1	Postcopulatory inbreeding avoidance in guppies
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23 Abstract

In many species the negative fitness effects of inbreeding have facilitated the 24 evolution of a wide range of inbreeding avoidance mechanisms. While those 25 operating prior to mating are well documented, evidence for postcopulatory 26 mechanisms of inbreeding avoidance remain scarce. Here, we examine the potential 27 for females to bias paternity in favour of unrelated males though postcopulatory 28 inbreeding avoidance mechanisms in the guppy, Poecilia reticulata. To test this 29 30 possibility, we used a series of artificial inseminations to deliver an equal number of sperm from a related (either full sibling or half sibling) and unrelated male to a female 31 while statistically controlling for differences in sperm quality between rival ejaculates. 32 This approach has the twofold advantages of (i) removing precopulatory processes 33 that can bias paternity and (ii) accounting for differences in sperm number and quality 34 between competing males. In this way we were able to focus exclusively on 35 postcopulatory mechanisms of inbreeding avoidance and account for differences in 36 sperm competitiveness between rival males. Under these carefully controlled 37 conditions, we report a significant bias in paternity towards unrelated males, although 38 this effect was only apparent when the related male was a full sibling. We also show 39 that sperm competition generally favours males with highly viable sperm, and thus 40 that some variance in sperm competitiveness can be attributed to difference in sperm 41 quality. Our findings for postcopulatory inbreeding avoidance are consistent with 42 prior work on guppies revealing that sperm competition success declines linearly with 43 the level of relatedness, but also that such effects are only apparent at relatedness 44 levels of full siblings or higher. Our study reveals evidence that postcopulatory 45 processes offer an effective mechanism of inbreeding avoidance. 46

- **Keywords:** sexual selection; relatedness; cryptic female choice; sperm competition;
- 48 genetic compatibility.

49 Introduction

Reproduction among close relatives can dramatically reduce offspring viability and 50 fitness, a phenomenon known as inbreeding depression (Charlesworth and 51 Charlesworth 1999; Keller and Waller 2002). To reduce the costs associated with 52 inbreeding, many species exhibit a wide range of inbreeding avoidance mechanisms. 53 For example, precopulatory mechanisms of inbreeding avoidance, such as dispersing 54 away from natal territories and/or recognizing kin, can represent effective methods 55 56 for reducing the likelihood of inbreeding (Pusey and Wolf 1996). However, postcopulatory inbreeding avoidance mechanisms can also evolve, particularly when 57 the risks and costs of inbreeding are high, precopulatory inbreeding avoidance 58 mechanisms are absent (e.g. Pitcher et al. 2008; Tan et al. 2012), or when 59 precopulatory processes can be undermined through forced matings (Kokko and Ots 60 61 2006). Thus, polyandrous females may avoid inbreeding depression by engaging in postcopulatory cryptic female choice to bias fertilizations towards unrelated males 62 (Stockley et al. 1993; Zeh and Zeh 1996; 1997). 63

Postcopulatory inbreeding avoidance mechanisms may bias paternity in favour 64 of genetically dissimilar males during competitive fertilizations. Accordingly, when 65 inseminated with sperm from both related and unrelated males, cryptic female choice 66 is thought to bias fertilization success towards unrelated males (Bishop 1996; Bishop 67 et al. 1996; Olsson et al. 1996; Wilson et al. 1997; Stockley 1999; Kraaijeveld-Smit et 68 al. 2002; Mack et al. 2002; Thuman and Griffith 2005; Jehle et al. 2007; Firman and 69 Simmons 2008; Brekke et al. 2012, but for counter examples see Kleven et al. 2005; 70 Sherman et al. 2008; Evans et al. 2008; Ala-Honkola et al. 2010; 2011). 71 72 Mechanistically, females can bias paternity by influencing the number of sperm

accepted during mating (or stored following insemination) in favour of unrelated 73 males (Pizzari et al. 2004; Welke and Schneider 2009; Bretman et al. 2004; Ala-74 Honkola et al. 2010; Tuni et al. 2013), or though interactive effects, for example 75 between ovarian fluid and sperm performance, that differentially influence sperm 76 quality in favour of unrelated sperm (Gasparini and Pilastro 2011; Butts et al. 2012). 77 Despite promising support for the idea that cryptic female choice 78 moderates inbreeding avoidance, very few studies have been able to exclude the influence of 79 precopulatory inbreeding avoidance mechanisms (Pusey and Wolf 1996), or 80 alternative postcopulatory processes, such as differential sperm allocation or 81 investment by males based on genetic relatedness (Pizzari et al. 2004; Fitzpatrick et 82 al. 2014). Moreover, most studies of postcopulatory inbreeding avoidance do not 83 account for differences in sperm quality (i.e. sperm traits such as swimming speed, 84 85 viability and morphology that predict fertilization success, Simmons and Fitzpatrick 2012) between competing males. Indeed, only a single study (Denk et al. 2005), which 86 failed to detect an effect of genetic relatedness on competitive fertilization success, 87 controlled for differences in sperm quality between competing males when assessing 88 postcopulatory inbreeding avoidance mechanisms. Consequently, examining the 89 90 potential for postcopulatory inbreeding avoidance requires both the influence of cryptic female choice and sperm competition to be assessed simultaneously within an 91 experimental framework that separates pre- from postcopulatory inbreeding 92 avoidance mechanisms. 93

