1 Inevitability of the emergence and persistence of genetic parasites caused by

2 thermodynamic instability of parasite-free states

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16

17 Abstract

- 18 Genetic parasites, including viruses and mobile genetic elements, are ubiquitous among cellular
- 19 life forms, and moreover, are the most abundant biological entities on earth that harbor the bulk
- 20 of the genetic diversity. Here we examine simple thought experiments to demonstrate that both
- 21 the emergence of parasites in simple replicator systems and their persistence in evolving life
- forms are inevitable because the putative parasite-free states are thermodynamically unstable.

24 Background

25 Nearly all cellular life forms are hosts to various types of genetic parasites that exploit functional systems of the host cells to replicate their own genomes [1]. Only some bacteria with highly 26 27 reduced genomes that themselves lead a symbiotic or parasitic lifestyle seem to lack genetic parasites that undoubtedly have been lost during the reductive evolution of these bacteria from 28 free-living ancestors. Genetic parasites include viruses, transposons, plasmids and other semi-29 30 autonomous genetic elements (SAGE) [2] that display a broad range of relationships with the hosts, from acute antagonism, whereby a virus rapidly kills the host, to symbiosis when SAGE 31 are not costly to the host and could even have beneficial effects [3, 4]. 32

33 Strikingly, virus particles appear to be the most common biological entities on earth. In most environments, the ratio between virus particles and cells varies between 10 and 100 [4-7]. This 34 enormous physical abundance of viruses is matched by vast genetic diversity so that most of the 35 gene repertoire of the biosphere appears to be concentrated in viruses, even as exact number 36 37 remain a matter of debate [8-10]. The prevalence of viruses in the biosphere is also paralleled by the abundance of SAGE integrated in genomes of cellular life forms. Integrated SAGE are 38 present in virtually all genomes of cellular organisms (again, missing only in some intracellular 39 40 symbionts and parasites), and in genomes of multicellular eukaryotes, SAGE-derived sequences quantitatively dominate the genome, comprising at least 50% of the DNA in vertebrates and up 41 to 90% in plants [11]. Recruitment of sequences from SAGE for cellular functions is a common 42 phenomenon that made substantial contributions to the evolution of cellular life forms [12-14]. 43

The entire course of the evolution of life is a history of host-parasite co-evolution [15-17]. Being 44 45 subject to the constant onslaught of genetic parasites, cellular life forms have evolved a plethora of defense mechanisms. A typical organism harbors and interacts with multiple types of genetic 46 parasites (e.g. viruses, different families of transposons, and plasmids) which it holds at bay 47 thanks to multiple defense strategies that include parasite exclusion, innate immunity and 48 49 adaptive immunity [18-23]. The SAGE respond with counter-defense mechanisms that range 50 from simple mutational escape from defense to dedicated multigene systems that specifically inactivate host defense systems. Notably, defense systems and SAGE including their counter-51 defense machineries are tightly linked in evolution. Enzymes involved in the mobility of SAGE, 52 53 in particular, transposons are often recruited by host defense systems for roles in parasite genome

inactivation and other functions, and conversely, SAGE recruit components of defense systems
that then evolve to become agents of counter-defense [24-26].

Thus, the arms race, along with cooperation, between genetic parasites and their hosts are 56 57 perennial features of the evolution of life. Why is this the case? Why do the parasites emerge in the first place? And, could some cellular organisms actually get rid of the parasites through 58 highly efficient defense systems? Empirically, the answer to the latter question seems to be 59 60 negative. Conceivably, the general cause of the inability of the hosts to eliminate the genetic parasites is the unescapable cost of maintaining sufficiently powerful defense systems [27-30]. 61 Analysis of theoretical models of parasite propagation suggests that an important source of this 62 cost, perhaps the primary one in microbes, could be that efficient anti-parasite defense has the 63 side effect of curtailing horizontal gene transfer (HGT), which is an essential process in 64 microbial evolution that allows microbes to avoid deterioration via Muller's ratchet [31, 32]. 65 66 Another major factor could be the effectively unavoidable autoimmunity [29, 33, 34]. However, what about the first, arguably, the most fundamental question: why do genetic parasites evolve to 67 68 begin with? Again, empirically, there is a strong impression that the emergence of such parasites is inevitable. Not only are they ubiquitous in cellular life forms but they also evolve in various 69 70 computer simulations of replicator system evolution [35-39]. Furthermore, it appears intuitive: genetic parasites can be considered cheaters, in game-theoretical terms, and as soon as, in a 71 72 replicator system, there is a distributable resource, such as a replicase, cheaters would emerge to 73 steal that resource without producing their share of it [40]. These, however, are informal considerations. Here we ask the question: is it possible to develop a theoretical framework that 74 would allow a formal demonstration of the inevitability of the emergence of genetic parasites in 75 76 evolving replicator systems, or else, that parasite-free replicator systems are after all possible?

