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Origin of cyanobacterial thylakoids via a non-vesicular glycolipid phase transition and their impact on the Great Oxygenation Event

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1 **Title**

2 Origin of Cyanobacteria thylakoids via a non-vesicular glycolipid phase transition and impact
3 on the Great Oxygenation Event

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31 **Highlight and Abstract**

32 The quest for thylakoid origin resists vesicular-based scenarios. An unexplored hypothesis is
33 based on Hexagonal II-forming glycolipids, turned within nanoseconds and without any
34 external energy source into membrane multilayers.

35 **Abstract**

36 Appearance of oxygenic photosynthesis in Cyanobacteria is a major event in the evolution of
37 Life. It had an irreversible impact on our planet, promoting the Great Oxygenation Event
38 (GOE), ~2.4 b.y.a. Ancient Cyanobacteria predating the GOE were *Gloeobacter*-type cells,
39 having no thylakoids. They hosted photosystems in their cytoplasmic membrane. The driver
40 of the GOE was proposed to be the transition from unicellular to filamentous Cyanobacteria.
41 However, the appearance of thylakoids expanded the photosynthetic surface by multiple logs:
42 this multiplier effect would be more coherent with an impact on the atmosphere. Primitive
43 thylakoids self-organize as concentric parietal uninterrupted multilayers. The quest for their
44 origin resists vesicular-based scenarios. This review reports studies supporting that *Hexagonal*
45 *II*-forming gluco- and galactolipids at the periphery of the cytosolic membrane could be
46 turned within nanoseconds and without any external source of energy into membrane
47 multilayers. Comparison of lipid biosynthetic pathways further shows that ancient
48 Cyanobacteria contained only one anionic *Lamellar*-forming lipid, phosphatidylglycerol.
49 Acquisition of sulfoquinovosyldiacylglycerol biosynthesis correlates with thylakoid
50 emergence, possibly enabling a sufficient provision of anionic lipids to trigger an *Hexagonal*
51 *II*-to-*Lamellar* phase transition. With this non-vesicular lipid-phase transition, a framework is
52 also available to reexamine the role of companion proteins in thylakoid biogenesis processes.

53 **Keywords**

54 Cyanobacteria; thylakoid; *Gloeobacter*; monoglucosyldiacylglycerol;
55 monogalactosyldiacylglycerol; Hexagonal II lipid; phosphatidylglycerol;
56 sulfoquinovosyldiacylglycerol; MGD; Great Oxygenation Event

57 **Abbreviations**

58 DGDG, digalactosyldiacylglycerol

59 MGDG, monogalactosyldiacylglycerol

60 MGlcDG, monoglucosyldiacylglycerol

61 SQDG, sulfoquinovosyldiacylglycerol

62 PtdCho, phosphatidylcholine

63 PtdEtn, phosphatidylethanolamine

64 PtdGro, phosphatidylglycerol

65

66 Main Text

67 1 Introduction

68 The appearance of oxygenic photosynthesis is a major event in the early evolution of Life and
69 had an irreversible impact on our planet. This bioenergetic and trophic innovation, coupling
70 H₂O splitting upon exposure to sun light with the reduction of atmospheric CO₂, occurred in
71 the Cyanobacteria ancestral lineage (Sanchez-Baracaldo and Cardona, 2020; Cardona, 2019,
72 2018; Cardona *et al.*, 2019). It deeply modified ecosystems, positioning Cyanobacteria as
73 prominent primary producers at the base of trophic networks, and allowed the development of
74 a tremendous biodiversity of secondary and tertiary consumers. At geological scale, the
75 production of O₂ as a byproduct of water splitting enabled the oxygenation of the atmosphere
76 during the Great Oxygenation Event (GOE), 2.4-2.32 billion years ago (b.y.a.) (Bekker *et al.*,
77 2004; Lyons *et al.*, 2014).

78 Later, oxygenic photosynthesis was acquired by Eukaryota of the Archaeplastida phylum, by
79 integration of an intracellular organelle called the ‘chloroplast’, deriving from the engulfment
80 of a close relative of the deep-branching *Gloeomargarita* cyanobacterium, combined with
81 components acquired by gene transfers from a variety of other sources (Ponce-Toledo *et al.*,
82 2019; Sato and Awai, 2017; Sato and Takano, 2017; Marechal, 2018). Following this unique
83 endosymbiotic event, the expansion of marine eukaryotic phytoplankton correlated with the
84 oxygenation of the oceans during the Neoproterozoic Oxygenation Event (NOE), 800-600
85 million years ago. This so-called ‘rise of Algae’ is thought to have created food webs with
86 even more efficient nutrient and energy transfers, driving ecosystems towards larger and more
87 complex organisms, including animals (Brocks *et al.*, 2017).

88 Access to increasing genomic data and refine reconstructions of molecular phylogenies have
89 improved our understanding of the early evolution of photosynthetic reaction center proteins
90 (Sanchez-Baracaldo and Cardona, 2020; Cardona, 2019, 2018; Cardona *et al.*, 2019).
91 Schematically, oxygenic photosynthesis requires two sets of dimeric reaction centers, one of
92 type II (in photosystem II, PSII) and one of type I (in PSI), all deriving from a unique origin
93 in an ancestral anoxygenic photosynthetic prokaryote. Whereas single PSII-like or PSI-like
94 reaction centers have evolved independently in various clades of anoxygenic phototrophic
95 Bacteria (Hohmann-Marriott and Blankenship, 2011), crown group Cyanobacteria inherited
96 both an heterodimeric versions of PSII, where water-splitting occurs, and an heterodimeric
97 PSI (Sanchez-Baracaldo and Cardona, 2020). Recent estimates of the age of PSII and PSI
98 gene families coincide with geological evidence of oxygen traces throughout a division of
99 Precambrian time called the Archean eon (4-2.5 b.y.a.). This implies that oxygenic
100 photosynthesis was established by 3.0 b.y.a., long before the GOE (Cardona, 2018; Cardona
101 *et al.*, 2019). It is still unresolved whether a ‘protocyanobacteria’ acquired the two sets by
102 gene duplication of anoxygenic photosystems (Martin *et al.*, 2018) or *via* gene transfers
103 (Raymond *et al.*, 2002). Amongst plausible scenarios, a versatile protocyanobacteria
104 containing two reaction centers, i.e. an H₂S splitting PSI (photolithotrophy) with an
105 expression controlled by fluctuating hydrogen sulfide concentrations, and a PSII
106 (photoorganotrophy), might have developed in shallow water at the vicinity of temporary
107 hydrothermal springs. This protocyanobacteria having a flexible metabolism adapted to
108 alternating redox conditions, might have acquired oxygenic photosynthesis by mutations in
109 the direction of a constitutive expression of both Types I and II reaction centers, and an
110 extraction of electrons, firstly from manganese and secondarily from water. This hypothesis
111 was termed the ‘Redox switch hypothesis for the first Cyanobacteria’ (Allen, 2016; Allen,
112 2014).

