Review

# Consequences of reproductive mode on genome evolution in fungi

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## A R T I C L E   I N F O

## A B S T R A C T

An organism's reproductive mode is believed to be a major factor driving its genome evolution. In theory, sexual inbreeding and asexuality are associated with lower effective recombination levels and smaller effective population sizes than sexual outbreeding, giving rise to reduced selection efficiency and genetic hitchhiking. This, in turn, is predicted to result in the accumulation of deleterious mutations and other genomic changes, for example the accumulation of repetitive elements. Empirical data from plants and animals supporting/refuting these theories are sparse and have yielded few conclusive results. A growing body of data from the fungal kingdom, wherein reproductive behavior varies extensively within and among taxonomic groups, has provided new insights into the role of mating systems (e.g., homothallism, heterothallism, pseudohomothallism) and asexuality, on genome evolution. Herein, we briefly review the theoretical relationships between reproductive mode and genome evolution and give examples of empirical data on the topic derived to date from plants and animals. We subsequently focus on the available data from fungi, which suggest that reproductive mode alters the rates and patterns of genome evolution in these organisms, e.g., protein evolution, mutation rate, codon usage, frequency of genome rearrangements and repetitive elements, and variation in chromosome size.

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## 1. Introduction

Reproductive lifestyles are believed to play a fundamental role in genome evolution. In particular, evolutionary theory predicts that an organism's reproductive mode, defined herein as sexual inbreeding or outbreeding and/or reproduction via asexuality, alters the rates and patterns of genome evolution by their influence on selection pressures, genetic variation, and rates of mutation fixation (Charlesworth and Wright, 2001; Charlesworth, 2006). Empirical data supporting/refuting these theories has been sparse. However, recently emerging data from fungi could provide important insights into the association between reproductive modes and genome evolution. Here, we review empirical data regarding the relationship between the mode of reproduction and genome

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evolution, with a focus on recent data from fungal systems. For this, we briefly review the theoretical predictions about the relationship between reproductive systems and genome evolution, and present examples of empirical data from plants and animals. We subsequently focus on the types of reproductive systems in fungi, and highlight specific empirical data revealing the relationships between the mode of reproduction and genome evolution in this kingdom, including data derived from the filamentous ascomycete Neurospora, yeasts and basidiomycetes.

## 2. Reproductive systems and evolution

### 2.1. Theoretical predictions

Theory predicts that an organism's mode of reproduction is a major factor affecting its genome evolution. Asexual and highly inbreeding species, i.e., species exhibiting low effective recombination rates, have small effective population sizes and thereby reduced selection efficiency compared to their outcrossing counterparts (Charlesworth and Wright, 2001; Haudry et al., 2008). As a result, genetic drift is predicted to play a greater role relative to selection in shaping their genomes. This reduced selection efficiency is expected to translate into accelerated evolution on both the chromosome level (e.g., repetitive elements, rearrangements) and the protein level, due to the accumulation of slightly deleterious mutations which otherwise would have been eliminated or minimized by purifying selection (Kimura, 1968; Charlesworth and Langley, 1989; Charlesworth et al., 1993; Charlesworth and Wright, 2001). Furthermore, asexual and inbreeding species with low effective population sizes are predicted to show a reduction in codon usage bias (Charlesworth and Wright, 2001), which has evolved for high translational efficiency (Akashi, 1994, 2001). This is consistent with a reduced rate of adaptive evolution (Charlesworth and Wright, 2001; Otto and Lenormand, 2002). The restriction of recombination in asexual and highly inbred species also makes the genome more susceptible to genetic hitchhiking via selective sweeps (wherein positive selection drags linked deleterious alleles/sites to fixation, Rice, 1987; Charlesworth and Charlesworth, 2000) and background selection (which may enhance the fixation of mildly deleterious mutations and/or result in the loss of beneficial mutations, Charlesworth and Charlesworth, 2000; Andolfatto, 2001). Furthermore, a reduced recombination level enhances the role of Muller's Ratchet (the stochastic losses of chromosome classes that have the fewest deleterious mutations, Muller, 1964). Both genetic hitchhiking and Muller's ratchet may further accelerate the rate of non-adaptive chromosome and protein evolution and reduce codon usage bias in genomes of organisms with low effective recombination rates (Charlesworth et al., 1993; Haudry et al., 2008). It has been postulated that as a result of low genetic diversity and the accumulation of deleterious mutations, highly inbreeding and asexual mating systems are evolutionary dead ends and thus are of recent origin (Takebayashi and Morrell, 2001).