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78 Thermodynamic instability of parasite-protected replicators

Let us try, as a gedunken experiment, to construct a self-replicating entity that is strictly resistant
to parasites. Consider a simple system consisting of a replicator, serving as a template for itself,
and the replicase it encodes (Figure 1). The replicator is assumed to contain the replicaseencoding signal (RES) (the replicase could be a protein, a ribozyme, under the RNA World

model, or, in theory, any other entity capable of catalyzing replication of a template) and the
replicase recognition signal (RRS).

Evolvability is a fundamental and inescapable property of such a replicator-replicase system 85 [41]. To be evolvable, a system must possess three basic properties: 1) heredity (whereby the 86 location of progeny in the phenotype space is correlated with that of the parents), 2) variability 87 (whereby the progeny is not identical to the parents), and 3) differential reproduction (whereby 88 89 the capability of a replicator to leave progeny is part of the phenotype). Heredity is ensured by replication with fidelity above the error catastrophe threshold. The replicator theory that was 90 developed primarily by Eigen and colleagues demonstrates that, under simple fitness landscapes, 91 there exists a replication fidelity threshold, below which the master sequence in a population of 92 93 replicators cannot be efficiently passed across generations, so that the entire population collapses 94 [42, 43]. Elucidation of the molecular mechanisms of primordial replication that could provide 95 for crossing the error catastrophe threshold remains a daunting task that is central to the entire origin of life field. However, for the purpose of the present discussion, we assume that a 96 97 sustainable replicator system with a minimally acceptable fidelity has evolved.

98 Variability is ensured because, at any temperature above 0 K, any process is subject to entropy99 increasing fluctuations and, therefore, replication is inherently error-prone, under the second and
100 third Laws of Thermodynamics.

Differential reproduction ensues from the fact that the replicator encodes the replicase that, in
 turn, copies the replicator itself. Mutations in both RES and RRS can affect the efficiency of
 replication.

104 If the resources that are available to the system are limited (i.e. the system does not support 105 unlimited growth of all possible constituent parts), competition between individual replicators 106 ensues and selection arises. In a system with finite memory storage, all information exchange, 107 transfer and utilization processes carry memory clearing cost of at least $kT \ln 2$ J/bit, where k is 108 Boltzmann constant and T is temperature (the existence and value of this minimum information 109 cost is known as Landauer's principle that is a corollary of the Second Law of 110 Thermodynamics); in all known systems, this cost is many orders of magnitude higher [44-46].

111 Therefore, selection for cost reduction acts not only on the constituent parts of the system, but

also on the information transfer processes themselves, effectively ensuring an upper limit on thefidelity of information recognition.

114 Selection acts on both RES (eliminating replicators encoding inefficient replicases) and RRS

(eliminating replicators that are inefficient as templates, e.g. are poor replicase-binders), but

these two selection processes act on the replicator through physically different agents (the

117 replicator-encoded replicase and the replicator itself, respectively).

118 The dual nature of the replicator (acting as both the template and, directly or indirectly, as the

replicase) necessitates that the information embedded in the RES and RRS is realized via

120 physically different processes. The RES guides the formation of the replicase which, in turn,

recognizes the RRS. Such recognition implies comparing the RRS in the replicator with some

form of memory encoded in or attached to the replicase (Figure 2).

123 A general, simple way of parasite emergence involves skipping part of the RES during

replication, resulting in a shorter replicator that consists of the RRS and, in the extreme, nothing

else (Figure 3). This straightforward mechanism for parasite evolution is inspired by and is

similar to the process of RNA shrinking that was observed during *in vitro* evolution in the classic

early experiments of Spiegelman and colleagues [47-49].