113 Since oxygenic photosynthesis predated the GOE by about 0.5 to 1 b.y., what was the actual
114 driver of this major atmospheric upheaval if not photosynthesis appearance *per se*? The extant
115 diversity of Cyanobacteria evolved after the GOE (Sanchez-Baracaldo and Cardona, 2020).
116 Most ancient Cyanobacteria are likely to have populated low salinity habitats and dry
117 environments (Blank and Sanchez-Baracaldo, 2010) as small unicellular forms close to
118 present-day *Gloeobacter* (Sanchez-Baracaldo and Cardona, 2020; Mares *et al.*, 2019; Raven
119 and Sanchez-Baracaldo, 2021). The GOE was proposed to be the consequence of the ability
120 of Cyanobacteria to form multicellular filaments, resembling extant *Pseudanabaena*,
121 facilitating the formation of microbial mats, a feature supposed to increase their ecological
122 dominance to such an extent that atmospheric O₂ underwent this dramatic increase (Sanchez-
123 Baracaldo and Cardona, 2020).

124 An alternative hypothesis based on studies reviewed here is that such an important
125 atmospheric change as the GOE requires an extraordinary multiplier effect that
126 multicellularity, introducing no additive effect, is not sufficient to explain. The transition from
127 *Gloeobacter*-type to other Cyanobacteria, is marked by the emergence of internal membranes
128 sacks, known as ‘thylakoids’, allowing a significant gain in the area of the ‘solar panels’
129 accommodating photosystems (Mares *et al.*, 2019). This review highlights the role of lipid
130 components in Cyanobacteria membranes, disregarded until now in the determinant processes
131 at the origin of thylakoids.

132 **2 Emergence of thylakoids in early Cyanobacteria had a multiplier effect on the** 133 **photosynthetic surface per cell.**

134 Thylakoids are evidently not required for oxygenic photosynthesis since *Gloeobacter* hosts its
135 photosystems in its cytoplasmic (or inner) membrane (Raven and Sanchez-Baracaldo, 2021).
136 The evolution of thylakoids starts with the appearance of continuous linear sacks with several
137 concentric, uninterrupted layers (Mares *et al.*, 2019). Based on a spherical cell with a 1 μm
138 diameter (volume = 0.53 μm³), a *Gloeobacter* membrane surface would be ~3.14 μm². Taking
139 into account that in *Gloeobacter*, photosynthetic proteins are concentrated in domains
140 representing less than a third of the cytosolic membrane (Rexroth *et al.*, 2011), the actual
141 photosynthetic surface is in the 1 μm² range. By contrast, in a *Cyanobium*-like coccid cell of
142 same size (Mares *et al.*, 2019), with four concentric thylakoids lining the plasma membrane
143 (so-called parietal thylakoids), the photosynthetic surface would reach ~20 μm². Parietal
144 thylakoid fascicules encountered in *Synechocystis*-like coccid or *Leptolyngbya*-like
145 filamentous cyanobacteria (Mares *et al.*, 2019) with four layers would reach about the same
146 photosynthetic surface per cell. Cyanobacteria containing parallel or radial arrangement of
147 thylakoids (Mares *et al.*, 2019) can increase the photosynthetic surface even further. An
148 *Arthrospira*-like cell with 50 radial thylakoids or a *Cyanothece*-like cell with 50 parallel
149 thylakoids can reach a photosynthetic surface in the range of 50-70 μm², based on the
150 summed area of flattened cisternae, within the same volume. In the course of evolution,
151 following chloroplast integration in Archaeplastida, thylakoids evolved in the direction of an
152 increased surface and organization in functional domains with the development of stacks and
153 grana, which do not form in Cyanobacteria. In the cells of eukaryotic microalgae, the volume
154 of the plastid is commonly higher than 10 μm³ (Uwizeye *et al.*, 2021) whereas in vascular
155 plants, such as maize, the volume of mesophyll cell chloroplasts can reach volumes higher
156 than 100 μm³ (Kutik *et al.*, 2004). Based on a 10-100 μm³ chloroplast containing 50
157 thylakoids, a gross calculation gives a photosynthetic surface of 10⁻³-10⁻² mm² per
158 chloroplast. Overall, a population of 1 million *Gloeobacter*-type cells harbors a global
159 photosynthetic surface of about 1 mm², whereas 1 million of *Arthrospira*- or *Cyanothece*-like

160 cells can easily exceed 50-70 mm². Because of this obvious multiplier effect, the appearance
161 of thylakoids seems therefore the most plausible determinant in the GOE.

162 One would naturally examine extant protein machinery(ies) involved in thylakoid biogenesis
163 to trace back its origin and look for evidence supporting this hypothesis. The difficulty lies in
164 the still unresolved process(es) governing the biogenesis of this membrane system, most
165 notably because this question is mainly posed considering protein components only. We
166 advocate here that spontaneous organization of lipids, following an appropriate biosynthetic
167 sequence, would be sufficient to produce very large amounts of membrane surfaces in nano-
168 to microseconds. This process does not require vesicles budding from the Cyanobacteria
169 plasma membrane or the chloroplast inner envelope membrane. Actually, the traditional
170 hypothesis for a ‘vesicular-based’ biogenesis of thylakoids finds little support in
171 ultrastructural analyses of Cyanobacteria and chloroplasts, where the observation of inner
172 membrane invaginations is extremely rare (Mares *et al.*, 2019; Botte *et al.*, 2011a; Boudiere *et*
173 *al.*, 2012; Bastien *et al.*, 2016; Gupta *et al.*, 2021). Some reports highlight the presence of
174 vesicles in eukaryotic proplastids prior their conversion into chloroplasts (Mechela *et al.*,
175 2019), but the lack of such vesicular compartment in Cyanobacteria disqualifies this
176 mechanism at the origin of thylakoids in ancient clades. Likewise, the focus on *Synechocystis*
177 ‘thylakoid convergence zones’ where thylakoids merge into high-curvature membranes in
178 close contact with the plasma membrane, also observed in some chloroplasts (Gupta *et al.*,
179 2021), do not account for the biogenesis of more primitive parietal thylakoids organized in
180 concentric and uninterrupted layers (Mares *et al.*, 2019). Here, we do not disregard the fact
181 that protein components evolved in the direction of helping, organizing, guiding, orchestrating
182 the process of thylakoid biogenesis, leading to the very sophisticated and efficient processes
183 observed today, but we assume that no evidence support their determinant role in the early
184 stages.

