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Biological evidence against the panspermia theory

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## Abstract

The following idea is analysed. Given that evolution on Earth seems to have passed through protocellular evolutionary stages of progenotes, this would appear to be incompatible with the panspermia theory because this observation would imply that the infection bringing life to the Earth started in these protocells, for which a low or null infective power is generally expected.

Key words: Progenote, tRNA split genes, biosynthetic pathways on tRNAs, evolutionary stages, evolutionary transitions, coevolution theory of the genetic code.

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## The panspermia theory

The panspermia theory, that is the possibility that life arrived on our planet transported by meteorites (lithopanspermia), was suggested in 1865 by the German physicist Hermann E. Richter (Raulin-Cerceau et al., 1998). In 1871, Lord Kelvin supported the same thesis that germs transported by meteorites might have infected the Earth (Thomson, 1971). In 1908, Arrhenius maintained that micro-organisms might have reached the Earth by means of an acceleration produced by stellar radiation pressure (radiopanspermia). A third possibility has also been explored, directed panspermia, which suggests that micro-organisms were deliberately transmitted to Earth by intelligent beings present on another planet (Crick and Orgel, 1973).

There is some evidence supporting panspermia and some observations that might favour it. For instance, Gold (1992) maintains that if life were only restricted to the surface of planetary bodies then panspermia would be highly unlikely because there would not have been any protection against the harmful effects of cosmic rays. He, instead, claims that panspermia is a much more realistic possibility if there had been abundant life in the depths of planetary bodies and, therefore, there would have been a potential protection of micro-organisms offered by the rock for an interplanetary journey of life (Gold, 1992). Crick and Orgel (1973) cite the enrichment of molybdenum instead of chromium and nickel in current organisms as possible evidence of panspermia, since the existence of an organism ought not to depend on an extremely rare element. This suggestion has been criticised (Gualtieri, 1977). Planetary microcosms models of asteroids and meteorites also suggest that protoplanetary nebulae might support and disperse micro-organisms (Mautner, 2002).

Wickramasinghe (2004) has been one of the great supporters of the panspermia theory and has gathered considerable evidence in its favour (Wallis et al., 1992; Sommer and Wickramasinghe, 2005). However, it seems to me that alongside the evidence presented by Wickramasinghe (2004), some of which seems truly weak, there is the view of Crick (1993) which seems to suggest that the implausibility of the RNA world might imply that life was

born not on our planet but on a planet where there might have been conditions that were particularly favourable for the evolution of RNA and much less adverse than those that seem to have existed on Earth and which would not have favoured the origin of the RNA world (Crick, 1993). Francis H.C. Crick is not the only great scientist to embrace the panspermia theory. More recently, eminent men of science like Stephen Hawking, Freeman Dyson, Richard Dawkins and Edward O. Wilson have all spoken in favour of the panspermia theory ([www.panspermia.org/intro.htm](http://www.panspermia.org/intro.htm)).

Although in some respects the panspermia theory might seem eccentric, it nevertheless represents one of the 'great' theories of the history of science. Therefore, the quest for its corroboration/falsification might seem to be an important issue, which is why I have undertaken the present analysis.

The tRNA split genes of *Nanoarchaeum equitans* and the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway are independent, plesiomorphic and domain-specific traits which define a progenotic stage for the LUCA and for the ancestors of Archaea and Bacteria

There are strong and specific arguments suggesting that the LUCA (last universal common ancestor) and the ancestors of Archaea and Bacteria were progenotes (Di Giulio, 2001, 2006a, 2010). These arguments have used two traits: the tRNA split genes of *Nanoarchaeum equitans* and the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway (Randau et al., 2005; Rajbhandary, 1994). Based on the hypothesis that a hairpin structure was the precursor of the tRNA molecule and that the assembly of two hairpin structures might have created this molecule, a theory was constructed predicting the existence of mini-genes codifying for these hairpin structures and, thus, for half tRNAs (Di Giulio, 1992, 1995, 1999a, 2004, 2006a, b, c, 2009a, b). This prediction of the existence of mini-genes codifying only for half tRNA has been completely confirmed by the identification in *N. equitans* of the split genes of tRNAs codifying solely and separately for the 5' and 3' halves of the tRNA molecule (Randau et al., 2005). It was first shown that the split genes of the tRNAs of *N. equitans* are the