128 Under the scheme in Figure 3, parasites emerge as long as the information content of the RRS is less than that in the full replicator, i.e. when the RRS is at least partially separable from the RES. 129 130 If this is the case, a replicator containing the full RRS, but omitting at least some of the RES $(RRS_p \equiv RRS, RES_p \rightarrow 0)$; the subscript 'p' denotes the respective signals in the parasite), would 131 not only serve as a template as efficient as the original replicator, but would also enjoy an 132 evolutionary advantage because replication of the smaller replicator is faster and requires less 133 resources (building blocks, such as nucleotides, and energy). This makes the parasite-free 134 equilibrium point of the replicator-parasite system unstable because deletion of any part of the 135 136 RES yields more efficient replicators (Figure 4). Therefore, the system is vulnerable to parasite invasion, and moreover, such an invasion is inevitable under a non-zero parasite emergence rate 137 (see Appendix for a more formal demonstration). 138

It appears that, under this scheme, the only way to render the replicase-producing replicatorparasite-protected is to make the RRS to include the entire RES (Figures 2 and 4). Such

141 RRS \equiv RES configuration evidently rules out the emergence of a parasite because any mutation 142 of the RES would also inactivate the RRS and prevent replication.

143 However, such a parasite-protected state is subject to the aforementioned instability (Figure 4).

144 In the absence of parasites, perfect protection does not carry any benefits, but incurs a greater

145 cost than less protected states. Given that the system is evolvable, an RRS < RES state will

inevitably arise and outcompete the RRS \equiv RES progenitors that are, as shown above, prone to

147 emergence of genetic parasites ($RRS_p \equiv RRS, RES_p \rightarrow 0$).

148 From a more abstract perspective, the fully protected $RRS \equiv RES$ system corresponds to the maximally constrained, i.e. minimum entropy, state. The second law of thermodynamics 149 150 effectively guarantees that it evolves into a higher entropy state, such that RRS < RES, and at least some parts of the RES can be mutated or deleted without compromising replication. The 151 ensemble of higher entropy states is obviously more robust than the unique RRS \equiv RES state. In 152 biological parlance, the higher entropy states are favored by selection via the 'survival of the 153 154 flattest' route [50]. They will necessarily prevail because there are plenty of such states with similar fitness values, whereas the RRS \equiv RES state is singular. However, the problem with the 155 'relaxed' states of the replicator is that they are no longer protected from parasites because a 156 157 parasite now can evolve that would exploit the RRS without producing the replicase (Figure 3). The Third Law of Thermodynamics dictates that the minimum (zero) entropy state can be stable 158 only at 0 K. Under the detailed correspondence between thermodynamics and population 159 genetics [51], the equivalent of temperature is the inverse effective population size, and 160 161 accordingly, 0 K corresponds to an infinite population, which can exist only as an abstraction. 162 Thus, in any realistic population, a parasite-free replicator system is inherently unstable and 163 either goes extinct or rapidly spawns parasites (Figure 4). The latter case inevitably triggers the host-parasite arms race, whereby in the simplest case, the hosts evolve by selection for changed 164 165 RRS allowing them to escape the parasites, whereas the parasites catch up. Furthermore, the competition also occurs between the parasites themselves and could eventually result in the 166 167 emergence of ultimate parasites, those that consist entirely of the RRS. Such (near) ultimate parasites were the end result of Spiegelman's experiments [49] and also exist in nature, namely 168 169 the viroids, small, non-coding parasitic RNAs that cause disease in plants and rely entirely on a 170 host-derived replication machinery [52, 53].

It should be noted that, because, at least in the simplest replicator system, the replication rate is
inversely proportional to the genome length, the parasite have an intrinsic advantage in the arms
race. In the well-mixed case, the preferential replication of parasites drives the host to extinction
which, obviously, results in the collapse of the entire system (no replicase is produced anymore).
However, compartmentalization can stabilize host-parasite systems. Thus, parasites, drive
evolution of biological complexity [37-39, 54].

