1	The genetics of mate preferences in hybrids between two young and sympatric Lake
2	Victoria cichlid species
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25 Abstract

26 The genetic architecture of mate preferences are likely to affect significant evolutionary processes, including speciation and hybridisation. Here, we investigate laboratory hybrids 27 28 between a pair of sympatric Lake Victoria cichlid fish species that appear to have recently 29 evolved from a hybrid population between in similar predecessor species. The species demonstrate strong assortative mating in the lab associated with divergent male breeding 30 31 colouration (red dorsum vs blue). We show in a common garden experiment, using DNA-32 based paternity testing, that the strong female mate preferences among males of the two 33 species are fully recovered in a large fraction of their F2 hybrid generation. Individual hybrid 34 females often demonstrated consistent preferences in multiple mate choice trials (≥ 5) across a 35 year or more. This result suggests that female mate preference is influenced by relatively few 36 major genes or genomic regions. These preferences were not changed by experience of a 37 successful spawning event with a male of the non-preferred species in a no-choice single-male 38 trial. We found no evidence for imprinting in the F2 hybrids, although the F1 hybrid females 39 may have been imprinted on their mothers. We discuss this nearly Mendelian inheritance of 40 consistent innate mate preferences in the context of speciation theory.

41

42 Key words

Assortative mating, hybridization, *Pundamilia nyererei*, *Pundamilia pundamilia*, sensory
drive, speciation-with-gene-flow

46 Introduction

47 Behavioural assortative mating is considered to play a significant role in the origin and maintenance of reproductive isolation among species [1, 2]. The rate of and constraints to the 48 evolution of behavioural assortative mating is likely often influenced by the genetic 49 50 architecture of mate preferences and the nature and strength of genetic and non-genetic influences, such as imprinting and experience. For example, modelling studies suggest that 51 52 sympatric and parapatric speciation starting from a monomorphic population is more probable in cases where assortative mating or female preference among male courtship genotypes is 53 54 influenced by relatively few genetic loci [3-5], although models starting from large standing 55 variation may not have this constraint of preference architecture [6]. However, a small 56 number of preference genes tends to facilitate speciation in many models of speciation with gene flow [7, 8]. Empirical studies of the genetics of species divergence in mating preferences 57 are still rare. Some of the empirical results are consistent with few genes having a major effect 58 59 on female assortative mating in cichlid fish and Heliconius butterflies [9-12]. In other 60 systems, mostly insects, female choice appears to have a more quantitative genetic 61 background [13-15]. 62

The Lake Victoria rocky-shore cichlid fishes of the genus *Pundamilia* have emerged as a significant model system for the study of speciation, being representatives of a spectacular hyperdiverse, rapid adaptive radiation and being relatively tractable as a laboratory species for breeding and mate choice experiments [16, 17]. Following the completion of their genome sequence [18], the evolutionary history of focal populations in the SE part of the lake has been reconstructed [19]. Analysis of genome-wide sequence data indicates that the species with red dorsum (*P*. 'nyererei-like') and blue (*P*. 'pundamilia-like') males at Python Island have

- 70 recently diverged in situ, following a period of massive introgression with resident *P*.
- *pundamilia* on the colonisation of the island by *P. nyererei* from elsewhere in the lake [19].
- 72

73	The Pundamilia species, like other haplochromine cichlid fishes, show strong sex role
74	differentiation and associated sexual dimorphism: the smaller, cryptic females are
75	mouthbrooders, caring for the offspring for several weeks, while the larger brightly coloured
76	males defend territories and display to attract females, but play no part in rearing the offspring
77	[20]. Such a breeding system is likely to generate strong sexual selection acting through
78	male-male competition and female preference for male courtship traits [21]. Closely-related
79	haplochromine species often differ markedly in male nuptial colour and it has been proposed
80	that this is associated with divergent female mate preferences [22], which have been
81	demonstrated in a number of experimental trials [23-25]. The resultant assortative mating
82	between females with a certain preference and males expressing the corresponding trait may
83	play a significant role in the maintenance and perhaps sometimes the origin of reproductive
84	isolation among sympatric species [16].
85	
86	In the Pundamilia red/blue system, increasing water depth is associated with differentiation in
87	alleles at the long wavelength sensitive opsin gene (LWS), female preferences and male
88	nuptial colour, and it is likely that the sensory environment along this microhabitat gradient
89	has influenced divergence through a process of 'sensory drive' [26]. Of course, mating signals
90	are often multimodal and subject to multivariate selection [27-29] which is most likely also
91	the case in Pundamilia [16, 17, 30]. However, in the Pundamilia system, female preferences
92	for male nuptial colouration – itself likely to be oligogenic [31] – appear to be necessary and
93	sufficient for assortative mating [30, 32, 33].

