1 2	Effect of the early social environment on behavioural and genomic responses to a social challenge in a cooperatively breeding vertebrate
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27 Abstract

The early social environment can have substantial, lifelong effects on vertebrate social 28 29 behaviour, which can be mediated by developmental plasticity of brain gene expression. Early 30 life effects can influence immediate behavioural responses towards later-life social challenges and can activate different gene expression responses. However, while genomic responses to 31 social challenges have been reported frequently, how developmental experience influences the 32 shape of these genomic reaction norms remains largely unexplored. We tested how 33 manipulating the early social environment of juvenile, cooperatively-breeding cichlids, 34 35 Neolamprologus pulcher, affects their behavioural and brain genomic responses when competing over a resource. Juveniles were reared either with or without a breeder pair and a 36 37 helper. Fish reared with family members behaved more appropriately in the competition than when reared without. We investigated whether the different social rearing environments also 38 39 affected the genomic responses to the social challenge. A set of candidate genes, coding for hormones and receptors influencing social behaviour, were measured in the telencephalon and 40 41 hypothalamus. Social environment and social challenge both influenced gene expression of egr-1 (early growth response 1) and gr1 (glucocorticoid receptor 1) in the telencephalon and 42 of *bdnf* (brain derived neurotrophic factor) in the hypothalamus. A global analysis of the 11 43 expression patterns in the two brain areas showed that neurogenomic states diverged more 44 strongly between intruder fish and control fish when they had been reared in a natural social 45 setting. Our results show that same molecular pathways may be used differently in response 46 to a social challenge depending on early life experiences. 47

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49 Keywords

50 Developmental plasticity, behavioural flexibility, social competence, early social 51 environment, genomic reaction norm, neurogenomic state, cooperative breeder, brain gene 52 expression, social challenge.

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61 Introduction

The early social environment can have important and persisting effects on the development of 62 an animal's emotional (reviewed in Champagne 2010) and behavioural phenotype (reviewed 63 in Kasumovic & Brooks 2011). Long-term effects of the early social environment have been 64 reported in all vertebrate classes (mammals: e.g. Harlow & Zimmermann 1959; Mireault & 65 Bond 1992; Liu et al. 1997; Bastian et al. 2003; Branchi & Alleva 2006; birds: Adkins-66 Regan & Krakauer 2000; Ruploh et al. 2013; Ruploh et al. 2014; Schmidt et al. 2014; 67 reptiles: Ballen et al. 2014; amphibians: Nicieza & Metcalfe 1999; fish: e.g. Arnold & 68 69 Taborsky 2010; Taborsky et al. 2012). The social conditions experienced early in life can 70 affect a remarkably broad array of traits including life history traits and reproductive 71 schedules (Kasumovic & Brooks 2011), coloration (Ballen et al. 2014) or learning and 72 memory (Liu et al. 2000), but most often it affects behaviours in the social domain (reviewed 73 in Taborsky 2016a). For instance, variation in the amount of received maternal care can affect maternal care behaviour of the next generation (Liu et al. 1997; Francis et al. 1999) or the 74 75 ability to use social information in effective hierarchy formation (Branchi et al. 2006). The sex composition of littermates or social groups during rearing can affect later mate choice 76 77 decisions (Adkins-Regan & Krakauer 2000) or aggressive tendencies (Benus & Henkelmann 78 1998).

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Lasting effects induced by the early social environment on social behaviours are thought to 80 result from developmental plasticity in the brain (e.g. Fischer et al. 2015) and can be mediated 81 by organizational effects of hormones or epigenetic modifications. Organizational effects of 82 the hormonal system (Phoenix et al. 1959; Soares et al. 2010) impact the neural structural 83 level, are slow and involve mechanisms such as neurogenesis, apoptosis and synaptic 84 plasticity (reviewed in Soares et al. 2010). Organizational effects are considered non-85 reversible and they usually affect a phenotype during specific sensitive periods of 86 development, for example in the perinatal period or during puberty (Rice & Barone Jr 2000; 87 Romeo 2003). Furthermore, early adversity can result in socially driven epigenetic 88 modifications (Champagne 2008). These lasting effects can often be measured by persistent 89 90 alterations of gene expression profiles in different brain areas, including effects on hormonal ligands and receptors related to the stress response and social recognition (e.g. corticosteroids, 91 serum oxytocin, and oxytocin and estrogen receptors; (Zimmer et al. 2013, Cao et al. 2014); 92 glucocorticoid receptors (gr, grl, Zimmer et al. 2014) and corticotropin-releasing factor (crf); 93 94 (Liu et al. 1997; McGowan et al. 2009; Banerjee et al. 2012; Taborsky et al. 2013)). The 95 early social environment might also have long lasting consequences for the individual by
96 influencing and modulating neuronal plasticity of the brain and related gene expression
97 pathways [brain-derived neurotrophic factor (*bdnf*) and nerve growth factor (*ngf*); (Zhang *et*98 *al.* 2002; Roceri *et al.* 2004)].

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Behavioural flexibility, a form of plasticity that should be distinguished from developmental 100 plasticity, is expressed as a response to an environmental trigger, and is immediate and 101 reversible (Taborsky & Oliveira 2012). For example, in the social domain, individuals 102 103 perceive and use social information to flexibly adjust their behaviour to the present social 104 context ('social competence', Taborsky & Oliveira 2012). Behavioural flexibility is mediated 105 in part by the activational effects of the hormonal system (Soares et al. 2010). Activational effects work at the functional level by changing the activity of neural circuits and are rapid 106 107 and transient. Social challenges and opportunities can activate different patterns of gene expression in specific brain areas, which can be measured as genomic reaction norms (Aubin-108 109 Horth & Renn 2009). For example, when previously subordinate cichlid fish, Astatotilapia burtoni, change their social rank, changes in behaviour and colouration are accompanied by 110 an activation of different brain areas through expression of the immediate early genes (IEG's) 111 egr-1 and c-fos (Burmeister et al. 2005; Maruska et al. 2013) and changed expression of 112 genes coding for hormones and their receptors in different brain areas associated with social 113 behaviour (Huffman et al. 2012a, 2015). 114

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We predict that developmental plasticity and behavioural flexibility will jointly shape social 116 behaviour, resulting in different slopes of behavioural reaction norms dependent on social 117 rearing conditions (e.g. Dettling et al. 2002). This means that the shape of an immediate 118 behavioural response towards a social challenge (e.g., the slope between baseline and 119 challenged condition) would differ depending on the early rearing environment. For example, 120 rhesus monkeys separated from their mothers early in life respond to peer presence with much 121 122 lower frequencies of affiliation behaviour than do mother-reared peers, even after years of living in normal social conditions (Feng et al. 2011). This difference in short-term 123 124 behavioural response of individuals that experienced divergent rearing environments should correspond to changes in components of the underlying control mechanisms, in particular 125 long-term and short-term alterations of gene expression. At the molecular level, this can best 126 be studied by measuring brain genomic reaction norms in response to an environmental 127 128 challenge (behavioural flexibility) of individuals reared in different environmental conditions