### 2.2. Reproductive systems and genome evolution in plants and animals

Empirical data supporting/refuting theoretical predictions about the influence of sexual mating systems on molecular evolution from plants and animals are rare, and the limited available data has not revealed clear trends. We highlight several examples here. First, data from the flowering plant genus Lycopersicon have uncovered that transposable elements (Lyt 1) are much more frequent in the genomes of red-fruited species than green-fruited species (Young et al., 1994). It has been proposed that these

differences might be attributable to mating systems as red-fruited taxa are highly inbreeding while green-fruited are outcrossing; thus, the data are consistent with theoretical predictions of elevated genomic changes in selfers (Charlesworth and Charlesworth, 1995). This trend is also supported by findings of higher levels of transposable elements in the inbreeding species Arabidopsis thaliana compared to its outcrossing close relative Arabidopsis lyrata (Lockton and Gaut, 2010). In contrast to what is expected from theory, however, A. thaliana was found not to have consistent evidence of accelerated protein evolution or reduced codon bias in its genome relative to A. lyrata (Wright et al., 2002). Findings from the plant tribe Triticeae have shown that codon usage bias is markedly lower for inbreeding than outbreeding species, consistent with elevated degeneration in codon usage for selfers within this taxonomic group (Haudry et al., 2008). In this case, however, it has been proposed that biased GC gene conversions might be elevated in outbreeders (due to elevated recombination rates), giving rise to enhanced codon usage bias towards GC ending codons, that could also explain the findings (Haudry et al., 2008; see also Wright et al., 2007). Similar to the data from the Triticeae, recent findings from the nematode genus Caenorhabditis reveal mild reductions in codon usage bias in the inbreeding species relative to obligate outbreeders, but show no consistent evidence of accelerated protein evolution (Cutter et al., 2008). In totality, these data are suggestive of a mild association between inbreeding and the accumulation of degenerative genomic traits, but is yet inconclusive.

It has been proposed that the findings of little/no observable effect of selfing on genomic traits in plants and animals might indicate that this mode of reproduction has recently originated, consistent with the dead end theory (Takebayashi and Morrell, 2001; Cutter et al., 2008). The data from Caenorhabditis support this theory. Specifically, it was found that the inbreeding species examined in this genus (Caenorhabditis elegans and Caenorhabditis briggsae) have likely originated less than 4 Mya while outcrossing species are of ancient origin (Cutter et al., 2008). Notably, a recent origin of selfing might also explain the weak or absent relationships between reproductive mode and genome evolution observed in plants (Wright et al., 2002, 2007; Haudry et al., 2008). For example, analysis of genomic data from the self-incompatibility locus (S) has revealed that selfing in A. thaliana originated approximately 1 Mya, consistent with too short of a time period to detect effects of relaxed selection on protein evolution or codon usage in this taxon (Wright et al., 2002; Tang et al., 2007). Thus, it is possible that many inbreeders have existed for too short-time period to substantially alter molecular evolutionary traits (Cutter et al., 2008).

Taken together, currently available data from plants and animals on the genomic consequences of mating systems remain largely inconclusive. Further insights that collaborate and/or refute trends reported in animals and plants may be obtained from fungi, wherein reproductive systems are highly variable within and among taxonomic groups. Thus, fungi serve as particularly effective systems to further reveal the association between reproductive systems and genome evolution.

## 3. Reproductive systems in fungi

In contrast to plants and animals wherein the vast majority of organisms reproduce sexually (Bell, 1982), fungi have complex life cycles exhibiting various modes of reproduction (see Heitman et al., 2007). In brief, sexual reproduction in the ascomycetic fungi can be divided into three major modes; heterothallic, homothallic and pseudohomothallic. Heterothallic (self-incompatible) species require a haploid partner with nuclei of a compatible mating type