



## Differential effect of genes in diverse environments, their role in local adaptation and the interference between genes that are physically linked

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Sebastián E Ramos-Onsins

Centre for Research in Agricultural Genomics CSIC-IRTA-UAB-UB -- Barcelona, Spain  
Correspondence to Sebastián E Ramos-Onsins ([sebastian.ramos@cragenomica.es](mailto:sebastian.ramos@cragenomica.es))

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**A recommendation – based on reviews by Tanja Pyhäjärvi and an anonymous reviewer – of**

Lotterhos KE, Yeaman S, Degner J, Aitken S and Hodgins K. 2018. Modularity of genes involved in local adaptation to climate despite physical linkage. bioRxiv 202481, ver. 4 peer-reviewed by Peer Community In Evolutionary Biology. doi: [10.1101/202481](https://doi.org/10.1101/202481)

The genome of eukaryotic species is a complex structure that experience many different interactions within itself and with the surrounding environment. The genetic architecture of a phenotype (that is, the set of genetic elements affecting a trait of the organism) plays a fundamental role in understanding the adaptation process of a species to, for example, different climate environments, or to its interaction with other species. Thus, it is fundamental to study the different aspects of the genetic architecture of the species and its relationship with its surrounding environment. Aspects such as modularity (the number of genetic units and the degree to which each unit is affecting a trait of the organism), pleiotropy (the number of different effects that a genetic unit can have on an organism) or linkage (the degree of association between the different genetic units) are essential to understand the genetic architecture and to interpret the effects of selection on the genome. Indeed, the knowledge of the different aspects of the genetic

architecture could clarify whether genes are affected by multiple aspects of the environment or, on the contrary, are affected by only specific aspects [1,2]

The work performed by Lotterhos et al. [3] sought to understand the genetic architecture of the adaptation to different environments in lodgepole pine (*Pinus contorta*), considering as candidate SNPs those previously detected as a result of its extreme association patterns to different environmental variables or to extreme population differentiation. This consideration is very important because the study is only relevant if the studied markers are under the effect of selection. Otherwise, the genetic architecture of the adaptation to different environments would be masked by other (neutral) kind of associations that would be difficult to interpret [4,5]. In order to understand the relationship between genetic architecture and adaptation, it is relevant to detect the association networks of the candidate SNPs with climate variables (a way to measure modularity) and if these SNPs (and loci) are affected by single or multiple environments (a way to measure pleiotropy).

The authors used co-association networks, an innovative approach in this field, to analyse the interaction between the environmental information and the genetic polymorphism of each individual. This methodology is more appropriate than other multivariate methods - such as analysis based on principal components - because it is possible to cluster SNPs based on associations with similar environmental variables. In this sense, the co-association networks allowed to both study the genetic and physical linkage between different co-associations modules but also to compare two different models of evolution: a Modular environmental response architecture (specific genes are affected by specific aspects of the environment) or a Universal pleiotropic environmental response architecture (all genes are affected by all aspects of the environment). The representation of different correlations between allelic frequency and environmental factors (named galaxy biplots) are especially informative to understand the effect of the different clusters on specific aspects of the environment (for example, the co-association network 'Aridity' shows strong associations with hot/wet versus cold/dry environments).

The analysis performed by Lotterhos et al. [3], although it has some unavoidable limitations (e.g., only extreme candidate SNPs are selected, limiting the results to the stronger effects; the genetic and physical map is incomplete in this species), includes relevant results and also implements new methodologies in the field. To highlight some of them: the preponderance of a Modular environmental response architecture (evolution in separated modules), the detection of physical linkage among SNPs that are co-associated with different aspects of the environment (which was unexpected a priori), the implementation of co-association networks and galaxy biplots to see the effect of modularity and pleiotropy on different aspects of environment. Finally, this work contains remarkable introductory Figures and Tables explaining unambiguously the main concepts [6] included in this study. This work can be treated as a starting point for many other future studies in the field.

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## Appendix

Reviews by Tanja Pyhäjärvi and an anonymous reviewer: <https://doi.org/10.24072/pci.evolbiol.100050>