Abstract

Sexual reproduction is an energetically costly process for organisms to accomplish in contrast to asexual reproduction. It requires organisms to compete for mates, exhibit pre-copulatory behaviors, and engage in the act of copulation, all of which are arduous behaviors that are not required in asexual reproduction. Nonetheless, sexual reproduction is evolutionarily conserved. The high prevalence of sexual reproduction among organisms remains unknown. Current literature supports the conservation of sexual reproduction due to its creation of genetic variation between organisms, which is particularly favored in unpredictable environments. One model which supports this is the Red Queen Hypothesis (RQH). The RQH states that organisms and their co-evolving parasites continually undergo genetic recombination in a positive-frequency dependent selection manner, to counter-adapt one another. Whereas, the parasite acts to evade the immune system of the host, the host's immune system acts to evade the entry and virulence of the parasite. As a result of the necessity for genetic variation in this evasion process, this parasite-host relationship reinforces sexual reproduction. In this review, I ýrst introduce the theory of the Red Queen and the type of selection that it models. I then tested the validity of the RQH against various models including computer-simulated bacterium such as Pseudomonas þuorescens SBW25 and their parasitic hosts, and ancestral genomes of Denisovans and Homo sapiens. Lastly, I will conclude whether there are limitations to the Red Queen. While this review will not begin to cover the breadth of possible beneýts to sexual reproduction, it will uncover real-world applications for how genetic variation is beneýcial in combating pathogens.

Introduction

Living organisms reproduce via two mechanisms, including asexual and sexual reproduction. Both modes achieve the same result, the passing down of genetic material to o spring and increasing ýtness within an individual. However, they di er in the percentage of genetic material that is passed along per parental genome, and the conditions necessary for each type of reproduction to occur. Asexual reproduction describes a parent cell duplicating its DNA to produce a genetically identical o spring. Asexually reproducing organisms will not yield genetic variation within a population's gene pool, unless in the case of random mutation. Modes of asexual reproduction typically include the duplication of the parental genome and cytoplasm within the cell, followed by a breaking away of the duplicate cell. Such modes include binary ýssion, snapping division, and budding (Bauman, 2016).

Alternatively, sexual reproduction is the generation of progeny via the gametic combination of two individuals, thereby creating genetically diverse o spring. This typically requires two haploid gametes fusing and fertilizing one another to create a diploid cell that is genetically diverse from the parental genomes. Recombination and crossing over of the parental chromosomes during fertilization allow for the zygote to remain genetically distinct from its parentsû genomes (Bauman, 2016). However, because the zygote's DNA was yielded from the parent's DNA, parent and daughter cells are genetically similar. Overall, asexual reproduction only requires one parent cell for the formation of progeny and guarantees the full genome of the parent cell will be duplicated and passed down for generations. Whereas sexual reproduction requires two separate parent cells and assures only half of each parental genome will be passed down to progeny. Sexual reproduction is viewed as an energetically costly process compared to that of asexual reproduction. Organisms that engage in sexual reproduction must outwardly exert energy seeking a mate, engaging in both pre- and post-copulatory behaviors, and engaging in the actual act of copulation. Furthermore, these acts themselves do not ensure the organism will be successf and Bender, 1981). Along this line of thought exists the Red Queen Hy

pothesis (RQH). The RQH states that species within predator-prey, or parasite-host associations are in a coevolutionary arms race with another, coevolving to counter-adapt the other organism. Because sexual reproduction yields high genetic variation within o spring, it may prevent both species from fully optimizing the weaknesses of their competitor, acting as ñmoving targets,û and thereby increasing ýtness Ĉ ȳ Z ᵐ ⁎ I ᶦ

growth of hosts (Ashby and King, 2015). These calculations require the probability of an epidemic to be inversely correlated with genetic diversity of a host population. If these calculations are true, as genetic host diversity increases, the likelihood of contracting a parasite decreases (Ashby and King, 2015). One could argue that on a short-term scale, if host genetic

models, as they incorporated density-dependent mortality, þuidity of recombination rates, and parasite immigration, all factors which may reþect population dynamics within the real-world (Ashby and King, 2015). They also properly addressed the idea that genetic variation of sexual individu-

Advancing Our Understanding of the RQH in Non-Predator-Prey or Parasite-Host Relationships

While the RQH surely acts on parasite-host and predator-prey models, evolutionary biologists questioned whether it can be observed between genetically similar parasite-host models. For example, cancer cells which feed o living hosts for nutrition (Aubier et al., 2020). This is a unique way of viewing the RQH because cancer cells are derived from host cells but mutate and replicate at faster rates (Aubier et al., 2020). In other words, cancer and host cells are one in the same. This is unlike a parasite-host relationship, as parasites and hosts are two di erent domains that inter-