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Evolution: Genomic Signatures of Mimicry and Mimicry of Genomic Signatures

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How new species form in the ocean, and thus what determines the diversity of fish in the sea, is not well understood. A study in Caribbean coral-reef fishes sheds light on the genomic underpinnings of diversification in the marine realm.

Paradoxically, although oceans cover a much greater portion of the Earth's surface than freshwater, the total number of teleost fish species is similar between the two habitats [1]. The exact reasons for the relatively low taxonomic diversity of teleost fish in the marine realm remain unknown. However, it appears plausible that factors conducive for local adaptation and rapid diversification in fishes thriving in rivers and lakes — such as a patchy distribution of suitable habitats, reduced dispersal ability and relatively small population sizes — are less effective in marine fishes [1]. The vastness of the oceans coupled with the passive dispersal of fish larvae via oceanic currents might also be the reason why rapid evolutionary radiations producing exceptional levels of endemism in freshwater ecosystems — as for instance in the cichlids of the East African lakes [2] — have no equal in marine fish [3]. However, fish inhabiting tropical coral reefs constitute a notable exception to the general trend of a lower fish diversity in marine environments. Many lineages of coral-reef fishes are characterized by a great deal of phenotypic and taxonomic diversity and often feature rapid rates of speciation [4]. In a recent study, Kosmas Hench and colleagues [5] focused on the underlying mechanisms of rapid diversification in coral-reef fishes, applying genome scan analyses to population samples of three common species of hamlets (genus *Hypoplectrus*; Figure 1) native to the coral reefs in the Caribbean and the Gulf of Mexico, the black hamlet (*H. nigricans*), the butter hamlet (*H. unicolor*) and the barred hamlet (*H. puella*).

With an estimated 18 species that have evolved within the last few million years, hamlets represent one of the best-documented cases of an adaptive radiation in the marine environment [5–7]. The different hamlet species are quite similar with respect to their ecology and overall morphology, but differ substantially in body coloration and pigmentation [7,8]. The diverse color patterns of hamlets have been implicated in aggressive mimicry, whereby predators imitate non-predatory model species to more readily get access to naïve prey [7–9]. At the same time, hamlets typically mate assortatively with respect to color patterns [7,8,10], making coloration in hamlets a trait that is likely to be under the influence of both natural and sexual selection. Interestingly, hamlets are simultaneous hermaphrodites and each mating partner takes over the role of both sexes during mating [8,11].

In their new study, Hench and colleagues [5] report the sequencing and *de novo* assembly of a high-quality reference hamlet genome and provide short-read-based genome resequencing data for another 110 specimens distributed across the three species and three populations each. By using F_{st} outlier analyses on the resequenced genomes, they identified four genomic regions with particularly high levels of differentiation between the three investigated hamlet species. These relatively narrow intervals are located on three different linkage groups (the equivalent to chromosomes in a genome assembly) and contain, in their most central regions, genes with known functions in coloration and vision. The kinds of genes identified are perhaps not surprising— after all, hamlet species are classified primarily according to color, so it might be expected that the underlying color genes are picked up in cross-species genome comparisons; and vision-related genes are regularly found as outliers in genome scans between closely related fish taxa [12,13]. However, the species-specific coupling of different gene versions across linkage groups in hamlets is surprising. Each species is thus given a unique molecular identity with respect to the arrangement of particular gene versions in just a handful of loci in the genome (Figure 1), whereby all but one of the identified mutations are non-coding or synonymous [5].

The black hamlet (*H. nigricans*), for example, possesses a unique version of *sox10*, a gene that is known to be involved in the development of dark pigment cells, the melanophores [14]. As the black hamlet mimics the similarly pigmented, non-predatory dusky and longfin damselfish (*Stegastes adustus* and *Stegastes diencaeus*, respectively), it is tempting to speculate that *sox10* is linked to the melanic phenotype of *H. nigricans*, which in turn is likely to be adaptive in the context of this species' aggressive mimicry. In addition, the black hamlet stands out in its unique version of a cluster of vision-related opsin genes (*sws2a*, *sws2b* and *lws*), suggesting that this region may have evolved in response to its dark pigmentation, too, for example to more efficiently recognize conspecifics or the mimicry models.

