The Trickster Microbes Shaking Up the Tree of Life

Mysterious groups of archaea — named after Loki and other Norse myths — are stirring debate about the origin of complex creatures, including humans.

Every mythology needs a good trickster, and there are few better than the Norse and Loki. He stirs trouble and insults other gods. He is elusive anarchic and ambiguous. He is, in other words, the perfect namesake for a group of microbes — the Lokiarchaeota — that is rewriting a fundamental story about life's early roots.

These unruly microbes belong to a category of single-celled organisms called archaea, which resemble bacteria under a microscope but are as distinct from them in some respects as humans are. The Lokis, as they are sometimes known, were discovered by sequencing DNA from sea-floor much collected near Greenland. Together with some related microbes, they are prodding biologists to reconsider one of the greatest events int eh history of life on Earth — the appearance of the eukaryotes, the group of organisms that includes all plants, animals, fungi and more.

The discovery of archaea in the late 1970s led scientists to propose that the tree of life diverged long ago into three main trunks, or 'domains'. One trunk gave rise to modern bacteria; one to archaea. And the third produced eukaryotes. But debates soon erupted over the structure of these trunks. A leading 'three-domain' model held that archaea and eukaryotes diverged from a common ancestor. But a two-domain scenario suggested that eukaryotes diverged directly from a subgroup of archaea.

## 搖晃生命之樹的騙子微生物

以洛基和其他北歐神話命名的神秘古菌群正在 引發關於包括人類在內的複雜生物起源的爭 論。

每個神話都需要一個好的騙子,沒有比北歐和 洛基更好的了。他惹事生非,侮辱其他神明。 他是難以捉摸的無政府主義和模棱兩可的。換 句話說,他是一群微生物的完美同名——洛基 古菌群——正在改寫一個關於生命早期根源的 基本故事。

這些不守規矩的微生物屬於一種叫做古細菌的單細胞生物,它們在顯微鏡下類似於細菌,但在某些方面與人類不同。 Lokis 有時被稱為 Lokis,是通過對從格陵蘭島附近大量收集的海底中的 DNA 進行測序而發現的。連同一些相關的微生物,它們正在促使生物學家重新考慮地球上生命史上最偉大的事件之一——真核生物的出現,真核生物是包括所有植物、動物、真菌等在內的生物群。

1970 年代後期古細菌的發現使科學家們提出生命之樹很久以前就分化為三個主要的樹乾或"域"。一根樹幹產生了現代細菌;一到古細菌。第三個產生了真核生物。但很快就這些樹幹的結構引發了爭論。一個領先的"三域"模型認為古生菌和真核生物與共同祖先不同。但是一個雙域場景表明真核生物直接從古細菌的一個亞群中分化出來。

The arguments, although heated at times, eventually stagnated, says microbiologist Phil Hugenholtz at the University of Queensland in Brisbane, Australia. Then the Lokis and their relatives blew in like "a breath of fresh air", he says, and revived the case for a two-domain tree.

These newly discovered archaea have genes that are considered hallmarks of eukaryotes. And deep analysis of the organisms' DNA suggests that modern eukaryotes belong to the same archaeal group. If that's the case, essentially all complex life — everything from green algae to blue whales — originally came from archaea.

But many scientists remain unconvinced. Evolutionary tree building is messy, contentious work. And no one has yet published evidence to show that these organisms can be grown in the lab, which makes them difficult to study. The debate is still rancorous. Stalwarts on both sides are "very hostile to each other, and 100% believe there's nothing correct in the other camp", Hugenholtz says. Some decline to voice an opinion, for fear of offending senior colleagues.

What's at stake is a deeper understanding of the biological leap that produced eukaryotes: "The biggest thing that happened since the origin of life," according to evolutionary biologist Patrick Keeling at the University of British Columbia in Vancouver, Canada. Where they came from "is one of the most fundamental questions in understanding the nature of biological complexity", he says. To answer that question, "we need to resolve who's related to who".

