On hydrogen transfer and a chimeric origin of eukaryotes

Our TiBS article was not intended as an exhaustive review of all chimeric models for the origin of eukaryotes. Rather, as can be readily deduced from its title, Metabolic symbiosis at the origin of eukaryotes1, we compared two recent hypotheses suggesting a metabolic interaction based on hydrogen transfer between bacteria and archaea as the driving force that triggered eukaryogenesis. In the engangement proposal by Gupta and Golding2, briefly summarized in Fig. 1 of our article together with previous chimeric models, no driving force or any symbiotic relationship (metabolic or other) was put forward, therefore it was not discussed further by us.

From his assumption that eukaryotes would be generated continuously from present-day methanogenic consortia, Gupta concludes that intermediates should be found and that eukaryotes would be polyphyletic. On the contrary, we believe that eukaryotes derived from a single, highly evolved, symbiotic association that, due to its innovative properties, conquered rapidly all colonizable ecological niches. This further facilitated the creation of novel (eukaryotic) adaptive features, while preventing the colonization by less efficient newcomers. Thus, putative new- forming eukaryotes would be outcompeted by already better adapted ones. In any case, anaerobic syntrophic consortia are far from being thoroughly studied and deserve further analysis.

Gene transfers might have occurred between partners, followed by gene displacements and losses, which, indeed, would help to explain why many of these symbioses are irreversible. Although such cases could not be considered as intermediate eukaryotes, they would attest for the probability of the process.

Gupta also provides specific arguments against hydrogen–syntrophy hypotheses, which we consider here.

(1) Retention of metabolic processes can be evidence for ancient symbiosis (e.g. different types of mitochondrial respiration) but the opposite is obviously false. For instance, hydrogenosomes have not retained oxygen respiration and have lost many pathways present in their common ancestor with mitochondria, and mitosomes (organelles of methanogenic origin found in certain amoebas) seem to have lost all functions related to core metabolism. Martin and Müller gave a good explanation for the loss of methanogenesis after the import of the heterotrophic metabolism from methanogenic ancestors3, avoiding futile cycling in the same cellular space. We proposed a metabolic displacement of methanogenesis by the more efficient bacterial heterotrophy4. Both arguments are indeed complementary.

(2) There is increasing evidence that bacteria radiated5: Even if some indels (insertions or deletions, or both) could suggest an earlier rise of cyanobacteria6, they provide by no means a molecular clock and, therefore, historical dates. Interestingly, the fossil record shows that methanogenesis, methanotrophy (e- and γ-proteobacteria) and sulfate reduction were already present in stromatolites (laminated microbial communities) 3.2 to 3.5 Ga old, in perfect coexistence with cyanobacteria7. The earth atmosphere was mostly anoxic for at least 1.5 billion years of cyanobacterial history (from 3.5 Ga, when they were first recorded, to 2–2.1 Ga ago, when atmospheric oxygen levels rose significantly)8. Therefore, the existence of oxygen-producing cyanobacteria is not necessarily linked to high oxygenic atmospheres.

Furthermore, recent evidence suggests that eukaryotes existed 2.7 Ga ago9, well before the oxygen rise. Finally, many stable anoxic environments have existed on earth continuously, and it is clear that anaerobes and anaerobic consortia are widespread today, living happily, regardless of atmospheric oxygen levels10.

(3) The rationale for the retention of the archaean informational genes was provided in the original formulation of the syntrophy hypothesis3. (4) Evidence for eocytes (crenarchaeota) being closer to eukaryotes comes essentially from an indel in the EF-1a gene. However, counter evidence is that, unlike euryarchaeota, they lack histones. In fact, compelling evidence for either sisterhood should come from total genomic comparison. The genome sequence of Aeropyrum pernix (crenarchaeota) has been recently made available11 and its analysis should help to clarify the matter.

In conclusion, we presented no dogma but only a hypothesis to stimulate further discussions on the origin of eukaryotes. We regard this as the only path towards the construction of a plausible history of eukaryotes consistent with the information from different research areas.

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References

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