Evolutionary dynamics of pre- and postzygotic reproductive isolation in cichlid fishes

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Supplementary information

Evaluation of premating isolation in cichlids (Figure 1)

We conducted a literature research in "Web of Science" using the keywords:

"cichlid*" AND "mating"; "cichlid*" AND "assortative mating"; "cichlid*" AND "mate choice"; "cichlid*" AND "random mating"; "cichlid*" AND "reproductive isolation". The literature search was conducted on 04.02.2020 between 13:31 and 13:45 o'clock (CET). Citation reports were exported and recurrent papers that were returned from more than one keyword search were removed. This resulted in a total of 803 studies (Supplementary Table S1). After removing theoretical papers, review articles and studies only citing cichlid literature but using focal species outside of the family Cichlidae, 497 relevant studies remained. Additionally, we added 21 studies that investigated assortative mating in cichlids but were not included in any of the keyword searches. Next, we filtered those papers for studies specifically testing for assortative mating between populations or species. This reduced the number of relevant studies to 39 (see Supplementary Table S1 and S2 for information on filtering). While some of those papers quantified the degree of assortative mating by the number of spawning events, eggs laid or other count data, others used preference scores (calculated as the difference in the proportions of females' positive responses to male courtship between con- and heterospecifics; 1) to describe the strength of premating isolation. We extracted those data from the literature. Due to the discrepancy in reporting the strength of premating isolation, Figure 1 in the paper only considers the studies reporting count data (since count data and preference scores provide different measures of premating isolation they could not be combined in our analysis), which reflects what the majority of studies reported (29 out of 39 studies). To obtain values for the frequency of expected assortative and disassortative mating for count data, as required for our meta-analysis, we assumed a scenario of random mating. Additionally, we considered the number of potential mates. Accordingly, if females could choose among two males in ten trials, the count data for expected assortative and disassortative under random mating would equal five, respectively. For the meta-analysis investigating the effect of manipulations on assortative mating, expected values were derived from results of respective experiments prior to manipulation.

Supplementary Figure S1 depicts the results of the meta-analysis conducted for the preference scores.

Meta-analysis was conducted using the software OpenMEE

To analyze the data, we conducted a series of analyses at the meta-analysis level using the software *OpenMEE* (2). For the count data we estimated the odd ratios of mating with a conspecific versus mating with a heterospecific and its associated variance (see above). These two estimated values were used in downstream analyses. We conducted a phylogenetically controlled meta-analysis by modelling phylogenetic variance as a random effect (2). For this analysis, we constructed a simplified phylogenetic tree based on the full mitochondrial genome (Supplementary Table S4 and Supplementary Figure S4). A maximum likelihood (ML) analysis was performed in *PAUP* version 4.0a, build 167 (3), using the BioNJ method under the GRT model of nucleotide substitution. Closely related species were grouped together in this tree. Further, we aimed at improving our understanding of the different drivers of phylogenetic and among-study variance $(\tau^{2}_{\lambda}, \tau^{2})$. For this we used the subgroup analysis module in *OpenMEE*. As categories, we used lineage (*Pundamilia cf. nyererei, Maylandia cf. zebra, Tropheus cf. moori,* other haplochromines and Neotropical species; see Supplementary

Table S2 and Supplementary Figure S2) and the geographic setting of the current diversity (e.g., sympatric versus allopatric) and the taxonomic status of the studied taxa (population versus species; see Supplementary Table S2 and Supplementary Figure S3).

