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Pauline Salis, Natacha Roux, Delai Huang, Anna Marcionetti, Pierick Mouginot, et al.. Thyroid hormones regulate the formation and environmental plasticity of white bars in clownfishes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118 (23), pp.e2101634118. 10.1073/pnas.2101634118 hal-03368778

HAL Id: hal-03368778 https://hal.science/hal-03368778v1

Submitted on 5 Nov 2021

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1 Thyroid hormones regulate the formation and environmental

2 plasticity of white bars in clownfishes

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22	Keywords: Pigmentation, Developmental plasticity, Clownfishes, Thyroid Hormones,
23	Metamorphosis
24	
25	Classifications: Biological sciences- Developmental Biology
26	
27	Authors contribution

P.S., N.R., M.R. and N.R. performed research. B.P., P.M. designed and performed the
inference approach. D.P. and D.H. performed CRISPR-Cas9 in *D. rerio*. O.S. and S.P.
performed sampling of *A. percula*. A.M. and N.S. analyzed transcriptomic data. P.S., S.P.
and V.L. designed research. P.S. and V.L. wrote the article.

32 Abstract

33 Determining how plasticity of developmental traits respond to environmental conditions is a 34 challenge that must combine evolutionary sciences, ecology and developmental biology. 35 During metamorphosis, fish alter their morphology and color pattern according to 36 environmental cues. We observed that juvenile clownfish (Amphiprion percula) modulate the 37 developmental timing of their adult white bar formation during metamorphosis, depending on 38 the sea anemone species in which they are recruited. We observed an earlier formation of 39 white bars when clownfish developed with Stichodactyla gigantea (Sg) than with Heteractis 40 magnifica (Hm). As these bars, composed of iridophores, form during metamorphosis, we 41 hypothesized that timing of their development may be thyroid hormone (TH) dependent. We 42 treated clownfish larvae with TH and found that white bars developed earlier than in control 43 fish. We further observed higher TH levels, associated with rapid white bar formation, in 44 juveniles recruited in Sg than Hm, explaining the faster white bar formation. Transcriptomic 45 analysis of Sg recruits revealed higher expression of duox, a dual oxidase implicated in TH 46 production as compared to Hm recruits. Finally, we showed that duox is an essential 47 regulator of iridophore pattern timing in zebrafish. Taken together our results suggest that TH 48 control the timing of adult color pattern formation and that shifts in *duox* expression and TH 49 levels are associated with ecological differences resulting in divergent ontogenetic 50 trajectories in color pattern development.

51 Significance statement

52 Developmental plasticity is defined as the ability of an organism to adjust its development 53 depending on environmental signals, thus producing alternative phenotypes precisely 54 adjusted to the environment. Yet the mechanisms underlying developmental plasticity are not 55 fully understood yet. We found that juvenile clownfish delay the development of their white 56 bars during metamorphosis, depending on the sea anemone species in which they are 57 recruited. To understand this developmental plasticity, we investigated roles for thyroid 58 hormones, the main hormones triggering metamorphosis in vertebrates. We found that 59 thyroid hormones regulate white bar formation and that a shift in hormone levels, associated 60 with ecological differences, results in divergent color patterns in different sea anemone 61 species in which the young fish is recruited.

64 Introduction

65 Understanding the origins of biodiversity is one of the major challenges of biology, but it 66 should not be limited to the species level, which is however already a formidable task (1). 67 Indeed, diversity is also present within species, as phenotypic variation between distinct 68 populations, and also within populations, depending on individual genotype and the extent to 69 which physiology, behavior, or development are influenced by the environment (1, 2). In 70 some instances, this phenotypic variation can reflect adaptive developmental plasticity that is 71 defined as the ability of organisms to change their developmental trajectories to generate 72 phenotypes precisely adjusted to the environmental conditions (1–3). Remarkable examples 73 of such plasticity are known in animals, giving rise to distinct color patterns and other 74 morphological traits, as well as life-histories (4). For instance, different generations of 75 butterfly can develop alternative color patterns on their wings, depending on the season in 76 which they emerge (5). Water fleas can grow large helmets and spikes as a response 77 induced by predator cues, such as the concentration of kairomones in the water (6). 78 Spadefoot toad tadpoles living in semi-arid environments accelerate their metamorphosis in 79 response to pond drying (7).

80

Determining how plastic developmental changes that occur in response to environmental conditions are coordinated at the physiological, cellular, and molecular levels is a challenge that must combine ecology with developmental biology (8, 9). The mechanisms that underlie the development of alternative phenotypes are still unclear for many systems and is one major goal of ecological developmental biology or Eco-Evo-Devo (1, 10).