95 In haplochromine cichlids, trait segregation in F2 hybrids has been shown for female 96 preferences [9, 12], male nuptial colouration [12, 31, 34] and male attractiveness to parental species [33, 35]. This includes the *Pundamilia* system, where, furthermore, studies suggest an 97 absence of physical linkage between male nuptial colour and female mate preference [36]. At 98 99 Python Island, gene flow between the species is estimated to be ongoing [19]. Therefore, the observed strong linkage disequilibrium between male colour and female preference is likely 100 101 to be maintained by divergent selection. A behavioural study on the second generation (F2) hybrid offspring of P. sp. "pundamilia-like" and P. sp. "nyererei-like" crosses by Haesler and 102 103 Seehausen [9] revealed that female mate preference has a genetic basis, and that there may be 104 as few as 1 to 5 major genes that contribute to the variation in this trait. That study, however, 105 used a behavioural assay to measure mate choice, which may not be entirely predictive of 106 actual mating decisions. Here, we used a 'common garden' approach with full-contact spawnings to examine female mate choice decisions in first and second-generation hybrids 107 108 (F1 and F2). Wild-type females were included as a control. We used molecular paternity 109 determination to measure directly the mating decisions of females in the laboratory [24] and 110 examined the repeatability (\geq 5 spawning decisions) of female mate choice over a year or more to estimate the segregation of mate preferences in the F2 hybrids of the sympatric sister 111 species of *Pundamilia* from Python island. In contrast to Haesler and Seehausen [9], we 112 examined if mate preferences are consistently maintained across many spawning events (the 113 114 fully cycle from egg maturation to spawning).

115

If female preference is a polygenic quantitative trait with an additive genetic basis, F2 hybrids
preferences is expected to be distributed in a Gaussian-like fashion with few individuals
expressing significant preferences in the tails of the distribution. In contrast, for a polygenic
trait with strong dominance effects, the preference distribution of the F2 will be skewed

120	towards either end of the distribution [37-39]. On the other hand, if preferences are not
121	genetically determined, the preference distribution of F2 females is predicted to be more
122	uniform across F2 females given that individuals shared the same common environment.
123	However, in the case of gene flow, linkage disequilibrium between alleles in a polygenic trait
124	will be broken up by recombination [40, 41] and polygenic mating preferences will be
125	difficult to maintain under such conditions. Because ongoing gene flow [17, 19, 26] and
126	recombination (J. Meier and O. Seehausen, unpublished data) have been shown in this young
127	[19] species pair, and because differentiation in polygenic mating preferences will be difficult
128	to maintain under such conditions, we predicted mate preferences to segregate as an
129	oligogenic trait in a nearly Mendelian fashion.
130	
131	Methods
132	The experimental fish
133	We used the sympatric sister species <i>Pundamilia</i> sp. "pundamilia-like" and <i>Pundamilia</i> sp.

"nyererei-like" (sensu Meier et al. [19]). These taxa show a striking difference in male nuptial 134 colours: P. sp. "pundamilia-like" males are grey on the flanks between black vertical bars and 135 have a metallic blue spinous dorsal fin, whereas P. sp. "nyererei-like" are orange on the 136 dorsum, dorsal head surface and dorsal fin and yellow on the flanks between black vertical 137 138 bars. It is estimated that there is currently a low to moderate level of gene flow between the 139 taxa at Python Island (The effective number of haploid immigrants per generation [2Nm] 140 forward in time is 0.7 from P. sp. "pundamilia-like" to P. sp. "nyererei-like" and 7.2 in the opposite direction [19]). Species differences in female mate choice and divergent alleles at the 141 LWS opsin gene are not completely fixed [17] and males with intermediate colouration are 142 found [26]. In contrast, at Makobe Island in the open lake the sympatric species pair P. 143 pundamilia and P. nyererei shows stronger genome-wide differentiation, is more ecologically 144

145 differentiated, intermediate phenotypes are not observed and no mismatches have been

reported between male colouration and *LWS* opsin allele [17, 19, 26]. Both species are diploid and have 22 chromosomes (2n=44) [18].