Evaluation of intrinsic incompatibilities in cichlids (Figure 2)

We scanned the literature for studies reporting interspecific crosses and their fitness consequences for the resulting F1 hybrid offspring. We extracted those crosses from the previously published literature (Supplementary Table S3). Viability was scored as 0 if F1s were reported to be viable and as 1 if F1 inviability or cumulative fitness of 1 (see 4) were reported. Sex ratio distortion was scored as 0 if no skew in F1 sex ratio was reported and as 1 if F1 sex ratio deviated from 1:1. D-loop sequences obtained from NCBI GenBank were used to compute pairwise genetic distances for interspecific crosses. For some species without available D-loop sequences in GenBank, we used sequences of closely related species (Supplementary Table S3). All sequences were aligned using the online version of MAFFT 7 (5). Pairwise genetic distances were calculated as uncorrected p-distances using MEGA version X (6). For interspecific comparisons with data on reciprocal crosses, we only included both cross directions when differences in viability or sex ratio distortion were reported and otherwise just included one of the crosses. We then analyzed intrinsic hybrid incompatibilities using a generalized linear model with binomial error distribution in R using F1 viability or sex ratio distortion as response variable and genetic distance as explanatory variable.

Supplementary Figures:



Supplementary Figure S1. Meta-analysis using preference scores. Evaluation of premating isolation in cichlids using preference scores shows the same qualitative trend as when considering count data: females prefer conspecific over heterospecific males (Figure 1). However, variation is more pronounced. The only lineage differing in the pattern of premating isolation when comparing meta-analyses based on count data and preference scores was *Tropheus cf. moorii.* Preference scores (difference in the proportions of females' positive responses to male courtship between con- and heterospecific males) are depicted with 95% CI as a behavioural proxy for premating isolation. Preference scores of 1 indicate preference for conspecific males and scores of -1 indicate preference for heterospecific males. l^2 = percentage of variability that is due to heterogeneity across studies rather than sampling variance, study IDs correspond to studies from which we extracted corresponding data (see Supplementary Table S2).

Study ID	Species	Neotropical	
		African	
Machado et al1	Amphilophus citrinellus	o mean	
Machado et al. 2	Amphilophus citrinellus		
Elmer et al. 1	Amphilophus sacittae		
Elmer et al. 2	Amphilophus sugatuc		
	Amphilophus xiloaensis		
Baylis	Amphilophus zaliosus		•
Romer et al2	Apistogramma cacatuoides		
Ready et al1	Apistogramma caetei		•
Ready et al2	Apistogramma caetei		•
Ready et al. 3	Apistogramma caetei		
Neotronical species (12=76.83 %***)	npierogramma edeter		
Neotropical species (1 -70.05 %)			
Deikey et al. 1	Astatatilania hurtani Kalamba laka		
	Astatotilapia burtoni Kalambo lake		
Theis et al2	Astatotilapia burtoni Kalambo lake		•
Theis et al1	Astatotilapia burtoni Kalambo river	•	—
Rajkov et al3	Astatotilapia burtoni Lufubu river	•	-
Theis et al. 3	Astatotilapia burtoni Lunza river		
Raikov et al. 2	Astatotilapia burtoni Ndole lake		
Types et al. 4	Astatotilania callintera "Chilingali"		
Tyors et al. 0	Astatotilapia calliptora "Ohimigai		
Tyers et al2	Astatotilapia caliptera Chizumulu		
Nichols et al1	Astatotilapia calliptera "Ruvuma"	1	•
Nichols et al2	Astatotilapia calliptera "Salima"		
Tyers et al1	Astatotilapia calliptera "Salima"	+	
Gerlai_2	Cynotilapia afra		· · · · · · · · · · · · · · · · · · ·
Pauers et al. 1	Labeotropheus fuelleborni Chipoka		
Tvers et al. 5	Lethrinons chilingalo		
Typers et al. 6			
Tyers et al6			
Genner et al1	Rhamphochromis chilingali		
Genner et al3	Rhamphochromis chilingali	1	•
Gerlai_1	Sciaenochromis fryeri	-	•
other haplochromines (I ² =86.13 % ***)			
.lordan et al −2	Mavlandia barlowi		_ '
lordan et al -1	Maylandia benetos		
Kidd et al1	Maylandia benetos	1	•
Knight et al1	Maylandia callainos		•
Plenderleith et al1	Maylandia emmiltos		•
Knight et al.5	Maylandia emmiltos		-
Blais et al. 1	Mavlandia emmiltos		
Knight et al 1	Mavlandia zebra Ruarwe		
Knight et al 2	Maylandia zobra Chiaumulu		
Knight et al.3	Maylandia zebra Mara Rocks	1	•
Knight et al.4	Maylandia zebra Nkhata Bay	-	•
Blais et al4	Maylandia zebra	•	
Jordan et al.−3	Maylandia zebra		- _
Kidd et al. 1−2	Mavlandia zebra		
Knight et al. 2	Metriaclima zebra gold		
Knight et al. 3	Metriaclima zebra gold		
Maylandia of $\pi a bra (l^2 = 52.2.9)$ **)	Wethacima zebra gola		
Maylandia cr. zebra (1=53.3 % **)			
Svensson et al2	Pundamilia "nyererei-like"		•
Selz et al.−4	Pundamilia nyererei		•
Selz et al.−1	Pundamilia nyererei Makobe		
Seehausen_1	Pundamilia nyererei Makobe	_	
Selz et al.−2	Pundamilia nyererei Python		• • • • • • • • • • • • • • • • • • •
Seehausen 3	Pundamilia nvererei Pvthon		
Selz et al -3	Pundamilia nvererei Senga		•
Svensson et al. 1	Pundamilia "pundamilia lika"		
Svensson et al1	Pundamina pundamina-like		
Seenausen_2	Pundamilia "pundamilia" Makobe		•
Seehausen_4	Pundamilia pundamilia Python		•
Pundamilia cf. nyererei (l²=8.23 %)			
Egger_et al2	Tropheus moorii blue "Nakaku"		•
Egger et al. 5	Tropheus moorii Chimba	•	_
Secf et al. 2	Tropheus moorii Mbita		
Egger et al. 3	Tropheus moorii Mbito		_
		•	
	i ropneus moorii Moliro		•
Egger_et al6	Tropheus moorii Moliro		
Secf et al3	Tropheus moorii Nakaku		
Egger_et al4	Tropheus moorii Nakaku	-	•
Egger_et al. 1	Tropheus moorii red "Moliro"	_	•
Tropheus cf. moorii (l²=77.61 % ***)	•		
Overall (12=83.81 % ***)			
			Y I
significance code: 0.05 *** 0.01**** 0.001****			
	()	4.26 1150.89