185 **3 Thylakoids emerged from a mixture of lipids allowing a non-vesicular biogenesis of** 186 **membranes**

187 Membrane bilayers are made of polar lipids, harboring a ‘polar head group’ exposed to the
188 surface, and hydrophobic ‘tails’ inside its core. How can a lipid bilayer form without any
189 source of vesicles, protruding or budding from a parent membrane, merging to produce large
190 surfaces? An answer developed here comes from the biophysical properties of polar lipids.
191 Depending on the equilibrium between polar head interactions and repulsive forces between
192 hydrophobic tails, each of the polar lipid can self-organize and form so called ‘phases’, either
193 with a positive curvature (e.g. micellar tubules, also known as ‘hexagonal I’, or *HexI*), or no
194 curvature (‘lamellar’, or *Lm*) or with a negative curvature (‘inverted hexagonal’, or *HexII*)
195 (Jouhet, 2013). These properties have attracted the attention for long, with a focus on lipids
196 promoting an *Lm* → *HexII* transition, since the disturbance introduced by inverted hexagonal
197 phase was considered essential for the promotion of highly bent and fused domains (Jouhet,
198 2013; Gawrisch *et al.*, 1992; Toombes *et al.*, 2002; Kuzmin *et al.*, 2001). Little
199 thermodynamic studies are available to evaluate all possible phase transitions in the different
200 lipid mixtures found in nature. Our knowledge relies on model lipids such as
201 phosphatidylethanolamine (PtdEtn), which organization in *Lm* or *HexII* phases depends on its
202 chemical structure, *i.e.* the length and desaturation level of acyl chains; physical properties,
203 such as hydration or temperature; and the presence of other lipids (Gawrisch *et al.*, 1992;
204 Toombes *et al.*, 2002; Mannock *et al.*, 2001; Harper *et al.*, 2001).

205 It is essential to keep in mind that so-called “*HexII* lipids” are also found in membrane
206 bilayers, either because in their pure state they can form both *HexII* or *Lm* phases depending

207 on temperature, hydration, etc., or because when mixed with *Lm* lipids, the lamellar phase is
208 the more stable organization. In past studies, *Lm* → *HexII* was the direction examined in the
209 search for plausible membrane fusion mechanisms. The enthalpy of dioleoyl-PtdEtn phase
210 transition (ΔH) measured by differential scanning calorimetry had a positive value (+0.3
211 kcal.mol⁻¹ = 1.255 kJ.mol⁻¹), meaning that energy external to the system had to be provided
212 (Gawrisch *et al.*, 1992). It was further showed that neither the *Lm* → *HexII* nor the *HexII* →
213 *Lm* kinetics had any significant deviation from a power-law relationship: a relative change in
214 the *Lm* phase results in a proportional relative change in *HexII* and *vice versa* (Toombes *et al.*,
215 2002; Garab, 2016). The *Lm* ↔ *HexII* transition is therefore remarkable for the symmetry
216 between forward and reverse dynamics (Toombes *et al.*, 2002). A corollary is that the *HexII*
217 → *Lm* transition for this pure lipid species may release some energy, and therefore occur
218 spontaneously. Same spontaneous *HexII* → *Lm* transition of dioleoyl-PtdEtn could occur by
219 changing the hydration level (Gawrisch *et al.*, 1992). The *HexII* → *Lm* phase transition
220 provides a solution to the unresolved question of the emergence of early membrane systems,
221 especially with such extended surface as thylakoids.

222 Let us first consider the lipid composition of Cyanobacteria in a simplified evolutionary
223 context. A variety of chemical structures can produce impermeable membranes delineating
224 cells (Jia *et al.*, 2019). We have evidence of two distinct options for the structure of polar
225 lipids in primordial membranes, based on their conservation in the three domains of life.
226 These primordial lipids are all built on a three-carbon glycerol scaffold (numbered *sn*-1, *sn*-2,
227 *sn*-3). On the one hand, Archaea are bounded by membranes made of isoprenoid hydrocarbon
228 chains linked *via* ether bonds to an *sn*-2,3-glycerol phosphate backbone, and multiple
229 derivatives with two polar heads, which can form lipid monolayers (Salvador-Castell *et al.*,
230 2021; Imachi *et al.*, 2020). On the other hand, Bacteria and Eukaryota are primarily bounded
231 by membranes made of acyl-glycerolipids, deriving from a precursor containing fatty acids
232 linked *via* ester bonds to an *sn*-1,2- glycerol phosphate backbone (Imachi *et al.*, 2020). It is
233 established that in Archaea, the presence of phytanyl chains, ether bonds and bipolar lipids
234 confer a high stability to their membranes (Guler *et al.*, 2009; Garcia-Arribas *et al.*, 2015;
235 Balleza *et al.*, 2014). By contrast, in Bacteria and Eukarya, acyl-glycerolipids may confer a
236 higher flexibility, especially *via* the controlled addition of double bonds to the acyl chains,
237 tuning the lateral fluidity of membranes, but also with the balance between *HexII* and *Lm*
238 lipids (Garab, 2016; de Kruijff, 1997). Increasing evidence support that Eukaryogenesis
239 originated from the merger between an archaeal host and a bacterial endosymbiont related to
240 modern α -proteobacteria (Imachi *et al.*, 2020). This raises the puzzling question of the loss of
241 Archaea-type lipids in Eukarya. An hypothesis is that the integrated α -proteobacteria gave
242 rise to a proto-mitochondrion, producing ATP by specific protein machineries preferring
243 Bacteria-type membranes, which were subsequently conserved (Sojo, 2019). In these initial
244 membrane matrices, other lipidic structures and hydrophobic polypeptides were integrated,
245 contributing to the multitude of functions harbored by cell membranes.