The guppy, *Poecilia reticulata*, is ideally suited to studies of postcopulatory inbreeding avoidance. Guppies are internally fertilizing, live-bearing freshwater fish characterized by high levels of polyandry (Neff et al. 2008; Evans and Pilastro 2011). In

their native tropical freshwater streams, guppies are likely to suffer periodic or 97 sustained periods of elevated inbreeding risk, as small populations can often become 98 isolated as water levels recede during the dry season (Griffiths and Magurran 1997). 99 Indeed, molecular data indicate that as many as 16% of randomly chosen pairs of 100 101 guppies in a Trinidadian stream reached levels of relatedness higher than those of half-siblings (Hain and Neff 2007). Moreover, inbreeding depression can be severe in 102 guppies, and studies have shown that inbred offspring have reduced survival 103 (Nakadate et al. 2003), vertebral deformities (Shikano et al. 2005), reduced 104 reproductive rates (Zajitschek and Brooks 2008), and for males, reduced courtship, 105 sexual colouration, sperm counts and semen quality (van Oosterhout et al. 2003; 106 Mariette et al. 2006; Zajitschek et al. 2009). However, despite the high potential for 107 inbreeding in wild populations, and associated costs, adult female guppies do not 108 109 appear to practice precopulatory inbreeding avoidance through active mate choice (Viken et al. 2006; Pitcher et al. 2008; Zajitschek and Brooks 2008). Instead, 110 polyandry, coupled with forced copulations by males (Magurran and Seghers 1994; 111 Pilastro and Bisazza 1999), suggest that females may have to rely on postcopulatory 112 inbreeding avoidance mechanisms (Gasparini and Pilastro 2011). 113

Here, we examine if genetic relatedness influences a males' competitive fertilization success using an established artificial insemination protocol (Evans et al. 2003) to assess the potential for postcopulatory processes to influence relative paternity of related and unrelated males. Artificial insemination effectively uncouples pre- from postcopulatory inbreeding avoidance mechanisms and allows for rigorous control over sperm numbers between competing males, mating order effects, and differential sperm retention by females, all of which have the potential to influence

competitive fertilization success in guppies (Evans and Magurran 2001; Pilastro et al.
 2004). In addition, our protocol accounts for differences in components of sperm
 quality (e.g. velocity and viability) between rival males when assessing postcopulatory
 inbreeding avoidance mechanisms.

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126 Methods

127 **Experimental animals and breeding protocols**

128 Experiments were performed on captive-bred guppies that were descendants (9-12 generations) of wild-caught fish collected from Alligator Creek in Queensland, 129 Australia. Stock populations were maintained in eight independent mixed-sex holding 130 tanks, each containing ~300-400 guppies. To minimize inbreeding in the stock 131 populations, random subsets of fish are transferred among holding tanks on a yearly 132 133 basis. Full and half siblings were generated by randomly pairing a sexually mature 134 male from one holding tank sequentially with two unrelated virgin females who originated from different holding tanks. Males and females were housed together for 135 a five-day mating period in a 3L tank, after which males were removed from the tank 136 and transferred to another 3L tank for a subsequent five-day mating period. Following 137 the mating period, females were left undisturbed until broods were produced. This 138 breeding protocol was repeated for 40 independent replicates (called 'family' 139 hereafter). Offspring from each family were separated by sex at the earliest sign of 140 141 sexual differentiation (when the male intromittent organ begins to develop) and reared in sex-specific family groups until reaching sexual maturity. The intention of 142 this breeding design was to generate full and half male siblings for each family. 143 144 However, due to a range of factors, including small brood sizes, the production of

mono-sex broods, the apparent absence of breeding and/or fertilizations during the 145 mating period in some pairs, unsuccessful artificial inseminations, or a combination of 146 these factors, we lacked sufficient replicates to evaluate both levels of relatedness for 147 every family. Instead, we divided the families into two groups: a focal virgin female 148 was either artificially inseminated with sperm from an unrelated male (R₀) and a full 149 sibling $(R_{0.5})$ $(R_{0.5} + R_0; n=16)$, or with sperm from an unrelated male (R_0) and a half 150 sibling $(R_{0.25})$ $(R_{0.25} + R_0; n=14)$. For all artificial inseminations, the unrelated male was 151 152 chosen randomly from a different family generated through the breeding protocol described above, thus ensuring all males were housed in similar conditions. However, 153 this design meant that some families (but not individuals from these family) were 154 represented in both the full and half sibling treatments, which we account for in the 155 statistical analyses (described below). 156

