

THERMODYNAMIC LIMITATIONS ON THE NATURAL EMERGENCE OF LONG CHAIN MOLECULES: IMPLICATIONS FOR ORIGIN OF LIFE

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Abstract

For a polymer of N -monomer-units long, or N -mer, which has a dimer decay time constant of τ , the polymer decay time constant is proved to be closely approximated by τ/N (under rather general assumptions). The implications of this for abiogenesis are profound, namely that there would be small amounts of time available (order of days) for a prebiotic sequence of a condensation polymer to serve as the primary information-bearing code for the last universal common ancestor. All three classes of prebiotically relevant polymers (polynucleotides, polypeptides and polysaccharides) are condensation polymers expected to be subject to these time constraints.

Keywords

quantitative geometrical thermodynamics • prebiotic synthesis • RNA • polymer stability • last universal common ancestor (LUCA)

Introduction

A problem that has received scant attention is how the limited natural lifetime of biomolecules relates to possible abiotic synthesis processes. For example, RNA consists of a chain of base-containing sugars linked through phosphate moieties. If the individual dimers have a finite lifetime, what will be the lifetime of the polymer? It is known that RNA is unstable in water; this is known as the 'Water Paradox' (1) [on which see, e.g., Lee et al. (2)] one of four other potentially fatal paradoxes, including the 'Probability Paradox' which is that RNA-catalysed *destruction* of RNA is more probable than its RNA-catalysed *replication*. Nevertheless, it seems that the 'RNA world' is the most common suggestion so far for the origin of life (3).

Ross and Deamer (4) call this '*question of how life-relevant polymers overcame the thermodynamic barriers to their formation*' a '*significant conundrum*'. They make detailed proposals for a resolution to this conundrum, but that a consensus has as yet not been achieved is shown by Whitaker

and Powner's (5) recent review of the field. That the question of the Origin of Life (OoL) is intricate is acknowledged by laneselli et al. (6), who say that the '*prebiotic replication of DNA and RNA is a complex interplay between chemistry and the environment*'. But their '*expectation*' is that it will only be in the future ('*in the near future*') that the OoL will be '*understandable and experimentally testable*'. For now, these problems remain baffling. On the '*complex interplay*', various speculative scenarios have been envisaged for the OoL, including: wet/dry cycling [e.g. Song et al. (7)], the '*hypercycle*' [Eigen & Schuster (8)], surface-mediated reactions [e.g. Riggi et al. (9)], and molecular '*crowding*' effects [e.g. Edri et al. (10)].

The famous Miller-Urey experiment of 1952 (11) for the (racemic) formation of many of the canonical and non-canonical amino acids breathed new life into OoL studies. Many thought that the laboratory creation of life would occur rapidly after that seminal experiment. Moreover, through

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that demonstration, a well-grounded proposal was expected to emerge to explain how life might have arisen upon an early Earth, shortly after the cooling following the late heavy bombardment. But after more than 70 years, no such proposal has arisen.

An even larger problem than the racemic small molecule difficulty was the polymerization of those small molecules into the required polypeptides (proteins and most enzymes), polysaccharides and polynucleic acids such as RNA. Indeed, there are no prebiotically relevant experiments to show the clean regiochemical synthesis of any of these polymerized structures [Okamoto *et al.* (12) show some reasons why].

Moreover (and aside from the regiospecificity problems), all of the polymerization reactions have a positive free energy so that the starting monomers are energetically favoured over the polymeric forms. Being all condensation polymerizations, these polymers all undergo hydrolysis in water.

Exacerbating the problem is that condensation polymerization (the chain coupling) requires ultrahigh purity of monomers and coupling yields for each reaction of >99.5% [see, e.g., Du *et al.* (13)]. Further, the sequence of the polymerization would have to embody the code for the use of these macromolecules to allow the building of a life-giving system. Random sequences would not provide the 'specified information' [a term used by Orgel (14)] necessary for life's prescriptive code.

Some have suggested that just a single polymer chain might randomly have formed that had the precise sequence to begin the synthesis of the life-requisite molecules. And that one properly specified molecule, for example that one RNA or polypeptide chain, was the genesis for life [an 'RNA world' was proposed by Rich in 1962 (15), an idea extended by many including Woese (16) and Orgel (17)]. If there had been long times available for life to begin, such as a few hundred million years, the probability of that one chain propagating its sequence information to other molecules might be probabilistically acceptable. But when the lifetime of the one chain is on the order of hours or a small number of days, there is insufficient time available for information transfer.