148

149 Wild-type females and two F1 hybrid families (one in each cross direction) used in the mate choice experiment were bred from wild-caught parents. The fry were raised in stock tanks 150 151 until large enough to be tagged with an integrated transponder (PIT tag), to enable individual identification. Using microsatellite DNA parentage analyses, we concluded that the 15 P. sp. 152 "pundamilia-like" females originated from 3 wild mothers and 1 wild sire and the 6 P. sp. 153 154 "nyererei-like" females from 3-6 wild mothers and 5 wild sires. 155 156 The two F2 families used in the mate choice experiment were bred from a lab stock collected in 1992 [42]. The F1 families were bred from the second to third lab generation. The F2 157 generations were bred by holding one F1 male (no replacement, N=3) together with not more 158 than 10 F1 females in the same aquarium. One F2 half-sib family (PN1-33) was bred from 159 160 fish from two F1 families bred in 1999 from a female P. sp. "pundamilia-like" x male P. sp. 161 "inverse inverse inverse in the same F2 family used by Haesler and Seehausen [9]. The F2 broods were kept separate and hence some broods in the electronic supplemental 162 material figure S3 may have had the same mother, whereas we know which of the two males 163 was the father. The other F2 family (PN34) was bred from fish from one F1 family bred in 164 2001 from a female P. sp. "pundamilia-like" x male P. sp. "nyererei-like". The offspring were 165 166 pooled into the same aquaria and hence the father is known but not the brood or mother. 167 When F2 offspring were large enough, they were PIT-tagged and pooled into the same aquaria. The breeding set-up is given in the electronic supplementary material, figure S1. 168 169

All females had been brooded in the mouth of their mothers until independently feeding and
were then raised apart from their mothers. In the data analyses we have included all spawning
wild type and F1 females and the 69 F2 females which spawned ≥5 times in the experiment.
Spawning decisions of females with ≤4 spawning decisions are given in the electronic
supplementary material (figure S3 and table S1) and were also used in the calculations of
paternal and brood effects.

176

177 Mate choice

Mate choice was tested using a "partial partition" design [24]. An aquarium measuring L 600 178 179 cm x W 80 cm x H 40 cm was divided into ten equally-sized compartments by plastic grids, 8 180 containing one male each, 4 of each species. Identical halved flower pots (D = 270 mm, L =220 mm) served as the focal point in male territories. Two chambers were accessible to 181 females only. We used several males of each species to decrease the chance that effects of 182 183 individual variation in male attractiveness could override female mating preferences for males of one species or the other. The mesh size of the plastic grids was adjusted to confine males in 184 185 their compartments, but to allow the smaller females to pass through. The complement of males was replaced every second month and the female-only compartments were relocated. In 186 total, 11 wild caught and 8 lab-bred P. sp. "pundamilia-like" males and 11 wild caught and 6 187 laboratory-bred P. sp. "nyererei-like" males were used in the experiment (Electronic 188 189 supplementary material table S3). Wild type females were tested as a control that species-190 specific mating preferences would be expressed in this setup. All females were tested with 191 wild type males; hybrid males were not used in these experiments. 192

To test whether experience altered mating preferences, 16 F2 females that had spawned 6
broods each and whose preferences were hence known were isolated in a tank with a male of

the non-preferred species. The 5 *P*. sp. "pundamilia-like"-preferring females had spawned 90100% with *P*. sp. "pundamilia-like" (mean= 98 %), and the 11 *P*. sp. "nyererei-like"preferring females had spawned 83 –100% with *P*. sp. "nyererei-like" (mean= 96 %). The
females that subsequently spawned with a male of the species they had not preferred (N=9)
were allowed to brood fry until final release and potential independence of the fry. Thereafter,
they were released back into the experimental tank and allowed to spawn again with a choice
of males.

202

203 All experimental fish were marked with PIT tags and a small piece of the dorsal fin was cut to

204 provide a DNA sample. Females with eggs were placed in a separate aquarium until the eggs

stored in 95% ethanol prior to paternity analyses. All females were released back into the

207 experimental tank after handling.

208

209 Paternity analyses

210 The experiment lasted 2.5 years. Five embryos from each brood were genotyped at 2-5 211 microsatellite loci, Ppun5, Ppun7, Pun17, Ppun21 and Ppun32. Methods for DNA extraction 212 and PCR reactions were as described previously [33] with additional optimizations for multiplex analyses. The amplified DNA samples were genotyped on a Beckman Coulter CEO 213 214 8000 capillary sequencer. Genotypes were received from the CEQ 8000 Series Genetic 215 Analysing System 8.0.52. Paternities were determined by direct inspection of the allele size 216 estimates on a spreadsheet, and males that possessed two alleles in a microsatellite locus that 217 were not present in the offspring were excluded as a possible father (electronic supplementary material, table S1-S4). We used the number of spawning decisions in figures and statistical 218 calculations i.e. if a brood was confirmed to be fathered by more than one male each male was 219

