

1 **Grandpaternal effects are lineage- and sex-specific in threespined sticklebacks**

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16 **Running head:** Lineage-specific grandpaternal effects

17 **Abstract**

18 Transgenerational plasticity (TGP) occurs when the environment encountered by one  
19 generation (F0) alters the phenotypes of one or more future generations (e.g. F1 and F2).  
20 Selective inheritance of ancestral environments, via specific lineages or to only male or female  
21 descendants, may be adaptive if it allows past generations to fine-tune the phenotypes of future  
22 generations in response to sex-specific life history strategies. Here, we reared F1 offspring of  
23 unexposed and predator-exposed threespined stickleback (*Gasterosteus aculeatus*) fathers under  
24 ‘control’ conditions and generated F2s with a predator-exposed maternal and/or paternal  
25 grandfather. Grandpaternal effects were both sex and lineage-specific: female F2s were heavier  
26 and reacted less strongly to a simulated predator attack when their paternal grandfather was  
27 exposed to predation risk while male F2s were bolder when their maternal grandfather was  
28 exposed to predation risk. Therefore, grandpaternal effects were mediated across sexes, from F1  
29 males to F2 females and from F1 females to F2 males. However, these patterns were only  
30 evident when one grandfather, but not both grandfathers, were exposed to predation risk. This  
31 selective inheritance may mean that grandparental effects are underestimated in the literature and  
32 raises new questions about the proximate and ultimate causes of selective transmission across  
33 generations.

34

35 **Key words:** phenotypic plasticity, paternal effect, *Gasterosteus aculeatus*, nongenetic

36 inheritance, maternal effect, intergenerational plasticity

## 37 **Introduction**

38           Transgenerational plasticity (TGP) occurs when the environment experienced by a parent  
39 influences the phenotype of one or more future generations [1]. In some cases, maternal and  
40 paternal environments (e.g. predation exposure, diet, stress) have consequences for offspring, but  
41 their effects do not persist into future (e.g. F2) generations [2-4]. In other cases, the effects of  
42 environments experienced by one generation (F0) persist for multiple generations [5-9], even  
43 when offspring (F1s) are raised under ‘control’ conditions, i.e. in the absence of the cue that  
44 triggered a response in the F0 generation. These different patterns of TGP raise questions  
45 regarding when and to what degree environmental effects become ‘biologically embedded’ into  
46 the germline and therefore, the extent to which TGP contributes to long-term evolutionary  
47 change. Recent evolutionary theory predicts that rates of environmental change influence the  
48 likelihood that experiences in one generation have multigenerational consequences [10, 11].  
49 However, this theory largely assumes that inheritance is non-selective (all or nothing). In reality,  
50 however, phenotypic changes in the F1 generation may persist selectively across generations in  
51 only a subset of individuals via, for example, sex-specific epigenetic changes to chromosomes or  
52 gametes [12, 13] that escape erasure at fertilization [14].

53           Indeed there is some evidence in the biomedical literature that transgenerational effects  
54 can persist in a lineage-specific (via either the paternal or maternal lineage) and/or sex-specific  
55 (to only male or female F2s) fashion through multiple generations [15-18]. In humans, for  
56 instance, grandsons are influenced by the diet of their paternal grandfather while grand-daughters  
57 are influenced by the diet of their paternal grandmother [19]. Studies of lineage and sex-specific  
58 effects have been conducted almost exclusively in mammals, where mechanisms such as sex-  
59 specific placental function and provisioning can generate sex-specific effects [20-22]. It is

60 unknown if these sex-specific and lineage-specific effects can arise in the absence of such  
61 mechanisms (e.g., in external fertilizers). Moreover, our understanding of lineage and sex-  
62 specific effects is limited because they are difficult to study, as they require measuring traits in  
63 both male and females F2s and tracking effects through both the maternal or paternal lineage  
64 (rather than comparing F2s with control grandparents to F2s with two or four experimental  
65 grandparents). This is problematic because it leaves us unable to know, for example, whether  
66 effects are passed only via either the male or female line (e.g., F0 males to F1 males to F2 males)  
67 or whether there are interactive effects across lineages. For example, receiving cues from both  
68 the maternal and paternal grandfather may result in different traits or more extreme trait values  
69 than receiving cues from only one grandfather. Given that there is strong evidence for  
70 interactions between maternal cues, paternal cues, and offspring sex [23-25], it is likely that  
71 empirical studies examining interactions between maternal lineage, paternal lineage, and the sex  
72 of the F2 generation are important for understanding the evolutionary implications of TGP and  
73 the ways in which the environment experienced in the F0 generation manifests in the F2  
74 generation.

75         Sex-specific and lineage-specific effects may have adaptive significance if they can allow  
76 past generations to fine-tune the phenotypes of future generations in response to sex-specific life  
77 history strategies or sex differences in the costs and benefits of attending to grandparental cues,  
78 which might contain outdated and inaccurate information about the environment. Here, we  
79 assessed whether grandpaternal experience with predation risk prior to fertilization affects the  
80 traits of their grandoffspring in lineage-specific or sex-specific ways in threespined stickleback  
81 (*Gasterosteus aculeatus*). Male and female sticklebacks are sexually dimorphic in several  
82 respects, such as habitat use [26] and diet [27]. Further, there are a variety of male-specific

83 reproductive traits that increase male vulnerability to predation risk [28, 29], including bright  
84 nuptial coloration, conspicuous territory defence and courtship behaviour, and paternal care of  
85 eggs and newly hatched fry [30]. These sex differences can alter the risks/costs of living in a  
86 high predation environment [31], likely altering the optimal phenotype for males versus females  
87 in response to cues of predation risk.