246 Acyl-glycerolipids with a polar head containing a phosphate group, such as the *HexII* lipid
247 PtdEtn, or phosphatidylcholine (PtdCho), an *Lm* lipid, are conserved in the majority of
248 Bacteria and Eukarya clades, with the notable exception of crown Cyanobacteria who only
249 contain one phospholipid, phosphatidylglycerol (PtdGro) (Petroustos *et al.*, 2014; Yuzawa *et al.*,
250 2012; Sato and Awai, 2016). PtdGro is anionic and its proportion is regulated in response
251 to phosphate availability (Boudiere *et al.*, 2014; Frentzen, 2004). The conservation of PtdGro
252 is consistent with its role in the assembly and functioning of photosynthesis components
253 (Boudiere *et al.*, 2014), supported by the lethality of PtdGro-less mutants of Cyanobacteria
254 (Kopečna *et al.*, 2015; Hagio *et al.*, 2000; Sakurai *et al.*, 2003a, b; Kobori *et al.*, 2018) and

255 plants (Babiyuchuk *et al.*, 2003; Xu *et al.*, 2002; Xu *et al.*, 2006). Such membrane composition
256 parsimonious in phospholipids supports the idea that early Cyanobacteria populated an
257 environment where phosphorous was limiting, at least to meet their basal metabolic demand.

258 The lipid composition of *Gloeobacter* membranes is simple, containing three lipid classes in
259 addition to PtdGro: monoglucosyldiacylglycerol (MGlcDG), monogalactosyldiacylglycerol
260 (MGDG) and digalactosyldiacylglycerol (DGDG) (Rexroth *et al.*, 2011; Yuzawa *et al.*, 2012;
261 Sato and Awai, 2016; Sato, 2015). MGlcDG and MGDG are *HexII* lipids, whereas DGDG
262 and PtdGro are *Lm* lipids (Jouhet, 2013). It is interesting to note that the addition of *HexII*-
263 forming MGlcDG could rescue a bacterial *Escherichia coli* mutant lacking *HexII*-forming
264 PtdEtn (Wikstrom *et al.*, 2004), indicating that an *HexII* lipid could replace another *HexII*
265 lipid, thus filling a vital role governed by its biophysical properties. The plasma membrane of
266 *Gloeobacter* has only traces of MGlcDG (Sato and Awai, 2016; Sato, 2015). It was shown to
267 contain segregated bioenergetic domains, some with low-chlorophyll content being MGDG-
268 rich (~70% MGDG, ~22% DGDG and ~8% PtdGro), whereas high-chlorophyll domains were
269 more balanced in their lipid composition (~55% MGDG, ~35% DGDG, ~10% PtdGro)
270 (Rexroth *et al.*, 2011). These latter domains also contain photosynthetic components, *i.e.* PSII,
271 PSI and ATP-synthetase. It is very important to note that the relative MGDG/DGDG ratio
272 differs in the two membrane domains: this indicates that although DGDG is produced from
273 MGDG, some regulatory mechanisms uncouple its final proportion from the available amount
274 of substrate. This is consistent with the multitude of roles played by DGDG which need to be
275 finely controlled, including the stability of the photosynthetic machinery (Boudiere *et al.*,
276 2014; Apdila and Awai, 2018; Sakurai *et al.*, 2007; Awai *et al.*, 2007). The MGDG-rich
277 domains at the plasma membrane appear therefore as ideal platforms to promote *HexII* → *Lm*
278 phase transition. Nevertheless, the $HexII_{(MGlcDG, MGDG)} / Lm_{(DGDG, PtdGro)}$ balance is still
279 insufficient in *Gloeobacter* to promote the formation of thylakoids. In addition, because
280 PtdGro is essential for the stability of photosystems (Kopečna *et al.*, 2015; Haggio *et al.*, 2000;
281 Sakurai *et al.*, 2003a, b; Koberi *et al.*, 2018; Babiyuchuk *et al.*, 2003; Xu *et al.*, 2002; Xu *et al.*,
282 2006), a minimal quantity of this anionic lipid should be included in thylakoids, and the
283 production of exceeding amounts of PtdGro in the bulk of membrane lipids appears difficult
284 to maintain in a phosphate-limiting environment.

285 How could thylakoids emerge from an *HexII* → *Lm* transition process? An absolute
286 prerequisite is a topological segregation of domains producing lipids in *HexII* phase from
287 those promoting *Lm* bilayers. MGDG-rich domains in *Gloeobacter* plasma membrane makes
288 this condition plausible. The enzymes synthesizing MGlcDG and MGDG should be distant
289 enough from those consuming them to produce the *Lm* forming DGDG. The galactolipid
290 biosynthesis pathway in *Gloeobacter* was shown to be similar to that in all other
291 Cyanobacteria. Firstly MGlcDG is produced by a monoglucosyldiacylglycerol synthase
292 (MgdA) (Apdila and Awai, 2018; Awai *et al.*, 2006), then the glucosyl polar head is
293 epimerized by an unknown mechanism into a galactosyl residue, thus forming MGDG;
294 eventually DGDG is formed by the action of a digalactosyldiacylglycerol synthase (DgdA)
295 similar to that identified in other Cyanobacteria (Apdila and Awai, 2018; Sakurai *et al.*, 2007;
296 Awai *et al.*, 2007). The activity converting MGlcDG into MGDG in *Gloeobacter* was
297 measured (Sato, 2015), but the corresponding enzyme is still uncharacterized molecularly. It
298 was tentatively called MgdX (Apdila and Awai, 2018). MGlcDG does not accumulate and
299 this lipid is barely detected in *Gloeobacter*, in support of a physical proximity between MgdA
300 and MgdX *in vivo*. With a few exceptions, major Cyanobacteria clades who have radiated
301 from a *Gloeobacter*-like ancestor contain another epimerase, called MgdE shown to convert
302 MGlcDG into MGDG (Awai *et al.*, 2014). Since MGlcDG can accumulate, even in small but

303 detectable amounts in MgdE-containing Cyanobacteria (Sato and Awai, 2016; Apdila and
304 Awai, 2018), one can suppose that MgdE is topologically separated from MgdA. The
305 galactolipid pathway thus evolved in the direction of a topological separation of each step
306 synthesizing each of its components, MGlCDG, MGDG and DGDG. Based on membrane
307 fractionation and enzymatic measurements, MgdA activity was detected in both thylakoid and
308 plasma membranes of *Anacystis* (Omata and Murata, 1986) and *Synechocystis* (Selao *et al.*,
309 2014), whereas DgdA appears restricted to the plasma membrane (Selao *et al.*, 2014). This
310 topological segregation of MGlCDG and MGDG synthesizing enzymes from DGDG
311 synthesizing ones may have enabled a transient accumulation of *HexII* lipids.