220	considered to be a spawning decision. F2 females in the analysed data had 4-8 broods each
221	and 5-15 spawning decisions. The complete datasets of the wild type females, F1 hybrid
222	females, F2 hybrid females and the males used in the experiment are included in the
223	electronic supplementary material, figure S2-3 and table S1-S4. We also provide pictures of
224	the F2 males from PN1-33 in figure S4.
225	
226	Statistics
227	When analysing between-group preferences (P. sp. "pundamilia-like vs. P. sp. "nyererei-
228	like"; F1 hubrid females with P. sp. "pundamilia-like" mother vs. F1 hybrid females with P.
229	sp. "nyererei-like" mother), we, for each female, subtracted the number of spawning decisions
230	with males of <i>P</i> . sp. "nyererei-like" from the number of spawning decisions with males of <i>P</i> .
231	sp. "pundamilia-like" and analysed the differences with Mann Whitney U-tests.
232	
233	Within-group preferences were analysed with Wilcoxon signed ranks tests on the individual's
	Within-group preferences were analysed with Wilcoxon signed ranks tests on the individual's number of spawning decisions with <i>P</i> . sp. "pundamilia-like" and <i>P</i> . sp. "nyererei-like". In one
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233 234	number of spawning decisions with <i>P</i> . sp. "pundamilia-like" and <i>P</i> . sp. "nyererei-like". In one
233 234 235	number of spawning decisions with <i>P</i> . sp. "pundamilia-like" and <i>P</i> . sp. "nyererei-like". In one F1 family, a binomial test was used due to the low number of spawning decisions per female.
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233 234 235 236 237	number of spawning decisions with <i>P</i> . sp. "pundamilia-like" and <i>P</i> . sp. "nyererei-like". In one F1 family, a binomial test was used due to the low number of spawning decisions per female. The preference of individual F2 hybrid females were also analysed with binomial tests. We could not estimate individual female preferences of wild type and F1 hybrid females given the
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express the level of deviation from randomness, we calculated the consistency of an

individual's mate choice and calculated the repeatability (R) of a female's spawning 245 246 decisions. In quantitative genetics, the repeatability can be used to determine the upper-bound estimate of the broad sense heritability ($H^2 = V_G/V_P$) [p. 136-138, 37]. The broad sense 247 heritability indicates the relative proportion of total phenotypic variation of a trait (V_P) that 248 249 has a genetic basis (V_G). Repeatability is an upper-bound estimate of this heritability, given that similarity in a trait value (in this case, consistent preference for males of one of the two 250 251 species) can both have a genetic and an environmental basis (e.g. a given female may prefer 252 males of a given species due to previous experiences). The model assesses the extent to which 253 a female's first spawning decision can predict her subsequent decisions, as this informs us on 254 how strong a mate preference has been expressed. In other words, the model assesses how significantly the pattern of spawning decisions deviates from a random pattern (i.e. no 255 256 preference) when analysed across all F2 females at the population level. In the simulations, each female is given a probability of mating with a Pp or a Pn male equivalent to the 257 258 proportion of P. sp. "pundamilia-like" and P. sp. "nyererei-like" spawning decisions 259 observed. This probability determines her first spawning decision. However, once a female has been allocated a mate preference, the strength with which this preference continues to 260 affect subsequent spawning decisions is given by the following formulae: 261 262

$$P(x_i = Pp) = Pp + R(1 - Pp)$$
$$P(x_i = Pn) = Pn + R(1 - Pn)$$

263

Here, $P(x_i = Pp)$ and $P(x_i = Pn)$ are the probabilities of spawning with a *Pp* and a *Pn* male at the *i*th spawning decision (*i* > 1), and *Pp* and *Pn* are the observed proportions of spawning decisions (across the entire population) with a *P*. sp. "pundamilia-like" and a *P*. sp. "nyererei-like" male, respectively. *R* is the repeatability coefficient ($0 \le R \le 1$). With *R*=0,

spawning is "random" and proportional to the observed proportion of *Pn* and *Pp* spawning 268 decisions. In this case, female choice will switch randomly between Pp and Pn males. With 269 R=1, however, spawning choice is fixed and all spawning decisions are for males of the same 270 species as the first choice. In this case, females will consistently choose either a Pp or a Pn271 272 male. With intermediate values of R, there is a preference for a species of male, but this preference will not completely determine a spawning decision. 273

274

275 Furthermore, we also calculated if the number of individuals with preference for one species differed from random. When categorizing female preference for males of either one of the two 276 277 species we used binomial tests and $\alpha = 0.05$ for the data set that included females with >6 spawning decisions. 278

279

To address potential parental and brood effects, all 100 F2 females were divided into two 280 categories: majority of spawnings with P. sp. "pundamilia-like" and majority of spawnings 281 with P. sp. "nyererei-like". Four females were omitted because they spawned equally many 282 283 times with males of the two species leaving 96 females (see the electronic supplementary material figure S3). We used Binomial tests to ask if the female offspring of each of the three 284 F1 fathers were biased in their spawning decisions towards one of the two species, and γ^2 to 285 test if there was a difference between F2 females fathered by different F1 males. When 286 analysing the brood effect we restricted the analyses to the 9 broods with \geq 4 F2 females and 287 performed 36 pairwise Fisher exact test comparisons and Bonferroni correction to correct for 288 289 multiple comparisons.