Here, we simply calculate the probability of scission, assuming that the polymer will be thereby rendered non-functional. Clearly, this is a crude approximation, but there are several well-documented examples of cases where proteolytic cleavage of a single peptide bond within an enzyme leads to its inactivation; including (recently) Zhang *et al.* (18) in connexion with the coronavirus disease of 2019 (COVID-19) virus.

We analyse here the stability of that singular precious life-generating polymer (LGP). Would the LGP indeed have billions of years to transfer its informational code to substrate molecules? For if one mole of a particular RNA has a half-life of 100 days in water at room temperature [see, e.g., the discussion of Benner *et al.* (19) and the detailed measurements of Wang and Liu (20)], then after some 80 half-lives (8000 days or about 24 years) we would not expect even one molecule of that mole to have survived. Similarly, if a polypeptide has a half-life of 7 years in water [as measured, e.g., by Kahne and Still (21)] then after 600 years, of an initial mole of material we would not expect even one molecule to have survived. Here, we outline limitations entailed (under certain plausible assumptions) by the stability of single polymer molecules.

Although polycyclic aromatic hydrocarbons are abundant in the observable universe, indicating that cosmic chemistry (22) is much more complex than one might have thought, and although it has been demonstrated that extra-terrestrial organic molecules may survive impact with earth (23), such polymeric molecules (polysaccharide, polypeptides or polynucleic acids) of any significant length have never been observed in such an inhospitable context. Hence, demonstrating a plausible process for the abiotic synthesis of RNA (24) remains problematic.

Sidestepping the enantiopurity challenge has been based on the suggestion that enantiopure small molecules, namely amino acids (peptides), carbohydrates (sugars or saccharides) and nucleotides (a phosphate, base and carbohydrate combined) might have arrived on meteorites. But few meteorites ever revealed the requisite molecules in >60% enantiomeric excess and they always arrive as grossly unusable mixtures (25).

Here, we calculate the polymer stability both probabilistically and thermodynamically, showing the two calculations to be in good agreement.

Polymer stability: calculated probabilistically from the half-life of an ensemble

We start with the simplest possible statistical (probabilistic) approach to the decay properties of an ensemble of the N bonds forming the polymer, assuming that a chemical bond (such as the amide bond in a peptide) exhibits an exponential decay where the exponential time parameter controlling the bond decay rate is given by α , and that any bond-breaking

events are independent of each other. Then the probability p_t of a bond surviving up to a time t is:

$$p_t = e^{-\alpha t} \quad (1)$$

This means that the probability of bond breaking up to a point in time t is simply given by:

$$1 - p_t = 1 - e^{-\alpha t} \quad (2)$$

We now consider an ensemble of N such bonds (which together describe the connections between the monomers so as to form the polymer). The polymer will be considered to have decayed when only a single bond (out of the N bonds) decays. In which case the probability that at least one of the N bonds has broken up to a point t in time can be expressed by the following equalities:

$$\begin{aligned} & \text{Probability of at least 1 } (\geq 1) \text{ bond out of } N \text{ breaking up to time } t \\ &= 1 - \text{Probability of zero bonds (out of } N) \text{ breaking up to time } t \\ &= 1 - \text{Probability of all } N \text{ bonds (out of } N) \text{ surviving up to time } t \end{aligned} \quad (3)$$

The latter probability expression, for the probability that all N bonds (out of N) surviving up to time t , is simply the N th product of Eq. (1) [i.e. the probability represented by Eq. (1) raised to the power N]:

$$p_{N,t} = e^{-N\alpha t} \quad (4)$$

and hence the probability of at least 1 bond out of N breaking up to a time t is given by:

$$1 - p_{N,t} = 1 - e^{-N\alpha t} \quad (5)$$

Thus, the decay rate of the polymer (N -mer) is also represented by a decaying exponential. The half-life of the polymer $t = t_{N/2}$ is simply:

$$\frac{1}{2} = 1 - e^{-N\alpha t_{N/2}} \quad (6)$$

which can be simplified thus:

$$t_{N/2} = \frac{\ln 2}{\alpha N} = \frac{\tau \ln 2}{N} = \frac{t_{1/2}}{N} \quad (7)$$

where $t_{1/2} \equiv \tau \ln 2$ is the half-life of a single bond (i.e. the dimer half-life) and $\tau \equiv 1/\alpha$ is the (exponential-decay) time constant of the dimer single bond, and simply given by the inverse decay rate. Thus, a simple probabilistic analysis indicates that the half-life of an N -polymer reduces by a factor N as compared to the half-life of the dimer.