177 There seems to be a symmetry between the hypothetical, minimum entropy, parasite-resistant

replicator and the ultimate parasite with $RRS_p \equiv RRS$, $RES_p \equiv 0$, another minimum entropy state,

this one being the theoretical end result of the competition between parasites (Figure 3). As a

180 minimum entropy state, the ultimate parasite cannot be evolutionarily stable either. The

181 gedunken experiment described above certainly is an idealization. Realistically, when the

182 minimum entropy state relaxes, the host-parasite arms race takes more complex forms. Most

parasites are far from this ultimate state but rather possess a number of genes and encode a

variety of functions. This complexity of parasites has to do with two strategies that parasites

evolve to maximize their evolutionary success, namely: 1) overcoming the defense systems

186 which the hosts evolve under the pressure for resistance to the parasites, and 2) surviving outside

the host and disseminating among hosts [4]. The question, then, emerges: even though the above

analysis shows that evolution of parasites in simple replicator systems is inevitable, is there a

189 chance that evolution of defense systems would exterminate parasites?

190

191 Costs and compromises of anti-parasite defense

192 The thought experiment described above also answers the question whether a perfect defense system can exist. A perfect self vs non-self discrimination, whereby a replicator possesses the 193 means to reject or destroy any potential cheater, that is, any sequence other than a perfect copy of 194 195 itself, is nothing but the same parasite-protected system with recognition based on the complete information on the self, i.e. $RRS \equiv RES$. We have already shown above that such a system is 196 evolutionary unstable from pure thermodynamic considerations because it provides no benefit in 197 the absence of parasites, and will inevitably devolve to an RRS < RES configuration ("leaky" 198 defense). 199

200 The existence of an unavoidable cost implies that maintenance of any form of defense is subject 201 to a cost-benefit tradeoff. Notably, a recent quantitative assessment of the selection coefficients 202 (a measure of fitness cost) associated with different classes of genes in microbial genomes has shown that defense systems are as costly as the more benign SAGEs, such as transposons [30]. 203 204 This result seems to be a genome-scale reflection of the intrinsic costliness of defense dictated by thermodynamics. In the actual biological context, this cost can be manifested in different forms, 205 206 such as autoimmunity or interference of defense systems with HGT. The curtailment of HGT, in particular, could be a key factor that makes defense systems costly and causes their repeated loss 207 [32]. However, at the bottom of it all seems to be the thermodynamic cost of information. 208 Certainly, defense is not the only process associated with an information cost. Such cost is 209 intrinsic to all processes of information transmission including replication, transcription, 210 translation, as well as signal transduction. However, loss of genes encoding those other functions 211 is often strongly deleterious to the organism, resulting in positive mean selection coefficients for 212 the respective classes of genes [30]. This is not the case for defense systems because, of which 213 the mean selection coefficient values for the defense genes are negative [30], and in accord with 214 215 this observation, defense genes are lost in the course of evolution significantly more often than genes of other functional categories [55]. Due to these fitness costs, evolving organisms cannot 216 217 build up defense systems to the extent that is required to eliminate parasites (Figure 4).

218

A quasi-formal demonstration of the inevitability of the emergence and persistence of parasites

- In the above, we demonstrate that a parasite-protected state, one in which RRS=RES, is
- thermodynamically unstable. The inevitability of the emergence of parasites and their subsequent
- 223 persistence follows from this demonstration. To present the argument succinctly and quasi-
- 224 formally:
- (1) The two signals that are essential in a replicator system, RRS and RES, are encoded in
 different genomic sequences.
- (2) Thus, at least some parts of the RES can be deleted without inactivating the RRS. Hence
 genetic parasites emerge.

(3) The shorter the genome sequence of a genetic element the more efficient its replication is.
Hence parasites accumulate in a replicator system and may bring it to collapse in a well-mixed case.

234

(4) A perfect defense system should, in the least, be able to recognize parasitic elements, i.e.
detect missing parts of the host genome. At the end of the replication cycle, this information
should be deleted. Under the Landauer principle, the cost of memory cleaning is at least *kTn*ln2 J
(*n* bits distinguish the host and the parasite). This cost makes defense systems evolutionary
unstable and precludes elimination of parasites.