290

Statistics were performed in SPSS v. 23. The individual-based model was constructed in 291 Minitab 12.1. 292

294 Ethics

- 295 This work was ethically reviewed and performed under a UK Government Home Office
- 296 Licence (PPL 60/3295).
- 297
- 298 Results
- 299 Wild type females spawned with their own species
- 300 There was a significant difference in spawning decisions between females of the two species
- 301 (Mann Whitney U test, n = 20, U = 0.00, p < 0.001, the electronic supplementary material
- figure S2a). The *P*. sp. "pundamilia-like" females had 1-3 spawning decisions each (median
- 2), and 14 out of 15 spawned only with conspecific males. One female mated once with *P*. sp.
- "'nyererei-like" and twice with conspecific males (Wilcoxon signed ranks test T = 0, n = 15, p
- 305 <0.001). The P. sp. "nyererei-like" females also had 1-3 spawning decisions each (median 3),</p>
- and all 6 spawned only with conspecific males (Wilcoxon signed ranks test T = 0, n = 6, p = 0
- **307** 0.024).
- 308

309 F1 hybrid females generally spawned with the species of their mother

- 310 There was a significant difference in spawning decisions between the two F1 families (Mann
- 311 Whitney U test, n = 16, U = 2.50, p = 0.002, the electronic supplementary material figure
- S2b). This was caused by F1 hybrid females spawning more often with the species of their
- mothers (*P.* sp. "pundamilia-like" mother, 2-3 spawning decisions per female, median 2; 2
- females spawned with both species, 9 with P. sp. "pundamilia-like" only, N = 11, Wilcoxon
- signed ranks test, z = 45, p = 0.004, *P*. sp. "nyererei-like" mother, 1 spawning decision each,
- all spawned with *P*. sp. "nyererei-like", two tailed Binomial test, n = 5, p = 0.063).
- 317

318 F2 hybrid spawning consistency suggests innate mating preference

319 When including females with ≥ 6 spawning decisions and $\alpha = 0.05$, 41 out of 59 F2 females had a significant preference for males of one of the two species, whereas we would have expected 320 <3 if females mated randomly (Fisher exact test, p<0.001; figure 1). The simulation model 321 322 showed that the pattern of spawning decisions significantly deviated from a random pattern when analysed at the population level. Spawning preferences segregated in an almost 323 324 Mendelian fashion and the majority of the females repeatedly spawned with one of the two 325 species (figure 1). The model estimates a repeatability of spawning decisions of R=0.7 (figure 326 2), which indicates that in our F2 population, 70% of the variation in spawning decisions is 327 explained by actual female mate preference. 328 To address potential parental effects, all 100 F2 females (the electronic supplementary 329 material figure S3) were divided into two categories: majority of spawnings with P. sp. 330 331 "pundamilia-like" and majority of spawnings with P. sp. "nyererei-like". The female offspring of the 3 F1 males were not significantly biased towards preferring either of the two 332

species (16:27, 12:16 and 11:14, Binomial tests p=0.072, p=0.57 and p=0.69) and there was

no difference in ratios between the offspring of the 3 males (χ^2 =0.384, df=2, p=0.82). The

experimental design of the present study did not allow us to confidently rule out that females

from different broods differed in preferences, because most broods were small. However, the

data rule out a general maternal effect. When restricting the analyses to broods with ≥ 4

females, 4 out of 36 pairwise comparisons between broods yield p < 0.05 with the lowest p

being p=0.015. All these are far from significant when correcting for multiple comparisons.

340 Furthermore, while their F2 brothers show considerable colour segregation within broods,

341 there is no indication of a strong correlation between a female's preference and the colour

342 phenotype of her brothers (electronic supplementary material figure S4).

344 There is no sign of copying of previous choice

Only 26 out of the 69 F2 females with ≥ 5 spawning decisions spawned with both species. Of
those females, 21 switched back and forth between species (figure 1). This demonstrates that
females do not simply copy their first mate choice or their most recent choice. In other words,
the high repeatability of mate choice decision is unlikely to be the result of copying a previous
choice.
Six of the 16 F2 females with a significant mating preference, which were enclosed with a

male of the non-preferred species, did not spawn at all, and one female that did spawn, did not
spawn again when reintroduced to the large choice experiment tank. The nine females that
had spawned in the no-choice situation against their preference and subsequently spawned
again in the choice experiment, all reverted to spawning with males of the previously
preferred species (*P*. sp. "pundamilia-like" preferring N=3, *P*. sp. "nyererei-like" preferring
N=6, Two tailed Binomial test p = 0.004) which highlights the innate strength of female mate
preference.