(developmental plasticity). With genomic reaction norms, we measure how an individual of a 129 particular phenotype responds to a specific situation at the gene expression level, within a 130 specific tissue, brain area or cell type, depending on the question asked. As a hypothetical 131 example, an individual that experienced benign early life conditions might respond by high 132 brain glucocorticoid receptor (gr) expression toward a social stimulus, whereas an individual 133 that grew up under adverse conditions may mount a much smaller gr response (or might not 134 respond at all). Individuals reared in socially more complex early environments generally 135 behave more socially competent in a range of different social challenges compared to when 136 137 reared in more simple environments (reviewed in Taborsky 2016a). Furthermore, in order to capture the change in the overall pattern of expression after a social challenge in individuals 138 139 from the two contrasting early rearing environments, a neurogenomic state can be defined using the expression of all genes in all surveyed brain regions at once (Robinson et al. 2008). 140 141 Such differences in molecular responses to a behavioural challenge between individuals that faced different early social environments have so far been only demonstrated in laboratory 142 143 strains of rodents (measured at the mRNA or protein level, Plotsky & Meaney 1993; Wigger & Neumann 1999; Ago et al. 2013). For example, male mice reared in isolation show higher 144 *c-fos* protein levels in the cortex when faced with a social challenge than group-reared males 145 (Ago et al. 2013). There is however no published explicit test of the effect of the early rearing 146 environment on gene expression levels in response to a short term challenge. 147

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Finally, the consistent finding that variation in the early social environment of animals results 149 150 in different behavioural responses to social challenges and opportunities (Taborsky 2016a) gives rise to the question whether changes in behaviour relate to changes in gene expression 151 152 patterns. Testing such a relationship is an important first attempt to decipher the functional significance of this variation at the gene expression level (Williams 2008). For instance 153 Cummings et al. 2008 show that specific genes are turned on in the females swordtail fish, 154 *Xiphophorus nigrensis,* interacting with attractive males but then turned off when interacting 155 156 with other females. Further aggressive behaviour in threespine stickleback, Gasterosteus aculeatus, was shown to be positively correlated with gene expression of glucocorticoid 157 receptors (Aubin-Horth et al. 2012). However, whether one always expects a linear 158 relationship between a phenotype and the underlying endocrine pathways, or whether 159 individuals from different context (age, sex, status, environment) should show the same 160 relationship is less certain (Williams 2008). 161

In order to understand how brain genomic reaction norms have evolved in the social domain 163 under natural conditions when confronted with biologically relevant challenges, we need 164 information from a broader array of taxonomic groups and, in particular, also from natural 165 study organisms (as opposed to organisms artificially selected for a certain purpose), because 166 they can be expected to display naturally evolved reaction norms (Groothuis & Taborsky 167 2015). Here we chose a highly social fish species as study system, the cooperatively breeding 168 cichlid Neolamprologus pulcher. This species, which has become a key organism for the 169 study of vertebrate social evolution (e.g. Wong & Balshine 2011; Taborsky 2016b), is now 170 171 also studied within an ecological genomics framework (Aubin-Horth et al. 2007; Taborsky et 172 al. 2013; Brawand et al. 2014; O'Connor et al. 2015, 2016; Reddon et al. 2015, O'Connor et 173 al. 2016). We investigated the association between behavioural and genomic reaction norms 174 in this species by comparing the response to a social challenge (a contest over a resource) of 175 individuals whose early rearing environment differed in levels of social complexity. Since previous experiments showed that N. pulcher reared in different social environments display 176 177 altered behavioural responses to social challenges (Arnold & Taborsky 2010; Taborsky et al. 2012), we predicted that social rearing and social challenge would jointly influence genomic 178 179 reaction norms in the brain of these fish.

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We aimed to answer two questions: (i) How do genomic reaction norms measured in fish 181 exposed to a social challenge or a control situation differ between fish reared in different 182 social environments? (ii) Is the observed behaviour and the early social environment related 183 to the genomic response? To answer the first question, we measured gene expression in the 184 telencephalon and hypothalamus of socially challenged and control fish. These two brain 185 areas play a key role in social behaviour and decision-making in fish (O'Connell & Hofmann 186 187 2011) and in their hypothalamic-pituitary-interrenal (HPI) stress axis. The HPI is homologous to the mammalian hypothalamic-pituitary-adrenal (HPA) stress axis, which has been shown to 188 be strongly impacted by the early social environment across different vertebrate classes 189 190 (Meaney & Szyf 2005; Banerjee et al. 2012; Taborsky et al. 2013). In the telencephalon we measured expression of egr-1, bdnf, gr1, crf, and neuroserpin, and in the hypothalamus the 191 expression of egr-1, bdnf, gr1, crf, avt and its V1a2 receptor (avtr). The product of these 192 genes are known to be involved in the modulation of social behaviour or social dominance 193 194 relationships and/or to be affected by early social experience in vertebrates (Liu et al. 1997; Young et al. 1999; Zhang et al. 2002; Madani et al. 2003; Burmeister et al. 2005; Branchi et 195 196 al. 2006; Aubin-Horth et al. 2007). To answer our second question, we analysed the relationship between social behaviours expressed during the social challenge and geneexpression.

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200 Methods

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202 *Study species*

Neolamprologus pulcher is a cooperatively breeding cichlid endemic to Lake Tanganyika, 203 East Africa. It lives in large family units of up to 25 fish consisting of a dominant breeder 204 205 pair, one or several related or unrelated helpers and fry from recent broods. Subordinates 206 provide help in form of direct brood care of the dominants' offspring and of territory defence 207 and maintenance. In turn they remain accepted by dominants at a territory, at which they have access to critical resources ('pay-to-stay'; Taborsky 1985; Balshine-Earn et al. 1998; 208 209 Bergmüller & Taborsky 2005; Stiver et al. 2005; Heg & Taborsky 2010; Zöttl et al. 2013b; Fischer et al. 2014). By being accepted at a territory, helpers benefit particularly from 210 211 protection from predators and access to high quality shelters (Balshine-Earn et al. 1998; Heg et al. 2004), and they might eventually get a chance to inherit a breeder position (Stiver et al. 212 213 2004). N. pulcher groups are organized in size-based linear hierarchies (Dey et al. 2013) and the fish have a large, fine-scaled repertoire of social behaviours to establish and maintain 214 these hierarchies (Taborsky 1984). Higher ranking fish show an array of open and restrained 215 aggressive displays towards lower ranking fish, which in turn show different submissive 216 217 behaviours.

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The early social environment influences the development of social behaviour and social 219 220 competence of *N. pulcher*. When young are reared either with the breeding pair, a helper, and their siblings (+F treatment), or with their siblings only (-F treatment), +F fish show more 221 adequate social behaviour and solve social conflicts more efficiently than -F fish (Arnold & 222 Taborsky 2010; Taborsky et al. 2012). Analysis of whole brain gene expression in adult 223 224 individuals has shown that the stress axis of these fish is stably reprogrammed by the early social rearing treatment. +F fish had a lower expression of gr1 and crf compared to fish from 225 the -F treatment (Taborsky et al. 2013). 226

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228 *Housing conditions*

The experiment was carried out at the 'Ethologische Station Hasli' of the Institute of Ecologyand Evolution, University of Bern, Switzerland, under licence number 52/12 of the Veterinary

Office of the Kanton Bern. The breeding pairs used to generate the experimental fish were 2^{nd} and 3^{rd} generation offspring of wild caught *N. pulcher* from Kasakalawe Point, Mpulungu, Zambia. Rearing tanks of 200 L were equipped with a 2 cm sand layer, and eight clay pot halves and two PET bottles serving as shelters. The light:dark cycle was set to 13:11 h with a 10 min dimmed light period in the morning and evening to simulate the light conditions of Lake Tanganyika. Fish were fed ad libitum 6 days a week (5 days commercial flake food, 1 day frozen zooplankton). Water temperature was held constant at 27 ± 1 °C.