86

87 Pigmentation is one of the conspicuous features of animals and often has clear ecological 88 and behavioral significance. It is thus an outstanding model for understanding links between 89 environment and developmental plasticity. There are several cases of teleost fishes 90 exhibiting phenotypic plasticity in pigmentation (11). This is the case in cichlids, for which 91 several species exhibit a conspicuous yellow-blue bright phenotype linked to social 92 dominance (12), in the platyfish in which melanic spots phenotypes are polymorphic within 93 and among populations of Xiphophorus variatus depending on stress status (13), in 94 salmonids with various pigmentation phenotypes linked to stress and social dominance (14) 95 and also in coral reef fishes such as the dottybacks depending on the presence of prey 96 species (15).

97

98 One of the most extraordinary life history transitions in vertebrates is metamorphosis which is 99 regulated by thyroid hormones (TH) (16). With the very large number of TH-regulated 100 morphological changes occurring during larval metamorphosis (17, 18), environmentally 101 induced alterations to TH status during this developmental period have the potential to affect 102 outcomes of the metamorphic process (19). TH is also required to shift the larval 103 pigmentation toward adult pattern (20). In zebrafish, for instance, TH promotes the 104 maturation of specific pigment cells, black melanophores and yellow xanthophores (21). 105 Whereas TH drives the terminal differentiation and proliferative arrest of melanophores, thus 106 limiting their final number, it promotes the accumulation of orange carotenoid pigments in 107 xanthophores, making the cells more visible (21, 22).

108

109 Here, we investigate the potential role of TH in a case of developmental plasticity in color 110 morphs of clownfishes and we tested the impact of two environments (e.g. sea anemone 111 species) on that kinetic. Among these coral reef fishes, two closely related allopatric species, 112 Amphiprion ocellaris and Amphiprion percula, live in mutualistic symbiosis with sea 113 anemones in the tropical Indo-pacific (23, 24). We observed that A. percula young juveniles 114 (referred to here as recruits) have a different rate of white bar formation depending on the 115 sea anemone species, their obligate symbiotic partner, in which they are recruited: white 116 bars develop more rapidly when fish are recruited in Stichodactyla gigantea than in 117 Heteractis magnifica. Because A. ocellaris acquire their adult color pattern during 118 metamorphosis (25, 26), we asked whether developmental plasticity in bar formation is 119 associated with alteration in TH status. Using A. ocellaris we found that blocking TH 120 production delayed white bar formation, whereas excess TH accelerated white bar formation, 121 revealing a role for TH in determining the rate at which color pattern shifts from larva to 122 juvenile form. To test the ecological significance of these findings, we assayed TH titers and 123 gene expression in wild-caught A. percula and found that young recruits associated with S. 124 gigantea exhibited a higher levels of TH and more abundant transcript of duox, a gene 125 implicated in thyroid function and TH synthesis, as compared to recruits associated with H. 126 *magnifica* (27). Further supporting a role for *duox* and TH in regulating the timing of 127 iridophore patterning, we found that zebrafish deficient for duox activity were delayed in 128 iridophore stripe formation relative to overall developmental progression. Taken together our 129 results suggest that TH regulates color pattern formation in clownfish and that shifts in 130 hormone levels are associated with ecological differences that result in divergent ontogenetic 131 trajectories in color pattern formation.

133 **Results**

134

Formation of white bars of *A. percula* new recruits is differentially influenced by age or size depending on anemone species

137 Amphiprion species acquire, in sequence, the head, body and finally peduncle white bars 138 during post-embryonic development (26). In Kimbe bay, Papua New Guinea, A. percula is 139 found in two different sea anemone hosts, Stichodactyla gigantea and Heteractis magnifica 140 and the fish leaving in these two hosts belongs to the same population (28). We observed in 141 the field that new A. percula recruits in S. gigantea have more white bars than new recruits in 142 *H. magnifica* for juveniles of the same age and developmental stage (juvenile stage). In fact, 143 33% of 148 new recruits (200–250 days old) in S. gigantea had 3 white bars, whereas only 144 5% of 118 new recruits of the same age in *H. magnifica* had this pattern (Fig. 1 A and B, Test 145 χ^2 p-value=0.0011).

146

We tested by multiple regression whether sea anemone species affects the timing of white bar formation of *A. percula* new recruits from Kimbe bay, while accounting for ecological and social structure variables. These results confirm our observations that new recruits had consistently more bars in *S. gigantea* than in *H. magnifica* for a similar age or size (Fig. 1C and D, Supp Fig 1A and B and Supp Table 1-4).

152

As illustrated Fig. 1C and Supp. Fig. 1A, the speed at which bands were acquired varies with age (or with size) and how the acceleration and deceleration of band acquisition varied with age (or size) also depends of the anemone species. Thus, our results indicate that anemone species differentially modulate the dynamic to which bars were acquired with age (or size). In fact, available data allow us to detect differences between anemone species in the shape of the relationship between bars and age (or size), but more data would be needed to fully characterize the shape of these relationships.