359

360 Discussion

The genetics of female mate preferences is likely to affect evolutionary processes, including speciation and hybridisation between species. We report a long term common garden study where we followed spawning decisions of F2 hybrid females between two sympatric sister species throughout a large part of their reproductive lives as well as spawning decisions of F1 hybrid females. Wild type females of both species were used as a control.

Using molecular paternity testing, our experiments indicated that wild-type females mostly 367 mated with conspecific males, although mating was not 100% assortative. This is consistent 368 with the results of previous studies on the same population using mating experiments [30] or 369 behavioural preference assays [9, 30, 42, 43], and indicates that either method can be used 370 371 reliably to estimate preferences. The occasional disassortative mating is also consistent with modelling based on population genomic data suggesting ongoing gene flow between the same 372 373 sympatric species in nature, as well as between allopatric populations [19]. 374 All F1 hybrid females mated with their maternal species, although a couple of them also 375 376 mated with the paternal species. This bias towards the maternal species is consistent with an 377 effect of imprinting, which had previously been demonstrated in Lake Victoria haplochromines using controlled cross-fostering experiments with mate preferences assayed 378 with a behavioural choice test [44, 45]. Our results are, however, also consistent with the 379 380 possibility that genes influencing species-specific preferences were not entirely reciprocally fixed between the wild-type individuals used to breed our F1 hybrids, e.g. as a result of 381 382 occasional introgression [19, 26]. It is not impossible that one of the parents of our two test F1 383 families may have been heterozygous at a mate preference locus, and that thus some of the F1 hybrid females were homozygous. 384 385 By contrast, the experimental design limited the potential for any imprinting of species-386 specific preferences in F2 hybrids, since their mothers were all F1 hybrids. Furthermore, we 387

found that siblings in most families exhibited consistent preferences for males of different

species, which is inconsistent with imprinting. Likewise, our experimental test of the

390 preferences of females following a 'no-choice' mating with the non-preferred male species

indicated that females retained their original preferences in a subsequent free choice

392 experiment, suggesting that experience did not disrupt their innate preferences. In general, 393 many F2 hybrid females were consistent in choosing males of a particular species, with 41 out of 59 females showing a significant preference, far more than the 3 expected if females had 394 mated by chance. This clear nearly Mendelian segregation in spawning preferences in the F2 395 396 generation is consistent with previous behavioural choice tests by Haesler and Seehausen [9]. The Mendelian segregation despite incomplete genetic isolation [17, 19, 26] and 397 398 recombination (J. Meier and O. Seehausen, unpublished data) in this species pair in the wild 399 implies that species-specific female mate choice among the *Pundamilia* sister species is 400 influenced by relatively few major genes or genomic regions containing several tightly linked 401 loci.

402

403 Repeatability and the heritability of mate choice

404 Our simulation indicated that the distribution of spawning decisions over F2 hybrid females 405 deviated significantly from expectations if mating was random when analysed at the population level. A large excess of females showed a significant preference for males of either 406 407 one of the two species. Female choice of certain type of males within a species often has low 408 repeatability and is subject to change depending on e.g. experience, age, condition, mate copying and the environment [46-48]. In our experiment, repeatability of spawning decisions 409 410 of F2 hybrid females was high (70%) and preferences did not change over time and over 411 successive reproductive cycles of females, nor after the experience of a successful spawning 412 event with a male of the non-preferred species. Repeatability is also often used to determine the upper-bound estimate of the broad sense heritability (H^2) in behavioural studies [46, 47]. 413 The results from our simulation therefore suggest that up to 70% of the variation in spawning 414 decisions observed among the F2 hybrid females may have a heritable basis. However, the 415 remaining 30% could simply be due to lack of a consistent preference in the class of 416

417 preference heterozygote F2 hybrid females – these are expected to mate randomly [9].

Therefore, heritability may be higher than the estimated 70% [9, 49]. In the experimental

design, we aimed to minimize environmental variation introduced by differences in condition

420 between males by providing a choice among eight males, four of each species in each trial.

421 Differences in territory quality were unlikely in the standardised conditions of our experiment.

422 Thus, we conclude that the observed among-female variation in preference is likely to be due

423 to genetic factors.

424

425 Sexual isolation by mate choice

426 Behavioural reproductive isolation is of key importance to understanding the rapid evolution

427 of genetically differentiated sympatric species [1, 41, 50], such as those in African cichlid fish

radiations. The species pair that we studied here has been estimated to have arisen in just

slightly more than 150 generations, facilitated by hybridisation between the local *P*.

