i>	<i>familiaris</i>		Brown Creeper
DCE	1	CERW	<i>Dendroica</i>	<i>cerulea</i>	<i>Setophaga cerulea</i>	Cerulean Warbler
DPA	1	PAWA	<i>Dendroica</i>	<i>palmarum</i>	<i>Setophaga palmarum</i>	Palm Warbler
DPI	1	PIWA	<i>Dendroica</i>	<i>pinus</i>	<i>Setophaga pinus</i>	Pine Warbler
DST	1	BLPW	<i>Dendroica</i>	<i>striata</i>	<i>Setophaga striata</i>	Blackpoll Warbler
EMI	1	LEFL	<i>Empidonax</i>	<i>minimus</i>		Least Flycatcher
PLD	1	RBGR	<i>Pheucticus</i>	<i>ludovicianus</i>		Rose-breasted Grosbeak
SDE	1	ECDO	<i>Streptopelia</i>	<i>decaocto</i>		Eurasian Collared-Dove
VBE	1	BEVI	<i>Vireo</i>	<i>bellii</i>		Bell's Vireo
VPH	1	PHVI	<i>Vireo</i>	<i>philadelphicus</i>		Philadelphia Vireo

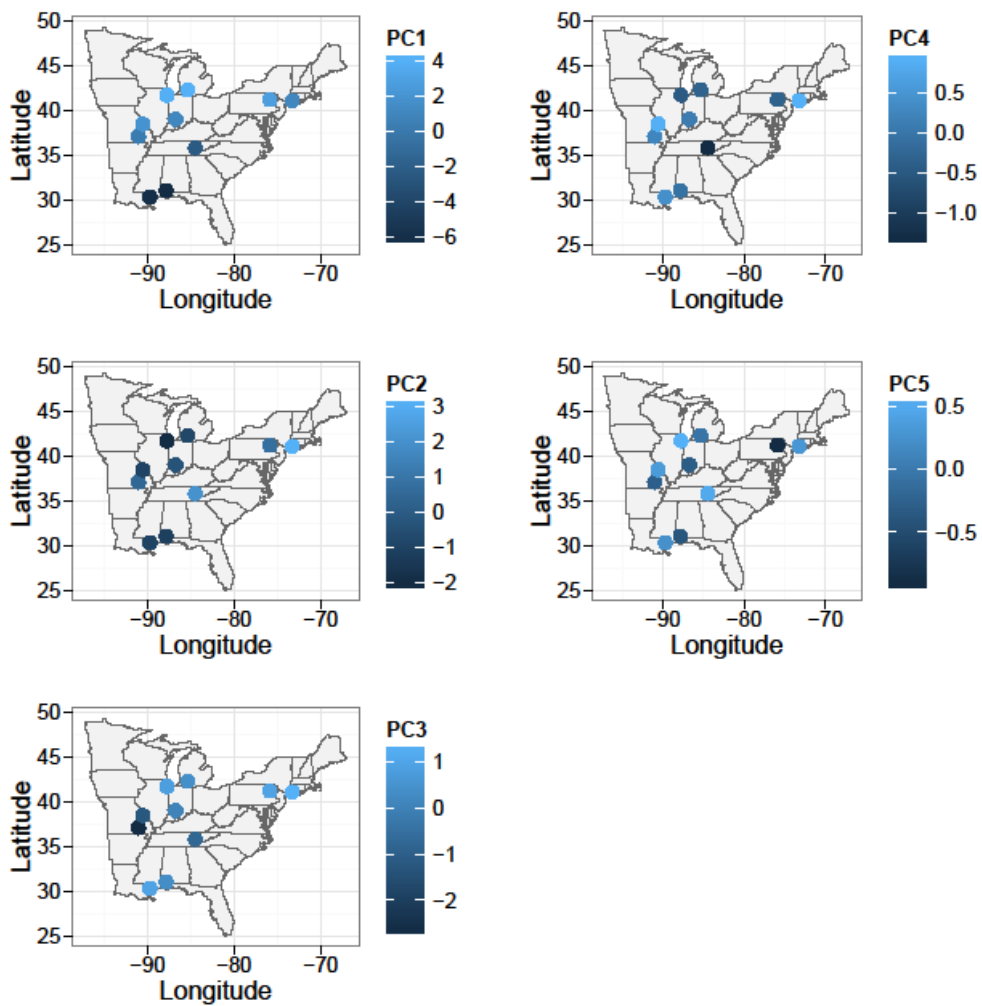


Fig. S1 The first five axes of a principal components analysis (PCA) ordinating 19 bioclim variables downloaded from <http://www.worldclim.org/> for each sampling location (Table S3).