160

161 Adult color pattern formation is linked to a switch in pigment cell specific gene 162 expression

Because we know that the sister species, *A. ocellaris* acquire their adult color pattern during metamorphosis (25, 26), we addressed whether TH is associated with developmental plasticity in color pattern using this species as a laboratory model (24, 25). *A. ocellaris* exhibits two pigmentation patterns during development: before stage 5 (around 9 dph; (25)), larvae have yellow larval xanthophores with a set of stellate larval melanophores forming two horizontal stripes covering the myotomes (Fig. 2A, B, C and D, red arrowheads). From stage 5, larvae acquire, in a rostro-caudal temporal gradient, three white vertical bars (Fig. 2E, F,
G, white arrowheads), orange xanthophores outside of the future white bars (Fig. 2E, orange
arrows) and melanophores dispersed all over the body (Fig. 2E and F, black arrows) (25,
29). These melanophores are present over the body and are at higher density at the border
of the white bars (Fig. 2F and G).

174 To better understand color pattern changes occurring around stage 4, we assessed the 175 expression of pigmentation genes across post-embryonic stages. We extracted RNA from 176 whole larvae at each of the seven A. ocellaris post-embryonic stages and performed 177 transcriptomic analysis (29). We focused on pigmentation genes defined by (30, 31) (Fig. 2H, 178 Supp Fig. 2A and Supp Table 5), and particularly on iridophore genes, as we showed 179 previously that white bars are formed by iridophores (29) (Fig. 2I and J and Supp Table 5). 180 We observed that stages 1 to 3 are clearly separated from stages 4 to 7 along principal 181 component 2 (PC2) (Fig. 2 H and I). Among those genes, *fhl2b, pnp4a* and *prkacaa* have a 182 highest fold difference at stages 5 to 7 compared to stages 1 to 3 whereas gbx2, trim33, 183 gmps and oca2 have a highest fold difference at stages 1 to 3 compared to stages 5 to 7 184 (Fig. 2J). We also observed a clear separation across stages for all the functional categories 185 described in (30) (Supp Fig. 2A): pigment cell specification (Supp Fig. 2B), xanthophore 186 development (Supp Fig. 2C), pteridine pigment synthesis of xanthophores (Supp Fig. 2D), as 187 well as melanophore development (Supp Fig. 2E), melanogenesis regulation (Supp Fig. 2F), 188 and at a later stage, melanosome biogenesis (Supp Fig. 2G). These outcomes are consistent 189 with changes across stages in pigmentation gene expression, complements of different 190 pigment cell types, or likely both. They suggest that an important switch in the development 191 of color pattern, involving each of the three pigment cells, occurs at stage 4.

192

193 White bar formation is controlled by thyroid hormone signaling

194 TH contributes to metamorphosis and the developmental program controlling pigmentation 195 pattern in zebrafish and other teleosts (21, 32, 33). We hypothesized that TH regulates the 196 timing of white bar formation during clownfish metamorphosis. To test this hypothesis, we 197 exposed stage 3 larvae (5 dph) to different concentrations $(10^{-6}, 10^{-7})$ and 10^{-8} M) of the active 198 thyroid hormone, T3. After 3 days of treatment with T3, we observed a more rapid 199 appearance of white bars than in control larvae. This effect was dose-dependent with, at 3 days post-treatment (dpt), 0 % of the fish exhibiting two bands in the control, 50% at 10⁻⁸ M 200 201 T3, 78% at 10⁻⁷ M and 73% at 10⁻⁶M (Fig. 3A to D; Fig. 3E).

We then tested the effect of decreasing TH signaling by blocking TH production with a mix of goitrogens (34). Larvae treated from stage 3 (5 dph) had a delay in white bar development compared to controls at 9 dpt (Fig. 3H compared to the control Fig. 3G; Fig. 3F): whereas 75% of controls had developed head and trunk white bars, only 15% of larvae treated with MPI (Methimazol, Perchlorate Potassium and Iopanoïc Acid) exhibited these bars and the remainder were devoid of any bars (Fig. 3F). It should be noted that after 25 days of treatment, white bars ultimately formed in MPI-treated fishes demonstrating that a delay, rather than blockade in bar formation is associated with TH inhibition (Fig. 3I).

210 Pigment cells other than iridophores were also affected by TH treatment, with melanophore

numbers increasing significantly within 48 h of treatment with 10⁻⁶ M T3 beginning at stage 3

212 (5 dph) (Fig. 3J- p-value_{48hpt} = 0.0299; p-value_{72hpt} = 0.0043). In contrast, MPI treatments led

213 only to a minor decrease (non-significant) in melanophore numbers at 48 or 72 hpt (Fig. 3J).

We did not observe gross differences in xanthophore development, and it was not possible to identify individual xanthophores or to quantify their numbers.

216 Taken together, these results suggest that TH controls the timing of white bar formation

217 relative to overall somatic development and may act on iridophores and melanophores.