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158 Sperm collection

Male guppies produce sperm bundles (spermatozeugmata) that are easily collected 159 manually (Matthews et al. 1997; Evans et al. 2003). Briefly, sexually mature males 160 were anaesthetized and placed on a glass slide under low-power magnification (Evans 161 2009). The ventral side of each male was dried before 60 μ l of an extender medium 162 (207 mM NaCl, 5.4 mM KCl, 1.3 mM CaCl2, 0.49 mM MgCl2, 0.41 mM MgSO4, and 10 163 164 mM Tris with pH 7.5) was pipetted to the base of the male's gonopodium. The use of the extender medium ensured that sperm remained quiescent prior to analyses 165 (Gardiner 1978). Gentle pressure was applied to the male's abdomen to release 166 sperm bundles into the extender solution. For each male (R_{0.5}, R_{0.25} and R₀) sperm 167 bundles were subdivided into four separate aliquots: 10 sperm bundles were 168

169 collected for artificial inseminations, 2-4 sperm bundles were collected for sperm 170 velocity analyses, 10 bundles were collected to assay sperm viability and the 171 remaining sperm bundles were used to assess sperm morphology. The order of sperm 172 collection was randomized based on relatedness for each competitive dyad to avoid 173 stripping order effects.

174

175 Artificial inseminations

Ten sperm bundles from each of the two rival males in each trial (i.e. $R_{0.5}$ + R_0 and $R_{0.25}$ 176 + R_0) were added to an Eppendoff tube in 20 μ l of extender solution and gently mixed 177 to ensure a homogenous distribution of sperm bundles. Because each sperm bundle 178 contains ~2.7 x 10⁵ sperm cells, performing competitive fertilization experiments with 179 an equal number of sperm bundles from each male effectively controls for differences 180 181 in sperm number between males (Evans et al. 2003). The mixed sperm bundles were taken up by a Drummond[®] microdispenser and artificially inseminated into an 182 anaesthetised virgin focal female viewed under low-power magnification. Fin clip 183 samples from females and males were collected and stored in absolute ethanol for 184 subsequent paternity analyses. Females were left undisturbed in 3L tanks for ~10 185 weeks, during which up to two broods per female were obtained for paternity 186 analyses. Offspring were euthanized within 48 hours of birth and placed in absolute 187 ethanol for subsequent molecular analyses (sample sizes are reported below). 188

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190 Sperm quality analyses

Sperm quality was assessed for each male by quantifying sperm swimming speed,
viability, and morphology. These are biologically important measures of sperm quality

that are associated with fertilization success in non-competitive and competitive 193 fertilizations in guppies and other taxa (reviewed by Simmons and Fitzpatrick 2012). A 194 3 µl aliquot of the extender medium containing two sperm bundles was placed on an 195 individual well of a 12-cell multi-test slide (MP Biomedicals, Aurora, OH), previously 196 coated with 1% polyvinyl alcohol to reduce sperm sticking to the glass (Wilson-Leedy 197 and Ingermann 2007). These quiescent sperm samples were then activated with 3 µl 198 of a 150 mM KCL solution (Billard et al. 1990) containing 2mg/L BSA to further prevent 199 200sperm from sticking to the slide (Pitcher et al. 2007). Computer-assisted sperm analysis (CASA) was used to assess sperm swimming speed for each sample using a 201 CEROS Sperm Tracker (Hamilton Thorne Research, Beverly, MA, USA) under 100x 202 magnification using the threshold values described in Evans (2009). Two sperm 203 velocity measures were determined for each male from different sperm 204 205 subpopulations within a sample and the mean of these values was used for analyses. 206 Sperm velocity measures were based on 68 ± 7.6 (mean \pm SE) motile sperm tracks per sample. CASA produces several highly co-linear measures of sperm velocity (Simpson 207 et al. 2013), including the average path velocity (VAP), which estimates the smoothed 208 path velocity, the curvilinear velocity (VCL), which is the actual velocity of the sperm 209 over the path, and the straight-line velocity (VSL), which measures the distance 210 between the start and end point of the path. To incorporate as much information as 211 possible in our analyses, these co-linear sperm velocity measures were collapsed 212 using principal component analyses (PCA) into a single principal component (PC1) 213 with an eigenvalue of 2.59, which explained 86.4% of the variance in sperm swimming 214 215 speed. PC1 was used as a measure of sperm swimming speed in all analyses (note, 216 however, that we obtained qualitatively similar results when using any of the

individual measures of sperm velocity). We were unable to quantify sperm swimming
speed for one male in the full sibling/unrelated male cross due to an experimental
handling error and consequently removed this replicate from analyses of sperm
quality (see below).