88         In a previous study we exposed male F0s to a cue of predation risk prior to fertilization  
89 and found sex-specific paternal effects on offspring brain gene expression and risk-taking  
90 behaviour [32]; namely, F1 sons, but not daughters, of predator-exposed fathers were more  
91 active relative to sons of control fathers. To understand the extent to which experiences in the F0  
92 generation alter the phenotypes of the F2 generation, in the current study we reared sons and  
93 daughters of control and predator-exposed fathers under ‘control’ conditions and used them to  
94 generate F2s with control grandfathers, a predator-exposed maternal grandfather, a predator-  
95 exposed paternal grandfather, or two predator-exposed grandfathers (Figure 1). We then assayed  
96 male and female F2s for a variety of traits related to predation defence, including behaviour in an  
97 open field assay, stress-induced cortisol levels, and body size.

98         Because mothers and fathers did not interact prior to fertilization nor with their offspring  
99 postfertilization, our experimental design allowed us to completely isolate TGP mediated via  
100 gametes while controlling for mate choice and differential allocation due to partner quality or  
101 parental care. Further, by using artificial fertilization, we controlled for the selective failure of  
102 males to court or parent successfully under stressful conditions, which may result in differences  
103 between control and predator-exposed lineages because of selective breeding of a nonrandom  
104 sample of individuals.

105

106 **Methods**

107 **Housing conditions.** In August-September 2016, adult threespined sticklebacks were collected  
108 from Putah Creek, a freshwater stream in northern California and shipped to the University of  
109 Illinois at Urbana- Champaign. This population has piscivorous predators, including the prickly  
110 sculpin (*Cottus asper*). To generate the F1 generation, F0 males were exposed to a clay model  
111 sculpin 6 times (over 12 days) or left undisturbed during an equivalent time frame. The day after  
112 the last exposure, F1 offspring were generated via *in vitro* fertilization using a split-clutch  
113 design: each female's clutch was split and fertilized by both a control and predator-exposed  
114 male. Offspring were artificially incubated, reared until adulthood and were not used in any  
115 behavioural assays nor exposed to predation risk (see Hellmann, Bukhari [32] for more details).

116 To generate the F2 generation, we housed adult F1 males singly in 26.5L tanks (36L x  
117 33W x 24H cm), visually isolated from the other males' tanks (August – October 2017). Each  
118 tank contained two plastic plants, a sandbox, a clay pot, and algae for nest building. Males were  
119 left undisturbed until they had completed their nest, at which point we euthanized the male to  
120 obtain sperm. We used a split-clutch design to generate four grandparental treatment groups.  
121 Each F1 females' eggs were fertilized by sons of control and predator-exposed fathers; similarly,  
122 each F1 male sired eggs from daughters of control and predator-exposed fathers (Figure 1). We  
123 successfully generated 32 clutches of half-siblings (some half clutches failed to fertilize or  
124 develop): F2s with control grandfathers (n=8 clutches), predator-exposed paternal grandfather  
125 (n=8 clutches), predator-exposed maternal grandfather (n=8 clutches), and two predator-exposed  
126 grandfathers (n=8 clutches). During this time, the F1 generation was maintained on a summer  
127 photoperiod schedule (16 L : 8D) at  $20^{\circ} \pm 1^{\circ}\text{C}$  and fed ad libitum daily with a mix of frozen  
128 bloodworm (*Chironomus* spp.), brine shrimp (*Artemia* spp.) Mysis shrimp, and cyclopez.

129           We incubated fertilized eggs in a cup with a mesh bottom placed above an air bubbler  
130 and fry were reared in 37.9 L (53L x 33W x 24H cm) tanks, with each half-clutch housed in a  
131 separate tank. By artificially fertilizing the eggs and incubating both the F1 and F2 embryos, we  
132 controlled for possible pre-fertilization effects mediated by interactions between mothers and  
133 fathers as well as the post-fertilization effects mediated by paternal care [33-36]. Offspring were  
134 switched to a winter light schedule (8 L: 16 D) at least one month prior to when assays were  
135 conducted. Fry were fed newly hatched brine shrimp for two months before transitioning to the  
136 mix of frozen food described above.

137  
138           *Open field assays*. When the F2 generation was 5 months (mean days post-hatching:  
139  $157.9 \pm 1.47$  s.e.), we measured emergence behaviour, activity, exploration, and antipredator  
140 (freezing) behaviour using similar methods described in Hellmann, Bukhari [32]. Briefly, the  
141 testing arena was a circular pool (150cm diameter) divided into eight peripheral sections with a  
142 circular section in the middle. Fish were placed in an opaque refuge in the centre of the arena  
143 with its entrance plugged. After a three minute acclimation period, we removed the plug from the  
144 refuge, measured the latency for fish to emerge, and then measured the number of different  
145 (exploration) and total (activity) sections visited for three minutes after emergence. Fish that did  
146 not emerge after 5 minutes were gently released from the refuge; whether fish emerged naturally  
147 or were released did not alter activity/exploration in the resulting periods (generalized linear  
148 model with binomial distribution (emerged or released), with activity/exploration difference  
149 score (see below) as a fixed effect:  $Z_{249}=-0.41$ ,  $p=0.69$ ).