218

219 Expression of pigmentation genes is modified by T3 treatment

220 To determine how TH affects iridophores, we assayed expression of iridophore genes (*fhl2a*, 221 fhl2b, apoda.1, saiyan and gpnmb; 27) after treating larvae with exogenous TH. Stage 3 222 larvae were treated with T3 at different concentrations (10⁻⁶, 10⁻⁷ and 10⁻⁸ M) for 12, 24, 48 223 and 72 hours and expression of these genes was monitored by nanostring in RNA extracted 224 from whole larvae. After T3 treatment, transcripts for all of these genes were significantly 225 more abundant compared to levels in controls (Supp Fig. 3). In some cases (apod1a and 226 gpnmb) this effect was evident by 12h and in others (fhl2a, fhl2b and saiyan) only after 24 or 227 48h. This suggests that TH affects expression of genes known to be expressed in clownfish 228 iridophores.

229

Treatments with thyroid hormones or goitrogens lead respectively to ectopic iridophores over the body and decrease in white hue in white bars

232 To determine whether TH promotes iridophore differentiation, we treated stage 3 larvae with 233 T3 at 10⁻⁶ M for a longer period to compare juveniles at stage 6, when fish have developed 234 both head and body bars. Interestingly, head and body bars were never fully formed in T3 235 treated juveniles compared to controls (Supp Fig. 4D compared to Supp Fig. 4A) and close 236 inspection of larvae revealed numerous ectopic iridophores across the flank of T3 treated fish 237 (Supp Fig. 4F compared to Supp Fig. 4C- white arrowheads). Moreover, orange coloration 238 was decreased in T3 treated juveniles compared to control (compare Supp Fig. 4B and Supp 239 Fig. 4E). MPI treatment led to bars with normal shapes that were, nevertheless, more translucent presumably owing to deficiencies in the numbers of iridophores or the deposition 240 241 of crystalline guanine within iridophores normally responsible for their white (or iridescent) 242 appearance (N=2, Fig. 3I).

Together, these results indicate that exogenous TH leads to reduced orange coloration and defects in white bar formation accompanied by ectopic iridophores on the body, whereas blockade of TH production leads to a reduced number of white iridophores or reflective guanine within white bars.

248

Ecological modulation in timing of white bar formation is linked to TH levels and *duox*expression.

As TH treatment accelerated white bar development in *A. ocellaris*, we asked whether the accelerated acquisition of bars in *A. percula* recruits in *S. gigantea* was linked to TH. We sampled a second set of new recruits of 12-27 mm (having one white bar either complete or being formed) living either in *S. gigantea* (N=6) or *H. magnifica* (N=6) and measured TH levels. Concentrations of T3 (in pg/ g of larvae) were significantly greater in new recruits sampled from *S. gigantea* compared to the those from *H. magnifica* (Fig. 4A).

257

258 To gain insight into mechanisms that explain these differences we compared gene 259 expression between A. percula new recruits found in H. magnifica (n=3) or S. gigantea (n=3) 260 by RNA-Seq of whole fish. Out of the 19063 analyzed genes, only 21 were significantly more 261 expressed in new recruits from S. gigantea (adj. P-value < 0.05, Log₂FC > 1), while 15 were 262 significantly more expressed in new recruits from H. magnifica (adj. P-value < 0.05, Log₂FC < 263 1) (Fig. 4B, Supp. table 6). Within the differentially expressed genes, we observed duox, 264 which encodes a dual oxidase implicated in TH production (27, 35). This gene was 265 significantly overexpressed in new recruits from S. gigantea (adj. P-value = 0.038, Log₂FC 266 =2.53) compared to those from *H. magnifica*. Together, these results suggest that the rate of 267 white bar formation in *A. percula* is linked to a differential level of T3, which is in turn linked to 268 a differential expression of *duox*.

269

270 Last, we wanted to directly test whether *duox* is required for iridophore patterning. For this 271 we used zebrafish Danio rerio, in which iridophores depend on TH for their maturation (22). 272 duox requirements have been described for somatic development and melanophore 273 numbers, but not iridophore pattern (27, 35). We therefore injected one-cell stage embryos of the iridophore reporter line Tg(pnp4a:palm-mcherry)^{wprt10Tg} with highly efficient Alt-R CRISPR-274 275 Cas9 (36) targeting *duox*, resulting in phenotypes concordant with those for this locus (27, 276 35) and other hypothyroid fish (21, 22). Figure 4C shows mCherry+ iridophores (dark cells; 277 pixel values inverted) in representative uninjected (wild-type) and duox-deficient larvae of the 278 same stage [10.6 mm standard length (SL)]. In wild-type, densely packed iridophores have 279 formed one complete interstripe and a second interstripe has started to form ventrally; some

280 loosely arranged iridophores occur in between, where a melanophore stripe develops (37). In 281 the duox-deficient larva only a single wider interstripe has developed and fewer stripe 282 iridophores are visible (Fig. 4C) suggesting that iridophore development is slowed in duox-283 deficient animals. Consistent with this interpretation, most wild-type fish greater than 11.0 284 mm SL had developed two complete interstripes (score=2.0), whereas equivalently staged 285 duox-deficient fish had developed only one complete interstripe and were still developing a 286 second interstripe (score=1.5) (Fig. 4D). Despite having fewer interstripes overall, duox-287 deficient animals had proportionally more of the flank covered by dense, interstripe 288 iridophores, as compared to the wild type (Fig. 4E). These data show that *duox*, presumably 289 acting through TH (27, 35), contributes to the timing of iridophore interstripe appearance and 290 the patterning of interstripes in zebrafish.