plesiomorphic forms of tRNA genes (Di Giulio, 2006a, b, 2009a, b). This also implied a polyphyletic origin for tRNA genes, i.e. these genes were assembled only when the main lines of divergence were defined (Di Giulio, 2006a, 2008c, 2008d). Therefore, the observation that in the stage of the ancestor of Archaea there must have been genes not yet fully evolved, i.e. immature genes constituted by the ancestors of the split genes of tRNAs, is certainly evidence of the progenotic nature of the LUCA and of the ancestor of Archaea (Di Giulio, 2006a, 2010). As the genes for the 5' and 3' halves of *N. equitans* are definitely an ancestral and primitive trait (Di Giulio, 2006a, b, 2009a), this should imply that the LUCA and the ancestor of Archaea were themselves primitive 'organisms' still rapidly evolving (Di Giulio, 2006a, 2010). That is, they were progenotes (Di Giulio, 2006a, 2010). Indeed, the immaturity of these genes seems to strongly corroborate the hypothesis of a progenotic state for these two evolutionary stages, for the very reason that split genes still in pieces might be direct witnesses of an evolutionary stage in rapid and progressive Darwinian evolution (Di Giulio, 2006a, 2010). Furthermore, the immaturity of tRNA genes should at least partially correspond to an immaturity of the tRNA molecule and, therefore, to an immaturity of translation (Di Giulio, 2010). This should make these evolutionary stages fall under Woese and Fox's definition of a progenote. These and other arguments show that both the LUCA and the ancestor of Archaea were progenotes (Di Giulio, 2010).

The other trait used to reach similar conclusions is the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway (Rajbhandary, 1994). This pathway should be an ancestral trait because it is one of the five known pathways on tRNAs representing the principal manifestation of the coevolution theory of genetic code origin (Wong, 1975, 2005; Di Giulio, 1999b, 2008b). Indeed, this theory maintains that the genetic code is a map of the biosynthetic relationships between amino acids (Wong, 1975; Di Giulio, 2008b). According to the coevolution theory, the development of the genetic code took place during the transfer of codons from the precursor amino acid to the product amino acid biosynthetically derived from it (Wong 1975, 1976, 2005; Di Giulio, 1999b, 2008b). This theory maintains that, during code origin, the biosynthetic transformations between amino acids occur on tRNA-like molecules and,

therefore, the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway is nothing other than a molecular fossil (Di Giulio, 2002), a simple manifestation of the predictions of this theory (Wong, 1976; Wachtershauser, 1988; Danchin, 1989; de Duve, 1991; Edwards, 1996; Di Giulio, 1999b, 2002). This might therefore define the ancestry of these pathways on tRNAs (Di Giulio, 2002).

This pathway is present only in the Bacteria domain (Rajbhandary, 1994) which, together with the differences existing between the three domains of life as far as the initiation of protein synthesis is concerned, lead us to believe that this pathway originated very late on in the evolution of the genetic code and only when the line of divergence leading to Bacteria was defined (Di Giulio, 2001, 2010). It must also be believed that when the phyletic pathway leading to Bacteria was defined, not only was the protein synthesis initiation apparatus still rapidly evolving (for the very reason that the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway is present only in the Bacteria domain) but also, and more generally, the entire translation apparatus must have been in rapid and progressive Darwinian evolution (Di Giulio, 2001, 2010). This is because the evolution of fMet-tRNA<sup>fMet</sup> must have caused problems in the translation of mRNAs as formyl-methionine might have been inserted even in other proteins positions and not only at its N-terminal end, thus generating a more tolerable translation noise if the entire translation apparatus was not yet fully mature, i.e. if was still in rapid and progressive Darwinian evolution (Di Giulio, 2001, 2010). Moreover, the simple observation that at the evolutionary stage of the ancestor of Bacteria it was possible to insert a new amino acid into the genetic code, albeit in an unusual way, indicates per se that this evolutionary stage possessed at least a mode, if not a tempo, different from today and more typical of a progenote than of a genote for the very reason that macroscopic changes of this nature have never been observed in the evolution of the genetic code (Di Giulio, 2010). This all indicates that the ancestor of Bacteria was a progenote and that the LUCA must also have been one since these arguments clearly imply a translation still in rapid and progressive Darwinian evolution which, in turn, by definition implies a progenotic state for this evolutionary stage (Di Giulio, 2001, 2010).

The rationale underlying the analysis: a falsification of the panspermia theory

The panspermia theory makes some predictions regarding how evolution on this planet began. It seems intuitive that, in order to be able to infect the Earth, a micro-organism must have been a complex organism comparable to current prokaryotes and could not have been a progenote, i.e. a protocell in which, by definition, the relationship between its genotype and its phenotype had not been definitively established, that is it was still evolving (Woese and Fox, 1977). This is because a progenote would evidently have had a very low likelihood of infecting a planet in that, for instance, (i) its growth capabilities in a context different from the one in which it normally lived could not have been such as to assure growth on another planet even if this is also partly true for present-day prokaryotes but in a less restrictive way than for a progenote; (ii) its resistance to the journey it would have been subjected to could not have been such as to assure the survival of the progenote, while present-day prokaryotes should be more resistant than a progenote because this is still a rapidly evolving protocell (Woese and Fox, 1977) with serious internal problems still to be solved and, thus, any external variation might have been fatal; (iii) the time that biological systems ought to spend in a progenotic stage should be shorter than that which these systems ought to spend in the 'prokaryotic' stage and, therefore, this too should reduce the likelihood that it was progenotes which infected a planet; (iv) in the progenotic stage, these protocells must have occupied only a very specific ecological niche and would not have been able to colonise the entire planet. This would have greatly diminished the infective potential of the progenotic stage; and, finally, (v) it is impossible to envisage a single situation in which a progenote might have been fitter than a generic prokaryote to infect a planet.

