and the emergence of human cultures. This can then aid efforts to determine the home of the speakers of an ancestral proto-language, when these people and their language dispersed and the different branches of the language family formed. However, the vagaries of history that have led to criss-crossing migrations, contact between different languages and cultures and other sociological factors have often meant that it is difficult to identify the family tree that correctly represents the history of a language family. Competing interpretations of the same data can lead to the generation of different trees and to different models of the origin and dispersal of a particular language. And it has previously been difficult to evaluate all of the possible trees that could be made on the basis of the available data.

Modern computers now make it possible to handle large amounts of data and calculations rapidly. Software developed for biosciences research that applies a particular model of probability testing known as Bayesian phylogenetic modelling can also be used in linguistics. This software can test the many possible language trees that could be made from a data set, and thereby determine the most likely tree and the most probable time frame for language diversification.

Zhang and colleagues focused on the Sino-Tibetan family, which encompasses hundreds of languages, including Chinese, Tibetan, Burmese and many other, less widely spoken, languages. The authors used data on cognate terms that have been assembled over the past 30 years in a project called the Sino-Tibetan Etymological Dictionary and Thesaurus (see go.nature.com/2uombqo). This provided a solid basis of relevant data for their calculations, and set Zhang and colleagues' study apart from earlier work that applied similar computational techniques but used random word lists from word families that had not been evaluated for cognacy, affecting the reliability of those studies.

The authors used these language data together with information from other fields, such as anthropology, and ran millions of iterations of their computer program. They determined the most likely location of the homeland of the ancestors of the modern Sino-Tibetan-speaking peoples, and the most probable time frame for when this language family began to diverge into subgroups as some members of the group of early Sino-Tibetan speakers migrated away from where the language originated. The authors also determined the most probable language family tree and which type of branching structures had the highest probability of representing the relationships between the languages.

Zhang *et al.* compared the two competing views of where the earliest Sino-Tibetan speakers originated. Their results support the theory that the homeland of the Proto-Sino-Tibetan language was in the Yellow River basin region (Fig. 1) of present-day northern China, and that the dispersal and diversification of this language family began around 5,900 years ago. At that time, this region was associated with the Yangshao culture and the later Majiayao (a culture thought to have arisen after a westward migration of people from the Yangshao culture)[7]. These cultures were associated with pottery and silk production, and the communities kept domesticated animals and had large, fixed settlements.

The results indicate that there was a major initial split between the Sinitic languages and the Tibeto-Burman languages before each of these two groups split further into linguistic sub-branches. This contrasts with one current model[3] suggesting that these two branches did not form from a major initial bifurcation. That model proposes instead that many branches formed at the same time. It suggests that the Sinitic languages do not form a major branch that is split from all of the other languages, and that what are commonly referred to as the Tibeto-Burman languages do not group into a single branch[3].

Zhang and colleagues' work is important in many ways. The history of the Sino-Tibetan languages has not been studied for as long as has the history of the Indo-European languages. Thus, by comparison, there has been much less certainty about some of the key points that provide a foundation for this area of research, such as the origins of the language. The authors' work provides more certainty on such fundamental issues, freeing researchers to build on this and to explore the history of this language family more deeply. The work should also help to identify connections between these language studies and findings from other related fields, such as archaeology and history. ■

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ORIGINS OF LIFE

A possible prebiotic basis for metabolism

Early life forms established a network of reactions for converting carbon dioxide into organic compounds. A non-biological system of reactions that could have formed the network's core on ancient Earth has been reported. SEE LETTER P.104

ROBERT PASCAL

All biological molecules used by living organisms are themselves synthesized by living organisms. The development of routes for making organic matter was therefore an essential early step in the emergence of life on Earth. A complex network of reactions must have arisen to make organic molecules from carbon dioxide, or possibly from other inorganic sources of carbon such as carbon monoxide or cyanides, but the process involved remains largely unknown. On page 104, Muchowska *et al.*[1] demonstrate experimentally that a suitable complex reaction network can develop from just two simple organic constituents, namely, glyoxylate ($HCOCO_2^-$) and pyruvate ($CH_3COCO_2^-$), in the presence of ferrous iron (Fe^{2+}).

