

Variation in fecundity among species and its evolutionary consequences

Predicting the evolutionary trajectories of living species give us the chance to develop informed management policies and preserve species at the brink of extinction. Also, the possibility to understand the consequences of climate change and of introduced, potentially invasive, species can allow us protecting local ecosystems from dramatic alterations. To this aim, conservation and population geneticists make use of sophisticated models tracing the past and future potential evolution of observed genetic variation. These models are able to reconstruct the past genealogies of related genes and infer key parameters from extant populations that help us determine their level of risk extinction and future loss of genetic variation. The development of appropriate models is under constant improvement, as we understand which biological features are most relevant to reconstruct and predict evolution and, also, as mathematical and computational tools are refined.

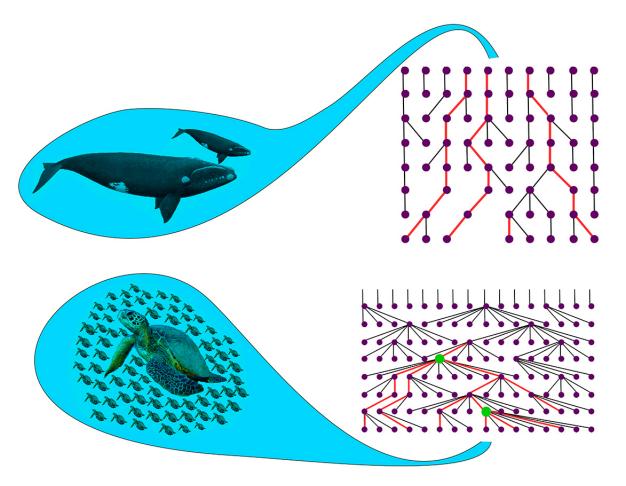


Fig. 1. Example of r- and k- strategist species and their hypothetical gene genealogies without overlapping generations. Green turtles (r-strategist) leave a high number of descendants per individual. Successful lineages (in black) will be sampled (in red) and tracked back in time to meet common ancestors. Sometimes more than two lineages will merge into the same parental one



(green dots). Whales (k-strategists) leave very few successful progeny per individual. The sampled lineages will meet common ancestors much back in time, compared to r-strategists, so that their genealogies are longer and no more than two lineages likely merge into a common ancestor.

Species reproductive strategies have been historically divided into two main ecological categories catching a blatant and substantial difference among the majority of known species. These categories are the so-called *r*- and *k*- reproductive strategies. *R*-strategists are individuals that produce a high amount of progeny per reproductive event and invest little to no energies in parental care so that each individual of any *r*-species has the potential to leave many progenies during the route of its life. As an alternative approach, *k*-strategists invest much energy in nurturing a limited number of offspring per reproductive event, while spending less energy to produce a high number. As an intuitive consequence, the gene genealogies of *r*- and *k*-strategist are likely to evolve following distinguishable paths (Fig. 1).

These differences in intrinsic reproductive strategies have been mostly neglected in conservation genetic inferences mainly for a matter of mathematical tractability, for which all species are usually approximated using a general model that neglects high reproductive variance and high differences in reproductive output among individuals of the same species. However, it has become clear that this simple model fails to capture the complexity of species where some individuals may by chance be incredibly successful in their reproductive effort and all the others very unlucky (Sweepstakes Reproductive Success hypothesis or SRS). Hence, more complex models, suitable for the scenario described above, have been recently developed and (mostly) theoretical studies have shown that they change substantially our predictions on the faith of observed genetic variation. To date, it is still unclear how to conciliate these new models with currently used ones, as their comparison is not straightforward in mathematical and thus biological terms. More empirical and simulation studies are needed to clarify and understand the relevance of models including high variance and skewness in offspring distributions, but once this step is taken, it will become a considerable improvement in our ability to carry out informative genetic inferences. The role of empiricists in this context must not be underestimated, as their contribution will likely accelerate the diffusion of new statistical tools already available.

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<u>Coalescent inferences in conservation genetics: should the exception become the rule?</u> Montano V



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