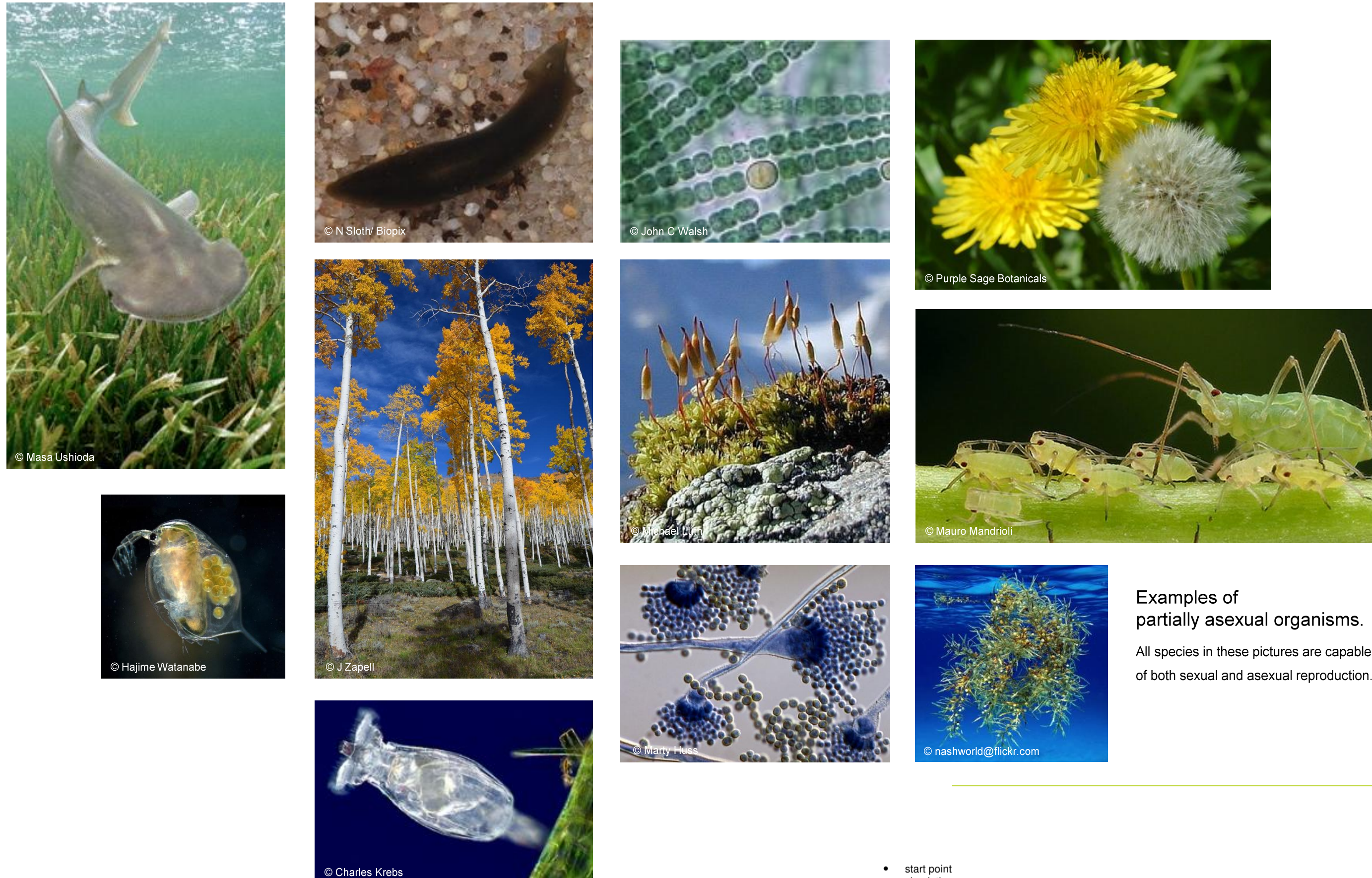


EXTENDING THE THEORETICAL BASIS OF POPULATION GENETICS FOR PARTIALLY ASEYUAL SPECIES

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Examples of partially asexual organisms. All species in these pictures are capable of both sexual and asexual reproduction.

INTRODUCTION

Partially asexual organisms have the ability to reproduce both sexually and asexually, either sequentially or in parallel. They occur throughout the earth's biomes and include many ecologically important species (parasites, invasives, colonizers, ecosystem engineers), yet also some which are under threat of extinction.

Population genetic analyses of partially asexual species have to deal with a number of challenges, e.g. defining sampling units and finding a representative sampling size and scheme. Moreover, since common methods for data analysis such as F-statistics rely on the Hardy-Weinberg equilibrium as a null model, asexual reproduction is a confounding effect and interferes with the interpretation of other factors.

