Evolution of Anisogamy

In primitive plants (where anisogamy evolved in the first place), the life cycle has two distinct stages. The sporophyte starts with a fertilised egg. We assume that the probability of survival of a zygote is an increasing function of its weight, *z*, which is in turn the sum of the weights of the two gametes that produced the zygote, for example of x_1 and x_2 . If the zygote survives, then it produces B(N) spores (spore number depends on population density in order to prevent exponential population growth, but does not depend on the size strategy). Half the spores carry the allele for weight x_1 and the other half carry x_2 . The spores develop into the gametophyte, which produces the gametes with weights according to the allele brought by the spore. Each individual in this stage has the same amount of resources, *R*, and hence it can produce R/x gametes of size *x*. We assume that there is a minimum size x_0 below which the gamete is not viable, and hence the set of possible size strategies is the interval $[x_0, R]$.

Assume first that any two gametes may unite to form a zygote and consider the fate of a mutant gamete of size y in a population with resident gamete size x. The expected probability of survival of the zygote derived from the focal gamete is f(y+x), where the function f(z) gives the probability of survival of a zygote of size z. If the zygote survives, then it will produce B(N)/2 spores with allele y, each of which will, in turn, make R/y gametes identical to the focal gamete. The number of gametes carrying allele y changes from generation to generation according to

$$n_{y}(t+1) = f(x+y)\frac{B(N(t))}{2}\frac{R}{y}n_{y}(t)$$
(1)

and the same equation for the gametes of the resident strategy x is

$$n_x(t+1) = f(2x)\frac{B(N(t))}{2}\frac{R}{x}n_x(t)$$
(2)

When y is a rare mutant in the resident population of x, $n_y \ll n_x$. In both equations,

$$N(t) = \frac{1}{2}n_x(t)f(2x)$$
(3)

is the number of sporophytes (division by 2 is because two gametes make one individual). It is simpler to concentrate on the frequency of the mutant strategy *y*,

$$q(t+1) = \frac{n_y(t+1)}{n_x(t+1)} = \frac{f(x+y)/y}{f(2x)/x} \cdot \frac{n_y(t)}{n_x(t)} = \frac{f(x+y)/y}{f(2x)/x} q(t)$$
(4)

because then R and the unknown function B(N) is cancelled. The dynamics of the mutant's frequency depends only on the shape of function f.

Investigate what types of functions *f* lead to evolutionary branching or to the evolution of a single gamete size. This can be done analytically, but illustrate the results also with PIPs. A locally linear trade-off $f(z) = \alpha + \beta z$ is a good starting point, but it needs to be truncated such that the probability of survival, *f*, is between 0 and 1 (truncation depends on the values of α and β). You can then perturb this function by adding a quadratic term $\gamma(z - z^*)^2$ (taking care that *f* remains an increasing function for the strategies of interest). A sigmoid function like $f(z) = c - \exp(-\alpha z^2)$ is a natural choice for the trade-off, since it assumes that the probability of survival saturates as a function of zygote size.

Construct examples for different types of PIPs and investigate dimorphic coevolution via isocline plots in examples which exhibit evolutionary branching.

Even in isogamous algal species, the gametes belong to two mating groups (often denoted by + and -, respectively) and two gametes can unite only if they are of different mating groups. If time permits, consider a species with +/- gametes where the sizes of + and - gametes evolve simultaneously as two different traits, x^+ and x^- . Assume that initially, x^+ and x^- are near one another (isogamy). Explore the joint adaptive dynamics of the two traits under various trade-offs f.