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239 *Early social environment treatments*

We used two early social environments: being reared (i) with parents, one helper and same-240 241 aged siblings (+F treatment), or (ii) with same-aged siblings only, but no older family members (-F treatment). We first created the experimental broods, by forming 20 social 242 243 groups in separate 200-L tanks, consisting of a breeder male, a breeder female and an immature helper by haphazardly selecting unfamiliar fish from the institute's breeding stock. 244 245 Ten days after a breeder pair had spawned a clutch, the offspring had reached the free swimming stage and were used to form 20 experimental groups. Each experimental group was 246 placed in a 100-L compartment of a 200-L tank, separated from neighbouring groups by an 247 opaque PVC sheet. Offspring of each experimental group were assigned randomly to one of 248 the two early social environment treatments. Mean group size was 32.6 fish \pm 3.8 SEM in the 249 +F treatment and 35.4 fish \pm 5.1 SEM in the –F treatment. Groups receiving the +F treatment 250 251 were moved to an empty 100-l compartment together with their parents and helper, whereas groups receiving the -F treatment were moved to another empty 100-1 compartment without 252 253 their parents and the helper. The early social environment treatment lasted for 62 days in accordance with earlier studies (Arnold & Taborsky 2010; Taborsky et al. 2012, 2013; 254 255 Fischer et al. 2015). Afterwards the parents and the helper were removed from the +F 256 treatment and were transferred back to the institute's breeding stock. During the following 72 257 ± 2 days ('neutral phase'), the sibling groups of both treatments were kept in their original 100-L compartments under identical, standard housing conditions (following Taborsky et al. 258 2012). 259

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261 Social challenge test

As a social challenge, we chose a test situation that juvenile fish encounter regularly in natural territories, where they have to defend a private shelter against other juvenile family members (Taborsky 2016b). On day 134 (\pm 2 days), four individuals per experimental group were used

in this social challenge test. Two fish were assigned to the challenge treatment and two fish to 265 266 a control treatment. Behavioural data were collected from a total of 80 fish (36 +F individuals from 9 groups and 44 – F individuals from 11 groups). Brain samples were taken from a total 267 of 71 fish; 36 challenged individuals (16 +F and 20 -F fish) and 35 controls (15 +F and 20 -F 268 fish). We staged an asymmetric contest over a shelter (for details see Arnold & Taborsky 269 2010). Briefly, a 20-L test tank (30 x 20 x 20cm) was divided into two compartments by an 270 opaque PVC wall. One compartment was empty and the other compartment contained a small 271 272 clay pot half placed in the centre, which served as a shelter. The focal individual of the 273 challenge test was always assigned the role of a territory intruder, that is, initially it did not own the shelter. Twenty-four hours before testing, a focal juvenile (2.303 cm \pm 0.012 SEM) 274 was removed from its home tank, measured, weighed and placed into the empty compartment 275 of the test tank (balanced between right and left side between trials). At the same time, an 276 277 unfamiliar N. pulcher of the same age was placed in the compartment with shelter to become 278 the pre-assigned shelter owner (2.303 cm \pm 0.645 SEM) and, thereby, the territory owner. Sizes were matched between the two individuals as close as possible (size difference 0.038 279 $cm \pm 0.006$ SEM). The shelter owner, which served only as an opponent for the focal fish, 280 was always a fish reared in a social group consisting of a breeder pair and a helper (+F 281 condition). Each shelter owner was used only once. In the control treatment, juveniles were 282 exposed to the same handling procedures as the challenged fish and placed in the empty 283 284 compartment of tanks equally equipped as the test tanks of the challenged fish, but without 285 any opponent present.

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The asymmetric competition trials were carried out on the day after the fish had been placed 287 288 in the experimental tank, between 12:00 and 14:00 h. Previous studies have shown that 24 h is 289 sufficiently long for N. pulcher individuals to occupy a novel shelter and defend it as its core territory (Arnold & Taborsky 2010; Taborsky et al. 2012). Before the start of a trial, the 290 divider between the compartments was lifted so that the pre-assigned intruder and the shelter 291 292 owner could interact. The starting point of the trial was set to the moment when either of the two fish crossed the virtual, vertical border between the two compartments (the place where 293 294 the PVC divider had been before) for the first time. From that moment onwards, the behaviour of the focal individual was recorded for 20 min from behind a black curtain with an 295 observation slit. The observer (CN) was blind to the rearing treatment of the focal fish. The 296 behaviour of both fish (submission, overt aggression, restrained aggression, hiding in shelter 297 and swimming activity) was recorded continuously using the Observer 5.0 software (Noldus, 298

The Netherlands). After 20 min the winner and loser of the contest were determined. A fish 299 300 was considered as winner when it stayed in or close (< 3 cm) to the shelter and when it was not attacked by its conspecific. Conversely, it was regarded as loser when it was evicted from 301 302 the vicinity of the shelter and showed submission, but no overt aggression, towards the other fish, or if it stayed close to the water surface (< 5 cm; see Taborsky et al. 2012). In seven 303 cases (2 +F fish and 5 -F fish) there was no clear winner or loser after 20 min, in which case 304 this contest was rated as 'undecided' and these trials were excluded from further behavioural 305 306 analysis. After 20 min the two fish were separated again by the divider and the winner was allowed to use the shelter for 10 min. For the control trials, we followed the same procedures 307 as in the challenge test, but the focal fish in the control situation was not exposed to a shelter 308 309 owner. In these trials, after the divider had been removed, the control fish could swim freely in the test tank for 20 min while we recorded its activity (swimming or in pot). At the end of 310 311 the observation the opaque wall was put back in and the control fish was left 10 min on the side with the shelter if it had entered the shelter during the experiment, otherwise it was left 312 313 on the opposite side in the aquarium.

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315 *Tissue sampling*

A 30-min interval from the start of the trial to brain collection was chosen since this protocol 316 has been used successfully before (Cummings et al. 2008). It could thus safely be assumed 317 that changes in gene activation patterns could be measured after this time. After the opaque 318 divider was put back in place following the 20-min behavioural recording, a 10-min period 319 without social contact followed for both the challenged and the control fish before the brain 320 tissue was sampled. In the challenge treatment, only brains of the intruder fish (the focal fish) 321 were sampled. In the control treatment, all control fish were sampled. Individuals were 322 sacrificed with an overdose of buffered Tricaine methanesulfonate (MS222; Sandoz, 323 Switzerland) within 30 s of catching and the brain was quickly dissected under a binocular 324 microscope (magnification: 16x). The brain was divided into five brain areas, telencephalon, 325 326 hypothalamus, cerebellum, optic tectum and hind brain. After the dissection each part was put into a 1.5 ml vial and immersed in RNAlater (Ambion). Further analysis focused on the 327 telencephalon and hypothalamus regions. Samples in RNA later were left overnight at +6 °C 328 and then moved to -20 °C for permanent storage. The sex of the individuals could not be 329 determined since in N. pulcher the sex can only be determined when the fish start to become 330 sexually mature, which occurs around lengths of 3.5 cm, while our test subjects ranged 331 332 between 2.1 - 2.4 cm standard length.

