Evolutionary dynamics of selfish genetic elements

Background

The genomes of many organisms in the tree of life are full of genetic material that is not directly required for operations necessary to live. In complex genomes, a large portion of this superfluous DNA is composed of parasitic elements or selfish genes. Selfish genetic elements (SGEs) are often detrimental to their host. As a result, an evolutionary arms race has driven the development of genome defense mechanisms to prevent the spread and proliferation of SGEs.

Transposable elements are well known examples of agents causing genomic conflict (Ågren and Wright 2015). A much less studied case is that of the so-called “meiotic drivers”. These SGEs “cheat” during (or immediately after) meiotic segregation, in order to favor their own transmission at the expense of the opposite allele (Lindholm et al. 2016). Consequently, meiotic drivers can increase their frequency (“drive”) in the population up to 100%, even if this entails deleterious effects for the host organism. By also increasing the frequency of linked mutations, a driver can lead to incompatibilities between populations, initiating or contributing to the process of speciation (Crespi and Nosil 2013).

The coprophilous fungus *Podospora anserina* is a model species for the study of molecular biology and evolution, e.g., for the molecular basis of ageing, meiosis, and prion biology (Espagne et al. 2008). It is also an interesting system to study meiotic drive, because several distinct driver elements (called “spore killers”) have been described in a single population in the Netherlands (van der Gaag et al. 2000). However, little is known on the ecology and evolution of *P. anserina*, which is needed to use it fully as a model for meiotic drive.

Research training project (forskningspraktik)

The Dutch population of *P. anserina* has been sampled a number of times between 1991 and 2010, making it a unique resource to study temporal shifts in allele frequencies and other traits over generations. To improve this system we sampled new populations in 2016 and 2017, with the aim of determining if the different killer genes are on their way to fixation, extinction, or if they maintain stable polymorphisms. The student will use microbiology and molecular techniques to investigate the newly sampled population for species identity and spore killing, and thereby participating in a project aimed at answering the following questions:

- Are there any changes in the frequencies of killers?
- Are there any new killers?
- What is the effect of the mating system (selfing) on the spore-killing dynamics of the population?
Master project (examensarbete)

_Podospora anserina_ has the potential to become a strong model system for the study of genomic conflict. It has an obvious morphological trait that can be identified in wild strains (spore-killing), comprehensive sampling, and high quality whole genome sequences. Nonetheless, the phylogenetic relationships of _P. anserina_ and related fungi remains entirely unresolved (Kruys _et al._ 2014), limiting the inferences on the prevalence of spore killing across taxa, as well as the evolution of mating systems in the group. For this thesis-project, the student will aim at:

- Resolving the phylogenetic relationships of _P. anserina_ and relatives using molecular markers
- Looking for homologs of the spore killer genes in other species to clarify their origin
- Infer the shifts in mating systems and morphological traits related to adaptations to the coprophilous life-style

The student will take an active part in planning the project and it can be adjusted to fit his/her specific interest.

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References
Espagne E., Lespinet O., Malagnac F., Silva C. Da, Jaillon O., _et al._, 2008 The genome sequence of the model ascomycete fungus _Podospora anserina_. Genome Biol. 9: R77.