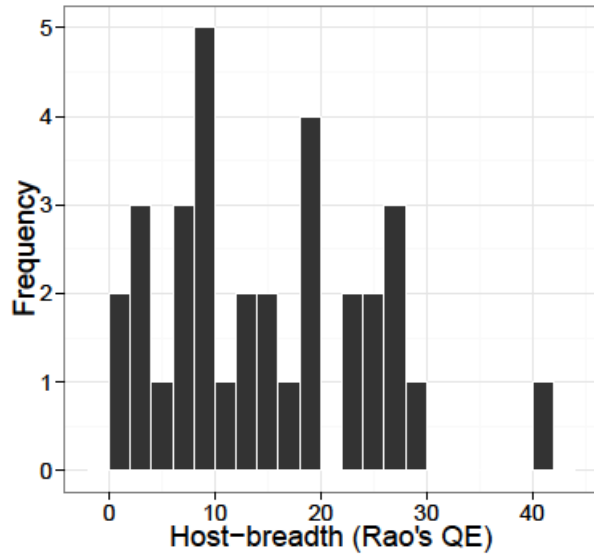


Fig. S2 Frequency distribution of parasite host-breadth (Rao's Quadratic Entropy) from parasite lineages sampled at least 10 times across all locations. It does not differ from a unimodal distribution (i.e., it is not bimodal; Hartigans' dip test, $D_{33} = 0.047$, $P = 0.87$).

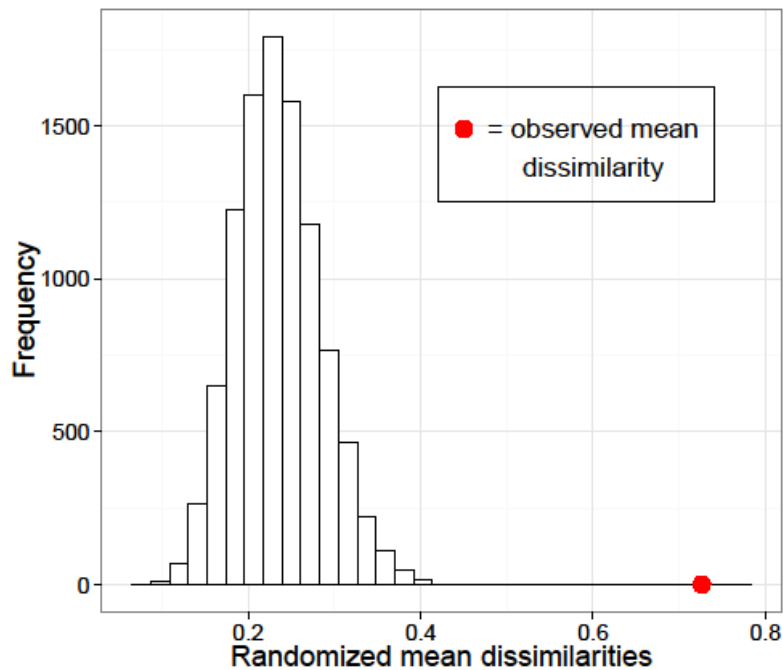


Fig. S3 The distribution of randomized mean dissimilarities between four locations where *Cardinalis cardinalis* was well-sampled in 2013 based on the prevalence of five parasite lineages at each location. Observed dissimilarity between locations was greater than the random distribution indicating that parasite by location combinations were more unique than expected by chance alone ($P < 0.001$).

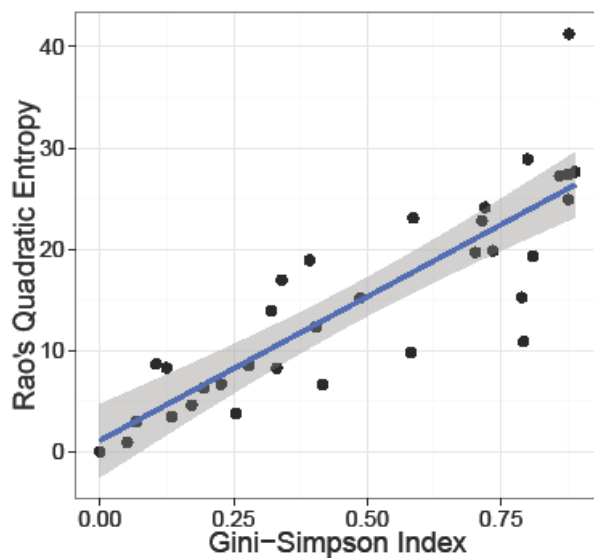


Fig. S4 The relationship between parasite host-breadth, calculated by Rao's Quadratic Entropy, and the Gini-Simpson Index for parasites sampled at least 10 times across community sampling locations ($R^2 = 0.724$, $P < 0.001$). The blue line is the predicted linear relationship and is surrounded by 95% confidence intervals.