334 *Sample preparation*

We performed RNA extraction from telencephalon and hypothalamus, for each brain part 335 separately, using a miRNeasy micro kit (Qiagen) using a modified manufacturer protocol (see 336 supplementary material) so that the miRNAs were discarded. The RNA concentration and 337 sample composition was checked with a Nanodrop microvolume spectrophotometer (samples 338 ranged between 27-139 ng/ul). Reverse transcription was done using the same amount of 339 RNA from each sample (200 ng RNA from hypothalamus and 304 ng RNA from 340 telencephalon) using a standard Superscript protocol (Invitrogen). To confirm the expression 341 342 of each candidate gene and success of RT, a small amount of cDNA from random samples from both treatments was used in a PCR using all the different candidate genes and visualised 343 344 using an electrophoretic gel.

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346 *Candidate genes*

We measured the expression of five genes in the telencephalon (egr-1, bdnf, gr1, crf and 347 neuroserpin) and six genes in the hypothalamus (egr-1, bdnf, gr1, crf, avt and avtr) of N. 348 *pulcher*. We were interested in the reaction norm of these genes, that is, if their expression 349 350 level is different in fish facing a control versus a challenge condition, and if these reaction norms differed between fish reared in +F or -F social conditions. The gene 18S was used as a 351 352 control gene. egr-1 (early growth response 1, also known as NGFI_A, Krox-24, zif268, ZENK and TIS8) is an immediate early gene coding for a transcription factor used as a 353 marker for neuronal activity (Desjardins & Fernald 2010) and plasticity (Morgan & Curran 354 355 1995). The gene is activated in different brain areas in response to a novel or changing social cue (Burmeister et al. 2005), and this property has been used to determine which brain areas 356 357 respond to a certain stimulus. In the lateral part of the dorsal telencephalon (Dl), which is thought to be the fish homologue of the mammalian hippocampus (Folgueira et al. 2004), egr-358 359 *I* has been proposed to act as a transcription factor targeting later-acting genes involved in 360 stress responses (Desjardins & Fernald 2010). bdnf (brain-derived neurotrophic factor) is a 361 molecule influencing neuronal proliferation, differentiation and synaptogenesis (McAllister et al. 1999) and is therefore assumed to impact brain function and structure (Branchi et al. 362 363 2004). Rat pups facing repeated maternal deprivation show persistently altered bdnf 364 expression in the hippocampus and prefrontal cortex compared to control (undisturbed) pups 365 (Roceri et al. 2004). In A. burtoni a higher bdnf expression was observed in the Dl of fish learning a task (finding shelter and a female) compared to non-learners (Wood et al. 2011). 366

gr1 (glucocorticoid receptor 1) is a ligand-activated nuclear receptor that is part of the HPI 367 368 stress axis in fish and is activated by glucocorticoids. Acting as a transcription factor, it is involved in modulating stress responses in different tissues and in the negative feedback of 369 370 corticosteroids on stress responses taking place in the hippocampus (Jacobson & Sapolsky 1991; Kloet et al. 1998). Previous work showed that adult N. pulcher reared in -F conditions 371 have higher gr1 expression in whole brain samples than +F individuals (Taborsky et al. 372 2013). crf (corticotropin-releasing factor) plays a role in activating the stress response, and in 373 374 modulating social behaviours associated with parental care, social memory, as well as 375 prosocial and affiliative behaviours (review in Hostetler & Ryabinin 2013). crf was higher expressed in whole brain samples of N. pulcher reared in -F conditions (Taborsky et al. 376 377 2013). Neuroserpin is a serine protease inhibitor that is assumed to play a role in synaptic plasticity and is most prominently expressed in areas of the brain that participate in learning, 378 379 memory and behaviour (review in Miranda & Lomas 2006). Thus this gene might be implicated in plastic behavioural responses in fish. The neuropeptide arginine vasotocin (avt), 380 381 the fish homologue to the mammalian arginine vasopressin (AVP), is involved in osmoregulation, the regulation of the stress response, and in reproductive and social 382 383 behaviours (reviewed in Godwin & Thompson 2012). Aubin-Horth et al. (2007) showed that dominant individuals of N. pulcher had higher levels of whole brain avt gene expression, 384 compared to subordinate conspecifics, and its expression is higher in wild-caught males of the 385 social cichlid N. pulcher than of the non-social cichlid Telmatochromis temporalis (O'Connor 386 et al. 2015), but this difference was not repeated in a laboratory study (O'Connor et al. 2016). 387 The V1a2 receptor for avt (avtr) is implicated in social behaviour in fish by mediating 388 aggressive and mating behaviour (Lema 2010; Kline et al. 2011; Huffman et al. 2012b; 389 390 Oldfield et al. 2013; Huffman et al. 2015).

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392 *Quantitative real time PCR*

Primers for gr1 and crf were as in Taborsky et al. 2013, the avt, avtr and 18S primers were as 393 in O'Connor et al. 2015, while primers for the other genes were designed using the sequences 394 available from of N. brichardi 395 the genome (http://cichlid.umd.edu/cichlidlabs/kocherlab/bouillabase.html). The sequences are as follows: 396 egr-1 (using the A. burtoni sequence as a search template, NCBI database ID number: 397 398 AY493348.1, N. brichardi NCBI database ID number XM 006781510.1, for-CGGCGATATATCCTAAAATC; rev-TCCCATGCCTATAAACACT), bdnf (using the A. 399 400 burtoni sequence as a template, NCBI database ID number: HQ398161.1, N. brichardi NCBI

database ID number XM 006780270.1, for-GGGTGACAGCTGTGGATAAAA; rev-401 GGGGTTGCATTTGGTCTCATA) and neuroserpin (using the Oreochromis mossambicus 402 sequence as a template, NCBI database ID number: HQ667766.1, N. brichardi NCBI 403 404 database ID number XM 006799864, for-GGATGGACCCTGTTCTCC; rev-TTGCCCTGACCAGGACTCT). To determine amplification efficiency, the absence of 405 primer dimers and the specificity of amplification for each primer pair, qPCR experiments 406 and melting curves (50 to 90 Celsius) were run using standard curves consisting of 5 x 10-fold 407 dilutions (of pooled samples) in duplicates (Aubin-Horth et al. 2012). The primers (Eurofins) 408 409 and 5 µl of sample cDNA were prepared on a 384-well plate (axigen) using an epMotion 410 liquid handler (Eppendorf) and used for a quantitative real-time PCR experiment following 411 the scaled-down version of the Quantitect SYBRGreen PCR kit manufacturer's protocol (Qiagen) using a 384-well plate qRT-PCR machine (Light Cycler, Roche). Each sample for 412 413 hypothalamus and telencephalon was run in triplicate for a given gene together with no primers and no template controls. To verify that only a single amplified product was present 414 415 and that no primer dimers were produced, a melting curve was also performed on each replicate. Relative gene expression for each individual-brain area combination was calculated 416 417 using the expression of a control gene (18S) (Pfaffl 2001).

