Towards an integrated scenario to understand evolutionary patterns in *A. thaliana*

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A recommendation of

Nobody can ignore that a full understanding of evolution requires an integrated approach from both conceptual and methodological viewpoints. Although some life-history traits, e.g. flowering time, have long been receiving more attention than others, in many cases because the former are more workable than the latter, we must acknowledge that our comprehension about how evolution works is strongly biased and limited. In the Arabidopsis community, such an integration is making good progress as an increasing number of research groups worldwide are changing the way in which evolution is put to the test.

This manuscript [1] is a good example of that as the authors raise an important issue in evolutionary biology by combining gene expression and flowering time data from different sources. In particular, the authors explore how variation in flowering time, which determines lifespan, and host immunity defenses co-vary, which is interpreted in terms of co-evolution between the two traits. Interestingly, the authors go beyond that pattern by separating lifespan-dependent from lifespan–independent defense genes, and by showing that defense genes with variants known to impact fitness in the field are among the genes whose expression co-varies most strongly with flowering time. Finally, these results are supported by a simple mathematical model indicating that such a relationship can also be expected theoretically.

Overall, the readers will find many conceptual and methodological elements of interest in this manuscript. The idea that evolution is better understood under the scope of life history variation is really exciting and challenging, and in my opinion on the right track for disentangling the inherent complexities of evolutionary research. However, only when we face complexity, we also face its costs and burdens. In this particular case, the well-known co-variation between seed dormancy and flowering time is a missing piece, as well as the identification of (variation in) putative selective pressures accounting for the co-evolution between defense mechanisms and life history (seed dormancy vs. flowering time) along environmental gradients. More intellectual, technical and methodological challenges that with no doubt are totally worth it.

Reference

[1] Glander S, He F, Schmitz G, Witten A, Telschow A, de Meaux J. 2017. Assortment of flowering time and defense alleles in natural *Arabidopsis thaliana* populations suggests co-evolution between defense and vegetative lifespan strategies. bioRxiv ver.1 of June 19, 2017. doi: 10.1101/131136

Appendix

Reviews by Xavier Picó and Rafa Rubio de Casas: http://dx.doi.org/10.24072/pci.evolbiol.100026