150           After the 3min period, we simulated a predator attack by quickly moving a clay sculpin  
151 toward the experimental fish. This attack elicited freezing behaviour from the fish; we measured

152 the latency for the fish to resume movement and then again measured the number of different  
153 and total sections visited for 3 minutes. If the fish remained frozen for greater than 10 minutes  
154 (n=25 fish), we ended the trial and considered activity and exploration after the simulated  
155 predation attack to be zero. We assayed n=63 F2s with control grandfathers (n=32 females, n=31  
156 males), n=64 F2s with predator-exposed paternal grandfathers (n=35 females, n=29 males), n=61  
157 F2s with predator-exposed maternal grandfathers (n=29 females, n=32 males), n=63 F2s with  
158 two predator-exposed grandfathers (n=30 females, n=33 males).

159 To measure cortisol in response to the predator attack [37], we netted the fish from the  
160 arena 15 minutes after the simulated predator attack and quickly weighed and measured it  
161 (standard length: from the tip of the nose to the base of the caudal fin). We euthanized the fish in  
162 MS-222 and drew blood from the tail of the fish using a heparinized microhematocrit tube. We  
163 centrifuged blood to separate the plasma (StatSpin CritSpin Microhemocrit centrifuge) and  
164 immediately froze the plasma at -80 °C. Because many fish had non-reproductively mature  
165 gonads, we visually sexed offspring when possible; we confirmed the accuracy of this method  
166 and sexed the remainder of the fish using a genetic marker [38].

167

168 ***Plasma cortisol.*** To measure circulating cortisol, we followed the manufacture's protocol (Enzo  
169 Life Sciences, Plymouth Meeting, PA, USA). All the plasma samples were prepared in 1:10  
170 steroid displacement reagent solution, then ran with a 1:120 dilution and in duplicate. Slopes of  
171 the standard curves and a serial dilution curve (1:20 to 1:320) were parallel ( $t_6=1.21$ ,  $p=0.27$ ),  
172 indicating that there was negligible matrix interference contributing to systematic measurement  
173 error. The intra-assay coefficients of variation were all within acceptable range (3.8%, 2.9%,  
174 4.4%, 4.7%, 4.8%, 3.8%). We ran common samples of pooled plasma on each plate (in



175 quadruplicate as the first two and last two wells of each plate) to calculate the interassay  
176 coefficient of variation (13.9%). Samples with a coefficient of variation greater than 15% ( $n = 2$ )  
177 were removed from the data set. Due to insufficient amount of blood drawn from some offspring,  
178 we sampled  $n=48$  F2s with control grandfathers,  $n=57$  F2s with predator-exposed paternal  
179 grandfathers,  $n=44$  F2s with predator-exposed maternal grandfathers, and  $n=49$  F2s with two  
180 predator-exposed grandfathers.

181  
182 ***Statistical analysis.*** For the activity and exploration, we found an interaction among observation  
183 period (before or after the simulated predator attack), grandmaternal treatment, grandpaternal  
184 treatment, and F2 sex. Because of the difficulty interpreting a 4-way interaction, we computed  
185 the difference between behaviour before versus after the attack (e.g. sections visited before -  
186 visited after the simulated predator attack); see the supplementary material for analysis of the full  
187 model with the raw data.

188 We then used a principal components analysis (R package factextra) to combine the  
189 activity and exploration difference score. We extracted one principle component with an  
190 eigenvalue of 1.65 that captured 82.5% of the variation, with smaller values indicating  
191 individuals who showed a smaller reduction in activity/exploration after the simulated predator  
192 attack compared to before the simulated predator attack. We then used a second principal  
193 components analysis to combine latency to emerge from the shelter and latency to resume  
194 movement after the simulated predator attack. We extracted one principle component  
195 (eigenvalue 1.10) capturing 54.8% of the variation, with high values indicating ‘bolder’  
196 individuals who were quick to emerge from the shelter and spent little time frozen. We ran  
197 activity/exploration and emergence/freezing behaviour as two separate PCAs, rather than one, to

198 maintain parallelism with our analysis of emergence/freezing behaviour in the F1 generation  
199 [32].

200 To test predictors of variation in activity/exploration, emergence/freezing behaviour,  
201 standard length (log-transformed), mass (log-transformed), and stress-induced cortisol (log-  
202 transformed), we used MCMC generalized linear mixed models (R package MCMCglmm).  
203 Because our data were heteroskedastic, we used a weak prior on the variance ( $V=1$ ,  $\nu=0.002$ ).  
204 We ran models for 200,000 iterations, with a burn-in of 3000 iterations,  $\text{thin} = 3$ , and Gaussian  
205 distributions. All models included fixed effects of maternal grandfather treatment, paternal  
206 grandfather treatment, and individual sex. The models testing predictors of activity/exploration,  
207 emergence/freezing behaviour, mass, and cortisol also included standard length (log-  
208 transformed). The model testing predictors of standard length also included tank density, age  
209 (days since hatching), and days since the first clutch hatched, to control for seasonal effects. All  
210 models included random effects of mother and father identity nested within maternal and  
211 paternal grandfather identity, as well as observer identity for the behavioural data. We tested for  
212 possible interactions between maternal grandfather treatment, paternal grandfather treatment, and  
213 F2 sex; we retained significant interactions. When significant interactions were present, we  
214 investigated those interactions by rerunning the models with male and female F2s analysed  
215 separately. We removed three outliers from the mass/length datasets (the same outliers) and two  
216 (different) outliers from the cortisol dataset; the significance of the results did not change with  
217 these removals.