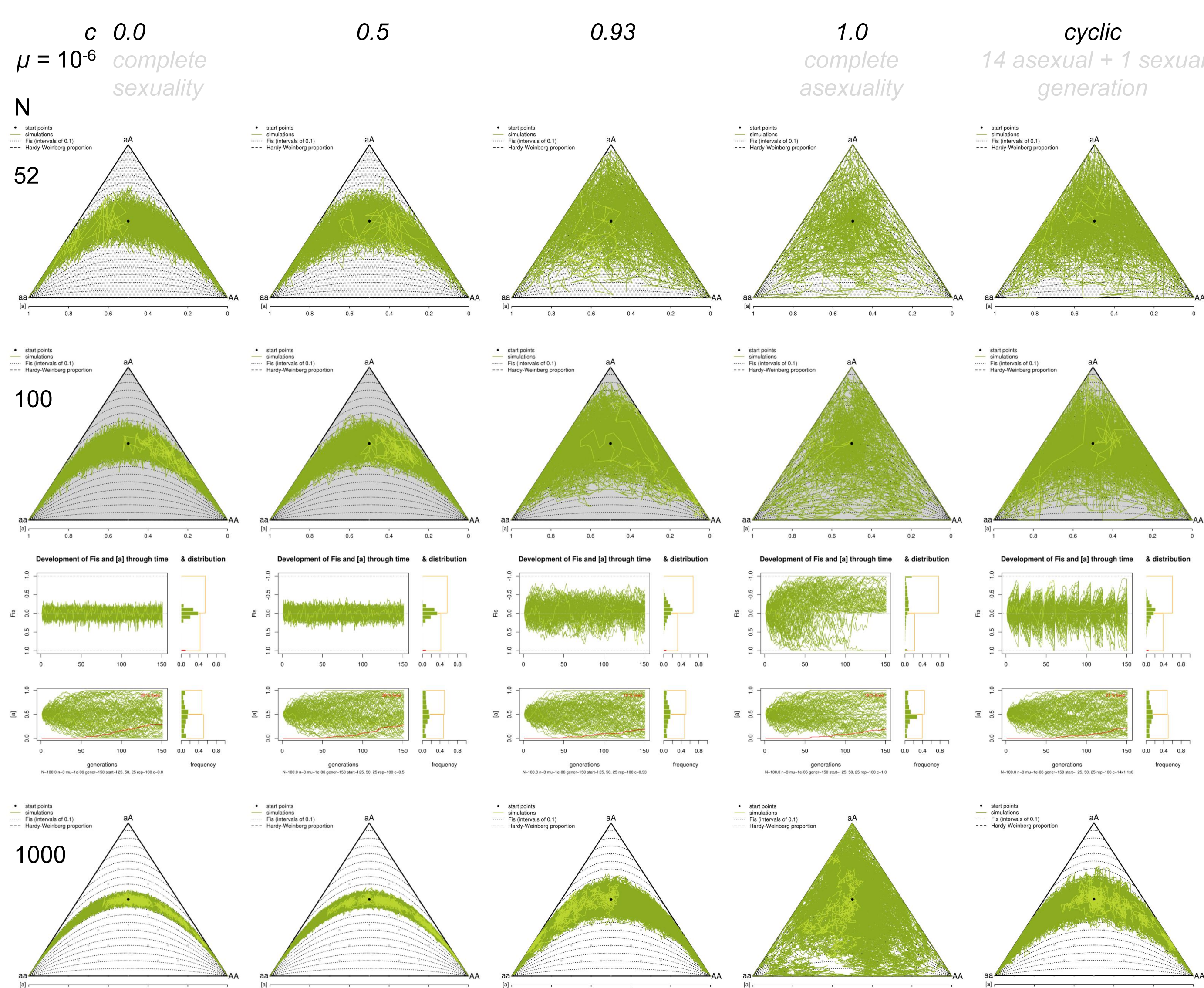
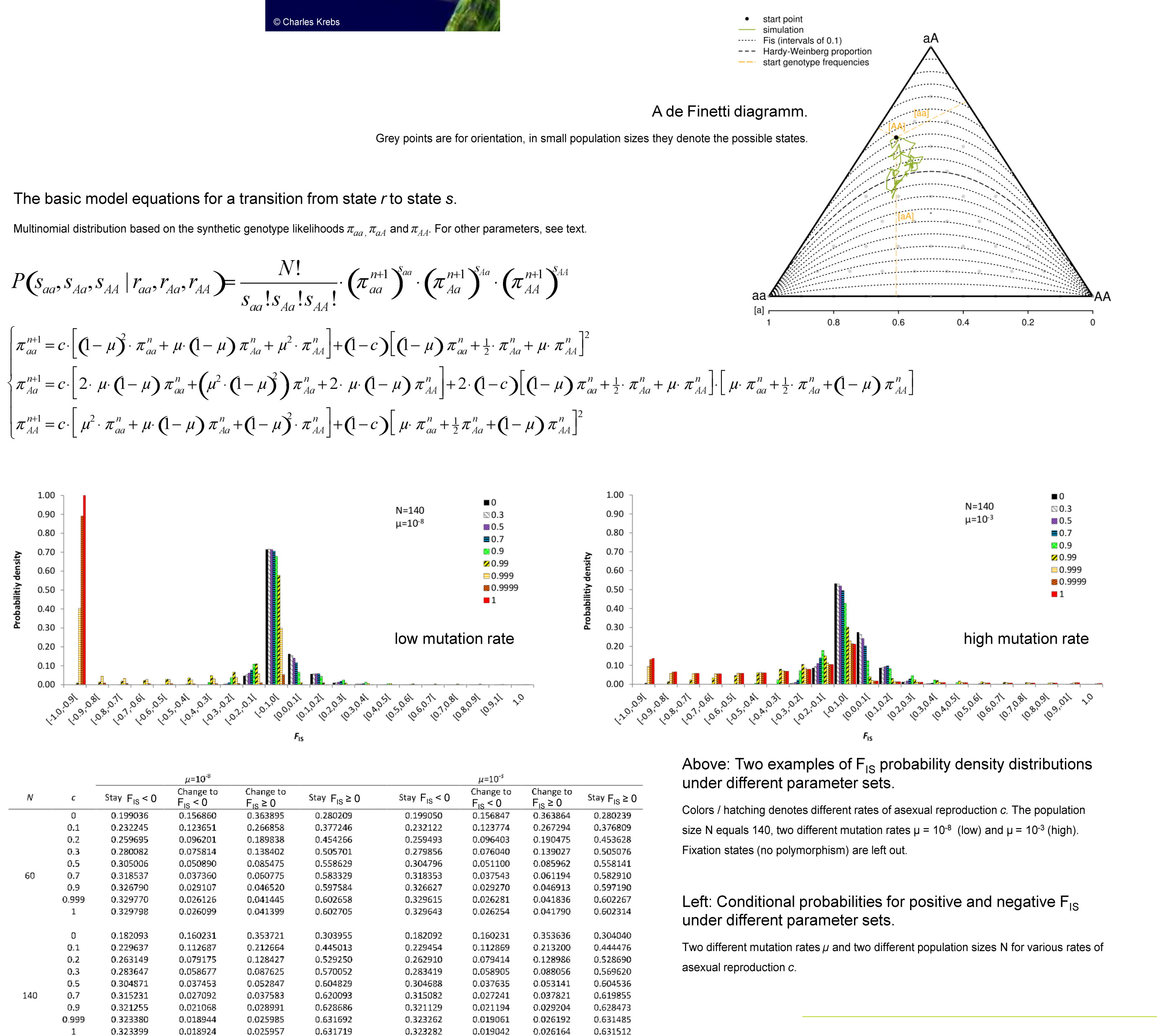
By modeling the population genetics of partially asexual organisms, we hope to provide a sound basis for analysis and bring light to the effects of this type of reproductive system on genetic diversity.

