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RECOMMENDATION

Genomic parallelism in adaptation to orthogonal environments in sea horses

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Based on reviews by: three anonymous reviewers

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A recommendation of

Riquet F, Liautard-Haag C, Woodall L, Bouza C, Louisy P, Hamer B, Otero-Ferrer F, Aublanc P, Beduneau V, Briard O, El Ayari T, Hochscheid S, Belkhir K, Arnaud-Haond S, Gagnaire PA, and Bierne N. Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. *bioRxiv*, 161786 ver. 4 peer-reviewed and recommended by *PCI Evol Biol* (2018)

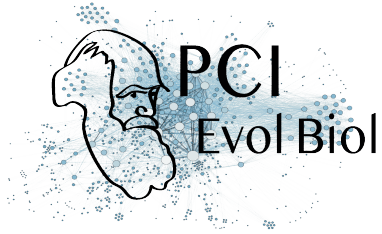
Studies in speciation genomics have revealed that gene flow is quite common, and that despite this, species can maintain their distinct environmental adaptations. Although researchers are still elucidating the genomic mechanisms by which species maintain their adaptations in the face of gene flow, this often appears to involve few diverged genomic regions in otherwise largely undifferentiated genomes. In this preprint [1], Riquet and colleagues investigate the genetic structuring and patterns of parallel evolution in the long-snouted seahorse.

Before investigating specific SNPs plausibly associated with adaptation, the authors first describe genome-wide population structure in the long-snouted seahorse. This species is split into five phenotypically similar, but genetically distinct populations. Two populations reside in the Atlantic Ocean and are geographically structured with one north of the Iberian peninsula and the other around the Iberian peninsula. Two other populations are found in the Mediterranean Sea and are structured by the environment as they correspond to marine and lagoon environments. The genetic clustering of lagoon populations in the Mediterranean, despite the substantial geographic distance between them is quite impressive, and worthy of further study. Finally, a fifth population resides in a lagoon-like habitat in the Black Sea.

The authors then investigate patterns of extreme genomic differentiation among populations, and uncover a remarkable pattern of parallel differentiation in these populations. In an

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outlier scan, Riquet and colleagues find numerous SNPs in one genomic region that separates northern and southern Atlantic populations. Quiet surprisingly, this same genomic region appears to differentiate populations living in marine and lagoon habitats in the Mediterranean. The idea that parallel patterns of genomic differentiation may underlie adaptation to differing environmental scenarios has not yet received much attention. This paper should change that. This paper is particularly impressive in that the authors uncovered this intriguing pattern with under three hundred SNPs. Future genome scale studies will uncover the genomic basis behind this unusual case of parallelism.

References

- [1] Riquet F, Liautard-Haag C, Woodall L, Bouza C, Louisy P, Hamer B, Otero-Ferrer F, Aublanc P, Beduneau V, Briard O, El Ayari T, Hochscheid S, Belkhir K, Arnaud-Haond S, Gagnaire PA, and Bierne N. Parallel pattern of differentiation at a genomic island shared between clinal and mosaic hybrid zones in a complex of cryptic seahorse lineages. *bioRxiv*, 161786 ver. 4 peer-reviewed and recommended by *PCI Evol Biol* (2018).

Appendix

Reviews by three anonymous reviewers, DOI: 10.24072/pci.evolbiol.100056