Polymer stability: calculated thermodynamically

The same result (an inverse relationship between the half-life of a dimer and the half-life of a polymer associated with it) is obtained more rigorously from the Conservation of Entropy Production [Parker and Jeynes (26)] as derived using the apparatus of quantitative geometrical thermodynamics [QGT; Parker and Jeynes (27)]. We start with the general expression for the *entropy production* Π (which is the rate of change of entropy, dS/dt) of any system, which may be a dimer molecule, or a more complex chemical system such as a polymer [see Eq. (2) of Parker and Jeynes (28)]:

$$\Pi = \frac{e^{-\Delta}}{\tau} S_0 \quad [\text{J/Ks}] \quad (8)$$

where S_0 is the initial entropy (expressed as a multiple of the Boltzmann constant, k_B), τ is the exponential-decay time constant (i.e. equivalent to the time constant of a bond, as discussed above), and Δ is the change in the number of degrees of freedom (DoFs) of the decaying system [DoFs are discussed extensively by Parker and Jeynes (28)] as it decays.

Here, the quantity S_0 [which, implicitly including k_B , has dimensionality (J/K)] represents the background or initial entropy of the system, where we note that, being entropic (and therefore logarithmic in nature), the value of S_0 is not absolute. S_0 is equivalent to a constant of integration which changes according to the boundary conditions: that is, S_0 represents the initial entropy of the system at the granularity (*length scale*) adopted to study the system entropy, such that the value of S_0 depends on the granularity chosen. The actual value of S_0 is not important in the context of the temporal characteristics of a system; rather its physical significance lies in the fact that it represents the *length scale* that is adopted for the particular chemical context. And such a reference length scale always needs to be explicitly defined, particularly in the entropic context, as expected from the principle of the relativity of scale: see the review of Auffray and Nottale (29), who regard multiscale integration to be a 'grand challenge' for systems biology, and Parker and Jeynes (30) who show both that scale relativity arises naturally in QGT and that it resolves some troublesome logical paradoxes. Moreover, Parker and Jeynes (31) have shown that the holographic principle (asserting that the entropy of a system is determined by its surface area) also requires a normalising length scale: Parker et al. (32) have given an important example of this.

Therefore, we assume that the same length scale applies to both the monomer and its polymer (even though the polymer

can be many orders of magnitude longer than the monomer unit) and that the same value of S_0 is used for both the dimer and polymer analyses. However, for considerations of bond breaking and chemical decay, the key thermodynamic quantity of interest here is the *entropy production*, an absolute measure, in contrast to *entropy*.

The exponential-decay time constant τ is simply related to the dimer half-life time parameter $t_{1/2}$ by $t_{1/2} = \tau \ln 2$. The parameter Δ represents the loss in the number of DoFs when the system decays. Note that, although the Entropy Production Π is a conserved quantity, the number of DoFs (which is also closely related to the entropy of the system) is *not* conserved; just as the *action* [Js] of a system is not conserved as the system evolves over time, neither is the entropy [see discussion in Parker and Jeynes (28)].

Whenever an identical pair of sub-systems unite holomorphically to create a resulting system exhibiting a C2 symmetry, the combined system exhibits an increase in its entropy of only a single unit [this is shown and discussed extensively in Parker et al. (32)]. That is to say, if the initial sub-system has an entropy of S_0 , then the resulting (daughter) system comprising the combined two identical subsystems has an entropy S_1 simply given by $S_1 = S_0 + 1$.

