Available online at:
www.afs-journal.org

Letter to the Editor

Adaptive potential in forest tree populations: what is it, and how can we measure it?

One of the most elusive concepts in population and evolutionary biology is "adaptive potential" (AP); yet we need to understand not only how organisms have adapted to extant environmental conditions, but also whether they can adapt to future changes. This issue has been discussed at the "Adaptive potential" workshop of the "Knowledge-Based Management of Tropical Rainforests" conference (Cayenne, French Guiana, November 2009). I summarise here a few conclusions.

There is no universal definition of AP, but a convenient consensus is "the ability of populations to maintain their viability in spite of environmental variations in space and time". This broad definition can be declined as several sub-definitions:

- Plasticity in, and genotype × environment interactions for, "key" traits, which can rapidly adjust so that survival and reproduction are maintained in spite of environmental change (Nussey et al., 2007).
- Ability of populations to maintain residual phenotypic/genetic diversity (and thus residual potential for local adaptation and for speciation) in spite of selection favouring optimal phenotypes (Jump et al., 2008). This can be realised by the capacity of populations and closely related species to remain connected by gene flow.
- "Evolvability" (Pigliucci et al., 2008; Sniegowski et al., 2006) i.e. the heritable potential for evolving new ontogenic equilibria through one of several mechanisms producing (and buffering) phenotypic variability.
- Capacity for a wide array of community-level interactions (e.g. in the case of "generalist" species) and for the expression of novel phenotypes and interactions (especially in the case of biological invasions) (Ghalambor et al., 2007).

These definitions do not indicate how to measure AP: the main challenge is to define a parameter that may be evaluated in natural populations and analysed experimentally. To get a precise definition of AP in forest trees, an operational definition of *fitness*, circumventing the long life cycle of trees, has to be defined; an efficient way to map fitness onto phenotypes, and phenotypes onto genotypes, in natural populations is required. AP can be realised through a variety of biological processes, from ecological adjustments to phylogenetic diversification: its characterisation belongs to the field of integrative biology and should inspire a research program involving the whole forest science commu-

nity. It is of course a matter of individual judgement to establish what the priorities of such a program should be, but addressing the following topics seems inescapable: (a) which ecophysiological, genetic, demographic factors, likely in interaction (Savolainen et al., 2007), affect long-term *viability* in tree populations? (b) Which environmental factors really matter when studying AP (Engelbrecht et al., 2007; John et al., 2007)? (c) At which spatio-temporal scales do these processes and factors matter most for the maintenance of AP in forest tree populations (Hedrick, 2006)? (d) How can we take advantage of increasingly high-throughput data collection (González-Martínez et al., 2006) to draw genotype-phenotype and phenotype-fitness maps? (e) Can we draw relevant evolutionary information directly from natural populations, e.g. by association mapping (Neale et al., 2008), in spite of the potential noise introduced by historical demography, hidden environmental variation and individual ontogeny?

Finding answers to these questions, and tackling the AP issue, will be difficult and exciting at the same time, and is the key to the success of actions to manage forests in the context of global change. Only tight collaboration among different research areas, and an effort to develop new analytical and theoretical frameworks, will make it possible.

Ivan Scotti[1]

REFERENCES

Engelbrecht B.M.J., Comita L.S., Condit R., Kursar T.A., Tyree M.T., Turner B.L., and Hubbell S.P., 2007. Drought sensitivity shapes species distribution patterns in tropical forests. Nature 447: 80–82.

Ghalambor C., Mckay J.K., Carroll S., and Reznick D., 2007. Adaptive versus non-adaptive phenotypic plasticity and the potential for contemporary adaptation innew environments. Funct. Ecol. 21: 394–407.

Hedrick P.W., 2006. Genetic polymorphism in heterogeneous environments: the age of genomics. Ann. Rev. Ecol. Evol. System. 37: 67–93.

John R., Dalling J.W., Harms K.E., Yavitt J.B., Stallard R.F., Mirabello M., Hubbell S.P., Valencia R., Navarrete H., Vallejo M., and Foster R.B., 2007. Soil nutrients influence spatial distributions of tropical tree species. PNAS 104: 864–869.

[1] INRA, Unité Mixte de Recherche "Écologie des Forêts de Guyane" (EcoFoG), Campus agronomique, Avenue de France, BP 709, 97387 KOUROU Cedex, French Guiana; ivan.scotti@ecofog.gf

Jump A.S., Marchant R., and Peñuelas J., 2008. Environmental change and the option value of genetic diversity. Trends Plant Sci. 51–58.

Neale D.B. and Ingvarsson P.K., 2008. Population, quantitative and comparative genomics of adaptation in forest trees. Curr. Opinion in Plant Biology 11: 149–155.

Nussey D.H., Wilson A.J., and Brommer J.E., 2007. The evolutionary ecology of individual phenotypic plasticity in wild populations. J. Evol. Biol. 20: 831–844.

Pigliucci M., 2008. Is evolvability evolvable?. Nature Reviews Genetics 9: 75–82.

González-Martínez S.C., Krutovsky K.V., and Neale D.B., 2006. Forest-tree population genomics and adaptive evolution. New Phytol. 170: 227–238.

Savolainen O., Pyhäjärvi T. and Knürr T., 2007. Gene flow and local adaptation in trees. Ann. Rev. Ecol. Evol. System. 38: 595–619.

Sniegowski P.D. and Murphy H.A., 2006. Evol. Curr. Biol. 16: R831–R834.