291

To conclude, our findings suggest that reduced abundance of *duox* transcript in *A. percula* recruits within *H. magnifica* in comparison with those that are recruited in *S. gigantea* leads to a delay in the development of their white bars. This effect of *duox* in regulating the timing of iridophore development is conserved between the distantly related clownfish and zebrafish.

298 **Discussion**

299 During post-embryonic development, A. ocellaris lose their larval color pattern and acquire in 300 a few days and in a rostro-caudal sequence the head, body and caudal peduncle white bars 301 of their final adult color pattern. We showed here that during clownfish metamorphosis the 302 formation of iridophore-containing white bars that are formed by iridophores is accelerated by 303 TH, and that TH also underlie environmental (e.g. sea anemone species) plasticity in bar 304 formation in wild populations. Interestingly a corresponding effect on iridophore patterning 305 was also seen in zebrafish: duox mutants are hypothyroid (27, 35), and we found that 306 iridophore patterning of *duox*-deficient animals was delayed. All these data converge toward 307 the notion that variations in TH levels control a plastic pigmentation phenotype observed in 308 clownfishes.

309

310 The observation that in both clownfish and zebrafish, TH affects white bar (clownfish) or 311 interstripe (zebrafish) formation strongly suggests that these hormones directly or indirectly 312 act on iridophores. Previous studies revealed that TH deficiency in zebrafish leads to an 313 excess of melanophores and a loss of visible xanthophores (21). Further analyses showed 314 that these hormones act differently on these two cell types, promoting maturation but via 315 distinct mechanisms. TH promotes terminal differentiation and limits the final number of 316 melanophores whereas it promotes accumulation of carotenoid pigments in xanthophores, 317 making initially unpigmented precursors visible. A similar role for TH in promoting iridophore 318 maturation was suggested by analyses of single cell transcriptomic states, though 319 consequences for iridophore number and pattern were not assessed (22). In our analysis we 320 observed that interstripe development is slowed in duox-deficient animals and that duox-321 deficient animals had proportionally more of the flank covered by dense, interstripe-322 iridophores, as compared to the wild type. Together these several observations support the 323 idea that TH signaling has an evolutionarily conserved role in regulating the timing of 324 iridophore development in two species having markedly different adult pigment patterns. TH 325 receptors are expressed in iridophores of both species but analyses to date cannot indicate 326 whether effects of TH are direct or mediated through other cell types (22).

327

We also observed an effect of TH on the shape of the trunk white bars in clownfish. Indeed, late in TH treated fishes, we observed abnormalities in this trunk white bar that is misshapen and incomplete (*e.g.* it does not cross the full body of the fish; see Supp Figure 4D). This is interesting as a similar phenotype is often observed in clownfish juveniles raised in the 332 laboratory and has been assumed to result from nutritional defects (38–40). In addition to 333 abnormalities in the shape of white bars, we observed ectopic iridophores. We cannot 334 exclude at this point that the defects in white bar shape could be linked to a role of TH on 335 pigment cells migration.

336 We have observed that A. percula developing in association with S. gigantea acquire white 337 bars and have higher levels of T3, than A. percula in H. magnifica. This difference can be 338 explained by higher expression of *duox* by *A. percula* recruited in *S. gigantea* as compared to 339 A percula recruited in H. magnifica. Indeed, duox, encodes a dual oxidase that has been 340 implicated in TH production both in mammals and zebrafish (27, 35). Beyond the effects of 341 duox inactivation we observed on zebrafish iridophore patterning, duox mutants have growth 342 retardation, ragged fins, thyroid hyperplasia and infertility and, a pigmentation phenotype with 343 increased melanophore and reduced xanthophore (27, 35) typical of hypothyroid fish (21). As 344 shown by Chopra et al., some of these defects can be rescued with T4 treatment, even when 345 initiated in adult fish (27). All these data allow us to suggest that in young juveniles which are 346 recruited in *S. gigantea* there is an increased expression of *duox* that led to a higher TH level 347 and a higher rate of white bar formation.