In the chemical context, the addition of two (identical) monomers to create a dimer is equivalent to *holomorphic pairing*, such that the entropy of the resulting polymer increases by a single unit for each added monomer. Each holomorphic addition of a monomer and a bond results in the entropy increasing by a single unit. Thus, for a dimer (assumed with initial entropy S_1) the entropy of the resulting N -fold polymer (featuring $N-1$ bonds connecting N monomers) is simply given by:

$$S_N = S_1 + N - 1 \quad (9)$$

For a 'complex' monomer (such as an RNA base) with a high intrinsic initial entropy S_0 (of the order 6^D where D is the number of atoms in the monomer, and we assume 3 linear translational and 3 rotational degrees of freedom for each atom), such that $S_0 \gg N$, we can approximate the entropy of the (N -mer) polymer S_N :

$$S_N \approx S_0 \quad (10)$$

Eq. (10) also justifies why the same length scale (as dictated by S_0 , see the discussion above) applies equally to the polymer as to its monomer constituent, since their two entropies are at least approximately equal when holomorphic

pairing is present. For example, adenine has 15 atoms so that $S_0 \sim 6^{15} \approx 5 \times 10^{11}$.

We first consider the dimerization of two monomers each with an entropy production Π_0 ; the dimer connecting the two monomers by a *single* bond, with the subscripts in the following analysis based on the number of bonds forming the polymer (rather than the number of component subunits). Using the general expression for the entropy production of a system as given by Eq. (1), and the dimer featuring a single connecting bond (with a time constant τ_1 of the dimer, representing the decay of its single connecting bond) and with dimer entropy S_1 , the entropy production Π_1 of the single bond associated with the dimer is given by:

$$\Pi_1 = \frac{e^{-\Delta}}{\tau_1} S_1 \quad (11a)$$

Using the approximation of Eq. (10) for the entropy, we approximate Eq. (11a) for the entropy production of the dimer bond as follows:

$$\Pi_1 \approx \frac{e^{-\Delta}}{\tau_1} S_0 \quad (11b)$$

We consider now the trimer consisting of *two* bonds connecting three monomers. We assume holomorphic addition of the monomer bond to the dimer system with its single bond, so that the trimer entropy S_2 is as according to Eq. (9). The resulting entropy production of the trimer is given by the scalar addition of the entropy productions associated with each of the two bonds, since entropy production is a conserved quantity [Parker and Jeynes (31)] and adds as a scalar, just as do energies because of the isomorphism of *entropy production* and *energy* [Parker and Jeynes (33)]:

$$\Pi_2 \equiv \frac{e^{-\Delta}}{\tau_2} S_2 = \Pi_1 + \Pi_1 = 2\Pi_1 \quad (12a)$$

where τ_2 is the decay time of the trimer.

Based on the assumption again that $S_0 \gg N$, then we can assume that the entropy of the trimer is closely given by S_0 , according to Eq. (10), where $N = 3$ in this case. Thus we re-write Eq. (12a) as:

$$\Pi_2 = 2\Pi_1 \approx \frac{e^{-\Delta}}{\tau_2} S_0 \quad (12b)$$

Comparison of equations Eqs. (11b) and (12b) allows us to express the time constant of the trimer (with its two bonds)

as a function of the time constant of the dimer (a single bond):

$$\tau_2 = \frac{\tau_1}{2} \quad (13)$$

The same analysis can now be extended to the N -fold polymer. In this case, assuming the ongoing approximation of Eq. (10), the polymer entropy production is given by the summation of the N individual entropy productions of each of the bonds:

$$\Pi_N = N\Pi_1 = \frac{e^{-\Delta}}{\tau_N} S_N \quad (14)$$

where the time constant of the polymer is given by τ_N , and the polymer entropy is given by S_N . Using the approximation of Eq. (10) for the entropy of the polymer, and the entropy production of each individual bond as given by Eq. (11b), we can re-write Eq. (14):

$$\Pi_N = N\Pi_1 \approx \frac{e^{-\Delta}}{\tau_N} S_0 = N \frac{e^{-\Delta}}{\tau_1} S_0 \quad (15)$$

Clearly the time-constant of the polymer is (approximately) given by:

$$\tau_N = \frac{\tau_1}{N} \quad (16)$$

in agreement with the probabilistic analysis of Eq. (7).

If an RNA dimer had a half-life of ~100 days in water at room temperature (a generous assumption) a 600-mer RNA molecule would have a half-life of ~4 hr, and if divalent ions such as Mg^{2+} were present, this would reduce by orders of magnitude [see, e.g., Chatterjee et al. (34)].

Considering abiotic molecules, if amide hydrolysis has a half-life of 7 years in neutral water [Kahne and Still (21)], a single 200-mer polypeptide in water has a half-life of ~13 days. If the water were slightly basic or acidic, the degradation would be faster [see, e.g., Sun et al. (35)].