澳大利亞布里斯班昆士蘭大學的微生物學家 Phil Hugenholtz說,這些爭論雖然有時很激烈, 但最終還是停滯不前。他說,然後 Lokis 和他 們的親戚像"呼吸新鮮空氣"一樣吹進來,並 恢復了兩域樹的案例。

這些新發現的古細菌具有被認為是真核生物標 誌的基因。對生物體 DNA 的深入分析表明,現 代真核生物屬於同一古菌群。如果是這樣的 話,基本上所有復雜的生命——從綠藻到藍鯨 的一切——最初都來自古細菌。

但許多科學家仍然不相信。進化樹構建是一項混亂、有爭議的工作。並且還沒有人發表證據表明這些生物可以在實驗室中生長,這使得它們難以研究。辯論仍然充滿敵意。 Hugenholtz說,雙方的堅定者"彼此非常敵對,並且 100%相信對方陣營沒有任何正確之處"。有些人拒絕發表意見,因為害怕冒犯資深同事。

加拿大溫哥華不列顛哥倫比亞大學的進化生物 學家帕特里克·基林 (Patrick Keeling) 表示,關鍵 在於對產生真核生物的生物飛躍有更深入的了 解:"自生命起源以來發生的最大的事情"。 他說,它們來自哪裡"是理解生物複雜性本質 的最基本問題之一"。要回答這個問題,"我 們需要解決誰與誰有關"。 For scientists half a century ago, life on Earth was split between two categories: eukaryotes, living things with cells that contain membrane- wrapped internal structures, such as a nucleus; and prokaryotes, single-celled organisms that generally lack internal membranes. Bacteria were the only prokaryotes that biologists knew about. Then, in 1977, evolutionary biologist Carl Woese and his colleagues described archaea as a third, distinct form of life — one that reached back billions of years 2. Life, Woese said, should be divided into three bins rather than two.

半個世紀前,對於科學家來說,地球上的生命分為兩類:真核生物,其細胞包含膜包裹的內部結構,如細胞核;和原核生物,通常缺乏內膜的單細胞生物。細菌是生物學家所知道的唯一原核生物。然後,在 1977 年,進化生物學家卡爾·沃斯 (Carl Woese) 和他的同事將古細菌描述為第三種獨特的生命形式——一種可以追溯到數十億年前。 Woese 說,生活應該被分成三個垃圾箱而不是兩個垃圾箱。

He was not without his detractors. In the 1980s, evolutionary biologist James Lake at the University of California, Los Angeles, proposed that eukaryotes are sisters to archaea that he called eocytes, which means dawn cells3,4. The idea evolved into the two-domain scenario.

他並非沒有批評者。在 1980 年代,加利福尼亞大學洛杉磯分校的進化生物學家 James Lake 提出真核生物是古細菌的姐妹,他稱之為卵細胞,即黎明細胞 3,4。這個想法演變成雙域場景。

Lake and Woese fought bitterly over their competing models, culminating in a legendary shouting match in the mid-1980s. After- wards, Woese "didn't want to meet with Jim Lake", says microbiologist Patrick Forterre at the Pasteur Institute in Paris. Lake does not dispute the acrimony. "That was really quite a debate, and there was an enormous amount of politics," he says. Woese died in 2012.

Lake 和 Woese 為他們的競爭模型進行了激烈的鬥爭,最終在 1980 年代中期進行了一場傳奇的大喊大叫。巴黎巴斯德研究所的微生物學家帕特里克·福泰爾 (Patrick Forterre) 說,之後,沃斯 "不想與吉姆·萊克見面"。萊克對尖刻沒有異議。 "那確實是一場激烈的辯論,涉及大量的政治,"他說。沃斯於 2012 年去世。

Today, the argument over where eukaryotes came from has matured. Many on both sides agree that the origin of eukaryotes probably involved a step known as endosymbiosis. This theory, championed by the late biologist Lynn Margulis, holds that a simple host cell living eons ago somehow swallowed a bacterium, and the two struck up a mutually beneficial relationship. These captive bacteria eventually evolved into mitochondria — the cellular substructures that produce energy — and the hybrid cells became what are now known as eukaryotes.

今天,關於真核生物來自何處的爭論已經成熟。雙方的許多人都同意,真核生物的起源可能涉及一個稱為內共生的步驟。已故生物學家林恩·馬古利斯 (Lynn Margulis) 支持的這一理論認為,生活在億萬年前的簡單宿主細胞以某種方式吞下了細菌,兩人建立了互惠互利的關係。這些圈養細菌最終進化成線粒體——產生能量的細胞亞結構——雜交細胞變成了現在被稱為真核生物的細胞。

The nature of the engulfing cell is where the two camps diverge. As the three-domain adherents tell it, the engulfer was an ancestral microbe, now extinct. According to Forterre, it was a "protoeukaryote" — "neither a modern archaeon nor a modern eukaryote". In this model, there were several major splits in early evolution. The first happened billions of years ago, when primeval organisms gave rise to both bacteria and an extinct group of microbes. This latter group diverged into archaea and the group that became eukaryotes.