218

219 ***Animal welfare note.*** All methods, including euthanasia techniques, were approved by  
220 Institutional Animal Care and Use Committee of University of Illinois Urbana-Champaign  
221 (protocol ID 15077).

222

## 223 **Results**

224 ***Female F2s were heavier and less responsive to a simulated predator attack when their***  
225 ***paternal grandfather, but not both grandfathers, was exposed to predation risk.*** We sought to  
226 understand how grandfathers' (F0) exposure to predation risk influenced the risk-taking  
227 behaviour, stress responses, and morphology of individuals in the F2 generation and whether  
228 these effects were transmitted in a lineage-specific (via the paternal versus maternal grandfather)  
229 and/or sex-specific (to either male versus female F2s) manner (n=251 F2s). We found that both  
230 F2 activity/exploration and mass (controlling for length) were influenced by a significant  
231 interaction between paternal grandfather treatment, maternal grandfather treatment, and F2 sex  
232 (Table 1). Specifically, relative to female F2s with control grandfathers, female F2s with only a  
233 predator-exposed paternal grandfather were heavier and showed a reduced change in  
234 activity/exploratory behaviour in response to the simulated predator attack; however, these  
235 patterns were not present for female F2s with both a paternal and maternal grandfather exposed  
236 to predation risk (interaction of maternal by paternal grandfather treatment in female F2s; mass:  
237 95% CI (-0.15, -0.02), p=0.02, Figure 2A; activity/exploration: 95% CI (0.39, 2.14), p=0.005,  
238 Figure 2B). For both mass and activity/exploration, we found no evidence of main or interactive  
239 effects of maternal or paternal grandfather treatment for male F2s (mass: paternal: 95% CI (-  
240 0.12, 0.04), p=0.28, maternal: 95% CI (-0.09, 0.07), p=0.75, interaction: 95% CI (-0.04, 0.13),  
241 p=0.27, Figure 2A; activity/exploration: paternal: 95% CI (-0.72, 0.76), p=0.95; maternal: 95%

242 CI (-0.61, 0.90),  $p=0.70$ , interaction: 95% CI (-1.41, 0.58),  $p=0.41$ , Figure 2B). It is likely that  
243 the results for mass and the difference in activity/exploration were similar because they were  
244 positively correlated (Wilcoxon signed-rank test:  $V=22321$ ,  $p<0.001$ ).

245

246 ***Male F2s were bolder when their maternal grandfather was exposed to predation risk.*** There  
247 was a significant interaction between maternal grandfather and paternal grandfather treatment, as  
248 well as between maternal grandfather treatment and F2 sex, on boldness (higher values indicate  
249 ‘bolder’ individuals who emerged quickly and stayed frozen after the predator attack for shorter  
250 periods of time; Table 1). Specifically, male F2s with a maternal grandfather exposed to  
251 predation risk were ‘bolder’ relative to offspring of control grandfathers (95% CI (0.13, 1.20),  
252  $p=0.02$ ), but this effect tended to be weaker when both the maternal and paternal grandfather  
253 were exposed compared to when just the maternal grandfather was exposed (interaction: 95% CI  
254 (-1.32, 0.11),  $p=0.09$ ; Figure 2C). We found no evidence of main or interactive effects of  
255 maternal or paternal grandfather treatment for female F2s (paternal: 95% CI (-0.19, 0.94),  
256  $p=0.18$ ; maternal: 95% CI (-0.48, 0.70),  $p=0.72$ ; interaction: 95% CI (-1.29, 0.28),  $p=0.21$ ;  
257 Figure 2C).

258

259 ***Neither offspring length, nor stress responses, were significantly altered by grandfathers’***  
260 ***predation exposure.*** We found no evidence that stress-induced cortisol varied with paternal  
261 (95% CI (-31, 0.29),  $p=0.95$ ) or maternal (95% CI (-0.56, 0.29),  $p=0.51$ ) grandfather treatment  
262 ( $n=196$  fish). Male F2s had lower stress-induced cortisol than female F2s (95% CI (-0.51, -0.07),  
263  $p=0.01$ ), but stress-induced cortisol did not vary with length (95% CI (-1.02, 1.92),  $p=0.56$ ).

264 We also found no evidence that paternal (95% CI (-0.04, 0.05),  $p=0.96$ ) or maternal (95%  
265 CI (-0.03, 0.06),  $p=0.41$ ) grandfather treatment altered length of the F2 generation ( $n=248$  fish).  
266 Although we found no effect of sex (95% CI (-0.01, 0.03),  $p=0.46$ ) or age (days since hatched:  
267 95% CI (-0.004, 0.005),  $p=0.86$ ) on length, F2s were larger when they were in a lower density  
268 tank (95% CI (-0.007, -0.003),  $p<0.001$ ) and when they were born later in the season (95% CI  
269 (0.001, 0.004),  $p=0.002$ ). We found no significant effect of size on activity/exploration or  
270 boldness (Table 1).

271

## 272 **Discussion**

273 Here, we demonstrate that grandpaternal effects, mediated via sperm, are transmitted  
274 selectively to their grandoffspring. Specifically, female F2s were heavier and reacted less  
275 strongly to a simulated predator attack when their paternal grandfather was exposed to predation  
276 risk. In contrast, male F2s were bolder when their maternal grandfather was exposed to predation  
277 risk. For both male and female F2s, this change was only significant when one grandfather, but  
278 not both grandfathers, were exposed to predation risk. These findings suggest that grandpaternal  
279 effects are both sex-specific and lineage-specific: grandfathers' experiences have different  
280 consequences for male and female F2s, and F2 traits depend on whether the paternal grandfather,  
281 maternal grandfather, or both grandfathers were exposed to predation risk.