A NOVEL APPROACH

We developed a Markov chain model based on the genotypic composition of partially asexual populations evolving through successive generations. Thus, we have a full view of all possible genotype frequencies which may ever occur in a given population, and the transition probabilities connecting them.

At the moment, we are looking at the "classical" case of a single locus with two alleles *a* and *A* in a diploid organism. Mutation between the alleles occurs with a constant universal rate μ . Populations are panmictic and have a constant, finite size *N*, and the potential clutch size of one individual exceeds the population size for both sexual and asexual reproduction. The rate of asexuality *c* describes the percentage of the offspring produced without gametic recombination. It is either constant throughout time (as in some plants), or changes in a cyclus (as in aphids, daphnia etc.). We use de Finetti diagrams to display our results, coupled with tools from network analysis.

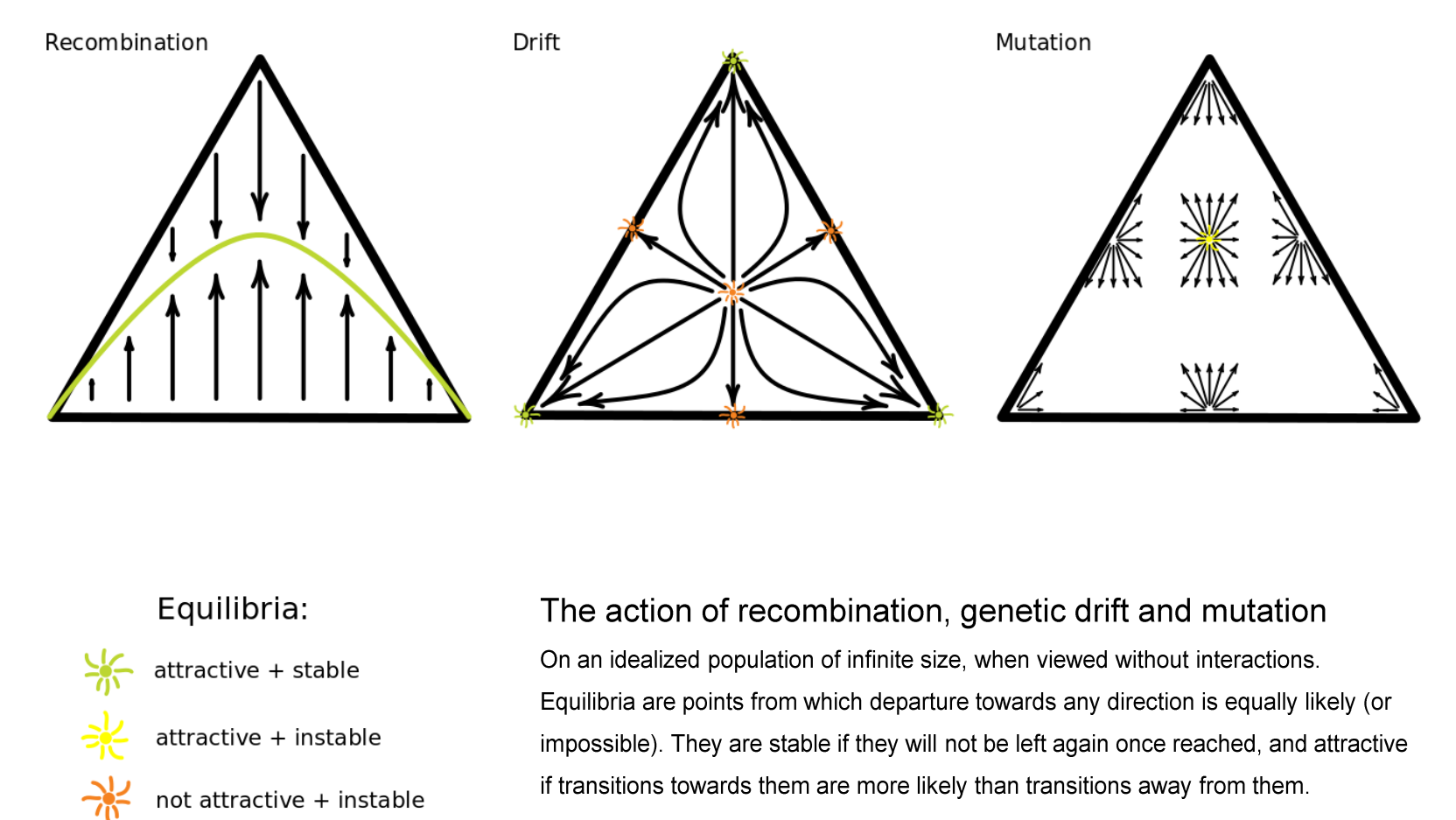
Based on our model, it is possible to obtain the full probability density distribution of commonly used population genetic parameters such as F_{IS} for a given set of parameters μ , *N* and *c*. By comparing field data to these theoretical distributions rather than just their mean values (which may not differ much from those for purely sexual reproduction), other effects such as selection, migration or preferential mating become easier to detect.



DYNAMICS

In changing natural environments, populations evolving under constant parameter sets for an infinite time may be an exception rather than the rule. However, the dynamics of genotypic composition under changing conditions (e.g. cyclic asexuality, population growth) can be simulated.

Our results show that partial asexuality changes the variance (and higher-order moments) of the F_{IS} distribution, depending on the background of mutation ($\sim \mu$) and genetic drift ($\sim 1/N$) in the population. Especially at small population sizes, it decreases the "pull" towards the Hardy-Weinberg equilibrium effected by gametic recombination, thus resulting in changed evolutionary trajectories.



USING A FULL DISTRIBUTION OF F_{IS} AS A NULL MODEL FOR PARTIALLY ASEYUAL SPECIES PROVIDES MORE ACCURATE RESULTS THAN JUST LOOKING FOR NEGATIVE F_{IS} VALUES