In the two-domain world, however, a primeval organism gave rise to bacteria and archaea. And the organism that eventually swallowed the fateful bacterium was an archaeon. That would make all eukaryotes a sort of overachieving branch of the archaea — or, as some scientists call it, a 'secondary domain' (see 'Domains in debate').

### **SCRAMBLED MESSAGES**

Without a wayback machine for microbes, sorting through these hypotheses is exceedingly difficult. The fossil record for the earliest eukaryotes is sparse, and examples can be inscrutable. Scientists must rely instead on the records that are written in the genomes of modern organisms, which themselves have been scrambled by the passage of time. "We're trying to resolve something that happened probably a couple billion years ago, using modern sequence data," says computational evolutionary biologist Tom Williams at the University of Bristol, UK. It is no easy task.

吞噬細胞的本質是兩個陣營的分歧所在。正如三域追隨者所說,吞噬者是一種祖先微生物,現已滅絕。根據 Forterre 的說法,它是一種"原始真核生物"——"既不是現代古細菌,也不是現代真核生物"。在這個模型中,早期進化中有幾個主要的分裂。第一次發生在數十億年前,當時原始生物產生了細菌和已滅絕的微生物群。後一組分化為古細菌和成為真核生物的組。

然而,在雙域世界中,原始生物產生了細菌和 古細菌。最終吞下這種致命細菌的生物體是古 細菌。這將使所有真核生物成為古細菌的一種 卓越的分支——或者,正如一些科學家所說, 一個"二級領域"(參見"辯論中的領域")。

## 加擾消息

如果沒有微生物的回歸機器,對這些假設進行 分類是非常困難的。最早的真核生物的化石記 錄很少,而且例子可能難以理解。相反,科學 家必須依賴現代生物基因組中的記錄,這些記 錄本身已經隨著時間的推移而被打亂。英國布 里斯托爾大學的計算進化生物學家湯姆威廉姆 斯說:"我們正試圖使用現代序列數據來解決 可能發生在幾十億年前的事情。"這不是一件 容易的事。 Current gene-sequencing technologies have pushed the debate forward. Until recently, scientists who sought to identify the bacteria or archaea in a particular habitat had to grow the organisms in the lab. Now, researchers can assess microbial diversity in a sample of water or soil by fishing out the DNA and analyzing it using mathematical tools, a technique called metagenomics. In 2002, scientists knew of two categories (or phyla) of archaea. Today, thanks to metagenomics, the number of groupings has exploded.

當前的基因測序技術推動了這場爭論。直到最近,試圖在特定棲息地識別細菌或古細菌的科學家還必須在實驗室中培養這些生物。現在,研究人員可以通過提取 DNA 並使用數學工具對其進行分析來評估水或土壤樣本中的微生物多樣性,這種技術稱為元基因組學。 2002 年,科學家們知道古細菌有兩類(或門)。今天,由於宏基因組學,分組的數量呈爆炸式增長。

Evolutionary scientists have been quick to take advantage of the growing bounty. Using the latest powerful modelling techniques, they have created a forest of evolutionary trees detailing the familial relationships among archaea. The results, in many cases, place eukaryotes within the archaeal ranks.

進化科學家很快就利用了不斷增長的賞金。使 用最新的強大建模技術,他們創建了一個進化 樹森林,詳細描述了古細菌之間的家族關係。 結果,在許多

"The weight of evidence, in our view, really did shift toward the two-domain, eocyte tree," says Williams. But for some, the debate was still short on data. 在這種情況下,將真核生物置於古菌群中。

Then, in 2015, a group led by Thijs Ettema, an evolutionary microbiologist at Uppsala University in Sweden at the time, published DNA sequences for Lokiarchaeota, found in sediments dredged up five years earlier1. Within two years, Ettema's team and other researchers had announced the discov- ery of three new archaeal phyla related to the Lokis5,6. The entire grouping of new phyla was named Asgard after the realm of the Norse gods.

"在我們看來,證據的權重確實轉向了雙域,即卵細胞樹,"威廉姆斯說。但對一些人來說,辯論仍然缺乏數據。

The Asgard archaea are tiny in size, but they have proved to be mighty. They have reinvigorated debate about the true number of life's domains. And they are providing tantalizing hints about the nature of the cells that gave rise to the first eukaryotes — at least to two-domain proponents.