Sperm viability (i.e. the proportion of live sperm in the male's ejaculate) was 221 determined using a live/dead sperm viability assay (Invitrogen, Molecular probes). 222 This assay uses fluorescent dyes that stain live sperm green with the membrane-223 224 permeant nucleic acid stain SYBR-14 and dead sperm red with propidium iodide. Sperm bundles (10 bundles in 20 μ l of the extender medium) were broken up by 225 thoroughly vortexing the sample. A 1:50 dilution of the SYBR-14 (1 mM) stain was 226 added to a 10 µl sample of the sperm/extender solution. Samples were left in the 227 dark for 10 min, followed by the addition of 2 μ l of 2.4 mM propidium iodide and an 228 229 additional incubation in the dark for 10 min. Samples were viewed under a Leica DM 230 1000 fluorescence microscope under 400x magnification and the number of live and dead sperm were counted from 200 sperm per sample as an estimate of sperm 231 232 viability.

To assess sperm morphology, sperm head, midpiece and flagellum length were measured from 20 sperm per male. Sperm were digitally photographed using a Leica DFC320 camera fitted to Leica DM 1000 phase contrast microscope under 400x magnification. Sperm lengths were measured using ImageJ (v1.37) and mean values were used in statistical analyses.

We did not expect any systematic differences in sperm quality measures between related and unrelated males given the breeding protocols outlined above. Nevertheless, we were concerned that any such systematic differences in sperm

quality generated by chance could bias our results. Therefore, we compared each of the sperm traits measured between related and unrelated males to account for any unintentional source of bias in our analyses and found no difference between competing related and unrelated males in any of the sperm traits assessed in this study (Table S1).

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247 Parentage analysis

248Genomic DNA was extracted from adult and offspring tissue samples using a standard salting-out protocol (Patwary et al. 1994). Paternity was determined by scoring up to 249 five polymorphic microsatellite loci that have been optimised previously for guppies: 250 TTA, KonD15, KonD21, Pret46, Pr39 (GenBank accession numbers AF164205, 251 AF368429, AF368430, AB100334 and AF467903, respectively). PCR amplifications 252 253 were performed on a GeneAmp PCR System 2700 Thermocycler (Applied Biosystems, 254 CA, USA) following methods described in Gasparini et al. (2010a). Amplified fragments were separated using an ABI 3100 sequencer (ABI PRISM, Applied Biosystems) and 255 PCR products were visualized using GeneMarker v1.91 (http://www.softgenetics.com). 256 Paternity was assigned to putative fathers, incorporating the known genotype of the 257 mother, using CERVUS v3.0.6 (Kalinowski et al. 2007). A total of 235 offspring were 258 scored (mean ± SE: 7.8 ± 0.9 per female, n=30, range 3-21). Families where only 259 considered in the analyses if more than two offspring were assigned to either of the 260 competing males; this criterion removed one family (consisting of three offspring 261 from the $R_{0.5} + R_0$ male treatment) from the analyses. Our final sample size therefore 262 263 comprised 232 offspring. CERVUS assigned paternity to 93% (n=216) of the offspring 264 at the strict (95%) level of confidence and assigned an additional two offspring (from

one brood) at the relaxed (80%) level of confidence. Our results remained qualitatively similar when we restricted our analysis to include only offspring assigned using the strict confidence level and when we included males assigned at both levels of confidence. Consequently, we only present data from the strict level of confidence. Seventeen offspring, from eight crosses, could not be assigned to either of the putative fathers (i.e. confidence <80%) and were therefore excluded from our analyses.

272

273 Statistical analyses

To determine if paternity differed between related and unrelated males, we used a 274 randomization test to compare the observed paternity share of the unrelated males 275 against a null expectation that assumes relatedness does not bias sperm use (i.e. 276 277 paternity probability = 0.5). Specifically, the observed difference in paternity success 278 between related and unrelated males was compared to the expected difference in paternity success between related and unrelated males for the given brood size under 279 the assumption that competing males had an equal probability of fertilizing eggs. 280 Random binomial probabilities were calculated and resampled 100,000 times to 281 obtain an expected distribution against which the observed binomial distributions 282 from each replicate were tested. Randomization tests were performed for the R_{0.5} + 283 R_0 and $R_{0.25}$ + R_0 crosses separately using an R script written by W. Black. 284