312 One could consider that the most important *HexII* lipid in this process would be the most
313 abundant one, *i.e.* MGDG, but Cyanobacteria genetic studies do not support this strict
314 requirement. The knock-out of *mgdA* was lethal in *Synechocystis* (Apdila and Awai, 2018;
315 Awai *et al.*, 2006), probably because this enzyme is the committing step for the formation of
316 three lipid classes, *i.e.* MGlCDG, MGDG and DGDG. The knock-out of the second enzyme,
317 *mgdE*, led to the hyper-accumulation of MGlCDG in *Synechocystis*, reaching nearly 70% of
318 the total proportion of lipids, replacing all MGDG and DGDG which could not be produced.
319 The *Synechocystis mgdE* mutant was viable and contained thylakoids (Awai *et al.*,
320 2006; Apdila and Awai, 2018). This indicated that MGDG was not strictly required for
321 thylakoid biogenesis, but that MGlCDG or MGDG, as *HexII* lipids, may be indistinctly usable.
322 *Synechocystis mgdE* mutation also indicated that thylakoid bilayers, if generated from
323 MGlCDG instead of MGDG, did not strictly require DGDG as a necessary *Lm* forming lipid.
324 Altogether, thylakoids might have emerged from a *Gloeobacter*-type Cyanobacteria, in which
325 a specific biosynthetic platform allowed the accumulation of an *HexII* lipid, most likely
326 MGDG, although MGlCDG might have been appropriate as well, reminiscent of the
327 complementation of viable *E. coli* PtdEtn mutants by external supply of MGlCDG (Wikstrom
328 *et al.*, 2004).

329 A 'trigger' should then be added to this system, to promote the transition of an *HexII* phase
330 into an *Lm* one. We discussed above that the model lipid PtdEtn could operate such transition
331 by discrete changes of its chemical structure, in particular the level of its acyl chains'
332 desaturation, by modulating temperature or hydration and that the enthalpy of *Lm* → *HexII*
333 transition was positive (Gawrisch *et al.*, 1992). Having in mind the mechanism of membrane
334 fusions, the modeling of the *Lm* → *HexII* transition showed that, given an initial multilamellar
335 configuration and with appropriate provision of external energy (increasing temperature), a
336 formation of so called 'stalks' (elongated structures) between bilayers could be observed in a
337 nanosecond timescale. The stalks were not stable and they subsequently elongated in a
338 cooperative manner, thus leading to the formation of an inverted *HexII* phase (Marrink and
339 Mark, 2004). Thylakoids may have simply emerged from the reverse process, from a
340 MGlCDG/MGDG *HexII* matrix converted within nano- to microseconds into piled multi-
341 lamellar membranes. It was reported that a decrease of double bonds per molecule of MGDG
342 was sufficient to promote the conversion from *HexII* structure to *Lm* phase (Gounaris and
343 Barber, 1983). The study of MGDG mixed with other thylakoid lipids has also shown that the
344 presence of various *Lm* lipids to MGDG triggered a spontaneous *HexII* to *Lm* transition upon
345 increasing hydration (Deme *et al.*, 2014). The trigger could therefore simply be an *Lm* lipid,
346 such as any of this type present in Cyanobacteria membranes. One should now identify which
347 of the *Lm* forming lipid would play this role at the beginning.

348 Another difference between *Gloeobacter*-type and subsequent Cyanobacteria is the absence of
349 a fifth lipid class, *i.e.* the anionic sulfoquinovosyldiacylglycerol (SQDG). The absence of the
350 equipment to synthesize SQDG in *Gloeobacter*, *i.e.* the *sqdB* and *sqdX* genes, was interpreted

351 as an ancestral trait (Sato *et al.*, 2016), although a secondary loss was also suggested (Sato
352 and Awai, 2016). Here, it may be interesting to remind one of the scenarios reported above for
353 the origin of oxygenic photosynthesis, starting from a protocyanobacteria containing two
354 reaction centers, one being an H₂S splitting PSI controlled by fluctuating hydrogen sulfide
355 concentrations (redox switch hypothesis for the first Cyanobacteria) (Allen, 2016; Allen,
356 2014). It may be that, in addition to living in a phosphorus-limiting environment, the proto-
357 cyanobacteria were exposed to reduced forms of sulfur such as hydrogen sulfide (H₂S), rather
358 than oxidized ones such as sulfate (H₂SO₄). The acquisition of the sulfolipid synthesis
359 pathway by horizontal gene transfer would then be a key event in the radiation of early
360 Cyanobacteria. In thylakoid-containing Cyanobacteria, mutants lacking SQDG are either
361 affected, such as in *Synechocystis*, or with no apparent phenotype under optimal growth
362 condition, such as in *Synechococcus* (Apdila and Awai, 2018), leading to the common idea
363 that this lipid could be to some extent dispensable (Sato *et al.*, 2016). It is now established in
364 Cyanobacteria, but also in chloroplasts of vascular plants that SQDG function is linked to that
365 of PtdGro, replacing temporarily this anionic phospholipid in case of phosphate shortage in
366 the environment (Boudiere *et al.*, 2014; Frentzen, 2004; Shimojima, 2011). The gain is clear:
367 Cyanobacteria with SQDG have acquired an anionic surrogate to replace PtdGro, and can
368 overcome stronger depletions of phosphorus in the environment. Thanks to SQDG, anionic
369 membrane lipids are no more limiting. This gain is an advantage when competing with
370 SQDG-missing Cyanobacteria, and in any case, when competing with Bacteria with
371 phospholipid-rich membranes in a phosphorus-deprived context. This also allows the
372 availability of sufficient amounts of an anionic *Lm*-forming lipid for the expensive formation
373 of an additional membrane system. Together, SQDG and PtdGro, and to some extent DGDG,
374 can be used as lipid triggers, some kind of catalysts, for the nanosecond-scale *HexII*_{(MGlCDG,}
375 _{MGDG)} → *Lm*_(MGlCDG, MGDG, DGDG, PtdGro, SQDG) transition.

