Evolution towards extinction in replicase models: inevitable unless....

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In the quest to understand biological evolution and to create artifical evolutionary systems, a useful paradigm is to focus on early supposedly simple (prebiotic) evolution. The RNA world hypothesis on early evolution, posits that initially coding and storage of information as well as the utilization of this information were embedded in the same polimeric molecule (RNA), and that only later a division of labor between these two essential aspects of evolutionary systems evolved.

In biological/chemical context RNA based models have been extensively studied, either by modeling RNA explicitly as a sequence of 4 nucleotides for information storage, and the (2D) folding as proxy for phenotype/function (e.g. [1]), or in a much simplified form as replicase (RP-like) models (e.g. the classical hyercycle model), in which template directed replication is catalyzed by a replicase, and the template/replicase are combined in one entity(variable) (e.g. [2, 3, 4]). All these RNA inspired models have in common that the actual process of template based replication is left implicit: it just happens; similarly, the occurrence (and rate) of certain types of mutations during replication is externally imposed.

In contrast in artificial life context, the emphasis has been on the replication process itself, by studying evolution of programs coding the copying (replication) of the programs (e.g. [5, 6, 7]. In these models, mutation changes

the program that a molecule executes, occasionally changing the replication process and introducing new (types of) mutations (e.g. a point mutation can lead to a large scale deletion during the next round of replication). Thus, evolution of the programs directly feeds back on the mutations and evolution of the programs, very directly embedding evolution of evolution EVOEVO within an experimental framework. Note that in the RNA based models EVOEVO emerges through the evolution of the genotype-phenotype mapping, whereby the effect of predefined mutational operators evolves, rather than the mutational operators themselves.

Evolution towards extinction of replicases

Unfortunately all these models which incorporate the dual function of information storage, and replication (as catalyzing replicase or as program) have in common that evolution tends to lead to extinction (*UNLESS....*, see below). For example the evolutionary artifical chemistry model Stringmol always evolves itself into extinction, as reported in [6]. One of the reasons for this is that replicating someone is a "strong altruistic" trait not only it benefits the one being replicated, but actually harms the replicase itself, by not being available as template during the process. Therefore selection will lead to minimize functioning as replicase, and therefor in the long run to extinction. Emergence of stronger binding templates which have lost replicase function altogether (i.e. strong parasites) also lead to rapid extinction of the whole system. Only if the probablity/rate of being replicated and replicating someone else are inseparably linked,(e.g. by both being dependent on reciprocal binding at the same site), this selection against being a replicase is overridden by the selection pressure to be replicated, and both functions are maximized.

The above explained selection pressure leading to minimizing replicase function (and maximizing the availability as template) has been extensively documented in the RP models [3, 4], and is stronger the longer the replication process takes. This selection pressure also explains the at first sight surprising zigzag pattern (down-up-down) of binding strengths observed in the Stringmol case-study detailed in[6] (fig 9,10). In Stringmol replication is initiated by complementary binding of two programs. Being template or being replicase depends on the relative localization of the binding site, i.e. both functions can evolve separately , and we should expect decrease of binding strength of the replicase-defining 3' binding site. This is indeed observed initially. At some point in time a second, shorter program arises in the

population which has lost its 5' (consensus) binding site. This means that now the 5' binding site of the ancestral and the novel species are complementary. Because relative localization is identical template and replicase roles are assigned 50-50 in this case. Thus for these interactions replicase and template roles are inseparably linked, and we expect maximization of binding, which is indeed observed. Simultaneously, and maybe unexpectedly, the 'self-binding' between two ancestral molecules also increases. This is entirely a side-effect of maximizing binding to the novel species (the same mutations are involved). Once the binding to the other program is maximized, self-binding decreases rapidly to zero, making replication of 'like' molecules impossible. The shorter, other molecule cannot self-replicate because the loss of reciprocal binding, and the end result is a hypercycle of 2 species mutually replicating each other. To complete the explanation, why is binding to the shorter molecule preferred. despite the fact that this lead in 50% of the cases to replicating the other program? In line with the process described above, this is exactly because it is shorter: it therefore needs less time to replicate that one, instead of one of similar length as 'self' (i.e. 210 steps instead of 240 steps), and therefore increases its avaibability as template.

Extinction, Unless... higher level selection prevents it

Higher level selection can counteract the vulnerability of 'altruistic' behaviour (like replicating others, at a cost to self) to non-altruistic 'cheaters' (parasites). Higher levels of selection may be imposed in the form of vescicles, or (partially) isolated groups, and tend to emerge automatically in spatially extended systems [1, 2]. The effectiveness of higher levels selection due to spatial pattern formation was first demonstrated in the context of protecting hypercycles to invading parasites [8], and later in various freely evolving RP models . In fact in spatially extended systems the evolution of parasites induce the formation of spatial patterns, and therewith higher levels of selection. Not only do these higher levels of selection prevent extinction due to parasites, they also generate novel selection pressures for the replicators/replicases, and therefore can reverse the selection pressure to less effecient replicases to a selection pressure to more efficient replicases [4]. A similar process can lead to the counterintuitive result that the higher the cost of altruism the more altruistic the evolving replicators become! [3]. Likewise in our sequence-based model of the RNA world, where being a replicase was dependent on secondary structure, the evolution of parasites was not only detrimental, but in fact essential for the evolution of complexity

[1].

Here we will investigate whether this 'solution' preventing evolution towards extinction is also effective in the Stringmol model, of which the evolutionary potential was sofar severely restricted due to premature evolutionary (parasitic) extinction.

Joyce [9] defines evolvability in terms of the number of bits which are constraint/predefined vs the number of bits which can evolve. In this sense Stringmol is likely to be more constraint by the need of executable replication program, than the RNA based models although in the sequence-based RNA world the replicase is also rare in sequence space [1]. On the other hand, it could be considered as more evolvable because the mutation profile can evolve.

Thus the here reported experiments will contribute to our insight to what extend different aspects of evolvability and the evolutionary robustness in interacting replacase systems are compatible, and even positively correlated as suggested by the RNA based models.

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