To determine the relationship between sperm quality, relatedness and paternity success we used a generalized linear mixed model (GLMM) with a binomial error distribution and a logit link function. Paternity was coded from the related males perspective, with offspring sired by the related male coded as successes and

offspring sired by the unrelated male coded as failures. All crosses were assessed in a 289 single model with difference in sperm trait values (i.e. sperm head length, midpiece 290 length, flagellum length, swimming speed PC1, and viability) between the related and 291 unrelated male (i.e. relate male sperm - unrelated male sperm traits) in each cross 292 added as covariates, the relatedness level of the related male (i.e. full sibling or half 293 sibling) included as a fixed effect, and all interactions between each of the sperm 294 traits and the relatedness level. To account for the use of individuals from the same 295 296 families in the artificial inseminations at different levels of relatedness we included family identity as a random effect in the model. Attempts to reduce the model by 297 removing non-significant interaction terms degraded the model fit, evidenced by 298 elevated Akaikie weight (AIC) values in the reduced model compared to the full model 299 (full model: df = 14, AIC = 104.50; reduced model: df = 9, AIC = 559.32). Consequently, 300 301 we only consider the full model in the analyses. All analyses were performed in R 302 v3.0.1 (R Development Core Team 2013). GLMM analyses were performed using the glmer function in the lme4 package (Bates et al. 2014). Significant values from the 303 glmer model were calculated from Type II Wald chi square tests using the 'Anova' 304 function in the car package. Overdispersion was assessed using the function 305 overdisp_fun in R, and this analysis revealed that overdispersion was not an issue in 306 the model. 307

308

309 Results

Paternity analyses revealed that fertilization success was skewed towards unrelated males, but only when females were inseminated with sperm from full siblings and an unrelated male competitor (i.e. $R_{0.5} + R_0$). When females were artificially inseminated

with an equal number of sperm from a full sibling and unrelated male, mean (±SE) 313 paternity percentage was 40.6 \pm 8.7% for R_{0.5} males. The mean difference in paternity 314 between R_{0.5} and R₀ males was -18.9% (n = 15, Figure 1), which differs significantly 315 from the null expectation of equal paternity between competing males (random 316 binomial probability, p = 0.038). In contrast, when females were artificially 317 inseminated with sperm from a half sibling and unrelated male, mean (±SE) paternity 318 percentage was 52.2 \pm 6.3% for R_{0.25} males. The mean difference in paternity between 319 $R_{0.25}$ and R_0 males was 4.3% (n = 13, Figure 1), which did not differ from the null 320 expectation (p = 0.35). 321

The paternity skew against related males observed in the R_{0.5} + R₀ treatment could 322 have been generated either by postcopulatory mechanisms of inbreeding avoidance 323 (e.g. cryptic female choice in favour of unrelated sperm) and/or or sperm competition 324 325 (i.e. differences in sperm quality between competing males where sperm quality was 326 consistently higher in unrelated males). To distinguish between these possibilities we determined whether the proportion of offspring sired by the related male (R_{0.5} and 327 R_{0.25}) was influenced by sperm quality while also controlling for the relatedness level 328 of the competing males. Relatedness level and difference in sperm viability between 329 males significantly influenced paternity success of related males in the full and 330 reduced model (Table 1, Figure 2). However, the significant relatedness level x sperm 331 viability interaction terms in the model revealed that while males with greater sperm 332 viability sired more offspring in both relatedness treatments, the effect of sperm 333 viability on competitive fertilization success was influenced by the level of relatedness 334 of male competitors (Figure 2). Specifically, the effect of sperm viability on 335 competitive fertilization success is more pronounced in the full sibling treatment than 336

337 the half-sibling treatment. Compared with the half sibling treatment, full sibling males sired more offspring when they had high sperm viability (relative to unrelated males) 338 and fewer offspring when they had lower sperm viability (relative to unrelated males) 339 in competitive fertilizations (Figure 2). No other sperm quality traits measured 340 predicted paternity success (Table 1). Thus, this analysis supports the paternity results 341 from our randomization tests while demonstrating the importance of considering 342 complex interactions between sperm traits, in this case sperm viability, and levels of 343 344 relatedness when examining paternity success.