376 Was DGDG necessary at the origin of thylakoids? This could make sense since SQDG and
377 PtdGro are anionic, and their use, although essential for photosystems, can thus introduce
378 repulsive electrostatic forces between membrane bilayers, which may prevent the formation
379 of tightly stacked membranes. Some arguments contradict this idea though, most importantly
380 since the *mgdE* mutant of *Synechocystis* can still make thylakoids whereas it has lost all of its
381 DGDG (Awai *et al.*, 2006; Apdila and Awai, 2018). One should admit that *Synechocystis*
382 thylakoids can organize as stacks in spite of the strong anionic charges harbored by the polar
383 head groups of its *Lm* forming lipids. Protein components may contribute to this stable
384 architecture in *Synechocystis*, but these proteins may have been missing in the original steps.
385 Indeed, DGDG was shown to stabilize membrane stacks, including in lipid mixtures
386 mimicking that of photosynthetic membranes (Deme *et al.*, 2014; Kanduc *et al.*, 2017). Thus,
387 we cannot assess with certainty the potential role of DGDG at the origin, but this lipid would
388 have been advantageous in the formation of stacked thylakoid primordia.

389 The hypothesis defended here relies on the fact that all the lipid actors but one, SQDG, were
390 present in *Gloeobacter*-type early Cyanobacteria. SQDG introduces a more flexible and
391 robust membrane lipid metabolism by the tuning of the SQDG/PtdGro balance in response to
392 phosphorus in the environment. *HexII* lipids, mostly MGDG, could be produced
393 concentrically toward the inside of the cell, followed by the transfer of *Lm* lipids, *i.e.* anionic
394 PtdGro and SQDG and neutral DGDG. These *Lm* lipids would then act as triggers of an *HexII*
395 → *Lm* phase transition. This gives an explanation to the non-vesicular biogenesis of
396 thylakoids, and to the initial formation of concentric, uninterrupted layers (Mares *et al.*,
397 2019).

398 4 Role of proteins

399 An *HexII* ↔ *Lm* phase transition is of ‘first-order’, *i.e.* involving a latent heat or phase
400 transition enthalpy, releasing or absorbing a fixed and typically large amount of energy, thus
401 differing from a ‘second order’, or ‘continuous phase transition’. The dynamics of the
402 dramatic lipid rearrangements occurring during this transition, although very rapid, has
403 limiting rate steps in topological transitions (Toombes *et al.*, 2002). Protein actors could have
404 played a role at the origin of thylakoid formation, by acting in the dynamics of *Lm* lipids’
405 transfers to an *HexII* matrix and the ‘nucleation’ of *HexII* → *Lm* transition.

406 *Gloeobacter* contains a homolog of Vipp1, found in all other oxygenic photosynthetic
407 organisms (Raven and Sanchez-Baracaldo, 2021). The Vipp1 protein has been functionally
408 associated to thylakoid biogenesis in a multitude of biological models, by various genetic,
409 structural or biochemical studies (Mechela *et al.*, 2019), but the precise understanding of its
410 role, at molecular level, still remains puzzling in spite of recent advances in the resolution of
411 its structural organization (Gupta *et al.*, 2021). *Gloeobacter* Vipp1 lacks a ~30 amino acid
412 extension found in thylakoid-containing organisms (Raven and Sanchez-Baracaldo, 2021),
413 and this protein plays a primitive function which is still elusive. In thylakoid-containing
414 *Synechocystis* or in the chloroplast of the green alga *Chlamydomonas reinhardtii*, *vipp1*
415 mutations lead to the formation of aberrant thylakoid convergence zones (Gupta *et al.*, 2021;
416 Nordhues *et al.*, 2012). This has led to the idea that Vipp1 had gained a new role in the course
417 of Evolution, acting at the level of highly bent regions of thylakoids (which are absent in
418 Cyanobacteria containing concentric thylakoids with uninterrupted layers). Of interest here,
419 Vipp1 has a strong affinity for lipids, particularly anionic lipids including but not restricted to
420 PtdGro, *in vitro* and *in vivo* (Otters *et al.*, 2013; Li *et al.*, 1994; Kroll *et al.*, 2001; McDonald
421 *et al.*, 2017; Heidrich *et al.*, 2016). Structural studies suggest a possible role of Vipp1 in
422 guiding some lipids from a donor membrane to thylakoid primordia (Gupta *et al.*, 2021). If
423 Vipp1 played this function for all thylakoid lipids, one should expect a detection of
424 innumerable complexes connecting the inner membrane, Vipp1 and thylakoids, but these are
425 instead very rarely observed (Gupta *et al.*, 2021). Little evidence are therefore available to
426 support that Vipp1 would act in the transfer of the bulk of thylakoid lipids, and in any case, a
427 role in a massive vesicular-based process is not supported. Vipp1 may have acquired a new
428 function in early Cyanobacteria, guiding some anionic lipids toward the light of the cell, thus
429 ‘helping’ the nucleation of thylakoid bilayer formation. The Vipp1 ancestral protein in
430 *Gloeobacter* might therefore have evolved in the direction of a guidance of thylakoid
431 biogenesis based on its initial biophysical properties, interacting with other lipids or proteins.

432 In this paper, we did not elaborate any scenario for the evolution of Vipp1 or others proteins
433 (Raven and Sanchez-Baracaldo, 2021). We simply suggest that proteins present in early
434 Cyanobacteria, completed with others acquired later on, following gene transfers, might have
435 been integrated based on their intrinsic biophysical properties. This is supported by studies
436 showing that Cyanobacteria Vipp1 C-terminal domain associates with lipid bilayers and
437 modulates membrane fusion and fluxes of lipids and proteins between membranes (Saur *et al.*,
438 2017; Hennig *et al.*, 2017; Hennig *et al.*, 2015). Here, we did not address the question of the
439 loading of thylakoids with all kinds of other components, proteins and cofactors, including the
440 photosystems and ATP-synthetase, also requiring guiding machineries. This could maybe rely
441 on *HexII* glycolipids, which are found in association with reaction centers from anoxygenic
442 photosynthetic Bacteria to Cyanobacteria, all algae and plants (Mizoguchi *et al.*, 2013). A
443 photosynthetic reaction center from *Blastochlorus viridis*, a species containing *HexII*
444 glycolipid, was thus shown to form a so-called ‘lipidic sponge phase’ crystal structure (Wohri
445 *et al.*, 2009). It is known for long that in energy-transducing membranes, *HexII* lipids are
446 preferentially associated with that part of the bilayers in which the coupling factors are

447 embedded, *i.e.* MGDG in the outer layer of plant thylakoids, PtdEtn on the cytosolic face of
448 *Rhodobacter sphaeroides* chromatophores, and both PtdEtn and cardiolipin in the inner
449 monolayer of internal mitochondrial membrane (Rawlyer *et al.*, 1987). In this context, a
450 parsimonious hypothesis is that at the origin, photosynthetic components were loaded during
451 the *HexII* → *Lm* phase transition.

