



RECOMMENDATION

## Pros and Cons of local adaptation scans

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**Based on reviews by:**  
Lucas Gonçalves da Silva and one anonymous reviewer

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### A recommendation of

Pratlong M, Haguenaer A, Brener K, Mitta G, Toulza E, Garrabou J, Bensoussan N, Pontarotti P, and Aurelle D. Separate the wheat from the chaff: genomic scan for local adaptation in the red coral *Corallium rubrum*. *bioRxiv* 306456, ver. 3 peer-reviewed and recommended by *PCI Evol Biol* (2018). doi: 10.1101/306456

The preprint by Pratlong et al. [4] is a well thought quest for genomic regions involved in local adaptation to depth in a species a red coral living the Mediterranean Sea. It first describes a pattern of structuration and then attempts to find candidate genes involved in local adaptation by contrasting deep with shallow populations. Although the pattern of structuration is clear and meaningful, the candidate genomic regions involved in local adaptation remain to be confirmed. Two external reviewers and myself found this preprint particularly interesting regarding the right-mindedness of the authors in front of the difficulties they encounter during their experiments. The discussions on the pros and cons of the approach are very sound and can be easily exported to a large number of studies that hunt for local adaptation. In this sense, the lessons one can learn by reading this well documented manuscript are certainly valuable for a wide range of evolutionary biologists.

More precisely, the authors RAD-sequenced 6 pairs of 'shallow vs deep' samples located in 3 geographical sea areas (Banyuls, Corsica and Marseille). They were hoping to detect genes involved in the adaptation to depth, if there were any. They start by assessing the patterns of structuration of the 6 samples using PCA and AMOVA [2] and also applied the STRUCTURE [5] assignment software. They show clearly that the samples were mostly differentiated between geographical areas and that only 1 out the 3 areas shows a pattern of isolation by depth (i.e. Marseille). They nevertheless went on and scanned for variants that are highly differentiated in the deep samples when compared to the shallow paired samples in Marseille, using an Fst outliers approach [3] implemented in the BayeScEnv software [1]. No clear functional signal was in the end detected among the highly differentiated SNPs, leaving a list of candidates

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begging for complementary data.

The scan for local adaptation using signatures of highly divergent regions is a classical problem of population genetics. It has been applied on many species with various degrees of success. This study is a beautiful example of a well-designed study that did not give full satisfactory answers. Readers will especially appreciate the honesty and the in-depth discussions of the authors while exposing their results and their conclusions step by step.

## References

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- [4] Pratlong M, Haguenaier A, Brener K, Mitta G, Toulza E, Garrabou J, Bensoussan N, Pontarotti P, and Aurelle D. Separate the wheat from the chaff: genomic scan for local adaptation in the red coral *Corallium rubrum*. *bioRxiv* 306456, ver. 3 peer-reviewed and recommended by *PCI Evol Biol* (2018). DOI: 10.1101/306456.
- [5] Pritchard JK, Stephens M, and Donnelly P. Inference of population structure using multi-locus genotype data. *Genetics* 155 (2000), 945–959.

## Appendix

Reviews by Lucas Gonçalves da Silva and one anonymous reviewer, DOI: 10.24072/pci.evolbiol.100061