345

346 **Discussion**

Our results demonstrate that competitive fertilization success was biased toward 347 unrelated male guppies, but only when females were inseminated with sperm from a 348 349 full sibling (R_{0.5}) and an unrelated male (R₀). In contrast, competitive fertilization 350 success was not influenced by genetic relatedness when females were artificially inseminated with sperm from a half sibling $(R_{0.25})$ and an unrelated male (R_0) . As our 351 experimental design prevented precopulatory mechanisms from biasing paternity and 352 controlled for postcopulatory processes known to influence competitive fertilization 353 success (i.e. mating order effects, differences in sperm number and quality), our 354 results provide strong support for the idea of postcopulatory inbreeding avoidance in 355 guppies. These findings support recent work showing that female guppies use 356 postcopulatory processes to bias paternity towards unrelated males following 357 artificial insemination by full sibling and non-sibling males (Gasparini and Pilastro 358 2011) or highly inbred (four generations of full sibling matings) and outbred males 359 360 (Zajitschek et al. 2009). However, our data also demonstrate that paternity biasing in

guppies is sensitive to the genetic relatedness of the competing males and is only 361 evident in matings involving full siblings (also see Zajitschek et al. 2009). Similar 362 inbreeding avoidance mechanisms appear to be in place in wild populations. For 363 example, Johnson et al. (2010) reported that unrelated males sired more offspring in 364 clutches from multiply mated female Trinidadian guppies, although this field result 365 could have resulted potentially from both pre- and postcopulatory processes. 366 Inbreeding avoidance mechanisms specifically targeting brothers are likely beneficial 367 368 for female guppies as a single generation of full sibling inbreeding can reduce juvenile survival (Nakadate et al. 2003) and delay the onset of sexual maturity (Pitcher et al. 369 2008) and reduce male courtship behaviours (Mariette et al. 2006). Consequently, 370 multiple mating by females coupled with postcopulatory inbreeding avoidance 371 mechanisms likely mitigate inbreeding depression in guppies. 372

373 The extensive use of guppies as a model system for studying postcopulatory 374 sexual selection and inbreeding offers a rare opportunity to evaluate how variance in male relatedness influences inbreeding avoidance exclusively at the postcopulatory 375 level. Together with the present study, seven other studies have used artificial 376 inseminations to assess sperm competitiveness in males of varying levels of 377 relatedness (Evans et al. 2003; Evans et al. 2008; Evans and Rutstein 2008; Zajitschek 378 et al. 2009; Gasparini et al. 2010a; Gasparini and Pilastro 2011; Boschatto et al. 2011). 379 Examining these studies together revealed two important patterns. First, significant 380 biasing of paternity in favour of unrelated males is only observed in artificial 381 inseminations involving relatedness levels of full sibling and above in guppies (e.g. this 382 study, Zajitschek et al. 2009; Gasparini and Pilastro 2011). Second, when we 383 384 combined these studies to examine the relationship between related male paternity

and level of relatedness (see Supporting Information for details), we observed a 385 significant decrease in paternity success of related males as male relatedness to 386 females increased (linear regression: n = 5, r = 0.91, p = 0.03, Figure 3). Thus, in 387 guppies postcopulatory inbreeding avoidance appears to be exaggerated when 388 inbreeding risk is elevated. A similar pattern of reduced paternity of related males 389 with increasing relatedness was observed in Drosophila melanogaster, where full 390 sibling males exhibited lower competitive paternity success than half siblings, cousins 391 392 and unrelated males (Mack et al. 2002; but see Ala-Honkola et al. 2011). Moreover, negative relationships between genetic similarity (i.e. band sharing) between males 393 and females and a males' paternity success in the sand lizard Lacerta agilis (Olsson et 394 al. 1996), ascidian Diplosoma listerianum (Bishop et al. 1996), and the marsupial 395 Antechinus agilis (Kraaijeveld-Smit et al. 2002) also suggest that cryptic female choice 396 397 for unrelated sperm intensifies as relatedness between males and females increases. 398 However, the accumulated evidence from guppies (Figure 3) represents the first evidence for a graded inbreeding avoidance response that can be attributed solely to 399 postcopulatory processes. This graded response may stem from the relative costs and 400 benefits of inbreeding, as females should only avoid inbreeding when the costs are 401 high (i.e. in full sibling matings), while potentially reaping inclusive fitness benefits 402 when the costs are low (i.e. in matings involving relatedness levels of half siblings or 403 lower) (Kokko and Ots 2006). 404

Our analysis accounted for differences in sperm quality between competitors when testing for postcopulatory inbreeding avoidance. However, this analysis also sheds light on how variation in sperm quality among males influences competitive fertilization success. Our results revealed that sperm viability is an important

