

Ad hoc support : #OpenDiv

A network for detecting and exploiting diversity and diffuse, weak, multi-dimensional marks of selection in open-managed agronomic and forestry ABSYSs

ABSTRACT

Adaptation of species, ecosystems and agrosystems is a multi-faceted process, calling into action Darwinian selection (including when operated by humans, i.e. so-called 'artificial' selection), individual plasticity, and the adaptation of practices by farmers and foresters, including changes in social organisation. When adaptation is realised at the local (regional, landscape, stand) level, it results in mosaics of locally adapted populations, landraces, and practices. The potential of micro-geographic adaptive processes to foster novel (and maintain current) adaptation has been identified early in the history of ecology and ecological genetics (1, 2) and the role of mosaics of local optima in maintaining genetic diversity has also been recognised (3, 4). Similarly, it has been shown that several combinations of functional traits, i.e. syndromes, may co-exist within a forest (5) or in crops (6–8), where adaptation to environmental variations can also be based on diversity of farmers practices, including sowing date, individual or variety selection and seed exchange (9–11).

Historically, large amounts of data have been gathered about the performances of varieties and provenances in variable ecological, agronomic and agro-climatic contexts, and accumulation of data has accelerated in some areas (particularly, genetics) made possible by the advent of high-throughput (particularly, genomic and phenotyping) methods. Within Labex Agro, the flagship project ARCAD has generated such data, including transcriptomic, genomic and socio-economic data which have been only partially analyzed and synthesized. Data collected in contexts with low barriers to migration and to mixing (either because of evolutionary and ecological reasons or because of the way genetic resources are managed) are of particular interest because they can contain unexplored / unexploited examples of adaptive processes. While differences among provenances for adaptive traits are regularly shown, within-provenance variation is often large but remains unexplained (12). These data were until recently not investigated, in terms of detection of adaptive signatures, because of lack analytical and modelling methods and of statistical and computational power, or because of outright scepticism about the possibility of micro-geographical scale divergence, because populations connected through gene flow are expected to have low phenotypic and genetic divergence. There was also a lack of interest in on farm dynamic management of local varieties by conventional breeders. A complementary source of multi-locus genetic variation for adaptive traits is introgression after interspecific hybridization (also a case of adaptive divergence with gene flow). The importance of the process of adaptive introgression, recently demonstrated in numerous systems, is reflected in the development of specific methods for its detection (13). Recently there was a strong development of new analysis methods across different disciplines. Advances in theoretical models of divergence with gene flow (14–16), as well as in testing local (17) and recent (18) adaptations have opened the way to a flurry of tests for genetic processes at fine scales (19–21). Considering on-farm management of local varieties as crop meta-population systems has also opened new avenues in analysing and testing for variety differentiation and local adaptation (22–24). The advent of finely-tuned modelling tools (25), some of which accounting for measurable mechanistic trait syndromes (26), permits predictions of responses to climate change. Models in population genetics have also strongly progressed, allowing more accurate inferences on population history (migration, demography, selection...) and traits' genetic architecture, especially under the approximate Bayesian computation framework (27, 28).

It has been proven that, in such contexts, adaptation is likely to be multi-trait and multi-locus (26, 29), making it more likely that finely-tuned adaptation is driven by weak processes affecting multiple targets (30) rather than by divergence in single characteristics. All these adaptive processes, characterised by the simultaneous maintenance of standing variation, are essential components of the resilience of eco- and agro-systems (31, 32) to CC.

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GOAL

Within #OPENDIV, we intend to screen existing data sets in genetics and genomics, functional ecology, agriculture, forestry with the goal of (1) detecting signatures associated to such adaptive processes, (2) modelling the impact of CC on adaptive diversity and (3) suggesting novel management strategies based on the use of such diversity to adapt agricultural and forest systems to CC, while maintaining the adaptive potential. We stress here the fact that, contrary to the typical research project, no collection of new data is planned. Instead, we insist on mining existing data, summoning scientists' imagination in finding ways to obtain information from data as "a judge, who compels the witnesses to reply to those questions which he himself thinks fit to propose" (33) and complying with the pressing need of reacting to CC here and now, with the tools we already have (while continuing to gather data in other research programs, which will feed #OPENDIV).