Discussion – chemical issues

There is an underlying chemical assumption in our analysis, that the decay rate of dimers is unaffected by being in a chain. But the stability measurements of Kahne & Still (21) were on hydrolysis of a polymer even though the results were expressed as a dimer decay rate. Other measurements have shown that in the presence of hydrolysis the lifetime of dimers

is indeed shorter than would be expected from Kahne & Still's results: that is, amides are stabilised (somewhat) by being polymerised. We allow for this by using the slower rates that are derived from the polymers.

Another underlying chemical assumption we employ is that a polymer becomes non-functional if any of its bonds break. Again, this is an approximation. But there now exists copious experimental justification for it. For example, peptide cleavage by Clp Protease has been surveyed by Beardslee et al. (36). The mechanisms and their systems are profoundly intricate, but much work has been done to reveal them. A cleavage near a polypeptide end will likely be less deleterious than further along the chain, nonetheless, we are stating this assumption.

The chemistry of hydrolysing condensation polymers is highly complex. Bruce Martin (37) collected some careful measurements (which are too rare, sadly) of the free energies of various peptide hydrolysis reactions (focussing on glycyl peptides, although other peptides are expected to behave similarly), showing that the hydrolysis of the dipeptide is the most exothermic (since it forms two zwitterions) where cutting a polypeptide without forming a zwitterion is the least exothermic (with free energies of 3.6 compared to 1.4 kcal/mol). Hydrolysis forming only one zwitterion needs an intermediate free energy (2.4 kcal/mol). Clearly, the dimer is the most weakly bound to hydrolysis: the average per-bond lifetime in polymers would be *longer* than for the dimer.

There is a problem with the uncertainty of lifetime measurements. It seems that Kahne & Still's estimates (21) are inconsistent with Radzicka and Wolfenden's (38); although both studies are still broadly consistent with the thrust of our analysis. But it highlights the urgent need for more reliable measurements.

Determining RNA half-life is tricky. Xu and Asakawa (39) have explored zebrafish RNA in a 'non-sterile aqueous environment' with the purpose of providing 'biological and ecological insights'. RNA in cells has a very short half-life (up to a few days in mammalian cells) because it is actively degraded by cell mechanisms, but outside the cells it is about 1 month.

There are a variety of possible OoL scenarios. Undoubtedly some catalytic action is involved: Brigiano et al. (40) have explored catalytic effects at silica interfaces, and Forsythe et al. (41) have explored the idea that '*peptides might have arisen from ester-based precursors*'.

There is also the 'translation' issue. DNA encodes information and RNA translates codons to amino acids in a process that is

deeply complex: as evidenced by the review of Zagrovic et al. (42). The question of how this all could have begun remains obscure, even though much detailed technical progress is being made. For example, Guo and Su (43) have shown how '*coded peptide formation without previously synthesized peptides*' is possible, although they conclude that '*the origin of translation is still a chemical and biological puzzle*'.

Discussion – QGT

QGT is a theoretical apparatus offering an alternative approach to the analysis of molecular structural *stability* from a *geometric entropy* perspective; the Conservation of Entropy Production [key in the QGT approach to the calculation of molecular half-life, as per Eq. (14)] is a direct consequence of the variational calculus (Euler–Lagrange equations) as applied within QGT. Here, the principle of least exertion (PLE) is exhibited by the *entropic* Lagrangian and is essentially equivalent to the more familiar Principle of Maximum Entropy (MaxEnt), but is articulated using the rigorous mathematical (Lagrangian) language of the variational calculus. Noether's theorem as applied to the PLE's Euler–Lagrange equations *entails* the existence of deep symmetry and conservation principles.

In calculating the half-life of a *N*-polymer we inevitably start confronting issues of stability: the *N*-polymer of time constant $\sim \tau/N$ is clearly a less stable molecule than its basic dimer which exhibits a time constant τ . In discussing this issue of stability, we can exploit the MaxEnt properties of (molecular) structures as described within the QGT theoretical framework: if a molecular structure is MaxEnt then this can be interpreted as it being the '*most likely*', or as the molecule having a '*preferred structural configuration*'. Molecules will adopt particular spatial configurations in order to maximise their *geometrical entropy*. This may surprise those more familiar with the concept that entropy is a measure of *disorder*. However, the conventional statistical mechanical framework for entropy ignores the geometrical (structural) aspects of entropy. This 'statistical mechanical' entropy as originally proposed by Ludwig Boltzmann is very well understood (and correct), but the geometric entropy articulated by QGT is only now being understood and applied in various contexts.