282 In a previous study, we found striking sex differences in paternal effects in response to  
283 predation risk [32]. These sex differences in paternal effects might help explain the lineage-  
284 specific effects in the F2 generation that were observed in this study: in Hellmann, Bukhari [32],  
285 F1 sons of predator-exposed fathers showed altered activity/exploration and in this study,  
286 differences in activity/exploratory behaviour were detected in the descendants of these F1 sons

287 (paternal line). In contrast, activity/exploration of F1 daughters was not affected by their fathers'  
288 experience with risk [32] and no changes in activity/exploration were detected in their  
289 descendants (maternal line) in this study. More generally, this finding suggests that offspring  
290 who do not respond to parental cues may be less likely to transmit information about those cues  
291 to future generations.

292         However, we also found that epigenetic transmission and phenotypic consequences can  
293 be decoupled: F2 boldness and mass were altered by grandpaternal exposure to predation risk,  
294 but not by paternal exposure to predation risk in the F1 generation [32]. Similar results have been  
295 found in other systems [39-41], which collectively suggests that individuals may be silent  
296 carriers of epigenetic information, transmitting altered phenotypes to their offspring without  
297 actually displaying the phenotype themselves. Differences between phenotypes in the F1 and F2  
298 generation may be linked to different transmission mechanisms from the F0 to F1 generations  
299 compared to the F1 to F2 generations [1, 8]. Alternatively, or in addition, cues from the F0  
300 generation may alter how F1s experience their environment (e.g. social interactions [42], habitat  
301 choice [43]), which could induce additional epigenetic changes [44] that are transmitted to the F2  
302 generation and result in different phenotypes between the F1 and F2 generation. Future work  
303 examining differences and similarities in the mechanisms of transmission across multiple  
304 generations would be highly useful.

305         Interestingly, we found no evidence for paternal transmission along sex-specific lines  
306 (e.g. fathers to sons); rather, we observed the opposite pattern, in which transmission was  
307 mediated across sexes from F1 males to F2 females and from F1 females to F2 males. This same  
308 pattern of transmission to female descendants (F2s and F3s) via the paternal lineage has been  
309 documented in mammals in response to a wide range of maternal experiences, such as high-fat

310 diets [15], chronic social instability [16], prenatal glucocorticoid exposure [17] and food  
311 availability [45]. It is remarkable that we see the same pattern as these mammalian studies, given  
312 that the cue originated in a different parent (F0 males versus females), that the mechanism of  
313 transmission is almost certainly different (e.g. sperm versus in utero effects), and that the  
314 triggering cue varies across studies (e.g. predation risk versus diet). These lineage effects may be  
315 generated by a number of different mechanisms including genomic imprinting regulated in a sex-  
316 specific manner [15] or sex-specific embryonic responses to differences in sperm content (e.g.  
317 small RNAs). An interesting possibility is that epigenetic changes to sex chromosomes are more  
318 faithfully transmitted via the F1 heterogametic sex (often males) due to lower rates of sex  
319 chromosome recombination [45]. Additional lineage-specific studies across a broader range of  
320 taxonomic groups, with diverse potential mechanisms of transmission, may determine the  
321 frequency of different patterns of transmission, whether these lineage-specific patterns of  
322 transmission are adaptive, and if these patterns are driven by mechanistic constraints on  
323 epigenetic erasure in males versus females.

324         In addition to distinct grandpaternal effects via maternal and paternal lineages, we also  
325 found strong interactive effects: grandpaternal effects were evident if one grandfather was  
326 exposed to predation risk, but not if both grandfathers experienced predation risk. Interestingly,  
327 this mirrors the interactive effects between maternal and paternal cues that were observed in the  
328 F1 generation: offspring of predator-exposed fathers showed reduced survival against a sculpin  
329 predator, but this pattern was not evident when both the mother and father were exposed to  
330 predation risk [32]. This suggests that maternal and paternal effects interact, both when mothers  
331 and fathers are directly exposed to the triggering environment (transmitted from predator-  
332 exposed F0s to the F1 generation) and when mothers and fathers inherit a cue about the

333 environment from their parents (transmitted from the offspring of predator-exposed parents to  
334 the F2 generation). These interactive effects also mean that if we had not isolated effects  
335 emerging in the paternal versus maternal lineage (e.g. compared controls to F2s with two  
336 predator-exposed grandfathers), we would have erroneously concluded that effects in the F1  
337 generation did not persist until the F2 generation. Consequently, previous studies that have not  
338 examined these lineage effects may have underestimated the extent to which transgenerational  
339 effects persist to the F2 generation.

340         Our experimental design allowed us to control for mate choice and differential allocation  
341 during gestation and parental care, which might underlie the sex-specific and lineage-specific  
342 effects observed in mammals in response to maternal experiences [20-22]. Here, we demonstrate  
343 that similar sex-specific and lineage-specific effects are observed when cues are transmitted via  
344 gametes alone (in the absence of these other mechanisms) and when cues are originally  
345 experienced by the father instead of the mother. This suggests that these lineage-specific patterns  
346 are robust, occurring across a variety of taxonomic groups and mechanisms, and may evolve in  
347 response to sex-specific life history strategies. This selective inheritance has significant  
348 implications for theory, raising new questions such as how and whether sex-specific selection  
349 pressures shape the evolution of transgenerational plasticity, the mechanisms underlying  
350 selective transmission of transgenerational information, and whether the mechanism of selective  
351 transmission affects the persistence of environmental effects across generations.