The identified network produces nine of the eleven main components of the tricarboxylic acid (TCA) cycle — the series of reactions by which present-day organisms metabolize organic matter to convert it into energy (Fig. 1), producing the nucleotide ATP as an energy carrier and CO_2 as a by-product. The TCA cycle can also work in reverse, in which case it is known as the reductive tricarboxylic acid (rTCA) cycle. The rTCA cycle could have been an early route by which CO_2 was converted (fixed) into the organic molecules that are used as the basic components of living organisms. Muchowska and colleagues' work suggests that the rTCA cycle, as well as other processes that are associated with the metabolism of carbon, could have emerged from a network of abiotic reactions that, at least partly, matched the pattern of the biological reaction network that is now catalysed by enzymes.

The authors also show that, in the presence

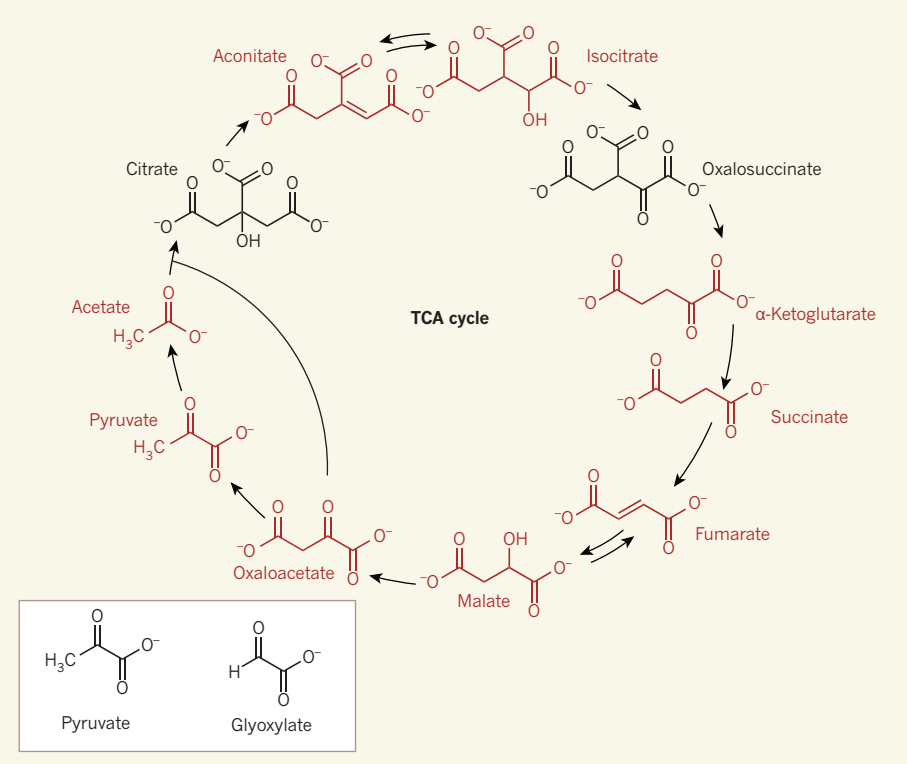

Figure 1 | The tricarboxylic acid (TCA) cycle. The TCA cycle is one of the core metabolic pathways in many present-day organisms. Muchowska *et al.*[1] report that nine (red) of the eleven intermediates in the TCA cycle are also formed in a complex network of reactions that is established when glyoxylate and pyruvate are combined in water with ferrous iron (Fe^{2+}). The authors propose that their network might have formed a non-biological framework for metabolic pathways when life emerged on early Earth. (Adapted from ref. 1.)

of hydroxylamine (NH_2OH) and metallic iron, their chemical network can be extended to include the formation of four kinds of amino acid, the building blocks of proteins. Both hydroxylamine and metallic iron could have been available on early Earth: hydroxylamine would probably have formed as a result of the rich, abiotic nitrogen chemistry that is known to have occurred early in the planet's existence[2], whereas metallic iron is abundant in certain meteorites that peppered our planet.