241

242 Conclusions

The problem of the ubiquity and persistence of genomic parasites throughout the evolution of life 243 can be broken into two parts: i) emergence of parasites in primitive replicator systems, ii) 244 persistence of parasites in evolving organisms. Our analysis of the basic aspects of host-parasite 245 coevolution presented here suggests that there are fundamental thermodynamic causes of the 246 247 inevitability of parasites on both stages. To put it most succinctly, both the hypothetical parasiteprotected state in a simple replicator system and the putative secondary parasite-free state 248 resulting from efficient action of evolved defense systems are thermodynamically unstable and 249 can only exist transiently. These conclusions certainly are compatible with a wealth of 250 251 observational data indicating that genetic parasites, along with defense systems, are enormously abundant in the biosphere and accompany virtually every cellular life form. The results of 252 253 numerous mathematical and computational modeling studies on replicator evolution, in which parasites invariably appear, lead to the same conclusion. The simple thought experiments 254 255 described here that start, effectively, from first principles emphasize the growing understanding that emergence as well as persistence of genetic parasites is an inalienable feature of evolving 256 257 replicators and, as such, one of the central principles of biology.

258

259 Appendix A.

260 Consider a simple system in which both the replicator and a parasite comprise single entities and

- the replicator entity can also function as the replicase (e.g., both the replicator and the parasite
- are single RNA molecules, and the replicator molecule in the native folded state can function as
- the replicase ribozyme). Replication of the replicator entity is governed by the second-order
- kinetics, where a template replicator meets an (identical) replicase to make a copy of the
- template. There is also a natural decay of both types of entities, occurring with the first-order
- kinetics. In an environment with a fixed carrying capacity (determined, e.g., by the influx of
- consumable resources), such a system behaves as a classical logistic model, with one exception:
- there exists a critical number of entities, below which the population is unsustainable due to the
- 269 (second-order) replication lagging behind the (first-order) decay.

Likewise, a parasite entity replicates upon meeting a replicator (acting as a replicase) and decays
spontaneously. The parasite population is subject to similar environmental restrictions as that of
the replicator due to the limitation by the same resources.

The more general model that we consider here also includes the existence of a (potentiallycostly) defense system:

275
$$\frac{dR}{dt} = \frac{1}{1+\alpha e^*} R^2 \left(1 - \frac{R+P/q}{K}\right) - e_R R$$

276
$$\frac{dP}{dt} = \frac{q}{1+e^*} PR\left(1 - \frac{R+P/q}{K}\right) - e_P P$$

where R and P are the concentrations of the replicator and the parasite particles, respectively, e_R 277 278 and e_P are the corresponding decay rates and K is the environment carrying capacity (the 279 replicator growth rate is taken to be 1 without loss of generality). The parasite enjoys an evolutionary advantage that is manifested in two ways: it both replicates faster and consumes 280 fewer resources by the same factor q (the simple conceptual model of this effect is based on an 281 RNA molecule that is shorter than the replicator by a factor of q). The parasite replication is 282 283 countered by the defense systems that are embedded in the replicase and discriminate against the parasites with an efficiency e^* . The action of the defense system is costly to the replicator, with 284 285 the cost coefficient α (according to the Landauer principle, $\alpha > 0$)

Upon introduction of the parasite to the population of the replicator near the equilibrium $(P \rightarrow 0, dR/dt \rightarrow 0)$, the host defense prevents the parasite invasion (dP/dt < 0) only if

288
$$\frac{1+e^*}{1+\alpha e^*} > q \frac{e_R}{e_P} \cong q$$

or, in other words, only if the effect of defense on the invading parasite relative to the cost of

290 defense to the host is greater than the parasite advantage q (assuming comparable decay rates).

Obviously, the replicator population lacking the defense system ($e^* = 0$) cannot resist the

292 parasite invasion. A defense system combining high efficiency with low cost is capable of

protecting the host population, but the maintenance of such defense depends on regular invasion

of parasites (otherwise, the evolutionary disadvantage due to the cost of defense would drive the

- defense system to extinction). In other words, a parasite-protected state of replicator system is
- unstable.