352



353 **Authors contributions**

354 JKH and AMB conceived of the study, JKH collected the data, ERC processed the cortisol  
355 samples, JKH analysed the data and wrote the first draft of the manuscript, and JKH and AMB  
356 edited the manuscript.

357

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364

365 **Table 1:** Results of MCMCglms testing predictors of activity/exploratory behaviour (higher  
 366 values showed a greater decrease in activity/exploration after the simulated predator attack;  
 367 n=251 fish), boldness (higher values are individuals that quickly emerged from the shelter and  
 368 spent little time frozen; n=251 fish), and offspring mass (log-transformed) at 5 months (n=248  
 369 fish). We tested fixed effects of maternal and paternal grandfather treatment, F2 sex, and  
 370 standard length, with random effects of maternal and paternal identity nested within maternal and  
 371 paternal grandfather, respectively. We also included observer identity in the behavioural models.

	Activity and exploration <sup>372</sup> behaviour		
	Mean	95% CI (L, U)	p
Maternal grandfather treatment	-0.37	-1.07, 0.29	0.28
Paternal grandfather treatment	-0.83	-1.48, -0.17	<b>0.01</b>
F2 sex	-0.21	-0.84, 0.43	0.51
Standard length (log-transformed)	-0.24	-2.05, 1.57	0.79
Maternal GF * paternal GF	1.09	0.20, 2.02	<b>0.02</b>
Paternal GF * F2 sex	0.77	-0.12, 1.69	0.09
Maternal GF * F2 sex	0.40	-0.50, 1.32	0.36
Maternal GF * paternal GF * F2 sex	-1.37	-2.67, -0.10	<b>0.04</b>
	Emergence and freezing <sup>373</sup> behaviour		
	Mean	95% CI (L, U)	p
Maternal grandfather treatment	0.12	-0.35, 0.59	0.61
Paternal grandfather treatment	0.40	0.001, 0.80	<b>0.046</b>
F2 sex	0.16	-0.19, 0.51	0.36
Standard length (log-transformed)	0.66	-0.74, 2.11	0.36
Maternal * paternal GF treatment	-0.55	-1.08, -0.05	<b>0.035</b>
Maternal GF * F2 sex	0.51	0.001, 1.01	<b>0.047</b>
	Mass (log-transformed) <sup>374</sup>		
	Mean	95% CI (L, U)	p
Maternal grandfather treatment	-0.008	-0.07, 0.07	0.99
Paternal grandfather treatment	0.048	-0.02, 0.12	0.18
F2 sex	0.05	0.005, 0.10	<b>0.03</b>
Standard length (log-transformed)	2.76	2.60, 2.92	<b>&lt;0.001</b>
Maternal GF * paternal GF	-0.07	-0.13, 0.002	0.06
Paternal GF * F2 sex	-0.01	-0.17, -0.03	<b>0.004</b>
Maternal GF * F2 sex	-0.17	-0.08, 0.05	0.62
Maternal GF * paternal GF * F2 sex	0.11	0.02, 0.21	<b>0.02</b>

377 **Figure Legend**

378 **Figure 1:** Males in the F0 generation were either left unexposed (white) or directly exposed to  
379 predation risk (dark grey) and their sperm was used to fertilize the eggs of an unexposed female  
380 using in vitro fertilization. The F1 generation was reared in the absence of predation risk and  
381 used to generate the F2 generation. For example, sons of predator-exposed fathers were mated to  
382 daughters of control fathers to generate F2s with a predator-exposed paternal grandfather.  
383 Similarly, daughters of predator-exposed fathers were mated to sons of control fathers to  
384 generate F2s with a predator-exposed maternal grandfather. Light grey indicates F1s/F2s whose  
385 lineage was exposed to predation risk (i.e. their parents or grandparents experienced predation  
386 risk). Juvenile F2s were then assayed for a variety of traits.