452 **5 The endosymbiotic origin of chloroplasts supports the conserved role of *HexII*** 453 **lipids in the formation of their thylakoids**

454 A vast array of evidence support an origin of the chloroplast in Archaeplastida cells
455 (Glaucomphyta, Rhodophyta and Chlorophyta) following a unique primary endosymbiosis
456 event, by engulfment of a Cyanobacteria-like ancestor related to extant *Gloeomargarita* inside
457 an unknown eukaryotic host cell (Ponce-Toledo *et al.*, 2019; Sato and Awai, 2017; Sato and
458 Takano, 2017; Marechal, 2018; Petroutsos *et al.*, 2014). This view is however simplistic,
459 since numerous genes coding for chloroplast proteins find no ancestor in crown
460 Cyanobacteria, but rather in other clades not discussed here (Ball *et al.*, 2013; Cenci *et al.*,
461 2017; Sato *et al.*, 2020). It is extremely important to note that all Cyanobacteria lipids have
462 been conserved, except one, MGLcDG (Sato and Awai, 2017; Petroutsos *et al.*, 2014; Sato and
463 Awai, 2016; Boudiere *et al.*, 2014). The four lipids MGDG, DGDG, PtdGro and SQDG are
464 thus present in all prokaryotic and eukaryotic thylakoids. Only when photosynthesis was lost
465 secondarily, could plastids ‘lose’ their glycolipids (Botte and Marechal, 2014; Botte *et al.*,
466 2018; Botte *et al.*, 2011b; Botte *et al.*, 2013).

467 How could galactolipids be synthesized in chloroplasts, if the committing step of MGLcDG
468 synthesis is not present? Chloroplast MGDG is not synthesized by a Cyanobacteria pathway,
469 but in one-step by the action of a monogalactosyldiacylglycerol synthase, or *MGD* acquired
470 secondarily by horizontal gene transfer from a bacterium (Sato and Awai, 2017; Petroutsos *et al.*
471 *et al.*, 2014; Yuzawa *et al.*, 2012). The production of DGDG is catalyzed by a Cyanobacteria-
472 type enzyme in Glaucomphyta and one branch of Rhodophyta, but, again, by another type of
473 digalactosyldiacylglycerol synthase, called *DGD*, also acquired secondarily (Sato and Awai,
474 2017; Petroutsos *et al.*, 2014). Some well-studied Archaeplastida models, like *Arabidopsis*
475 show clear topological separation between the *MGD* enzyme involved in thylakoid
476 biogenesis, called *MGD1* in the inner envelope membrane, and the *DGD* acting at the outer
477 envelope membrane (Froelich *et al.*, 2001; Boudiere *et al.*, 2012; Petroutsos *et al.*, 2014;
478 Awai *et al.*, 2001), supporting that *HexII* lipids can transiently accumulate. In models where
479 such topological separation is not fully demonstrated, like *Chlamydomonas* chloroplasts, most
480 representations show *MGD* in the inner envelope separated from *DGD* in the outer envelope
481 membrane (Hurlock *et al.*, 2014; Li-Beisson *et al.*, 2015). In *Chlamydomonas*, other strategies
482 were also shown to ensure an accumulation of a MGDG pool, by the rapid desaturation of
483 MGDG fatty acids, generating molecular species, which cannot be used by *DGD* enzymes
484 (Yang *et al.*, 2015). Such ‘locking’ of specifically unsaturated MGDG species, more prone to
485 form *HexII* structures (Gounaris *et al.*, 1983) is also observed in *Arabidopsis* and other
486 photosynthetic eukaryotes (Dolch and Marechal, 2015). Thus, all chloroplasts present in cells
487 of the immense biodiversity of photosynthetic Eukaryota conserved Cyanobacteria lipids,
488 without the corresponding Cyanobacteria genes, and the new biosynthesis pathway retained
489 initial important features, even improved, like mechanisms ensuring that *HexII* MGDG can
490 accumulate.

491 The molecular characterization of plant chloroplast *MGD1* is remarkably coherent with the
492 hypothesis elaborated here. In biomimetic membranes, it was shown that *Arabidopsis* *MGD1*
493 had unique biophysical properties. *MGD1* is soluble and its membrane binding is promoted

494 by the presence of its product, MGDG (Sarkis *et al.*, 2014) supporting the existence of a
495 positive-feedback loop leading to a local over-accumulation of *HexII* lipids. MGD1 binding is
496 inhibited by DGDG, reinforcing this initial segregation of MGDG from DGDG detailed above
497 (Sarkis *et al.*, 2014). The activity of MGD1 requires the presence of anionic lipids, including
498 PtdGro and phosphatidic acid (Makshakova *et al.*, 2020; Dubots *et al.*, 2010; Dubots *et al.*,
499 2012), reminiscent of the activation Cyanobacteria MgdA enzyme by another anionic lipid,
500 SQDG (Selao *et al.*, 2014). This stresses the likely role of anionic lipids as triggers for
501 thylakoid biogenesis. When lowering MGD1 activity with a specific inhibitor, the proportion
502 of *HexII* MGDG decreases and some membrane invagination appear at the inner envelope
503 membrane (Botte *et al.*, 2011a), not indicating a vesicular-based formation of thylakoids, but
504 rather an excess of *Lm* forming lipids. Similar results were obtained in a null *MGD1* mutant of
505 *Arabidopsis*, germinating as small albinos only in the presence of sucrose, with seedlings
506 containing traces of galactolipids (Kobayashi *et al.*, 2007). Invaginations of the inner
507 envelope, which were not seen in mature WT chloroplasts, were also observed in this mutant,
508 simply due to an excess of *Lm* lipids over *HexII* ones (Kobayashi *et al.*, 2007). Although this
509 phenomenon was initially suggested as an evidence for formation of thylakoids from the
510 budding of inner envelope membrane, it fits with the non-vesicular model developed here,
511 reflecting an uncontrolled excess of *Lm* lipids in this membrane. Consistently, the growth of
512 the *MGD1* mutant in low phosphate conditions, activating the expression of the MGDG
513 synthase isoforms *MGD2* and *MGD3*, allowed a synthesis of *HexII* lipids in chloroplasts and
514 the formation of thylakoid structures (Kobayashi *et al.*, 2013). Nevertheless, the level of
515 MGDG remained low under these conditions, and photosynthetic activity was still abolished,
516 (Kobayashi *et al.*, 2013), indicating that the production of the right amount of MGDG at the
517 right place, by MGD1 located in the inner envelope membrane, could not be reached by the
518 action of MGD2 and MGD3 located at the outer envelope membrane.