The butter hamlet (*H. unicolor*), on the other hand, is differentiated from the other two species in a cluster of Hox genes

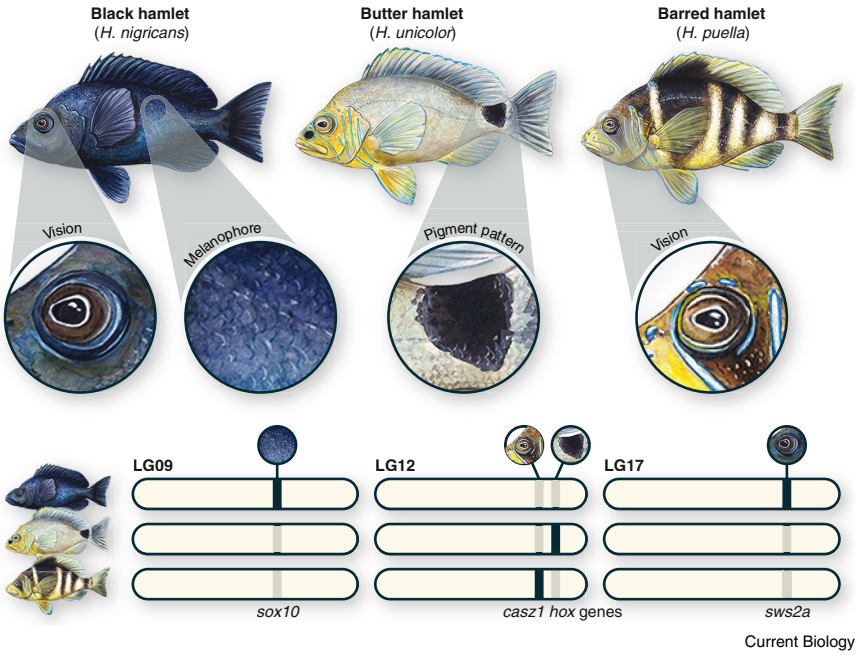

Figure 1. The genomic architecture of divergence in hamlets.
A genomic exploration of populations of three species of hamlets native to the Caribbean and the Gulf of Mexico revealed that the black hamlet (*H. nigricans*), the butter hamlet (*H. unicolor*) and the barred hamlet (*H. puella*) primarily differ in four genomic regions located on three linkage groups (9, 12, and 17; illustrated as rounded rectangles) [5]. Versions of these regions unique to one of the hamlet species are marked in black, alternative versions are shown in gray; gene names refer to candidate loci in these regions. Drawings by Alexandra Viertler, Zoological Institute, University of Basel.

(*hoxc10a*, *hoxc11a*, *hoxc12a* and *hoxc13a*). Like the black hamlet, the butter hamlet also performs aggressive mimicry, in this case imitating the color pattern of the non-predatory four-eye butterflyfish (*Chaetodon capistratus*) [7,15]. The four-eye butterflyfish is characterized by a large eye-spot at the base of its tail fin— a pattern matched by the butter hamlet. Again, a potential link can be established between the genomic region in question and the conspicuous phenotype of the eye-spot involved in mimicry: One of the genes within this cluster (*hoxc12a*) has previously been associated with the formation of another circular marking in fish, the so-called egg-spots on the anal fins of male haplochromine cichlids [16]. Even outside vertebrates, such pigment patterns are produced by Hox genes, as exemplified by the eye-spots on the wings of butterflies [17].

Finally, the barred hamlet (*H. puella*) is primarily separated from the other two species through its version of the *casz1* gene, which is known to be involved in the development of photoreceptors [18]. While not as clearly linked to aggressive mimicry as the differentiated gene regions of the other two hamlet species investigated by Hench and colleagues [5], it is possible that, just like in the black hamlet, this vision-related gene evolved in response to color-pattern changes mediated by (less prominent) differentiation in other genes.