430 *pundamilia* and migrants of *P. nyererei* from around Makobe island [19].

431

432 The male trait (red dorsum vs. blue colour) that species-assortative female mating preferences 433 are based on [30] is likely oligogenic itself [31]. Theoretical work suggests that it is easier for divergent selection to overcome homogenizing gene flow if traits under divergent selection 434 435 are due to relatively few genes, because the fewer genes that are responsible for a trait under 436 divergent selection, the higher are the selection coefficients for each locus [51-53]. Hence, the 437 genetic architecture of mate choice and mating traits in *Pundamilia* may facilitate speciation 438 in the face of gene flow, perhaps in combination with other selection pressures, as might be 439 generated by adaptation to divergent microhabitats, particularly water depths: field studies have shown that red dorsum males tend to be found in deeper water than the blue males [26]. 440

442 Candidate genes for mate choice

443 Candidate genes relating to species-specific mate preferences are likely to include those

444 affecting vision. Divergence has been shown in the long wavelength sensitive opsin gene

445 (LWS) [26]. In the red vs. blue species pair at Makobe Island, there is also divergence in the

short wavelength sensitive opsin gene (SWS2A) but this is not currently known in the species

447 pair of the present study [26]. At Makobe Island, there is also divergence in other putative

448 coding regions [18], some of which may be related to vision.

449

450 Many small genomic 'islands of differentiation' were found to differentiate *P. pundamilia* and

451 *P. nyererei* from Makobe Island [18]. However, the Python Island species pair having

452 recently (around 150 generations ago) re-emerged after a period of massive introgression

453 might be expected to be divergent at fewer regions, more directly related to divergent

454 selection pressures, which should make traits directly related to reproductive isolation easier

to detect. Malinsky et al. [54] identified several genomic regions with high differentiation in

456 two young ecomorphs of crater lake haplochromine cichlids (genus Astatotilapia) with partial

457 assortative mating. Candidate adaptive genes in these so called 'genomic islands of

458 differentiation' included rhodops in and other twilight-vision-associated genes. Differentiation

in such 'islands' can resist ongoing gene flow, as shown in < 150 year old incipient

460 *Gasterosteus* stickleback species pairs in two Swiss lakes [55, 56].

461

462 To conclude

463 We show in a common garden long term mating experiment that strong female mating

464 preferences for males of either one of two sister species are recovered in large fractions of the

465 F2 hybrid generation. The genetic assays of mate choice in F2 hybrids between *P*. sp.

466 "pundamilia-like" and P. sp. "nyererei-like" show high repeatability and consistency in

467	female choice across many reproductive cycles, and we argue that the variation is influenced
468	by the segregation of a few genes with large effects. We propose that a simple genetic basis
469	could help facilitate stable phenotypic differentiation in sympatry in the face of gene flow.
470	
471	Data accessibility
472	The complete datasets of the wild type, F1 and F2 females, and the males used in the
473	experiment are included in figure 1 and the electronic supplementary material, figure S2-3
474	and table S1-S4. The raw data in the electronic supplementary material, table S1-S4 are also
475	available from the Dryad Digital Repository <u>http://dx.doi.org/10.5061/dryad.q58hr[</u> 57]. The
476	Minitab 12.1 macro to test the repeatability of mate choice is deposited at GitHub
477	https://github.com/Ward9250/FishSpawn
478	
479	
480	Authous? contribution
400	Authors' contribution
480	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments,
481	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments,
481 482	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments,
481 482 483	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments, O.Sv. carried out microsatellite paternity analyses and processed the data, C.v.O. wrote the
481 482 483 484	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments, O.Sv. carried out microsatellite paternity analyses and processed the data, C.v.O. wrote the simulation model, O.Sv. and C.v.O. analysed the data, O.Sv. wrote the manuscript with
481 482 483 484 485	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments, O.Sv. carried out microsatellite paternity analyses and processed the data, C.v.O. wrote the simulation model, O.Sv. and C.v.O. analysed the data, O.Sv. wrote the manuscript with important contribution from C.v.O, G.F.T. and O.Se. All authors have provided critical
481 482 483 484 485 486	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments, O.Sv. carried out microsatellite paternity analyses and processed the data, C.v.O. wrote the simulation model, O.Sv. and C.v.O. analysed the data, O.Sv. wrote the manuscript with important contribution from C.v.O, G.F.T. and O.Se. All authors have provided critical
481 482 483 484 485 486 487	G.F.T. and O.Se. conceived the project, O.Sv., G.F.T. and O.Se. designed the experiments, K.W. and A.S. carried out the crosses, O.Sv., K.W. and A.S. performed the experiments, O.Sv. carried out microsatellite paternity analyses and processed the data, C.v.O. wrote the simulation model, O.Sv. and C.v.O. analysed the data, O.Sv. wrote the manuscript with important contribution from C.v.O, G.F.T. and O.Se. All authors have provided critical revision of the manuscript and approved the final version.