348 The results of our study leave two major questions unanswered: why is there an increased 349 duox expression in S. gigantea recruits, and is there ecological significance to faster white 350 bar formation in those fish. The regulation of *duox* gene expression in fish is still poorly 351 known but it has been shown that *Duox1* and *Duox2* expression in mammals in tightly 352 controlled and regulated by TSH, that is the hypothalamo-pituitary-thyroid axis (41). As S. 353 gigantea has been shown to be a much more toxic sea anemone than H. magnifica by 354 hemolytic and neurotoxicity assays (42), it is conceivable that clownfish recruited in this sea 355 anemone perceive this harsher environment and hence activate their neuroendocrine axis to 356 compensate. It is important to note in that respect that several anemonefish adults (A. 357 percula but also A. clarki, A. polymnus or A. chrysopterus) exhibit a similar polymorphic 358 melanistic morph when present in *Stichodactyla* vs. *Heteractis* (43). It is tempting to propose 359 that these melanistic morphs are also linked to TH signaling in these species. The white bar 360 phenotype we discussed here is therefore likely to be only one of a series of changes linked 361 to the differential recruitment in various sea anemone species that allow the physiological 362 adjustment of the fish in these distinct environments (44). However, the adaptative 363 significance of this plastic phenotype is still only a hypothesis that remains to be tested 364 experimentally in the field (44). It is interesting to note that A. ocellaris can also live in the 365 same two sea anemone species but does not exhibit a melanistic morph when present in 366 Stichodactyla (45). The rate of white bar appearance in young recruits of A. ocellaris living in 367 the two sea anemone species is unknown. It will be interesting to study in the future the differences in pigmentation plasticity between the two sister species, *A. ocellaris* and *A.percula.*

In conclusion, our study of white bar formation in clownfish highlight the interest of this new emerging system to investigate the cellular, molecular endocrine and developmental basis of alternative phenotypes that are detected in natural situation (24, 46). Combining analysis in the wild as well as in the lab, as we have done here using clownfish as model, offers great promises to understand the evolutionary and developmental basis of plastic phenotypes often observed in nature.

376 Acknowledgments

This study was supported by Agence Nationale de la Recherche (ANR-19-CE34-0006-Manini and ANR-19-CE14-0010-SENSO) as well as by National Institute of Science (NIH R35 GM122471). We thank Valentin Logeux, Remi Pillot, Nancy Trouillard and Pascal Romans from the Aquariology Service at Observatoire Océanologique de Banyuls-Sur-Mer for expert technical help for clownfish husbandry. We also thank the Centre de Recherches en Cancérologie de Toulouse (CRCT UMR 1037 INSERM, Plateau Génomique et Transcriptomique) for the Nanostring experiments.

384

387 Materials and methods

388

389 See extended methods provided in *SI Appendix*.

390

A. ocellaris larval rearing and ethics. A. ocellaris were maintained as described in (25).
We have approval for these experiments from the C2EA - 36 Ethics Committee for Animal
Experiment Languedoc-Roussillon (CEEA-LR), number A6601601. The experimental
protocols were following French regulation.

395

396 RNA extraction and transcriptomic analysis. Transcriptomic data of developmental stages 397 of A. ocellaris larvae were taken from the transcriptomic analysis of A. ocellaris post-398 embryonic stages performed in (29). For more information see SI Appendix. Individuals of A. 399 percula new recruits were sampled, euthanized in a MS222 solution (200 mg/l) and 400 conserved in RNAlater. Total RNA of each individual was extracted using (Trizol Reagent 401 15596-026 kit, Ambion) followed by DNase treatment (DNA-free AM1906 kit, Ambion) and 402 then purified with 0.025 µm dialysis membranes. RNA-Seg libraries and sequencing were 403 performed on a Illumina HiSeq4000 sequencer using a stranded protocol as Paired-end 50 404 base reads. Transcriptomic analysis is described in SI Appendix.

405

406 Drug treatment of A. ocellaris larvae. T3 (3,3',5-Triiodo-L-thyronine) and IOP (lopanoic 407 Acid) were both diluted in dimethylsulphoxyde (T3: T2877, IOP: 14131, DMSO: D8418; 408 Sigma-Aldrich Louis, MI, USA) to a final concentration 1 mM. To analyze the effect of a 409 reduction of TH signaling we used a mix of goitrogens called MPI (Methimazole, Potassium 410 Perchlorate and Iopanoic Acid) as in reference (47). Methimazole, Potassium Perchlorate 411 and IOP (Methimazole: M8506, Potassium perchlorate 460494, Sigma-Aldrich Louis, MI, 412 USA) were also diluted in DMSO to a respective final concentration of 100 mM, 10 mM and 1 mM. Larvae were treated from 5 until 18 dph in 0.005% DMSO with T3+IOP at 10^{-6} , 10^{-7} and 413 414 10⁻⁸ M (respective dilutions of 1/1000, 1/10000 or 1/100000) or MPI (dilution of 1/1000) or 415 without (controls). For each condition, five larvae were treated in 500-mL fish medium in a 416 beaker. One hundred milliliters of solution were changed every day.