297

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315 **Competing interests**

316 The authors declare that they have no competing interests.

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References

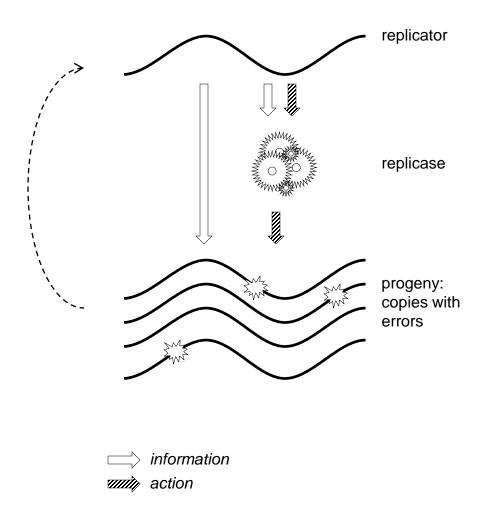
323	1.	Koonin EV, Wolf YI: Evolution of microbes and viruses: a paradigm shift in evolutionary
324		biology? Front Cell Infect Microbiol 2012, 2 :119.
325	2.	Woese C: The universal ancestor. Proc Natl Acad Sci U S A 1998, 95 (12):6854-6859.
326	3.	Jalasvuori M, Koonin EV: Classification of prokaryotic genetic replicators: between selfishness
327		and altruism. Ann N Y Acad Sci 2015, 1341 :96-105.
328	4.	Koonin EV, Starokadomskyy P: Are viruses alive? The replicator paradigm sheds decisive light
329		on an old but misguided question. Stud Hist Philos Biol Biomed Sci 2016, 59:125-134.
330	5.	Suttle CA: Viruses in the sea. Nature 2005, 437 (7057):356-361.
331	6.	Suttle CA: Marine virusesmajor players in the global ecosystem. Nat Rev Microbiol 2007,
332		5 (10):801-812.
333	7.	Brum JR, Sullivan MB: Rising to the challenge: accelerated pace of discovery transforms marine
334		virology. Nat Rev Microbiol 2015, 13 (3):147-159.
335	8.	Rohwer F: Global phage diversity. Cell 2003, 113(2):141.
336	9.	Kristensen DM, Mushegian AR, Dolja VV, Koonin EV: New dimensions of the virus world
337		discovered through metagenomics. Trends Microbiol 2010, 18(1):11-19.
338	10.	Ignacio-Espinoza JC, Solonenko SA, Sullivan MB: The global virome: not as big as we thought?
339		Curr Opin Virol 2013, 3 (5):566-571.
340	11.	Koonin EV, Dolja VV: Virus world as an evolutionary network of viruses and capsidless selfish
341		elements. Microbiol Mol Biol Rev 2014, 78(2):278-303.
342	12.	Jordan IK, Rogozin IB, Glazko GV, Koonin EV: Origin of a substantial fraction of human
343		regulatory sequences from transposable elements. Trends Genet 2003, 19(2):68-72.
344	13.	Bowen NJ, Jordan IK: Exaptation of protein coding sequences from transposable elements.
345		Genome Dyn 2007, 3 :147-162.
346	14.	Rebollo R, Romanish MT, Mager DL: Transposable elements: an abundant and natural source of
347		regulatory sequences for host genes. Annu Rev Genet 2012, 46:21-42.
348	15.	Forterre P, Prangishvili D: The great billion-year war between ribosome- and capsid-encoding
349		organisms (cells and viruses) as the major source of evolutionary novelties. Ann N Y Acad Sci
350		2009, 1178 :65-77.
351	16.	Stern A, Sorek R: The phage-host arms race: shaping the evolution of microbes. <i>Bioessays</i> 2011,
352		33 (1):43-51.
353	17.	Koonin EV, Dolja VV: A virocentric perspective on the evolution of life. Curr Opin Virol 2013,
354		3 (5):546-557.
355	18.	Labrie SJ, Samson JE, Moineau S: Bacteriophage resistance mechanisms. Nat Rev Microbiol
356		2010, 8 (5):317-327.
357	19.	Samson JE, Magadan AH, Sabri M, Moineau S: Revenge of the phages: defeating bacterial
358		defences. Nat Rev Microbiol 2013, 11 (10):675-687.
359	20.	Makarova KS, Wolf YI, Koonin EV: Comparative genomics of defense systems in archaea and
360		bacteria. Nucleic Acids Res 2013, 41(8):4360-4377.
361	21.	Rimer J, Cohen IR, Friedman N: Do all creatures possess an acquired immune system of some
362		sort? Bioessays 2014, 36(3):273-281.
363	22.	Koonin EV, Zhang F: Coupling immunity and programmed cell suicide in prokaryotes: Life-or-
364		death choices. Bioessays 2017, 39(1):1-9.
365	23.	Koonin EV, Makarova KS, Wolf YI: Evolutionary Genomics of Defense Systems in Archaea and
366		Bacteria. Annu Rev Microbiol 2017.