387

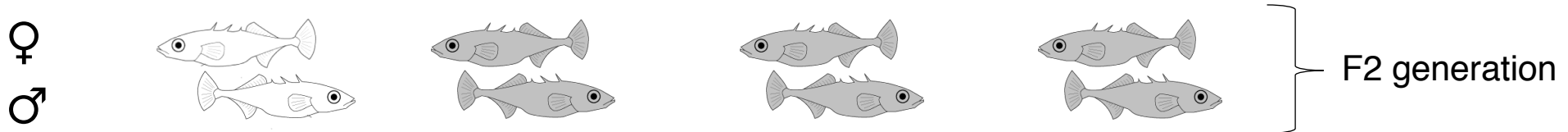
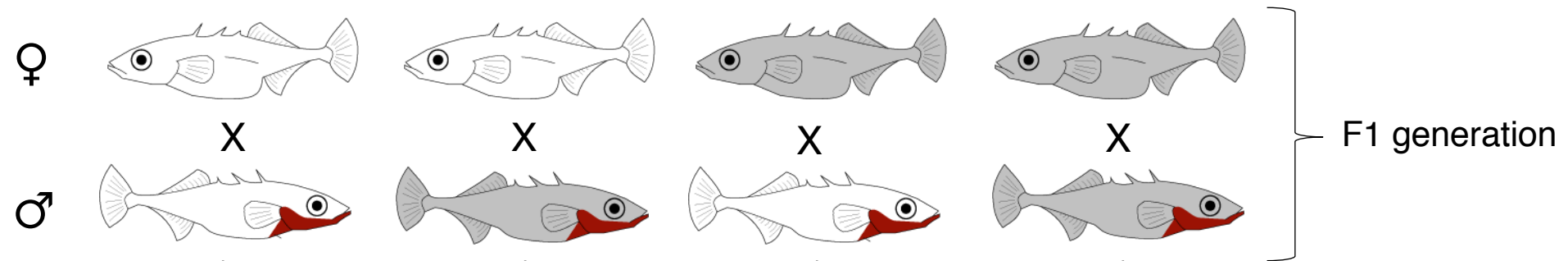
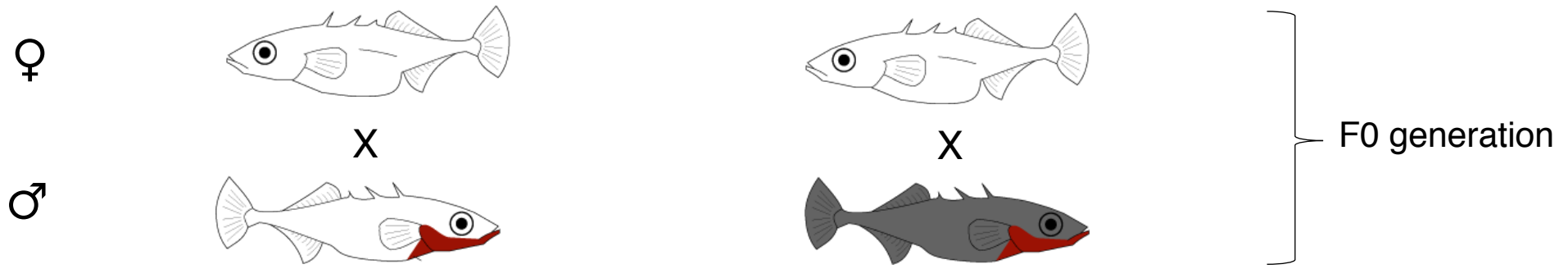
388 **Figure 2:** A) Mass (log-transformed) of female (red, circles) and male (blue, triangles) F2s with  
389 control grandfathers, predator-exposed paternal grandfather, predator-exposed maternal  
390 grandfather, or two predator-exposed grandfathers (5 months post-hatching). Plotted on the y-  
391 axis are the residuals of the regression model, with grandparental treatment and sex removed  
392 (mean  $\pm$  s.e.). B) Difference score in activity/exploratory behaviour (PCA) of female and male  
393 F2s, with higher values indicate individuals who showed a greater change in activity/exploration  
394 behaviour before versus after the predator attack (mean  $\pm$  s.e.) in the open field assay. All  
395 treatment groups were less active/exploratory after the simulated predator attack compared to  
396 before (Supplementary Figure 1). C) Emergence time and freezing behaviour (PCA) of female  
397 and male F2s across the four grandpaternal treatments. Higher values indicate 'bolder'  
398 individuals who were quick to initially emerge from the shelter and who spent a reduced amount  
399 of time frozen after the simulated predator attack (mean  $\pm$  s.e.).