Therefore, we can rationally conclude that if it can be shown that evolution on Earth passed through a progenotic stage, then we would obtain strong evidence against the panspermia theory and, in particular, against the directed panspermia theory in that intelligent beings sending micro-organisms to infect a planet would certainly not have sent progenotes.

In order to complete this argument, the following needs to be added. The split genes of tRNAs and the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway are two independent, ancestral (i.e. possessed by the LUCA) and domain-specific traits (present only in the domain of Archaea or only in that of Bacteria), as summarised above. Are two independent, ancestral and domain-specific traits per se able to establish that the panspermia theory is false? One trait alone is not, because it might be maintained that the fully evolved (i.e. not progenotic) infecting organism possessed it. Whereas, the second trait implies, given its specificity and ancestrality, that if there was only one infecting organism then the panspermia theory is false because the second trait could not have evolved. If it had evolved, this would imply that (i) the two infecting organisms were progenotes (thus capable of evolving these ancestral traits) or (ii) there cannot have been an evolution of the second trait as it was already an ancestral trait which could not evolve at that evolutionary stage because the evolution of a trait by a fully evolved organism (which is, instead, typical of ancestral evolutionary stages) is impossible. Therefore, either the ancestrality of these traits is false or the panspermia theory is. This theory predicts that evolution on Earth started from a very complex (i.e. already evolved) organism that could not undergo this type of evolution in that the very nature of the trait would imply an ancestral evolutionary stage that is impossible for an already complex and evolved organism. Thus, for the panspermia theory to continue to hold, it would be necessary for the Earth to have been infected by two different progenotes (or one alone that evolved into the others) which originated two of the domains of life, namely Archaea and Bacteria. The latter condition seems too restrictive and unusual to be true in that it would require the infection bringing life to Earth to be obtained not from one but from two different progenotes which, as we have seen, ought to have been highly unlikely, if not impossible, given the very limited infective capabilities and possibilities of these protocells.

However, an important specification must be made. According to the panspermia theory, the two independent, ancestral and domain-specific traits might have been brought to Earth as molecular fossils from two different prokaryotes and not from progenotes. In other words, two different prokaryotes might have housed these traits, which would not therefore

reflect progenotic stages but merely prokaryotic cells. This criticism is true, i.e. it rehabilitates the panspermia theory, only if both traits were not subjected to a strong and permanent selective pressure to remove them. But if at least one of these traits had been subjected to this selective pressure aiming to make it evolve into a different evolutionary stage, then the panspermia theory would be false because this trait would never have been observed after about 3.5 billion years of evolution as selective pressure would have removed it because it was rare at the start. (This property is possessed by the split genes of tRNAs which tend to evolve towards a single gene (Di Giulio, 2006a, b, 2008c, 2009a, b,)). Therefore, finding the split genes of tRNAs in two organisms today, i.e. a trait with this additional feature, would imply that it was possessed by a progenote and not by a prokaryote in that, if it had been possessed by a progenote, this trait would have been widespread at that time and extremely rare today, as is the case. However, if it had been possessed by a prokaryote then it ought to have been rare or extremely rare at that time because, by definition, it was a molecular fossil with a tendency to pass on to a new evolutionary stage and hence no longer identifiable today, after 3.5 million years of evolution. Therefore, we would not have been able to prove a progenotic stage for the first stages of the evolution of life on Earth simply because one of these traits was never observed in natural populations because it evolved (disappeared) into its subsequent evolutionary stage (as is thought to have happened for the split genes of tRNAs (Di Giulio, 2006a, b, 2008a, c, 2009a, b,)).

In conclusion, this shows that the infection, if there was one, could not have been caused by two different prokaryotes, but by progenotes, which deny the infection.

## Conclusions

In the above sections we have seen that since the two traits (the split genes of tRNAs of *Nanoarchaeum equitans* and the Met-tRNA<sup>fMet</sup>->fMet-tRNA<sup>fMet</sup> pathway) are independent, ancestral and domain-specific and as they imply progenotic stages for the LUCA and for the ancestors of Archaea and Bacteria (Di Giulio, 2001, 2006a, 2010), they have the

potential to falsify the panspermia theory in that the infection of the Earth by one or two different progenotes ought to have been a highly unlikely event. In other words, the conclusion that evolution on Earth passed through progenotic stages (Di Giulio, 2001, 2006a, 2010) has the consequence of significantly reducing the truth of the panspermia theory.

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