predictor of competitive fertilization success in guppies, although levels of relatedness 409 of the competing males modulated this effect. Although sperm viability is commonly 410 expected to influence male fertility and to be shaped by sperm competition, there is 411 relatively little evidence that sperm viability influences competitive fertilization 412 success (Simmons and Fitzpatrick 2012). For example, sperm viability predicts 413 competitive fertilization success in the cricket *Teleogryllus oceanicus* (Garcia-Gonzalez 414 and Simmons 2005) and the swordtail Xiphophorus nigrensis (Smith 2012), but in two 415 416 species of frogs (Crinia georgiana and Litoria peronii) sperm viability does not influence male fertility under competitive conditions (Sherman et al. 2008; 2009; 417 Dziminski et al. 2009). Therefore, our findings contribute towards a relatively scarce 418 body of literature revealing the importance of sperm viability during sperm 419 competition. Interestingly, however, the remaining sperm traits assessed in this study 420 421 (sperm morphology and velocity) did not predict sperm competitiveness. This is surprising as sperm viability is negatively genetically correlated with sperm 422 morphology (head, flagellum and total length) in the study population (Evans 2011). 423 Yet, our finding is partially in keeping with recent work on guppies and other poeciliid 424 fishes that did not find an effect of sperm morphology and only weak effects of sperm 425 swimming speed on competitive fertilization success (Gasparini et al 2010b; 426 Boschetto et al. 2011; Smith 2012). Nevertheless, it remains unclear why sperm 427 morphology and swimming speed appear to be unrelated to male fertility in this and 428 other studies of poeciliid fishes, as there is growing evidence that these sperm traits, 429 particularly sperm swimming speed, predict male fertilization success during sperm 430 competition (Simmons and Fitzpatrick 2012). 431

Our results, and those summarized from recent studies of guppies (Figure 3), 432 highlight the importance of postcopulatory inbreeding avoidance mechanisms as a 433 means of mitigating inbreeding. Although we cannot entirely rule out the possibility 434 that differences in ejaculate traits (not measured here) may have contributed towards 435 our findings, we suggest that our results are more consistent with the notion that 436 females exert some form of postcopulatory selection that favours unrelated males. 437 One potential mechanism to account for the paternity biases detected in our study is 438 439 that offspring arising from consanguineous matings (i.e. >R=0.5) exhibit impaired survival compared to those sired by unrelated parents. However, in the case of 440 guppies, this explanation seems unlikely as Gasparini and Pilastro (2011) 441 demonstrated that under non-competitive fertilization conditions females produced 442 equivalent sized broods when artificially inseminated with sperm from full siblings or 443 444 unrelated males. Instead, we suggest that our findings are more likely to be explained 445 by fertilization biases that favour sperm from unrelated males when they compete to fertilize eggs. This conclusion is supported by the previous observation that female 446 guppies exert cryptic female choice via the differential action of their ovarian fluid on 447 the sperm swimming velocity of ejaculates from related and unrelated males 448 (Gasparini and Pilastro 2011). Moreover, Gasparini and Pilastro (2011) showed that 449 under conditions of sperm competition, this differential effect of ovarian fluid on 450 sperm velocity generated a significant bias in paternity in favour of unrelated males, 451 leading them to hypothesize that such effects may be attributable to interactions 452 between peptides in the ovarian fluid and sperm membrane (e.g. major 453 histocompatibility (MHC) peptides). Indeed, the MHC complex mediates fertilization 454 455 success in mice (e.g. Wedekind et al. 1996; Rulicke et al. 1998) and may play a similar

role in guppies. Thus, avenues for future examination would be to experimentally validate the role of MHC in postcopulatory inbreeding avoidance mechanisms in guppies and to assess if the graded response in paternity biasing observed across various levels of relatedness is mirrored by increasing effects of ovarian fluid on sperm performance as relatedness increased. Elucidating the mechanisms driving paternity biasing based on relatedness promises to be both a challenging and stimulating future research endeavour.

463

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729	Table 1. The proportion of offspring sired by related males in relation to differences
730	in sperm traits between the competing males and level of male relatedness.
731	Relatedness refers to the level of relatedness of the related sperm competitor ($R_{0.5}$ or
732	$R_{0.25}).$ Test parameters ($\chi^2)$ and significance levels (p) are generated from generalized
733	linear mixed-effects models. Significant parameter values are presented in bold text.

Parameter	χ ²	р
Sperm head length	2.37	0.12
Sperm midpiece length	1.16	0.28
Sperm flagellum length	1.94	0.16
Sperm viability	14.88	<0.001
Sperm swimming speed (PC1)	0.00	0.99
Relatedness	14.52	<0.001
Relatedness x Sperm head length	1.16	0.28
Relatedness x Sperm midpiece length	0.00	0.99
Relatedness x Sperm flagellum length	0.01	0.91
Relatedness x Sperm viability	10.20	<0.01
Relatedness x Sperm swimming speed (PC1)	1.58	0.21



Figure 1. Proportion of offspring sired (mean \pm SE) by related males when females were artificially inseminated with equal numbers of sperm from a related and unrelated male. Males were related at the level of half sibling (R_{0.25}) or full (R_{0.5}) sibling, resulting in artificial inseminations of half sibling and unrelated male (R_{0.25} + R₀) or a full sibling and unrelated male (R_{0.5} + R₀). The dotted line represents the null expectation of equal paternity between competing males. The * indicates a significant difference in paternity success between males based on randomization tests.