418

419 *Data analysis*

We used two different data sets to answer our questions. To analyse genomic reaction norms 420 421 and neurogenomic states of individuals from the different early social environment and social challenge treatments, we included all intruder and all control fish (data set 1). To analyse (i) 422 the expressed behaviours during the challenge of intruders and owners and (ii) the 423 relationship between intruder behaviour and gene expression, we only analysed intruder fish 424 that either won or lost the contest over the shelter (data set 2). Furthermore we analysed only 425 the interactions between the start and the end of a contest. Contests were considered to be 426 427 terminated when the loser did not aim to gain access to the shelter and retreated either to the upper parts of the water column or to a distant corner of the tank. As the duration of these 428 429 periods varied between trials, we analysed behavioural rates (per min). We used this subset of 430 the data (data set 2) for two reasons. (i) Controls could not be included because they could not 431 show any social behaviour; (ii) Contests which were still undecided after 20 min observation time were excluded, because behavioural frequencies are expected to vary with the eventual 432 433 fight outcome (e.g., the loser should show submission). By including fights that were ongoing

434 at the end of the observation time behaviours would be biased towards higher aggression435 relative to submission rates.

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Statistical analyses were conducted with R 3.0.2 (R Core Development team 2013) including 437 the package 'lme4' (Bates et al. 2013) and 'afex' (Singmann et al. 2015). Linear mixed 438 models (LMM) were built to analyse the influence of the two rearing treatments (+F and -F 439 fish) on fish behaviour. We used intruder behaviour as our dependent variable and rearing 440 treatment (+F / -F) as our independent variable. In the LMM with intruder submission as 441 442 dependent variable owner aggressive behaviour was included as covariate, as in N. pulcher 443 submission is often an immediate response to received aggression. In the LMMs with intruder 444 overt aggression and restraint aggression as dependent variable the contest outcome (winning/losing) was included as covariate. In a further set of LMMs, we analysed the 445 446 influence of the two rearing treatments (+F and -F fish), the social challenge treatments (intruder vs control fish) and their interactions on the expression levels of each single gene. If 447 448 the interaction term "rearing treatment x social challenge" was significant we conducted post 449 hoc analyses by testing for gene expression differences between the two social challenge 450 situations, separately within +F fish and -F fish, respectively. For all post-hoc analyses we present adjusted P-values after applying the Benjamini-Hochberg false-discovery rate method 451 (Benjamini & Hochberg, 1995) to correct for multiple testing. For some individuals, gene 452 expression data were missing for one or more genes because the coefficient of variation (CV) 453 of the three replicates was too large. A CV cutoff of 5% was used for all genes. The sample 454 sizes for each gene are as follows: in telencephalon: egr-1, bdnf, gr1, crf, neuroserpin N=57 455 (of them -F control = 14, -F intruder = 16, +F control = 13 and +F intruder = 14) and in 456 457 hypothalamus: egr-1 N=40 (of them -F control =12, -F intruder = 12, +F control = 6 and +F intruder = 10), *bdnf*, *gr1*, *crf*, *avtr* N=56 (of them –F control =17, –F intruder = 17, +F control 458 = 10 and +F intruder = 12) and avt N=54 (of them -F control = 17, -F intruder = 17, +F 459 control = 9 and +F intruder = 11). In addition, a principal component analysis (PCA) was 460 461 performed in order to reduce the complexity of the gene dataset and thus to obtain a "neurogenomic state" (Robinson et al. 2008) for each individual that summarises the 462 information on all genes in both brain areas. The PCA was done with 70 individuals as 463 464 observations and expression levels of 7 different candidate genes, with a total of 11 measures 465 of gene expression (5 in telencephalon, 6 in hypothalamus) as variables using the R package "psych" (function "principal"). A correlation matrix for the 11 measures of gene expression 466 467 was used as input (Pearson correlation coefficients). To be able to include individuals with

missing data (see above) in the analysis, the mean gene expression of that gene for a given 468 469 combination of rearing environment and social challenge was used in the data analysis for these individuals (Zar 1999). A varimax rotation was applied to the data. Loadings of 470 471 individual genes on each principal component (PC) were determined and the PC scores for individual fish were calculated. LMMs were built to analyse the influence of the early social 472 environment and social challenge treatments and their interactions on the first two principal 473 components (see below). All models assumed a Gaussian error structure, which was validated 474 by visual inspection of the distributions of residuals, predicted vs. fitted values and Quantile-475 476 Quantile (Q-Q)-plots. Some variables were log-transformed in order to achieve a normally 477 distributed error structure. Experimental group was included as random factor in each model. 478 To account for possible effects of intruder size, the intruder standard length (I_SL) was included as covariate in all behavioural models. For significance testing each term was singly 479 480 removed from the model and the reduced model was compared to the full model. To do so we used the command 'mixed' in the R package 'afex', which calculates type 3 p-values using a 481 482 Kenward-Roger approximation for degrees-of-freedom (Singmann et al. 2015). Models were fitted with sum contrasts. These are orthogonal contrasts, where every level of a factor is 483 484 compared to the overall factor mean, which is represented by the intercept.

485

486 *Ethical note*

Fish interacted directly with each other in the asymmetric competition. We observed carefully 487 that no fish was injured during the experiment, in which case the trial would have been 488 489 immediately interrupted. This never happened. Some fish showed overt aggression towards each other (i.e. aggression that involves body contact, Taborsky 1984). Probably due to the 490 491 small size and low weights of the fish, these direct body contacts never caused any injuries in 492 the opponent. A fish subject to overt aggression usually responded by showing submissive tail quivering and/or by retreating out of reach of the aggressor, which stopped aggression 493 immediately. 494

495

496 **Results**

497

498 *Effect of early social environment on behavioural phenotype*

To test whether our early social environment treatment was effective to influence the phenotypic development of the fish, we tested whether the rearing treatment influenced the later-life social behaviour of our experimental fish. Intruder fish of the +F treatment displayed

more submissive behaviour relative to the amount of received owner aggression than did fish 502 503 from the -F treatment (Fig. 1, LMM, interaction term: F = 7.2413, P = 0.013, treatment: F =1.269, P = 0.270, received aggression: F = 22.599, P < 0.0001, N = 31). In contrast, intruder 504 505 overt aggression did not differ between the rearing treatments but winners showed more overt aggression than losers (LMM, treatment: F = 0.759, P = 0.397, contest outcome: F = 4.381, P 506 = 0.048, N = 31). Intruder restraint aggression (i.e., threat displays towards the opponent 507 without body contact) was not influenced by the rearing treatment or by contest outcome 508 (LMM, treatment: F = 0.203, P = 0.658, contest outcome: F = 0.001, P = 0.992, N = 31). 509