519 A very recent work has shown that MGD enzymes could also play roles outside of the
520 chloroplast, in the cytosol. During the development of *Arabidopsis* pollen tube, it was thus
521 shown that MGD2 accumulated in the cytosol, following the expression of mRNAs controlled
522 by a specific RNA-binding protein (Billey *et al.*, 2021). This raises questions, since pollen
523 tubes do not contain chloroplasts. Nevertheless pollen tubes are known to accumulate
524 galactolipids (Botte *et al.*, 2011a; Nakamura *et al.*, 2009). In green tissues, *Arabidopsis*
525 MGD2 had been localized at the outer envelope membrane of the chloroplast, but some
526 cytosolic localization had also been observed based on the imaging of proteins fused with a
527 fluorescent reporter (Awai *et al.*, 2001). It is therefore plausible that in addition to its role in
528 chloroplast architecture, the soluble eukaryotic MGD enzymes may have introduced a
529 powerful system for integrating lipid metabolism from different compartments. One
530 possibility is that MGD2 might be able to bind its diacylglycerol substrate from one cytosolic
531 membrane and cargo it to another one, including the chloroplast where MGDG synthesis
532 should occur or possibly other cell compartment.

533 Altogether, the chloroplast MGD biosynthesis system performs much better than the primitive
534 MgdA/MgdE system of the *Gloeomargarita*-type cyanobacterium integrated following
535 primary endosymbiosis. It may be one of the reasons for the substitution of the
536 MgdA/MgdE/DgdA pathway by a MGD/DGD pathway early in the radiation of
537 Archaeplastida. An *HexII* → *Lm* phase transition is therefore the most likely scenario for the
538 non-vesicular biogenesis of thylakoids in chloroplasts as well (Bastien *et al.*, 2016). Protein
539 actors, such as VIPP1, have become more and more important in the orchestration of
540 thylakoid biogenetic processes, possibly guiding anionic lipids, including chloroplastic lipids
541 such as PtdGro, but also extraplastidial lipids such as phosphoinositides (Gupta *et al.*, 2021).

542 The increase in size of chloroplasts compared to Cyanobacteria, the development of larger
543 photosynthetic surfaces per cell, some structural innovations like the appearance of pyrenoids
544 or grana, the bioenergetic coupling of chloroplast within eukaryotic metabolism, etc, led to a
545 supplementary multiplier effect, likely determinant for the ‘rise of Algae’ during the
546 Neoproterozoic period, and the oxygenation of oceans known as the NOE.

547 **6 Concluding remarks**

548 The origin of internal membrane compartments is one of the most fascinating and difficult
549 questions in the evolution of cells. Textbooks highlight that one of the differences between the
550 three Domains of Life, Archae and Bacteria on the one hand, and Eukaryota on the other
551 hand, lies in the level of subcellular compartmentalization, absent or poor in the former,
552 prolific, sophisticated and dynamic in the latter. Such statement suggests that cell
553 compartmentalization should be accomplished the way it is described in a model Eukaryota,
554 *i.e.* either by vesicles budding from one parent membrane merging to form a novel
555 compartment, and/or by various membrane protrusions, fusion mechanisms, etc. The
556 biophysical rearrangements of membrane lipids during a fusion process were shown to have a
557 positive enthalpy and require an external source of energy, usually provided by ATP or GTP.
558 Such reorganizations of membrane architecture are not spontaneous and involve dedicated
559 protein machineries.

560 The formation of thylakoids in Cyanobacteria resists vesicular-based scenarios, firstly because
561 of the lack of any ultrastructural observation of vesicles supposed to protrude from the plasma
562 membrane toward the inside of the cell, but also because primitive thylakoids are concentric,
563 and we do not see where thylakoid biogenesis could be initiated. Here, we reviewed studies
564 converging into a simple hypothesis based on the stepwise production of *HexII* lipids, at the
565 inner periphery of the cytosolic membrane of an early cyanobacterium, turned within
566 nanoseconds and without any external source of energy into multilayered pro-thylakoids.
567 Comparison of lipid biosynthetic pathways suggests that most ancient Cyanobacteria could
568 not achieve thylakoid biogenesis due to the lack of anionic *Lm* lipids, only represented by a
569 minor phospholipid with a proportion controlled by phosphorus level in the environment. The
570 acquisition of the biosynthesis pathway producing a sulfolipid seemed critical for a regular
571 provision of sufficient amounts of anionic lipids, allowing the *HexII* → *Lm* phase transition to
572 occur thus forming parietal thylakoids. We designed this model before the very recent
573 description of the spatio-temporal biogenesis process of thylakoid membranes in the rod-
574 shaped cyanobacterium *Synechococcus elongatus* PCC 7942 (Huokko *et al.*, 2021). In this
575 cyanobacterium, the plasma membrane and concentric thylakoid layers have no physical
576 connections and newly synthesized thylakoid membrane fragments emerge between the
577 plasma membrane and pre-existing thylakoids (Huokko *et al.*, 2021). This is strikingly
578 reminiscent of the model described in Figs. 2A and 4 and illustrates the power of the *HexII-to-*
579 *Lm* phase transition not only at the origin of early thylakoids, but also in biogenetic processes
580 observed today. With this non-vesicular lipid-phase transition, a framework is therefore also
581 available to reexamine the role of companion proteins, such as Vipp1, which characterization
582 in a hypothetical vesicular-based biogenetic process remains unsatisfying in both Cyanobacteria
583 and chloroplasts. It is time to address these questions by considering lipids and proteins
584 together, with additional challenging issues, such as the integration of membrane proteins and
585 cofactors in the course of thylakoid biogenesis. Eventually, first-order phase transitions are
586 not restricted to changes in lipid phases. They are also involved in RNA and protein structural
587 changes between liquid phases (Hardenberg *et al.*, 2020; Guo *et al.*, 2021; Rhine *et al.*, 2020),
588 which might provide clues on extremely rapid, nearly instant processes, which cannot be
589 comprehended yet with more classical biochemical, structural or cell biology approaches.

590 Taking into consideration all these phase transitions might improve our understanding of
591 other steps in cell evolution.

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599 NG and EM contributed to the development of the hypothesis developed in this paper. NG
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