

BIOLOGICAL SYSTEMS OF INTEREST TO RESEARCHERS OF CULTURAL EVOLUTION

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Cultural evolution has played an important role in the evolution of language (e.g. see Kirby & Hurford, 2002; Kirby, Cornish, & Smith, 2008). This cultural process is however far less well understood than its biological equivalent, which has led to the proposal of various analogies between biological and cultural evolution (Serenio, 1991). These analogies, however, have been rightfully criticised as misleading (e.g. Smith, 2012). Despite this, we argue much insight can still be gained from the study of biology, and in this paper survey several lesser-known biological systems that are informative for the study of cultural evolution.

The first class of systems we discuss are species which undergo an *alternation of generations* between two distinct reproductive forms as part of their life cycles. Examples of such species include those of the phylum *Cnidaria* (Collins, 2002), which includes jellyfish and corals, and the parasitic fungi of the genus *Gymnosporangium* best known for causing cedar-apple rust (Petersen, 1974). A parallel is drawn with the inherently two-stage replication of cultural information from brains to the environment and then back from the environment to brains.

Second, we consider *prions*, misfolded variants of the mammalian PrP protein which can cause transmissible neurological diseases. Li, Browning, Mahal, Oelschlegel, and Weissmann (2010) have shown that, without changes in the genetic encoding of the base protein, changes in the secondary (folding) structure of prions can be selected and evolve via a darwinian process. We argue prions are therefore interesting from a cultural evolution perspective due to their replication via direct copying of form, without the separation of genotype and phenotype found in other biological systems (which is also absent in cultural transmission).

Next we introduce *clonal transmissible cancers*; infectious cancers evolved from a species' own cells (Murchison, 2008; Metzger, Reinisch, Sherry, & Goff, 2015). Both the inter-cellular selection process leading to the emergence of these cancers, as well as their subsequent evolution as pathogens (and the host response), are suggested as a model for the often proposed evolution of maladaptive cultural variants. This host-parasite relationship is briefly contrasted with the sym-

biosis between ants and certain epiphytes (plants that grow on other plants) which are known to grow structures specifically to house ant colonies (Huxley, 1980). It is suggested that, in the general case, this is likely a better model for thinking about linguistic gene-culture interactions.

And finally, we discuss the species *Oxytricha trifallax* which is claimed to have the most complex genome architecture of any known eukaryote (Chen et al., 2014). Possessing two nuclei per cell, and undergoing large-scale genome remodeling during reproduction (including deletions, rearrangements and inversions), it is argued to provide a good test ground for theories concerning the nature and necessary properties of generalised darwinian replicators.

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