510

511 Genomic reaction norms in response to early social environment and social challenge 512 treatments

Telencephalon. The early social environment (+F/-F) and the social challenge 513 514 (intruder/control) treatments interactively influenced the expression of egr-1 and gr1 in the telencephalon (Fig. 2, table 1). Post hoc analysis revealed that -F fish had a lower egr-1 515 516 expression in the control than in the intruder situation (LMM, -F fish: F = 11.372 adjusted P = 0.006, N = 30), whereas in +F fish there was no difference in egr-1 expression with respect 517 518 to the social challenge (LMM, +F fish: F = 0.215, adjusted P = 0.648, N = 27). In +F fish gr1 expression tended to be lower in the intruder than in the control situation (LMM, +F fish: F =519 5.355, adjusted P = 0.063, N = 27), whereas -F fish did not differ with respect to the social 520 challenge (LMM, -F fish: F = 0.124, adjusted P = 0.728, N = 30). The early social 521 environment and social challenge did not significantly influence gene expression levels of 522 bdnf, crf and neuroserpin in the telencephalon (Fig. 2, table 1 and S1, Supplementary 523 material). 524

525

Hypothalamus. The early social environment (+F/-F) and the social challenge 526 (intruder/control) treatments interactively influenced the expression of bdnf in the 527 hypothalamus (Fig. 3, table 1). Post hoc analysis showed that +F fish had a higher bdnf 528 529 expression in the control than in the intruder situation (LMM, +F fish: F = 5.815, adjusted P =0.029, N = 22), whereas the reverse was found in -F fish, which had a higher *bdnf* expression 530 in the intruder than in the control situation (LMM, treatment: F = 15.007, adjusted P = 0.001, 531 N = 34). Moreover, fish reared in the +F social environment had a higher expression of egr-1 532 than in the -F condition, whereas the social challenge did not influence its expression (Fig. 3, 533 table 1). The early social environment and social challenge did not influence the expression of 534 535 gr1, CFR, avt and avtr in the hypothalamus (Fig. 3, table 1 and S1, Supplementary material).

537 Neurogenomic states

We used a PCA analysis to define a neurogenomic state that synthetises gene expression 538 patterns in the two brain areas studied for each individual. The first two principal components 539 of the PCA accounted for a total of 45% of the variance in gene expression (PC 1: 27 %; PC 540 2: 18%, table 2). All genes analysed in the telencephalon (egr-1, bdnf, gr1, crf 541 and neuroserpin) loaded positively on PC1. The genes analysed in the hypothalamus loaded 542 negatively (egr-1, gr1) or positively (bdnf, crf, avt and avt) on PC2 (table 2). We extracted the 543 544 individual PC scores for each fish for the two first principal components and investigated the 545 effects of early social environment and social challenge treatment on these two components 546 by LMMs (Fig. 4). For example, a positive score for an individual on PC1 indicates higher expression in the telencephalon of the five genes studied. The early social environment and 547 548 the social challenge jointly influenced PC1 and PC2 (table 3). This significant interaction was reflected in a larger divergence of neurogenomic state (PC scores) between control and 549 550 intruder fish from the +F rearing treatment as compared to -F fish, along both PC axes (Fig. 551 4).

552

553 Behaviour and gene expression

The expression levels of two of the analysed genes were associated with behavioural variation 554 among individuals (table 4). In the telencephalon, *crf* expression was interactively influenced 555 by the early social environment and intruder submission. In +F intruders the expressed *crf* 556 557 levels decreased with increasing amounts of displayed submissive behaviours, whereas no such relationship was present in -F intruders (Fig. 5a). In the hypothalamus, grl expression 558 559 decreased with intruder submission, with no effect of early social environment (Fig. 5b). Gene 560 expression was not influenced by intruder overt and restrained aggression. Winning or losing the contest did not impact expression of any of the genes, nor was gene expression of winners 561 vs. losers influenced by the social treatment. None of the other analysed genes were 562 563 significantly related to any social behaviour.

564

565 Discussion

In this experimental study, we aimed to understand how the early social rearing environment of a cooperatively breeding fish species influences brain genomic responses to a short-term social challenge. We found that early social environment and social challenge treatments interactively influenced the expression of an immediate early gene (egr-1) and a

glucocorticoid receptor (grl) in the telencephalon, and of a neural plasticity gene (bdnf) in the 570 571 hypothalamus. Moreover, egr-1 in the hypothalamus was more expressed in fish reared in the +F environment, independently of their exposure to a social challenge. A global analysis of 572 573 the 11 measures of gene expression patterns in the brain showed that the neurogenomic state 574 diverged more between intruder fish and control fish from the +F rearing treatment than in -F fish. Finally, we showed that with increasing submissive behaviour of intruders the expression 575 of crf in the telencephalon decreased, but only in fish from the +F rearing treatment. In the 576 hypothalamus, grl expression decreased with increasing amounts of submissive behaviour of 577 578 the intruder.

579

580 We first established that the behavioural response of a fish to a social challenge was markedly affected by the rearing treatment. During the social challenge, intruder fish reared with 581 582 parents and a helper showed more submissive behaviour per received aggression. If in a 583 natural context an intruder cannot monopolize its own shelter, the adequate response is to 584 submit towards other shelter owners (Taborsky 1985, Zöttl et al. 2013a). The latter are then willing to tolerate the subordinate fish close to the shelter (Taborsky et al. 2012), which 585 586 would enable the subordinate to share the access to the shelter in case of a predator attack. 587 Our result therefore suggests that +F fish showed better social competence, confirming earlier findings by Arnold & Taborsky (2010) from a similar behavioural experiment. 588

589

The early rearing environment influenced the gene expression response to a social challenge 590 591 of several genes in both the telencephalon and the hypothalamus. First, the telencephalon expression of egr-1 was relatively high in +F fish in both social situations (control or 592 593 intruder), while in -F fish this gene was highly expressed only after taking part in the contest 594 over a shelter. Environmental stimulation activates the expression of egr-1 (Burmeister & 595 Fernald 2005, Goerlich et al. 2012). Higher egr-1 expression of -F intruders after the challenge compared to the -F control suggests a short term response to the challenge, while 596 597 there is a lack of an *egr-1* response to the challenge in the +F intruders which keep a higher baseline egr-1 expression. Similarly, isolation-reared, but not group-reared, male mice had a 598 599 significant rise in expression levels of *c*-Fos, another immediate early gene, in the prefrontal 600 cortex two hours after facing a social challenge (Ago et al. 2013). Together, these studies suggest that the transcription response of egr-1 to a social challenge can be affected by the 601 early social environment in vertebrates. These changes can have far-ranging consequences. 602 603 Since *egr-1* is a transcription factor mediating the expression of downstream genes belonging

to many different pathways, it is likely that entirely different networks are activated under the
two social rearing conditions. Higher *egr-1* expression measured in +F fish and in challenged
-F fish could increase their behavioural and neuronal plasticity (Donovan *et al.* 1999),
activate effector genes downstream (for example by regulating GR expression by binding to
its promoter (Weaver *et al.* 2007; Weaver *et al.* 2014) and increase learning and memory
capabilities (Joëls *et al.* 2006; Roozendaal & McGaugh 2011).