然後,在 2015 年,當時瑞典烏普薩拉大學的 進化微生物學家 Thijs Ettema 領導的一個小組 發表了 Lokiarchaeota 的 DNA 序列,該序列是 在五年前挖掘的沉積物中發現的。在兩年內, Ettema 的團隊和其他研究人員宣布發現了三個 與 Lokis 相關的新古菌門 5,6。整個新門群以北 歐諸神的領域命名為 Asgard。

Asgard 古菌體積很小,但已被證明是強大的。 他們重新激發了關於生命領域真實數量的爭 論。他們提供了關於產生第一個真核生物的細 胞性質的誘人暗示——至少對雙域支持者來說 是這樣。 Like their namesake, Lokiarchaeota and their kin evade easy description. They are unquestionably archaea, but their genomes include a smorgasbord of genes that are similar to some found in eukaryotes. Loki DNA, for example, contains genetic instructions for actins, proteins that form a skeleton-like framework in eukaryotic cells. The genes seemed so out of place that the researcher who spotted them initially worried that contamination was to blame. "I said, 'Hmm, how is that possible? Can it be that this is really an archaeal genome?'" recalls evolutionary microbiologist Anja Spang at the Royal Netherlands Institute for Sea Research in Texel.

就像他們的同名一樣,Lokiarchaeota 和他們的 親屬避免了簡單的描述。它們無疑是古細菌, 但它們的基因組包含大量與真核生物中發現的 基因相似的基因。例如,Loki DNA 包含肌動蛋 白的遺傳指令,肌動蛋白是在真核細胞中形成 骨架樣框架的蛋白質。這些基因看起來很不合 適,以至於發現它們的研究人員最初擔心污染 是罪魁禍首。 "我說,'嗯,這怎麼可能?難 道這真的是一個古細菌基因組嗎?'"特塞爾 荷蘭皇家海洋研究所的進化微生物學家 Anja Spang 回憶道。

Evolutionary modelling reinforced the tight linkage between the Asgard archaea and eukaryotes. The trees built by Ettema's team place all eukaryotes in the Asgard grouping. 進化模型加強了阿斯加德古細菌和真核生物之間的緊密聯繫。 Ettema 團隊建造的樹木將所有真核生物都歸入了 Asgard 組。

Now, many researchers are using data from these archaea to formulate a better picture of the eukaryotic precursor. It might already have had some features typical of eukaryotes before it took in the mitochondrial predecessor. "It probably had some very primitive membrane-biology processes going on," Ettema says.

現在,許多研究人員正在使用來自這些古細菌 的數據來更好地了解真核前體。在吸收線粒體 前身之前,它可能已經具有一些典型的真核生 物特徵。"它可能有一些非常原始的膜生物學 過程,"埃特瑪說。

According to an analysis published this year7, the ancestor of the Asgard archaea probably fed on carbon-based molecules, such as fatty acids and butane. This diet would have generated byproducts that could nourish partner bacteria. Such foodsharing agreements — common among microbes — could have evolved into a more intimate relation- ship. An archaeon might have snuggled up next to its bacterial partner to ease nutrient exchanges, leading eventually to the ultimate embrace.

根據今年發表的一項分析 7 ,阿斯加德古細菌的 祖先可能以脂肪酸和丁烷等碳基分子為食。這 種飲食會產生可以滋養伴侶細菌的副產品。這 種在微生物中很常見的食物共享協議本可以演 變成一種更親密的關係。古細菌可能會依偎在 它的細菌夥伴旁邊以促進營養交換,最終導致 最終的擁抱。 Such scenarios still provoke doubts, however. Chief among the unconvinced is Forterre. After combing through the Asgard paper, he and his colleagues published an exhaustive rebuttal8 of the work.

#### MISLEADING MARKERS?

In a charge that infuriates Ettema, Forterre and his group suggested that some eukaryotic-like sequences found in the Lokis were a result of contamination. A Loki protein called elongation factor 2, for example, was "likely contaminated by eukaryotic sequences", Forterre's team wrote in its critique. Forterre now says he's uncertain about this point.

But he and his colleagues still stand by their criticism of the Asgard evolutionary trees. Even those who are master tree-builders concede that it is tricky to untangle how organisms living two billion years ago were related to each other. Biologists reconstruct these relationships by modelling how a particular 'marker' — usually a protein or a gene — has changed over time in the organisms of interest.

Forterre's group says that Ettema's team unintentionally chose misleading markers to build its tree. Forterre and his group did their own tree analysis using two large proteins as markers because, by virtue of their size, big proteins are more likely to record the desired information. The result was a three-domain tree.