417

418 Nanostring gene expression analysis. 400 ng of total RNA were analyzed using the
419 Nanostring Counter. Each sample was analyzed in a separate multiplexed reaction including
420 8 negative probes and 6 serial concentrations of positive control probes. Data were imported

into nSolver software (version 2.5) for quality checking and data normalization according to
NanoString guidelines. Analysis was done using the R package TTCA1 (R version 3.5.1).

423 Effect of ecological factors on the number of bars in new recruits of A. percula. At the 424 time of the sampling in Kimbe bay (5°12'22.56" S, 150°22'35.58" E), West New Britain Prov-425 ince, Papua New Guinea, we characterized the new recruit size, age (see SI appendix) eco-426 logical variables (geographic zone, primary host anemone species, depth), and the social 427 structure of the new recruits within its sea anemone (total number of conspecifics inhabiting 428 the sea anemone, size difference between the new recruit and the last subadult in the social 429 hierarchy, female size) (28, 48). In the studied A. percula colonies located in Kimbe 43% are 430 in S. gigantea and 57% in H. magnifica. To assess what factors affect the number of bars on 431 new recruits, we modelled the number of bars as a response variable depending upon either 432 size or age, their squared value, and ecological and social structure independent variables. 433 We followed a multi-model inference approach (49, 50) to estimate predictors effect sizes 434 and their 85% confidence interval (51). This approach was conducted independently in each 435 anemone species to avoid confounding effects between anemone species and depth (see 436 Supp. Methods for details of the statistical analysis). All analyses were performed with the 437 MuMIn v1.43.6 package (52) in the statistical software R v3.6.3 (53). 438

Thyroid hormones extraction and dosage. TH were extracted individuals from *A. percula*new recruits sampled in Kimbe Island, dry-frozen (previously euthanized in a 200 mg/l
solution of MS-222) following the protocol described in (32). More details are described in *SI Appendix*.

443

444 Zebrafish duox CRISPR-Cas9. Zebrafish D. rerio were reared under standard conditions 445 (28 °C, 14L:10D) and staged according to (54). Embryos Tg(pnp4a:palm-mcherry)^{wprt10Tg} 446 expressing membrane-targeted mCherry (mem-Cherry) (55, 56) were injected at the one-cell 447 stage with Alt-R CRISPR-Cas9 (36) targeting duox, and reared on a thyroid hormone free 448 diet of brine shrimp and marine rotifers (21). Images of *duox* AltR-injected fish and uninjected 449 controls were acquired on a Zeiss Axio Observer inverted microscope equipped with a 450 Yokogawa CSU-X1M5000 laser spinning disk with Hamamatsu ORCA-Flash 4.0 camera. 451 Regions of interest were defined by the anterior and posterior margin of the anal fin, and 452 proportional coverage of dense interstripe iridophores relative to this region of interest were 453 analyzed using ImageJ software. Numbers of completed or developing interstripes were 454 scored qualitatively. Display levels were adjusted and inverted for visualization in Adobe 455 Photoshop 2021.

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589 Figure legends

590

591 Figure 1. Formation of white bars of *Amphiprion percula* new recruits is differentially 592 influenced by age depending on the anemone species

593 (A-B) Histograms representing percentage of new recruits having 1 (blue), 2 (green) or 3 594 white bars (yellow) depending on their age, in new recruits living in H. magnifica (A) or S. gigantea (B). Statistical tests were done using χ^2 tests at each age between H. magnifica or 595 596 S. gigantea and show statistical difference at 150-200 dph and 200-250 dph (respective p-597 value: 0.0032 and 0.0011). (C) Number of bars (85% CI) depending on age of individuals 598 predicted from full averaging of the model candidates (D). Blue and orange represent 599 respectively A. percula new recruits sampled in H. magnifica and in S. gigantea. Dots are 600 observed data and are shifted around their number of bars for graphical representation. 601 Predicted regressions of the number of bars are presented for the reference level "lagoon 0". 602 (D) Full model averaged estimates (85% CI) of linear regression parameters from models 603 including age for each anemone species. Parameter estimates after model averaging of 604 treatment were compared with "Lagoon 1" as reference for the geographic zone. A 605 parameter estimate whose 85% CI includes zero is considered uncertain and parameter 606 estimates whose 85% CI do not overlap are considered different.