610

Second, like egr-1 expression, expression levels of gr1 in the telencephalon were influenced 611 612 by the combined effect of rearing environment and social challenge treatments. In +F fish, gr1 was downregulated in the intruder challenge group compared to the control situation, whereas 613 614 in -F fish, grl expression was generally low and unaffected by the social challenge. Fewer glucocorticoid receptors in specific brain regions are known to reduce the efficiency of 615 616 negative feedback to return cortisol levels to normal, pre-stress levels (Ladd et al. 2004). In rats, for instance, decreased quality of maternal care leads to life-long reduction of gr 617 618 expression (the functional homologue of the grl gene in fish, Bury et al. 2003) in the hippocampus and prefrontal cortex (telencephalon in fish), impairing their negative feedback 619 620 inhibition of the HPA axis (Liu et al. 1997; Ladd et al. 2004; Navailles et al. 2010). 621 Interestingly, after the social challenge, +F and -F fish had similarly low grl levels. Poststress down-regulation of glucocorticoid receptor gene expression has been recently 622 quantified in mammals. A 15-min forced swim test in rats quickly resulted in lower levels of 623 gr mRNA in the hippocampus, which was suggested to be a mechanism protecting neurons 624 from repeated stress (Mifsud et al. 2016). The response to the social challenge observed in +F 625 fish is similar suggesting that this could be a "normal" vertebrate-wide transcriptional 626 response to challenging situations, which is disturbed by early rearing in a socially-deprived 627 628 environment, as seen in –F fish.

629

Finally, *bdnf* expression levels in the hypothalamus showed crossing reaction norms, as there 630 631 were both developmental and short-term environmental effects. After the contest, +F fish had a lower *bdnf* expression than in the control situation, whereas the reverse pattern was present 632 633 in –F fish. Thus the response in –F individuals was opposite to that of +F fish, suggesting that the same activational pathways were used differently in the same situation by fish from the 634 two rearing treatments. *bdnf* is implicated in several important functions, including the stress 635 response. Rats subjected to stress show increased hypothalamic bdnf mRNA levels (Smith et 636 637 al. 1995) and conversely, strong cerebral bdnf inhibition decreases HPA activity in mice

(Naert et al. 2015). Our results would thus suggest that -F fish may be subject to a higher 638 stress response when socially challenged. Moreover, +F fish might have been more stressed 639 while being alone in the control situation. However, increased *bdnf* expression is also 640 expected to enhance synaptic plasticity (Alder et al. 2003). Therefore we would have 641 predicted +F fish, which are known to behave more flexibly in social encounters (Taborsky & 642 Oliveira 2012, this study), to show higher expression when socially challenged. +F 643 individuals had a higher *bdnf* expression only in the control situation, suggesting that their 644 basic state, that is, before a social challenge, may be inherently more amenable to plasticity. 645 646 However, the fact that we found lower expression after the challenge may mean that the role 647 of *bdnf* in the stress response is more prominent in this system. Measuring *bdnf* levels after a 648 non-social stress could help disentangle these two effects.

649

650 Gene expression was not always influenced by both the early rearing environment and the short term social challenge. In the hypothalamus, egr-1 was only influenced by the rearing 651 652 treatments. The hypothalamus is a key area regulating many different social behaviours, including aggression, parental care, sexual behavior and social cognition, and the activity of 653 654 the HPA axis (O'Connell & Hofmann 2011; Wolkers et al. 2015). Because of the broad effect of egr-1 on many different pathways the higher egr-1 hypothalamus expression in +F fish 655 compared to -F fish might indicate that +F fish are able to show a greater extent of plasticity 656 than -F fish in a wide array of social behaviours and social contexts. Furthermore, contrary to 657 our expectations, the early social environment and social challenge did not influence gene 658 expression of crf, bdnf and neuroserpin in the telencephalon, or gr1, crf, avt and avtr in the 659 hypothalamus. There are several possible reasons to explain the lack of treatment difference 660 in expression of these genes. First the timing of sampling is crucial (see Liu et al 2000). If we 661 662 sample the brain too early, some later acting genes have possibly not been activated yet, whereas when sampling too late we might miss the window for early-activated genes. 663 Furthermore, it is possible that differential gene expression in opposite directions in different 664 665 sub-regions of the complex 'social decision making (SDM) network' might have masked an effect (Greenwood et al. 2008). The telencephalon contains six important nodes of the SDM 666 667 network and the hypothalamus holds two nodes (O'Connell & Hofmann 2011). Since we sampled the whole telencephalon and hypothalamus, we might have lost some valuable 668 669 information on gene expression at the level of the subregions (Wood et al. 2011) Finally, while the control fish in our experiment did not meet an opponent in the control situation, we 670 671 nevertheless cannot exclude that they perceived the control environment as novel experience, 672 which influenced brain gene expression.

673

The pattern of expression of several genes can define the neurogenomic state associated with 674 a particular behaviour (Robinson et al. 2008, Aubin-Horth et al. 2009). In addition to our 675 analysis of effects on single genes, we investigated the neurogenomic state of fish reared in 676 each type of environment. Fish reared in the more natural +F environment showed a larger 677 shift in neurogenomic state when faced with a social challenge compared with fish that 678 experienced a -F rearing environment. The principal component analysis suggests that the 679 680 expression of candidate genes is strongly coordinated within each of the targeted brain areas. 681 The larger overall change observed in fish reared in the natural, +F environment thus suggest 682 that the social challenge we chose has significant consequences for the coordinated activation of the molecular networks of these genes. This result also raises the intriguing possibility that 683 684 -F fish do exhibit a genomic response, but that it is delayed. Quantifying such a potential time shift in genomic response was beyond the scope of the study but could also potentially result 685 686 in the altered behavioural response observed in these fish. In any cases, these concerted genomic modifications may by linked to the modulation of behaviour in response to the social 687 688 challenge (reviewed in Robinson et al. 2008, Taborsky & Oliveira 2012).

689

690 The observation that a behavioural response to a social challenge is accompanied by changes in the average level of gene expression can reasonably lead to the prediction that behaviour 691 and gene expression will covary at the individual level (Williams 2008). This is supported by 692 693 our results on the link between gene expression and the expression of submissive displays, a social behaviour, which is of particular importance for N. pulcher to maintain the stability of 694 695 its social system. The amount of submissive displays by intruders decreased with the 696 expression of crf in the telencephalon, and grl in the hypothalamus. Showing more 697 submissive displays represents an adequate behavioural response when being in the intruder role, as most intruders were not able to take over the shelter. For crf the interaction between 698 699 social rearing and amount of submission was significant; intruders of +F treatments showing 700 more submission had lower crf expression, while in -F intruders this trend was absent. For 701 grl, intruders from both rearing treatments showed more submission with a lower expression 702 of the gene. It is possible that the amount of submission an intruder shows influences the 703 expression of these genes, or that the gene expression itself regulates the submissive behaviour. The lower *crf* expression in intruders showing more submission could be related to 704 705 social defeat stress (SDS) as seen in rats (Panksepp et al. 2007), as submissive intruders are the defeated contestants in our social challenge test. Rats facing SDS have lower hippocampal *crf* mRNA expression 6 hours after an encounter compared to non-defeated rats (Panksepp *et al.* 2007). *N. pulcher* intruders with higher *gr1* expression might be more bold and risk-prone,
as it has been observed in sticklebacks (Aubin-Horth *et al.* 2012), which might explain their
lower submission tendencies.

