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BIOGENESIS: DIVERSITY, SELECTION AND FRACTALITY*

by

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ABSTRACT

Recent renormalization group and computational simulation approaches of the prebiotic growth of codified self-replicating polymers can be brought into consistency if finite size effects and possible fractality are taken into account.

Key-words: Biogenesis; Diversity; Selection; Fractality.

Dedicated to a fascinating person,
Ricardo Ferreira,
who introduced me in a fascinating subject,
Biogenesis.

Biogenesis refers to the (possibly) spontaneous appearence of life in one or more places of the Universe, since, from all our present cosmological knowledge, it seems reasonable to think that in very remote times (say 20×10^9 years ago) matter was present only in the form of elementary particles. Life seems to have started on Earth (in very primitive virus–like forms) about 3.8×10^9 years ago. If it started spontaneously on Earth, we are refering to that; if life arrived to Earth from elsewhere, we are then refering to processes which might have occured in some other place (or places) of the Universe.

It seems clear that Biogenesis must have occured through various important steps, named prebiotic stages. Among them, a crucial one is the appearence of codified self–replicating polymers starting from a random assembly of oligomers (dimers, trimers, etc...). We shall concentrate on this particular stage (see details in [1] and references therein), and our stand point will be to look for plausibility for this stage to have happened essentially as a thermodynamical equilibrum critical phenomenon using, as central growth mechanism, autocatalysis through Crick and Watson–like complementary pairs. We have presented, along this line, two different approaches, namely a real space renormalization group (RG) treatment [1,2] and a computer simulation (CS) [3]. Both approaches use, as central variables, the chemical strengths of the A–T and C–G hydrogen–bridges, where A,T,C and G denote the well known nucleotides or their precursors. In the RG case we have used the chemical fugacities K_{AT} and K_{CG}, whereas in the CS case we rather used the link probabilities p_{AT} and p_{CG}. It is the former we shall adopt herein, being understood that their connection is simple and such that when K varies from zero to infinity, p varies from zero to one (p=K/(1+K), for instance). Both approaches are consistent with a microscopic darwinian picture, presenting diversity and selection (see [1–3] for details). However, they yield phase diagrams (in the (p_{AT}, p_{CG}) space) which look different : see Fig. 1. It is the purpose of the present note to show how they can be compatible among them.

If the growing polymeric ADN–like double–chain is assumed strictly one–dimensional (from the topological point of view) the correct phase diagram has to be that of Fig. 1(b) for all codes, since [4] no infinite chains are possible at any finite temperature for finite couplings (i.e. $p_{AT} < 1$ or $p_{CG} < 1$). Why then the RG approach

has led to Fig. 1(a)? The reason is in fact very simple : the calculations are only approximate since the renormalizations have been done among cells with finite size. The exact answer can only be achieved in principle in the limit of cells with infinite size. Therefore for RG cells which are increasingly larger we should except the critical lines if Fig. 1(a) to shrink onto the $p_{AT} = p_{CG} = 1$ corner, thus reproducing Fig. 1(b). In fact we have numerically observed [1 and 2] this shrinking tendency while considering larger and larger oligomers to perform the renormalization.

Is it then the phase diagram of Fig. 1(b) the ultimate form we can expect? The answer is no. Indeed, if we take into account the chemical cross–links which do exist between different parts of the real folded polymer (see, for example, [5]), the system may become a fractal object with fractal dimensionality d_f higher than 1. Consequently, the system not being strictly one–dimensional anymore, the statments developed in [4] do not apply, and we are in right for expecting critical lines like those appearing in Fig. 1(a).

To say it in other words, in the CS approach we did one approximation, namely we neglected the cross–links of the polymer. In the RG approach we did that approximation plus another one, namely not considering infinite large RG cells. It is our belief that the real phenomenon might have occured in a manner which is closer to that of Fig. 1(a) rather than that of Fig. 1(b). Consequently, we verify once more that in Science it might happen to be preferable to do two mistakes rather than only one!

It is a pleasure to acknowledge interesting discussions with R. Maynard, who called my attention on the content of Ref. [4], and with H.J. Herrmann, my co–author in the CS approach. Unnecessary to express how much I am indebted to my friend R. Ferreira who has greatly influenced my views on Biogenesis, either by agreeing with some of them... or by disagreeing with some others!

CAPTION FOR FIGURE

Fig. 1 Phase diagrams within the RG (a) and CS (b) approaches. FG and IG respectively denote the finite growth and infinite growth phases. The various critical lines in (a) correspond to various codes along the chains. The dot • in (b) indicates the critical point for all codes.

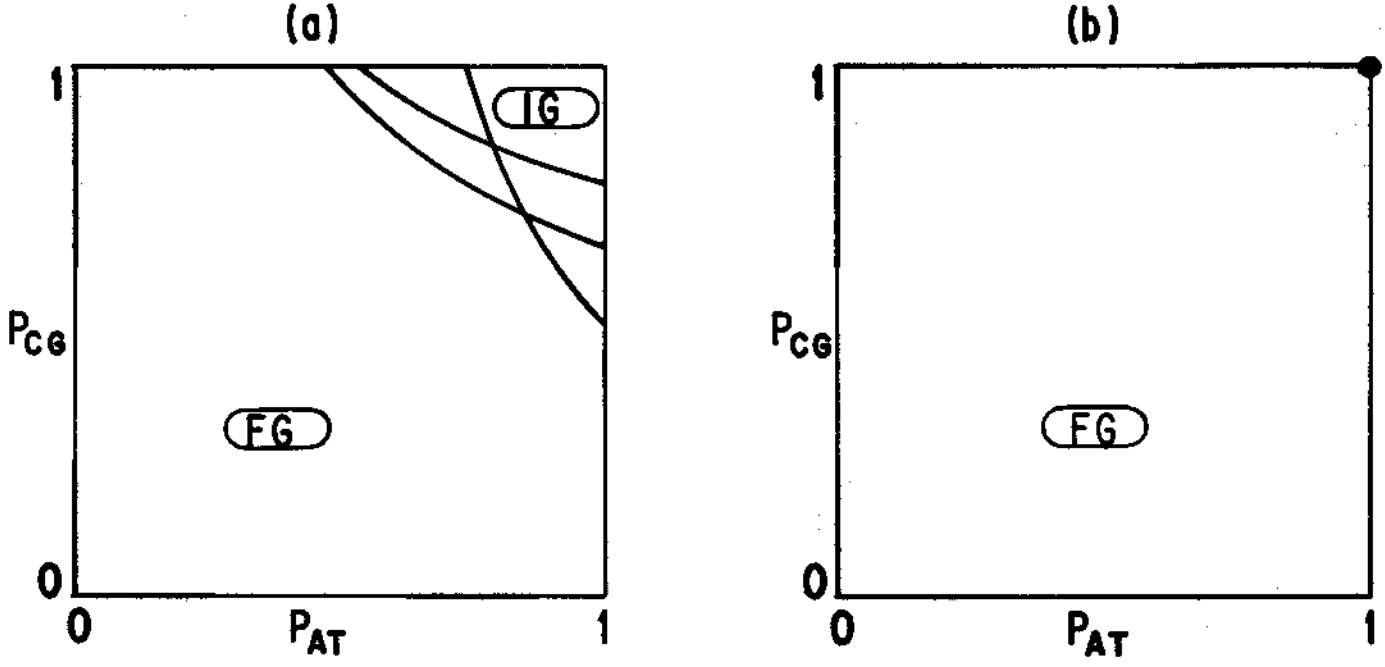

FIG. 1

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