

W633**Detecting Selection Along Environmental Gradients: Analysis of Eight Methods and Their Effectiveness for Outbreeding and Selfing Populations***Date: Saturday, January 11, 2014**Time: 4:20 PM**Room: Pacific Salon 3**Stéphane De Mita , INRA, Nancy, France**Anne-Céline Thuillet , IRD, Montpellier, France**Laurène Gay , INRA, Montpellier, France**Nourollah Ahmadi , Cirad, Montpellier Cedex 5, France**Stéphanie Manel , Université Aix-Marseille, Aix en Provence, France**Joelle Ronfort , INRA, Montpellier, France****Yves P. Vigouroux** , IRD, Montpellier, France*[PDF file](#)

Thanks to genome-scale diversity data, present-day studies can provide a detailed view of how natural and cultivated species adapt to their environment and particularly to environmental gradients. However, due to their sensitivity, up-to-date studies might be more sensitive to undocumented demographic effects such as the pattern of migration and the reproduction regime. In this study, we provide guidelines for the use of popular or recently developed statistical methods to detect footprints of selection. We simulated 100 populations along a selective gradient and explored different migration models, sampling schemes and rates of self-fertilization. We investigated the power and robustness of eight methods to detect loci potentially under selection: three designed to detect genotype-environment correlations and five designed to detect adaptive differentiation (based on F_{ST} or similar measures). We show that genotype-environment correlation methods have substantially more power to detect selection than differentiation-based methods but that they generally suffer from high rates of false positives. This effect is exacerbated whenever allele frequencies are correlated, either between populations or within populations. Our results suggest that, when the underlying genetic structure of the data is unknown, a number of robust methods are preferable. Moreover, in the simulated scenario we used, sampling many populations led to better results than sampling many individuals per population. Finally, care should be taken when using methods to identify genotype-environment correlations without correcting for allele frequency autocorrelation because of the risk of spurious signals due to allele frequency correlations between populations.

[Back to: Population & Conservation Genomics](#)[<< Previous Abstract](#) | [Next Abstract >>](#)**Meeting Information****When:**