odds ratio (log scale)

Supplementary Figure S2. Details of Meta-analysis considering different lineages. Detailed meta-analysis investigating if premating isolation differs among lineages (Figure 1B). Log odds ratios depicted with 95% CI indicate likelihood of premating isolation. Ratios of 1 indicate mating with con- versus heterospecifics is equally likely, values higher than one express the fold increase in likelihood of mating assortatively and values lower than one express the fold increase in mating disassortatively. I^2 = percentage of variability that is due to heterogeneity across studies rather than sampling variance, study IDs correspond to studies from which we extracted corresponding data (see Supplementary Table S2).



Rhamphochromis longiceps



Genner et al._1 Genner et al. 3

allopatric species (I2=39.92 %)

Overall (I2=83.81 % ***)

significance code: 0.05 " 0.01"" 0.001

Supplementary Figure S3. Details of Meta-analysis considering geographic settings. Detailed meta-analysis investigating if premating isolation differs among geographic settings and among populations and species (Figure 1C). Log odds ratios depicted with 95% CI indicate likelihood of premating isolation. Ratios of 1 indicate mating with con- versus heterospecifics is equally likely, values higher than one express the fold increase in likelihood of mating assortatively and values lower than one express the fold increase in mating disassortatively. l^2 = percentage of variability that is due to heterogeneity across studies rather than sampling variance, study IDs correspond to studies from which we extracted corresponding data (see Supplementary Table S2).



Supplementary Figure S4. Ultrametric tree based on mitochondrial genomes. A simplified phylogenetic tree was constructed based on full mitochondrial genomes (Supplementary Table S4). A chronogram was fitted to the tree using a strict clock model with the function chronos in package ape in R(7).

References:

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