607

Figure 2. Adult color pattern formation in *Amphiprion ocellaris* is linked to a switch in expression of pigment cells specific genes during post-embryonic development

610 (A-B) Stereomicroscope images of entire larvae and the associated zoom of the trunk at 611 stage 1 (A), 2 (B), 3 (C), 4 (D), 5 (E), 6 (F) and 7 (G) (Adapted from (25)). White and red 612 arrowheads point white bars and black larval melanophores, black and orange arrows point 613 respectively melanophores and xanthophores. (H and I) PCA analysis of the pigmentation 614 genes (H) and iridophores genes (I) expression from transcriptomic analysis from entire 615 larvae over post-embryonic stages. The two PCA exhibit a clear separation between stage 1 616 to 3 and stage 4 to 7. The ellipses were arbitrarily drawn around arrays to help resolution: 617 stages 1 to 3 (orange) and 4 to 7 (blue) arrays. All stages had 3 replicates. (J) Heatmap of 618 the 7 iridophore genes having the highest fold change between stage 1-3 and stages 5-7. 619 Color represents the intensity of the centered (but unscaled) signal that goes, for each gene, 620 from low (blue) to medium (white) to high (red).

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624 Figure 3. White bars in Amphiprion ocellaris form earlier and later respectively after

625 treatments with thyroid hormones or goitrogens

626 (A-D) Stereomicroscope images of larvae treated at stage 3 during 3 days (dpt) in DMSO (A)

627 or T3 at 10^{-6} M (B), 10^{-7} M (C) and 10^{-8} M (D).

628 (E-F) Histogram showing the percentage of larvae having 0 (red), 1 (blue), 2 (green) or 3

629 (yellow) white bars. (E) Larvae are treated at stage 3 for 3 days with DMSO, T3 10⁻⁶ M, 10⁻⁷

- 630 M and 10⁻⁸ M (nDMSO=16, nT3 10⁻⁸ M=20, nT3 10⁻⁷ M=18, nT3 10⁻⁶ M=15 individuals). Chi2
- 631 tests are significant between T3 10⁻⁶ M and DMSO (p-value <0.0001). (F) Larvae are treated
- at stage 3 for 9 days with DMSO or MPI 10^{-6} M (nDMSO=12, nMPI 10^{-6} M= 13 individuals).
- 633 Statistical test was done using χ^2 tests (p-value <0.0029).
- (G-I) Stereomicroscope images of larvae treated at stage 3 during 9 days in DMSO (G) and
 MPI 10⁻⁶ M (H) and MPI 10⁻⁶ M stage 3 larvae treated for 25 days (I).

(J) Graphic showing the number of melanophores in a specific area of the trunk in DMSO
(black), T3 10⁻⁶ M (green) and MPI 10⁻⁶ M (red) at 12, 24, 48 and 72 hpt (nDMSO>9, nT3>9,
nMPI>9 individuals). Statistical tests were done using ANOVA between the T3 or MPI
treatments and DMSO (control) at each time. Tests are significant between T3 and DMSO at
48 hpt and 72 hpt (p-value are respectively equal to 0.0299 and 0.0043).

- Bars correspond to the mean and crosses correspond to one experiment. hpt = hours posttreatment. Scale bar = 1mm.
- 643

644 Figure 4. *duox* requirement for the timing of color pattern formation in zebrafish

645 (A) Graph representing T3 level (in pg.g-1 of fish) in A. percula new recruits sampled in H. 646 magnifica or S. gigantea (Non-parametric Mann Whitney Test, p-value=0.0022). (B) Volcano 647 plot of differentially expressed genes between new recruits living in H. magnifica or S. 648 gigantea. Positive Log2FC values correspond to an increased expression in recruits from S. 649 gigantea, while negative Log2FC corresponds to increased expression in recruits from H. 650 magnifica. Green and red points correspond to significantly differentially expressed genes. 651 The vertical black lines delimit the Log2FC threshold of 1, while the horizontal line 652 corresponds to the corrected p-value threshold. (C) Inverted fluorescence images show 653 iridophores (dark cells) marked by pnp4a:mem-mCherry expression at 10.6 mm standard in 654 wild-type (left) and duox CRISPR/Cas9 mutants (Right). (D) Numbers of interstripes were scored qualitatively over Standard Length (SL) in wild-type (blue, N=61) and duox 655 656 CRISPR/Cas9 mutants (yellow, N=51). Complete interstripes received a score of 1 and 657 developing interstripes received a score of 0.5. Each circle represents a single individual and 658 points are jittered vertically for clarity, and equivalently smoothed splines are shown for ease 659 of visualization. Differences in total numbers of interstripes and tractories of interstripe addition resulted in significant effects of genotype (likelihood ratio test, x²=91.7, p-660

value<0.0001, d.f. = 1) and genotype x standard length interaction (χ^2 =21.9, p-value<0.0001, d.f. = 1). (E) Despite having fewer interstripes overall, *duox*-deficient animals had proportionally more of the flank covered by dense, interstripe-iridophores, as compared to the wild type ($F_{1,43}$ =76.1, *P*<0.0001). Bars indicate means ± 95% confidence intervals. Scale bar in A = 200 µm.

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Salis et al. Fig 1





Salis et al.,

Fig 3



ТЗ 10⁻⁷М







<u>T3 10⁻⁶M</u>





Treatment









Salis et al., Fig 4