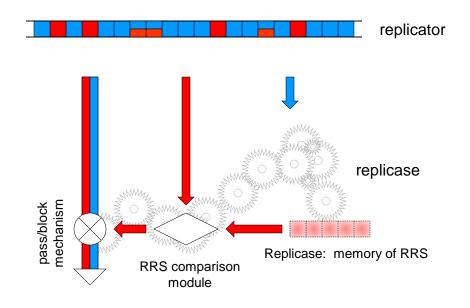
367	24.	Koonin EV, Krupovic M: Evolution of adaptive immunity from transposable elements combined
368		with innate immune systems. Nat Rev Genet 2015, 16 (3):184-192.
369	25.	Koonin EV, Krupovic M: A Movable Defense. The Scientist 2015(january 1).
370	26.	Shmakov S, Smargon A, Scott D, Cox D, Pyzocha N, Yan W, Abudayyeh OO, Gootenberg JS,
371		Makarova KS, Wolf YI et al: Diversity and evolution of class 2 CRISPR-Cas systems. Nat Rev
372		Microbiol 2017, 15 (3):169-182.
373	27.	Read AF, Allen JE: Evolution and immunology. The economics of immunity. Science 2000,
374		290 (5494):1104-1105.
375	28.	Westra ER, van Houte S, Oyesiku-Blakemore S, Makin B, Broniewski JM, Best A, Bondy-Denomy
376		J, Davidson A, Boots M, Buckling A: Parasite Exposure Drives Selective Evolution of Constitutive
377		versus Inducible Defense. Curr Biol 2015, 25(8):1043-1049.
378	29.	Hartmann G: Nucleic Acid Immunity. Adv Immunol 2017, 133:121-169.
379	30.	Iranzo J, Cuesta JA, Manrubia S, Katsnelson MI, Koonin EV: Disentangling the effects of selection
380		and loss bias on gene dynamics. Proc Natl Acad Sci U S A 2017, 114(28):E5616-E5624.
381	31.	Takeuchi N, Kaneko K, Koonin EV: Horizontal gene transfer can rescue prokaryotes from
382		Muller's ratchet: benefit of DNA from dead cells and population subdivision. G3 (Bethesda)
383		2014, 4 (2):325-339.
384	32.	Iranzo J, Puigbo P, Lobkovsky AE, Wolf YI, Koonin EV: Inevitability of Genetic Parasites. Genome
385		Biol Evol 2016, 8 (9):2856-2869.
386	33.	Stern A, Keren L, Wurtzel O, Amitai G, Sorek R: Self-targeting by CRISPR: gene regulation or
387		autoimmunity? Trends Genet 2010, 26 (8):335-340.
388	34.	Koonin EV: Evolution of RNA- and DNA-guided antivirus defense systems in prokaryotes and
389		eukaryotes: common ancestry vs convergence. <i>Biol Direct</i> 2017, 12 (1):5.
390	35.	Szathmary E: The evolution of replicators . <i>Philos Trans R Soc Lond B Biol Sci</i> 2000,
391		355 (1403):1669-1676.
392	36.	Szathmary E, Demeter L: Group selection of early replicators and the origin of life. J Theor Biol
393	501	1987, 128 (4):463-486.
394	37.	Takeuchi N, Hogeweg P: Evolution of complexity in RNA-like replicator systems. <i>Biol Direct</i>
395	571	2008, 3 :11.
396	38.	Takeuchi N, Hogeweg P, Koonin EV: On the origin of DNA genomes: Evolution of the division of
397	50.	labor between template and catalyst in model replicator systems <i>PLoS Comput Biol</i> 2011, in
398		press.
399	39.	Takeuchi N, Hogeweg P: Evolutionary dynamics of RNA-like replicator systems: A bioinformatic
400	55.	approach to the origin of life. Phys Life Rev 2012, 9(3):219-263.
400	40.	Maynard Smith J: Evolution and the Theory of Games . Cambridge: Cambridge Univ Press; 1982.
401	40. 41.	Koonin EV: The Logic of Chance: The Nature and Origin of Biological Evolution Upper Saddle
402	41.	River, NJ: FT press; 2011.
403	42.	Eigen M: Selforganization of matter and the evolution of biological macromolecules.
	42.	
405	40	Naturwissenschaften 1971, 58 (10):465-523.
406	43.	Biebricher CK, Eigen M: The error threshold . <i>Virus Res</i> 2005, 107 (2):117-127.
407	44.	Landauer R: Irreversibility and Heat Generation in the Computing Process. <i>IBM Journal of</i>
408	4 -	Research and Development 1961, 5 :183-191.
409	45.	Bennett CH: Demons, engines, and the Second Law . <i>Sci Am</i> 1987, 257 :108-117.
410	46.	Bennett CH: Notes on Landauer's principle, reversible computation, and Maxwell's Demon.
411		Studies in History and Philosophy of Science Part B: Studies in History and Philosophy of Modern
412		Physics 2003, 34 :501-510.
413	47.	Haruna I, Spiegelman S: Autocatalytic synthesis of a viral RNA in vitro. Science 1965,
414		150 (3698):884-886.