711

In conclusion, our results highlight the importance to incorporate the environmental 712 conditions experienced during development when we aim to understand the genomic basis of 713 714 social behaviour. Furthermore it shows how integrative biology approaches can help understanding the evolution of complex social behaviour, by jointly investigating molecular, 715 716 neuroendocrine and behavioural responses to environmental conditions in ecologically relevant contexts (Aubin-Horth & Renn 2009; Taborsky & Taborsky 2015). Future studies 717 718 should aim to obtain a more complete picture of the genes and the gene networks involved in the development and regulation of social behaviour. 719

720

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- 1011

1012 Data accessibility

Behavioural observation files and gene expression values have been deposited to Dryad,
 doi:10.5061/dryad.9c2j1

- 1016 Information on primers is provided in the Methods section
- 1017
- 1018 Supplementary material
- 1019 RNA extraction protocol
- 1020 Results of the full linear mixed models including non-significant interactions testing the
- 1021 effect of rearing environment and social challenge on the expression of candidate genes.
- 1022
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- 1024

Figure legends 1

2

3 Fig. 1: Intruder submission (log transformed) in relation to received owner aggression (log transformed). Behaviours are expressed as rates per minute. Circles and black lines represent

- 4
- the –F treatment; triangles and red lines represent the +F treatment. 5
- 6
- 7 Fig. 2: Gene expression for control and intruder fish for 5 genes in the telencephalon. (A)
- immediately early gene egr-1, (B) brain-derived neurotrophic factor (bdnf), (C) glucocorticoid 8
- 9 receptor (gr1), (D) corticotropin releasing factor (crf) and (E) neuroserpin. Gene expression
- of egr-1 is log-transformed as it was done in the linear mixed model. Black circles represent 10
- F treatment, red triangles represent +F treatment. Figures display means ± SE. 11
- 12 Fig. 3: Gene expression for control and intruder fish for 6 genes in the hypothalamus. (A)
- immediately early gene egr-1, (B) brain-derived neurotrophic factor (bdnf), (C) glucocorticoid 13
- 14 receptor (gr1), (D) corticotropin releasing factor (crf) (E) arginine-vasotocin (avt) and (F)
- arginine-vasotocin receptor V1a2 (avtr). Gene expression of egr-1, gr1, crf and avt is log-15
- 16 transformed as it was done in the linear mixed models. Black circles represent –F treatment,
- 17 red triangles represent +F treatment. Figures display means±SE.
- 18 Fig. 4. Relationship between individual PC1 and PC2 scores representing the neurogenomic
- states of individuals from each combination of early social environment and social challenge. 19
- 20 Triangles represent +F rearing treatment fish and circles -F individuals. Open symbols
- 21 represent control individual in the social challenge and filled symbols represent intruders.
- 22
- 23 Fig. 5: Association of intruder submission and gene expression of (A) crf in the telencephalon
- 24 and (B) grl in the hypothalamus. Gene expression of grl is log-transformed as it was done in
- the linear mixed model. Sample sizes crf. N=22, gr1: N=21. Circles and black lines represent 25
- 26 -F treatment; triangles and red lines represent +F treatment.
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Brain area	Factors	Estimate ± SE	F-value	p-value
Telencephalon	<i>egr-1</i> (log)			
	Rearing	- 0.064± 0.025	6.473	0.023
	Challenge	- 0.034±0.025	1.787	0.189
	Rearing x			
	Challenge	-0.055±0.025	4.684	0.036
	bdnf			
	Rearing	-0.016±0.049	0.101	0.756
	Challenge	0.030±0.044	0.457	0.503
	gr1			
	Rearing	-0.080±0.037	4.627	0.048
	Challenge	0.062± 0.036	2.959	0.093
	Rearing x	-0.077±0.036	4.577	0.038
	Challenge			
	Crj		2 260	0 000
	Challenge	-0.101±0.056	3.200	0.090
	Challenge	0.022±0.040	0.315	0.578
	neuroserpin	0.020+0.042	0.425	0 5 2 4
	Rearing	-0.028±0.043	0.425	0.524
	Challenge	-0.001±0.041	0.001	0.980
Hypothalamus	egr-1 (log)	0.457.0.070	4 0 0 0	
	Rearing	-0.15/±0.0/0	4.880	0.044
	Challenge	0.060±0.068	0.756	0.392
	bdnf			
	Rearing	0.036±0.045	0.643	0.435
	Challenge	-0.023±0.042	0.281	0.600
	Rearing x	-0.181±0.042	18.195	0.0001
	challenge			
	gri (log)	0.011+0.010	0.260	0 5 5 7
	Challange	0.011 ± 0.019	0.300	0.557
	challenge	-0.010±0.017	0.352	0.550
	Crj (log)	0.015+0.020	0 1 9 1	0 676
	Challenge	0.015±0.029	0.181	
	Challenge	0.025±0.025	1.077	0.3055
	avt (log)	0.076+0.400	0.070	0 - 1 -
	Rearing	U.U/6±U.123	0.379	0.547
	Challenge	0.084±0.076	1.199	0.280
	avtr			
	Rearing	-0.057± 0.052	1.196	0.291
	Challenge	-0.022± 0.050	0.191	0.665

Table 1: Results of the linear mixed models testing the effect of rearing environment (-F or +F) and social challenge (intruder or control situation) on the expression of candidate genes in *N. pulcher*. For sample sizes see section "Data analysis". P-values <0.05 are highlighted in bold.

Table 2: Factor loadings for the 7 different candidate genes, with a total of 11 measures of gene expression (5 in telencephalon, 6 in hypothalamus) on the first two principal components (PC). The respective higher loadings among the two PCs are highlighted in bold. N=70.

Brain area	Gene	PC1	PC2
Telencephalon	egr-1	0.66	-0.04
	bdnf	0.80	-0.13
	gr1	0.79	0.05
	crf	0.74	-0.14
	neuroserpin	0.83	-0.11
Variance explained		27%	
Hypothalamus	egr-1	0.11	-0.22
	bdnf	0.15	0.78
	gr1	0.08	-0.21
	crf	0.03	0.43
	avt	-0.14	0.56
	avtr	-0.03	0.86
Variance explained			18%

Table 3: Results of the linear mixed models testing the effect of rearing environment (-F or +F) and social challenge (intruder or control situation) using the PC scores of the first two principal components. N= 70. P-values <0.05 are highlighted in bold.

Factors	Estimate ± SE	F-value	p-value
PC1			
Rearing	-0.234±0.128	3.337	0.09
Challenge	0.059±0.109	0.290	0.59
Rearing x challenge	-0.313±0.109	8.262	0.006
PC2			
Rearing	0.156±0.117	1.766	0.2
Challenge	0.250±0.114	4.794	0.03
Rearing x challenge	-0.231±0.114	4.126	0.05

Brain area	Factors	Estimate ± SE	F-value	p-value
Telencephalon				
crf				
	Rearing	-0.318±0.101	9.002	0.009
	Submission	-0.003±0.002	2.832	0.128
	Intruder size	-1.241±0.968	1.381	0.263
	Rearing x submission	0.006± 0.002	8.995	0.014
Hypothalamus				
gr1				
	Rearing	-0.060±0.042	1.917	0.191
	Submission	-0.003±0.001	8.121	0.012
	Intruder size	0.171±0.494	0.097	0.759

Table 4: Effect of rearing environment, submissive behaviour and size of intruders on brain gene expression in fish facing a social challenge. *crf*: N=22, *gr1*: N=21. P-values <0.05 are highlighted in bold.