Ettema says that the two markers used by Forterre are insufficient for tracking events that took place so long ago — a criticism echoed by other scientists. And when Ettema's team tried to replicate Forterre's finding, even with the two proteins Forterre used, the result was still a two-domain tree, he says. Ettema hasn't published the results.

然而,這種情況仍然引起懷疑。不服氣的人中最主要的是 Forterre。在梳理了 Asgard 的論文後,他和他的同事們發表了對這項工作的詳盡反駁 8。

# 誤導性標記?

在一項激怒 Ettema 的指控中,Forterre 和他的 團隊提出,在 Lokis 中發現的一些真核樣序列 是污染的結果。例如,一種名為延伸因子 2 的 Loki 蛋白 "可能被真核序列污染",Forterre 的團隊在其批評中寫道。 Forterre 現在說他不確定這一點。

但他和他的同事們仍然支持他們對阿斯加德進 化樹的批評。即使是那些造樹大師也承認,要 弄清楚 20 億年前生活的生物之間是如何相互 關聯的,是一件很棘手的事情。生物學家通過 對特定"標記"(通常是蛋白質或基因)在感 興趣的生物體中如何隨時間變化進行建模來重 建這些關係。

Forterre 的團隊表示,Ettema 的團隊無意中選擇了誤導性標記來構建其樹。 Forterre 和他的團隊使用兩種大蛋白質作為標記進行了他們自己的樹分析,因為憑藉它們的大小,大蛋白質更有可能記錄所需的信息。結果是一個三域樹。

Ettema 說 Forterre 使用的兩個標記不足以追踪 很久以前發生的事件——其他科學家也提出了 同樣的批評。他說,當 Ettema 的團隊試圖複製 Forterre 的發現時,即使 Forterre 使用了兩種 蛋白質,結果仍然是一個雙域樹。 Ettema 尚未 公佈結果。 Ettema chalks up some of the differences to disciplinary background. "Patrick Forterre is a brilliant scientist in his field," he says, but with the Lokis, "he overstepped his expertise a little bit." Forterre says that he has some skills in phylogenetics and that his co-authors have more.

Nevertheless, not all two-domain supporters dismiss Forterre's trees. Williams, for example, is building a tree using the latest analytical tools and folding in new varieties of archaea. He hopes that this effort will help him to understand some of Forterre's results.

The three-domain tree also has a high-profile ally in microbiologist Norm Pace of the University of Colorado, Boulder, who pioneered some of the methods that are essential for placing microbes on the tree of life. Pace says that over vast spans of time, some markers will undergo change that is difficult to track. Ettema and others use statistical methods to account for such stealthy change, but Pace dismisses them. "Ettema and colleagues claim they can calculate unseen change. I claim that's a stupid assumption," Pace says. But the methods are widely used. And Ettema counters that scientists can use various tests to determine whether such changes are affecting their data.

Other scientists are reserving judgement: "Trees change," is a com- mon refrain. Keeling says he's "totally on the fence". And Hugenholtz agrees that "the jury's out", although both scientists say they think that the evidence for two domains is growing.

Ettema 將一些差異歸結為學科背景。 "Patrick Forterre 在他的領域是一位傑出的科學家,"他說,但對於 Lokis,"他有點超出了他的專業知識。" Forterre 說他在系統發育學方面有一些技能,而他的合著者則擁有更多技能。

儘管如此,並非所有的雙域支持者都拒絕 Forterre 的樹。例如,威廉姆斯正在使用最新的 分析工具建造一棵樹,並折疊新的古細菌品 種。他希望這項工作能幫助他了解 Forterre 的 一些成果。

三域樹還有一位備受矚目的盟友,他是科羅拉多大學博爾德分校的微生物學家 Norm Pace,他開創了一些將微生物置於生命之樹上必不可少的方法。 Pace 表示,在很長一段時間內,一些標記會發生難以追踪的變化。 Ettema 和其他人使用統計方法來解釋這種隱秘的變化,但 Pace 駁回了他們。 "Ettema 和同事聲稱他們可以計算出看不見的變化。我聲稱這是一個愚蠢的假設,"佩斯說。但這些方法被廣泛使用。 Ettema 反駁說,科學家可以使用各種測試來確定此類變化是否影響了他們的數據。

其他科學家持保留意見:"樹木在變"是一種常見的說法。基林說他"完全在圍欄上"。 Hugenholtz 也同意"沒有定論",儘管兩位科學家都表示,他們認為關於兩個領域的證據正在增加。 As they wait for the rustling trees to settle, researchers are turning to other lines of evidence that might support a two-domain tree. Bacteria and eukaryotes have one set of lipids in their cell membranes, whereas archaeal membranes contain a different set. A mixture of the two was thought to be unstable. This 'lipid divide' has been a sore spot for the two-domain proponents, because it implies that if eukaryotes came from archaea, they would have had to switch from using archaeal lipids to producing bacterial versions.