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Control  
grandfather

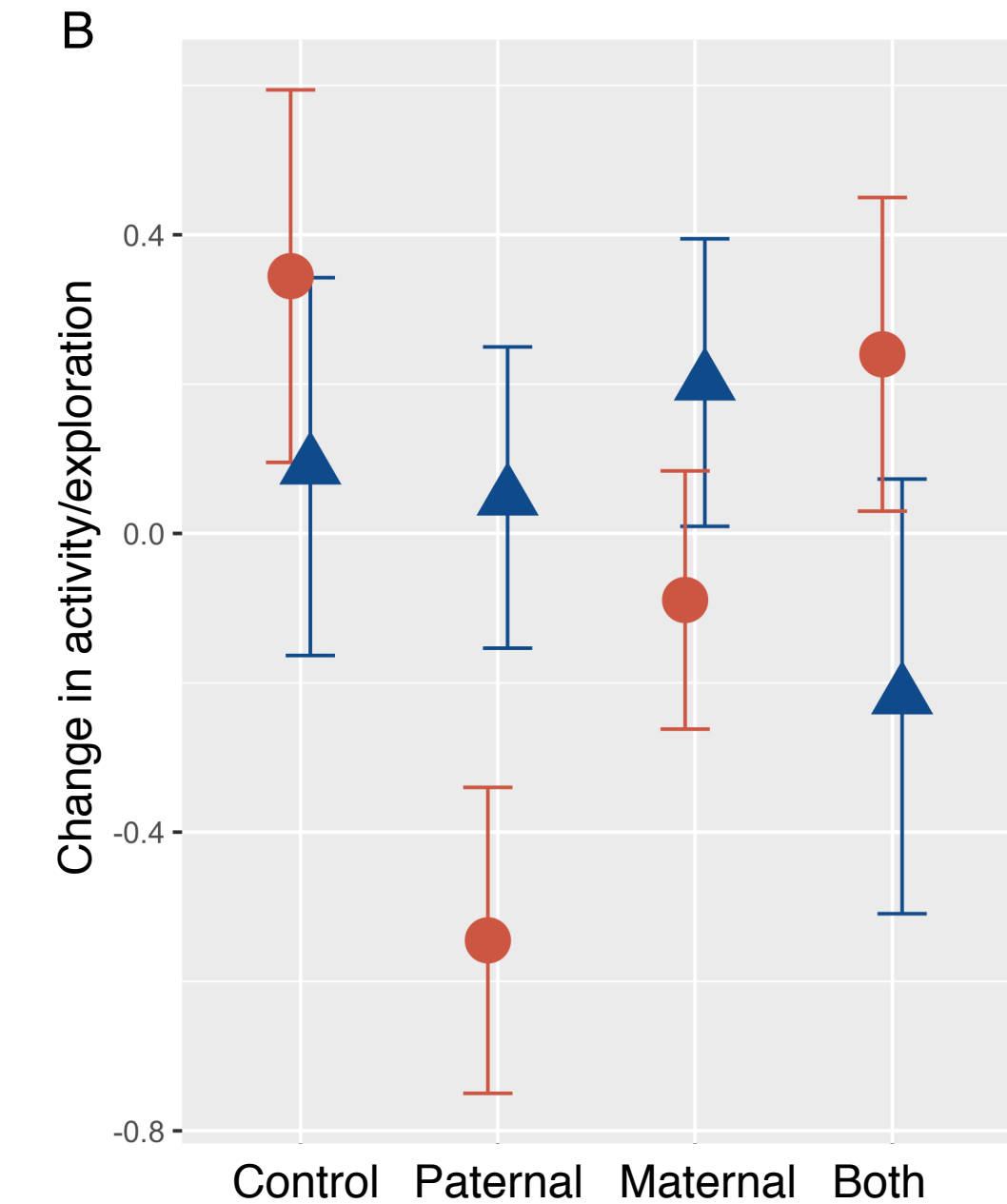
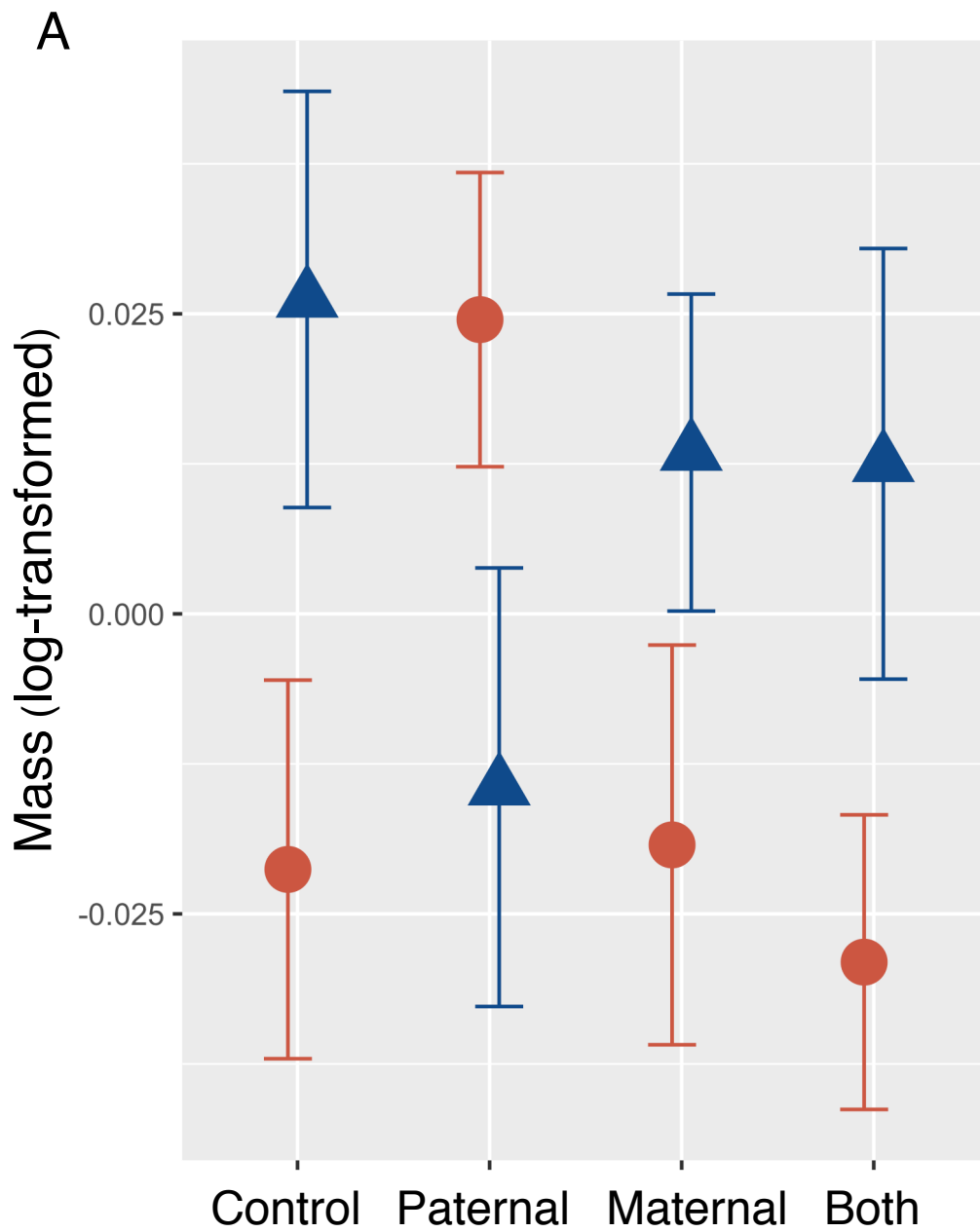
Paternal  
grandfather

Maternal  
grandfather

Both  
grandfathers

Predation exposure

- Control
- Directly exposed
- Lineage exposed



Lineage of grandfather predation exposure