In the context of this paper, the QGT description of molecular stability requires a molecule to exhibit itself as a conjugated pair: it must be paired up with a copy of itself in a C2 symmetry. This is the configuration for the DNA (polymer) molecule which is highly stable despite its vast length. DNA was proved stable using the theoretical apparatus of QGT in 2019 [Parker and Jeynes (27)], Buckminsterfullerene was also proved stable in 2020 (44), and the relative stability of the

'halo' isotopes of helium (${}^6\text{He}^{++}$ and ${}^8\text{He}^{++}$) was explained by QGT in 2022 [Parker et al. (32); with decay lifetimes correctly calculated by QGT in 2023: Parker and Jeynes (28)].

We have proved, other things being equal, that an *N*-polymer is less stable than its constituent dimers. This is also true for a *single-stranded* molecule, such as RNA: but in the (unlikely) event of the *N*-polymer pairing up with a copy of itself, so that the overall molecule exhibits a C2 symmetry, then QGT suggests that the resulting molecule may be more stable (as is DNA). However, it is important to also note that while holomorphic pairing increases stability, it inhibits utility. Duplexes need to be unpaired to be useful for information transfer: single-stranded RNA is used for protein synthesis. The duplex formation slows subsequent reactions, retarding the utility of the parent polymer.

We also note here that the entropic Hamiltonian–Lagrangian equations of state for QGT require the theatre of *hyperbolic spacetime*, in accordance with Roger Penrose's assertion that the universe exhibits a 'hyperbolic overall geometry' (see §2.7, p.48 of '*The Road to Reality*' 2004). What this means in the context of origin of life studies has not been intensively investigated: but note that the discussion of stability in terms of a 'half-life' (with its logarithmic behaviour) is itself indicative of the hyperbolic nature of the *temporal* aspect of spacetime geometry. That the *natural clock* of physical phenomena (including radioactivity, or chemical reactions) is measured using a half-life suggests the universal hyperbolic nature of the passage of time. In addition, this hyperbolic nature of spacetime geometry is also attested by the fractal self-similarity of the double logarithmic spiral (instanced by spiral galaxies, hurricanes, cyclones, and also living organisms such as the nautilus shell, sunflower heads, or *Romanesco broccoli*). Indeed, helical molecular structures are therefore also seen to be a favoured (i.e. most likely and MaxEnt) geometry in QGT, and this might therefore also have a constructive bearing on the statistical probabilities of certain molecular configurations.

It is not yet clear how one should compare the passing of long periods of time with shorter, more local time frames within such an overall hyperbolic spacetime framework. How does one effect a 'length comparison' in such a non-rectilinear, non-Euclidean geometry? More specifically, whether the hyperbolic geometry of QGT may compress the 'statistical barriers' highlighted earlier remains an open question suggesting that there continue to be basic unknown aspects to the thermodynamics. In addition, recent work on *entropic purpose* (45) also suggests that the creation of (specified) information has both teleological and time-dilation aspects, either of which could, thermodynamically, affect the height of the 'statistical barriers'. But the fact that *conservation of*

entropy production (a profound result only available from QGT) leads to essentially similar conclusions as a ‘back-of-the-napkin’ probability calculation is encouraging: science’s unity and integrity is frequently demonstrated both by its self-consistency and the multiplicity of independent yet mutually coherent explanations for a phenomenon.

Summary

An intuitive (statistical) treatment indicates that the decay time of the polymer (N -mer) is expected to be much shorter ($1/N$) than that of the dimer (Eq. 7): a more rigorous thermodynamic treatment based on considerations of geometrical entropy shows that this same result (Eq. 16) is also (approximately) obtained, where the approximation is explicit and can be assessed. (This treatment ignores the possible stabilising of long polymers, the location of the bond-breaking along the polymer length, and effectively neglects any influence of *entropic purpose*).

We should point out that there are very large uncertainties in measurements of average bond half-life, and that we badly need better lab experiments to clarify these parameters.

Currently proposed mechanisms for the origin of life’s essential molecules do not take such short expected lifetimes for organic condensation polymers into account. We have demonstrated fundamental thermodynamic limitations on the time available for the abiotic processes needed to precede the emergence of life.

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