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503

504 **References**

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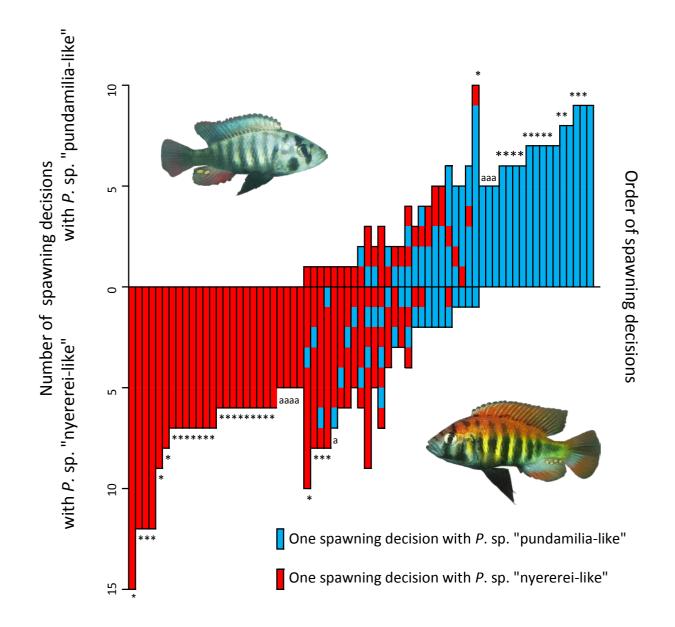
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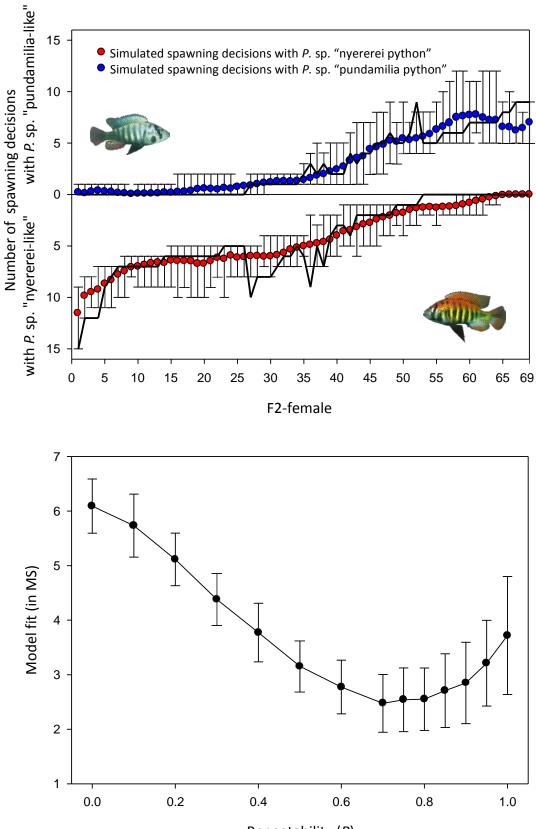
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672	Figure 1. Individual spawning decisions by the 69 F2 hybrid females. Spawning decisions
673	were determined by microsatellite DNA paternity analyses. Above the line y=0 is the number
674	of spawning decisions with P. sp. "pundamilia-like", and below the line is the number of
675	spawning decisions with P. sp. "nyererei-like". The order of spawning decisions is arranged
676	with the first spawning on the top, and the last on the bottom with a spawning decision with
677	<i>P</i> . sp. "pundamilia-like", marked in blue and a spawning decision with <i>P</i> . sp. "nyererei-like"
678	marked in red. *p<0.05, ^a 0.05 <p<0.1.< td=""></p<0.1.<>

681	Figure 2. (A) Simulated (means and 5-95% error bars) spawning decisions of F2 females with
682	P. sp. "pundamilia-like" (blue dots), and with P. sp. "nyererei-like" (red dots) based on a
683	repeatability of an individual's spawning decision of $R=0.7$. Observed ratio of spawning
684	decisions is shown by the solid black lines. (B) The best fit of the model is with $R=0.7$, which
685	minimises the mean squares (MS) between the observed and simulated spawning distribution.
686	Lower values of R produce a more random spawning pattern, whilst higher values of R
687	increase the consistency of a females' spawning choices above those observed, which reduced
688	the fit of the model by inflating the MS.





Repeatability (R)