Figure 2. The relationship between the proportion of offspring sired by a half sibling ($R_{0.25}$, grey circle and fit line) or full sibling ($R_{0.5}$, black circle and fit line) male when in sperm competition with an unrelated male and the difference in sperm viability (%) between the related and unrelated males.



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Figure 3. Paternity success (mean ± SE) of focal males in studies where female guppies 756 757 were artificially inseminated with equal numbers of sperm from two unrelated males (R₀ + R₀) or from an unrelated and related male at varying degrees of relatedness (first 758 cousin: R_{0.125} + R₀; half sibling: R_{0.25} + R₀;, full sibling: R_{0.5} + R₀;, four generations of full 759 sibling mating: R_{0.59} + R₀). When females were artificially inseminated with sperm from 760 two unrelated males (R₀ + R₀) the mean paternity success of a randomly chosen male 761 is presented. When females were artificially inseminated with sperm from a related 762 and unrelated male the mean paternity success of the related male is presented. The 763 dotted line represents the null expectation of equal paternity between competing 764

- 765 males. See Supporting Information for details on how data was extracted from
- 766 published work and combined in this analysis.

768 **Postcopulatory inbreeding avoidance in guppies**

- 769 John L. Fitzpatrick and Jonathan P. Evans
- 770

771 Supporting Information

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773 Appendix S1: Additional Methodological Details

Data from the present study and seven other recent studies using artificial 774 inseminations to assess sperm competitiveness in males of varying levels of 775 relatedness were combined. Published studies include: Evans et al. (2003; 2008), 776 Evans and Rutstein (2008), Zajitschek et al. (2009), Gasparini et al. (2010a), Gasparini 777 778 and Pilastro (2011), and Boschatto et al. (2011). In all cases, females were artificially inseminated with equal numbers of sperm from two males, with the focal male in 779 each artificial insemination exhibiting varying levels of relatedness with the female. 780 Sperm competitiveness was assessed from two unrelated males in four studies (R₀ + 781 R₀: Evans et al. 2003; Evans and Rutstein 2008; Gasparini et al. 2010a; Boschatto et al. 782 2011), a first cousin and unrelated male in one study (R_{0.125} + R₀: Evans et al. 2008), a 783 784 half sibling and unrelated male in two studies (R_{0.25} + R₀: this study, Zajitschek et al. 2009), a full sibling and unrelated male in two studies (R_{0.5} + R₀: this study, Gasparini 785 and Pilastro 2011), and males following four generations of full sibling mating and an 786 unrelated male in one study (R_{0.59} + R₀: Zajitschek et al. 2009). In cases where only one 787 study was available we used the mean paternity of focal or related males in our 788 789 analyses. In cases where two or more studies were available we generated a mean values by calculated a sample size weighted mean from each study. When mean 790

- values were not presented in the text but were plotted instead, data was extracted
- 792 from published figures using GraphClick[®] (Ariozona software, <u>http://www.arizona-</u>
- 793 <u>software.ch/graphclick/</u>).

794	Table S1. Comparison between sperm traits of related and unrelated males
795	competing to fertilize eggs in artificial inseminations. Paired t-tests were used to
796	compare sperm traits between the unrelated male in the artificial insemination and
797	the a) related males from the $R_{0.5}$ or $R_{0.25}$ treatments. Differences in sperm traits
798	between the unrelated male and the related male were also examined for the b) $R_{0.5}$
799	and c) R _{0.25} relatedness treatment separately.

Comparison	Sperm trait	t	df	р
a) All males: R _{0.5} and R _{0.25}				
Related vs. Unrelated	Sperm viability	0.69	25	0.49
	Sperm head length	0.82	25	0.42
	Sperm midpiece length	1.81	25	0.08
	Sperm flagellum length	-0.48	25	0.64
	Sperm swimming speed (PC1)	-0.18	25	0.86
b) R _{0.5} treatment				
Related vs. Unrelated	Sperm viability	-0.19	13	0.85
	Sperm head length	0.49	13	0.63
	Sperm midpiece length	1.05	13	0.31
	Sperm flagellum length	-0.55	13	0.59
	Sperm swimming speed (PC1)	-1.21	13	0.25
b) R _{0.25} treatment				
Related vs. Unrelated	Sperm viability	1.06	11	0.31
	Sperm head length	0.68	11	0.51
	Sperm midpiece length	2.03	11	0.07
	Sperm flagellum length	-0.12	11	0.91
	Sperm swimming speed (PC1)	0.74	11	0.48

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