Taken together, it appears plausible that the observed species-specific differentiation in all four genomic intervals is adaptive in hamlets and linked to their aggressive-mimicry behavior, and that the relatively simple genomic architecture of species-specific differences has facilitated rapid diversification. The study by Hench and colleagues [5] therefore provides important new insights into the processes shaping species differences in a recent adaptive radiation in marine fish.

It is a bit less clear, at this stage, whether the species-specific patterns observed in the hamlets' genomes are indeed directly linked to the speciation process. Hench and colleagues [5] favor a 'speciation-with-gene-flow' scenario, in which the genomic landscape of differentiation is shaped by strong divergent selection on a few loci, whereas the rest of the genome becomes homogenized due to occasional interbreeding between species. Alternatively, however, selective sweeps after speciation could mimic the genomic signatures of locally high differentiation [19]. In this 'divergence-after-speciation' scenario, speciation initially occurs due to other (unknown) factors promoting reproductive isolation, and the observed low levels of differentiation across the rest of the genome stem from unsorted ancestral variation. Both scenarios can, in principle, explain the occurrence of genomic intervals featuring strong differentiation, but they differ in other, testable predictions: the speciation-with-gene-flow model predicts that genomic regions with high differentiation also show greater absolute divergence compared to the genome-wide background. Unfortunately, the hamlet genomes are only moderately informative regarding this prediction, as absolute divergence in the four genomic intervals appears higher than the genome-wide average, but not significantly so. The divergence-after-speciation model, on the other hand, predicts that gene flow between the newly formed species is absent or massively reduced [19], which seems to be in conflict with reports of hamlet species hybridizing and backcrossing in the wild [5,10,20].

To discriminate conclusively between the speciation-with-gene-flow and the divergence-after-speciation scenarios and to corroborate the putative role of aggressive mimicry as major driver of diversification in hamlets, it will be important to examine the effects of hybridization among species in more detail. In particular, it would be interesting to test the viability and fitness of hybrids explicitly with regard to their combinations of genotypes at the four highly differentiated regions. The findings of Hench and colleagues [5] — as important as they are — only scratch the surface of the insights that the genomic exploration of the entire hamlet adaptive radiation could provide, especially when coupled with functional analyses. With as many as 18 closely related species that largely occur in sympatry, many more divergence events and many more interactions between species following divergence could be investigated in hamlets. Without doubt, this would greatly increase our understanding of species diversification in the marine realm.

