

Effect of partial selfing on local adaptation

Project description

Local adaptation reflects the fact that local populations tend to have a higher mean fitness in their native environment than in other environments and than other populations introduced in their home site. Local adaptation is widespread, especially in plant species, and the conditions and mechanisms promoting local adaptation have been studied for a long time, both theoretically and empirically [1,2]. A key ingredient is the existence of spatially heterogeneous selective pressure favouring locally specialised genotypes, balanced by other evolutionary forces such as migration and random genetic drift, which have been integrated in many population genetics models. However, most models of local adaptation assume local random mating [but see 3]. The effect of partial selfing thus remains unclear because of its antagonistic effects on key evolutionary forces mentioned above, and a meta-analysis of empirical studies lead to inconclusive results [4].

Selfing strongly affects population genetic parameters such as homozygosity, effective size and effective recombination rate, which should globally reduce the efficacy of selection [reviewed in 5]. This should limit the possibility for local adaptation. However, selfing also reduces pollen gene flow, which should promote local adaptation. In addition, selfing maintains linkage disequilibrium and should avoid the breakdown of locally co-adapted combinations.

The aim of the project is to develop theoretical predictions on the effect of partial selfing on local adaptation. First we propose to study a simple single-locus model in two biological contexts:

- (i) An island/mainland model, corresponding to the colonization of a new peripheral environment; the allele adapted to the new environment will be considered as deleterious in the old environment. We will determine the frequency of the beneficial allele in the new environment and the migration load. This could be done by the extension of [6].
- (ii) A two-patch model where an allele is favoured in one environment and the other in the other environment. This corresponds to the classical Bulmer's model [7], extended by Yeaman and Otto to take genetic drift into account [8]. This model will be extended by adding partial selfing. It will help determining the conditions under which polymorphism, hence local adaptation, can be maintained and whether selfing reduces or increases the range of conditions for local adaptation.

Second, two-locus models could be studied to take into account the effect of selfing on genetic linkage. The approach will rely on the development of analytical models using classical population genetics modelling tools such as diffusion methods that will be compared to stochastic simulations.

Contact

Supervisor: Sylvain Glémin – sylvain.glemin@ebc.uu.se

Co-supervisor: Martin Lascoux – martin.lascoux@ebc.uu.se

More info: <http://sylvain.glemin.pagesperso-orange.fr/sylvain-glemin/Home.html>

Group at EBC: <http://www.ieg.uu.se/plant/lascoux-group/>

Department: Plant Ecology and Evolution, IEG, UU

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