當他們等待沙沙作響的樹木安定下來時,研究 人員正在轉向可能支持雙域樹的其他證據。細 菌和真核生物的細胞膜中含有一組脂質,而古 細菌細胞膜中含有一組不同的脂質。兩者的混 合物被認為是不穩定的。這種"脂質鴻溝"一 直是雙域支持者的痛處,因為這意味著如果真 核生物來自古細菌,他們將不得不從使用古細 菌脂質轉變為生產細菌形式。

But the lipid divide no longer looms as large. Last year, Dutch researchers succeeded in engineering bacteria with cell membranes that contain both archaeal and bacterial lipids9. Scientists have also found bacteria in the Black Sea that have genes for making both types of lipid10. Microbes could have had such mixed membranes during the transition from archaea to eukaryotes, says microbiologist Laura Villanueva of the Royal Netherlands Institute for Sea Research, who is a member of the team that studied the Black Sea bacteria.

但脂質鴻溝不再那麼大。去年,荷蘭研究人員成功地用含有古菌和細菌脂質的細胞膜設計細菌。科學家還在黑海發現了具有製造兩種脂質的基因的細菌 10。荷蘭皇家海洋研究所的微生物學家勞拉·維拉紐瓦 (Laura Villanueva) 是研究黑海細菌的團隊成員,她說,在從古細菌到真核生物的過渡過程中,微生物可能具有這種混合膜。

But analyses of the Asgard archaea, including the Lokis, remain limited. "What people are really waiting for is the isolation of a member of these lineages," says evolutionary microbiologist Simonetta Gribaldo at the Pasteur Institute. "We need to grab them, we need to culture them."

但是對包括 Lokis 在内的 Asgard 古菌的分析仍然有限。巴斯德研究所的進化微生物學家西蒙內塔·格里巴爾多(Simonetta Gribaldo)說:"人們真正在等待的是這些譜系成員的分離。" "我們需要抓住他們,我們需要培養他們。"

Some have sluggish metabolisms and are slow to multiply — "exactly what you do not want if you're trying to grow an organism", Ettema says. Only a few other scientists admit to even trying.

Microbiologist Christa Schleper at the University of Vienna, who is attempting to culture the Asgards, calls it "the craziest project I've ever applied for money for".

有些新陳代謝緩慢,繁殖緩慢——"如果你想培育有機體,這正是你不想要的",埃特瑪說。只有少數其他科學家承認嘗試過。試圖培養阿斯加德的維也納大學微生物學家 Christa Schleper 稱其為"我申請過的最瘋狂的項目"。

Elusive though the microbes might be, one team has captured what it says are the first images of Asgard organisms. Pictures of one type show rounded cells, each containing a compacted bundle of DNA that resembles that defining feature of all eukaryotes, a nucleus. The images are "intriguing" but inconclusive, says microbiologist Rohit Ghai at the Biology Centre of the Czech Academy of Sciences in České Budějovice, who is a co-author of the preprint containing the images.

The overall picture is still unclear. In Norse legends, Loki often sows mayhem — and then sets everything right again. As the Lokiarchaeota and their relatives emerge from the shadows, two-domain supporters would like them to settle the long-standing debate over the origin of complex life. But that could take a while. "When we discovered the Asgard archaea, we thought that would convince everybody," says Spang with a laugh. "That wasn't the case."

儘管微生物可能難以捉摸,但一個團隊已經捕捉到了據稱是 Asgard 生物的第一張圖像。 一種類型的圖片顯示圓形細胞,每個細胞都包含一束緊密的 DNA,類似於所有真核生物的特徵,即細胞核。 捷克科學院生物中心的微生物學家 Rohit Ghai 說,這些圖像"很有趣",但還沒有定論,他是包含這些圖像的預印本的合著者。

整體情況還不清楚。 在北歐傳說中,洛基經常製造混亂——然後一切又恢復原樣。 隨著 Lokiarchaeota 及其親屬從陰影中出現,兩個領域的支持者希望他們能夠解決關於復雜生命起源的長期爭論。 但這可能需要一段時間。

"當我們發現 Asgard 古細菌時,我們認為這會讓所有人信服," Spang 笑著說。 "事實並非如此。"