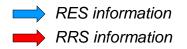
- 415 48. Spiegelman S: An approach to the experimental analysis of precellular evolution. Q Rev 416 Biophys 1971, 4(2):213-253. 417 Mills DR, Kramer FR, Spiegelman S: Complete nucleotide sequence of a replicating RNA 49. 418 molecule. Science 1973, 180(89):916-927. 419 50. Wilke CO, Wang JL, Ofria C, Lenski RE, Adami C: Evolution of digital organisms at high mutation 420 rates leads to survival of the flattest. Nature 2001, 412(6844):331-333. 421 Sella G, Hirsh AE: The application of statistical physics to evolutionary biology. Proc Natl Acad 51. 422 Sci U S A 2005, 102(27):9541-9546. 423 52. Diener TO: The viroid: biological oddity or evolutionary fossil? Adv Virus Res 2001, 57:137-184. Tsagris EM, Martinez de Alba AE, Gozmanova M, Kalantidis K: Viroids. Cell Microbiol 2008, 424 53. 425 **10**(11):2168-2179. 426 Koonin EV: Viruses and mobile elements as drivers of evolutionary transitions. Philos Trans R 54. 427 Soc Lond B Biol Sci 2016, **371**(1701). 428 Puigbo P, Makarova KS, Kristensen DM, Wolf YI, Koonin EV: Reconstruction of the evolution of 55. 429 microbial defense systems. BMC Evol Biol 2017, 17(1):94. 430
- 431

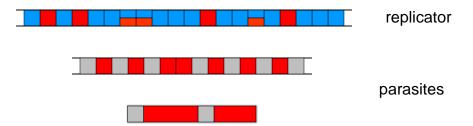
433 Figure legends

- 434 Figure 1. A replicator-replicase systems with heredity, variability and differential reproduction.
- The dotted arrow denotes differential reproduction of the copies of the original replicator that carry mutations.
- 437 Figure 2. The replicase-encoding signal (RES) and replicase-recognition signal (RRS) in
- 438 replicator-replicase systems. For generality, the RRS is shown as being distributed along the
- 439 length of the replicator although in real genomes, this signal is often localized such that, for
- 440 example, short terminal sequences are sufficient for the replication of a virus genome. The
- 441 replicase structure carries memory of the RRS allowing recognition of competent templates
- 442 ("pass/block mechanism").
- 443 Figure 3. Emergence of parasites in replicator systems via deletion of portion of the RES.
- Figure 4. A conceptual phase diagram of the evolution of replicator systems.











RES RRS replicase