REFERENCES

1. Vega, G.C., and Wiens, J.J. (2012). Why are there so few fish in the sea? Proc. R. Soc. B. *279*, 2323–2329.
2. Salzburger, W. (2018). Understanding explosive diversification through cichlid fish genomics. Nat. Rev. Genet. *19*, 705–717.
3. Matschiner, M., Hanel, R., and Salzburger, W. (2010). Phylogeography and speciation processes in marine fishes and fishes from large freshwater lakes. In Phylogeography: Concepts, Intraspecific Patterns and Speciation Processes, D.S. Rutgers, ed. (Nova Science Publishers), pp. 1–29.
4. Rocha, L.A., and Bowen, B.W. (2008). Speciation in coral-reef fishes. J. Fish Biol. *72*, 1101–1121.
5. Hench, K., Vargas, M., Höppner, M.P., McMillan, W.O., and Puebla, O. (2019). Inter-chromosomal coupling between vision and pigmentation genes during genomic divergence. Nat. Ecol. Evol. *3*, 657–667.
6. Puebla, O., Birmingham, E., and Guichard, F. (2008). Population genetic analyses of *Hypoplectrus* coral reef fishes provide evidence that local processes are operating during the early stages of marine adaptive radiations. Mol. Ecol. *17*, 1405–1415.
7. Puebla, O., Bermingham, E., Guichard, F., and Whiteman, E. (2007). Colour pattern as a single trait driving speciation in *Hypoplectrus* coral reef fishes? Proc. R. Soc. B. *274*, 1265–1271.
8. Fischer, E.A. (1980). Speciation in the hamlets (*Hypoplectrus*: Serranidae) - a continuing enigma. Copeia *1980*, 649–659.
9. Thresher, R.E. (1978). Polymorphism, mimicry, and the evolution of the hamlets (*Hypoplectrus*, Serranidae). Bull. Mar. Sci. *28*, 345–353.
10. Puebla, O., Bermingham, E., and Guichard, F. (2012). Pairing dynamics and the origin of species. Proc. R. Soc. B *279*, 1085–1092.
11. Fischer, E.A. (1980). The relationship between mating system and simultaneous hermaphroditism in the coral reef fish, *Hypoplectrus nigricans* (Serranidae). Animal Behav. *28*, 620–633.
12. Malinsky, M., Challis, R.J., Tyers, A.M., Schiffels, S., Terai, Y., Ngatunga, B.P., Miska, E., Durbin, R., Genner, M.J., and Turner, G.F. (2015). Genomic islands of speciation separate cichlid ecomorphs in an East African crater lake. Science *350*, 1493–1498.
13. Rennison, D.J., Owens, G.L., Heckman, N., Schluter, D., and Veen, T. (2016). Rapid adaptive evolution of colour vision in the threespine stickleback radiation. Proc. R. Soc. B. *283*, 20160242.
14. Singh, A.P., and Nüsslein-Volhard, C. (2015). Zebrafish stripes as a model for vertebrate review colour pattern formation. Curr. Biol. *25*, R81–R92.
15. Robertson, D.R. (2013). Who resembles whom? Mimetic and coincidental look-alikes among tropical reef fishes. PLoS One *8*, e54939.
16. Santos, M.E., Baldo, L., Gu, L., Boileau, N., Musilova, M., and Salzburger, W. (2016). Comparative transcriptomics of anal fin pigmentation patterns in cichlid fishes. BMC Genomics *17*, 712.
17. Saenko, S.V., Marialva, M.S.P., and Beldade, P. (2011). Involvement of the conserved Hox gene Antennapedia in the development and evolution of a novel trait. EvoDevo *2*, 9.
18. Mattar, P., Ericson, J., Blackshaw, S., and Cayouette, M. (2015). A conserved regulatory logic controls temporal identity in mouse neural progenitors. Neuron *85*, 497–504.
19. Cruickshank, T.E., and Hahn, M.W. (2014). Reanalysis suggests that genomic islands of speciation are due to reduced diversity, not reduced gene flow. Mol. Ecol. *23*, 3133–3157.
20. Puebla, O., Bermingham, E., and McMillan, W.O. (2014). Genomic atolls of differentiation in coral reef fishes (*Hypoplectrus* spp., Serranidae). Mol. Ecol. *23*, 5291–5303.

Learning and Memory: Mind over Matter in *C. elegans*

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The capacity to respond to adverse conditions is key for animal survival. Research in the nematode *Caenorhabditis elegans* demonstrates that retrieval of aversive memories, stored within sensory neurons, is sufficient to induce a protective systemic stress response that improves fitness.

Does the mind have the power to control systemic physiological processes? For example, could enhanced conscious awareness, through the practice of meditation, help us to relieve pain? In 1863, geologist Sir Charles Lyell postulated that the mind's ability to control body physiology, termed mind over matter, is a *bona fide* function that emerged as brains expanded in size over evolutionary time [1]. In this issue of *Current Biology*, a new study by Eliezer and colleagues [2] suggests that even the free-living soil nematode *Caenorhabditis elegans*, with its 302-neuron nervous system, may be endowed with the capacity to modify its physiology merely by recalling past experiences.

Like most animals, *C. elegans* must adjust its behavior and physiology in response to dire conditions. When food resources are limited, protective programs, which enhance somatic maintenance and repress reproductive development, are activated [3]. These systemic stress-induced pathways are thought to act, in part, through transcription of genes that promote stress resistance, fat metabolism, pathogen protection, and entry into a protective developmental state called dauer. Many of these transcriptional events are mediated by the DAF-16/FOXO forkhead transcription factor [4], which rapidly translocates from the cytoplasm to the nucleus following exposure to stressful conditions [5]. Activation of these transcriptional programs can take anywhere from minutes to hours. It would therefore be advantageous for *C. elegans* to have the ability to predict and prepare in advance for impending adversity. Associative learning is a mechanism that could underlie such an early warning system, predicting future events based on