Muchowska *et al.* suggest that their pathway could have developed further to facilitate the subsequent emergence of functional polymers, including peptides and nucleic acids. This would require that abiotic processes that fix CO_2 fed the system with glyoxylate and pyruvate. The authors identify evidence from the scientific literature that supports the existence of such processes, but it is unclear whether these processes could have produced sufficient concentrations of glyoxylate and pyruvate to sustain emergent living organisms. This does not invalidate the authors' reaction network as a potential key player in the origins of life, however.

We are unlikely ever to know for certain whether present-day processes for metabolizing compounds that contain carbon are a purely biochemical innovation, or are instead derived from a prebiotic chemical network. This is because no remnant of the evolutionary processes involved could have persisted for billions of years. Nevertheless, Muchowska and co-workers' results strongly support the latter possibility. It seems realistic for a rudimentary biological system to have harnessed a pre-existing network by sharing intermediates, and then for it to have gradually become more efficient by evolving genetically encoded catalysts (such as enzymes that directly facilitate the necessary reactions).

The other possibility is that a full set of enzymes that catalyse the essential metabolic steps emerged from scratch. However, this seems highly improbable, because there would have been no selective evolutionary pressure for this to happen in the absence of a pre-existing, analogous system.

Other general themes have been debated by those working in this field. For example, most researchers reject the idea that life began as the result of a sharp transition in complexity from a mixture of organic compounds to a highly organized, self-reproducing entity that looked like a living cell[3,4]. Instead, life is thought to have originated as the result of gradual improvements to an evolving system that were introduced at separate times[5]. In this scenario, the distinction between life and non-life is fuzzy, rather than clear-cut[6].

Another model builds on the concept of systems chemistry. It suggests that primordial, chemical equivalents of metabolic systems and self-replicating systems could initially have coexisted, but then combined into more-complex systems, perhaps as the result of some kind of compartmentalization process, thereby giving rise to the essential features of life[7]. But it is unknown whether all three components — metabolism, self-replication and compartmentalization — needed to have coexisted before life emerged. Chemists can contribute to these debates by uncovering a wide range of abiotic processes that might feasibly have occurred on early Earth, as Muchowska and colleagues have done. The authors' reaction network could have integrated into the process of life's emergence after the appearance of functional polymers, or contributed to the metabolic component in the systems-chemistry model.

The mystery of the origins of life is not simply a question of how the molecular components of biological systems were formed. If that had been the case, then the puzzle would have been solved soon after 1953, when amino acids were identified as the product of an experiment in which electric sparks were fired into a mixture of simple molecules, to simulate the effects of lightning flashes on early Earth[8].

In fact, the most important aspect of life's emergence was the first implementation of a 'physical principle' for natural selection[9] — a process by which inheritable improvements can be selected from a population of variants. This, in turn, required molecules or molecular assemblies that can reproduce under certain kinetic constraints, and resulted in the development of a specific kind of stability (known as dynamic kinetic stability[10]) that is associated with the dynamics of reproduction. This stability has characterized the living state on Earth for billions of years. Nevertheless, life's requirement for self-replicating molecules does not mean that the contribution of other molecular subsystems (such as reaction networks) was unimportant, if only because such systems might have needed to reach certain concentrations so that self-replicating systems could emerge.

If research on the origins of life is to reach the next level[5], several approaches will be needed to provide insight into the process by which life emerged. Identifying abiotic pathways that could have contributed to the overall process is highly valuable, regardless of the stage in life's evolution at which they were incorporated. Combining systems-chemistry and evolutionary views might be the most productive way forward. ■ SEE ALSO BOOKS & ARTS P.36

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NUCLEAR PHYSICS

A doubly magic nucleus that has two faces

The neutron-rich nickel nucleus ^{78}Ni is difficult to excite and, once excited, has competing spherical and deformed shapes. These intriguing properties make ^{78}Ni a valuable testing ground for nuclear theory. SEE ARTICLE P.53

GAUTE HAGEN & THOMAS PAPENBROCK

Not all atomic nuclei are created equal. 'Doubly magic' nuclei have fully occupied shells of protons and neutrons, the subatomic particles known generically as nucleons. Such nuclei are therefore more strongly bound together and more difficult to excite than their neighbours on the Segrè chart — a 2D grid in which nuclei are arranged by their proton and neutron numbers. The simple structure of doubly magic nuclei makes them the cornerstone of our understanding of nuclear physics. This is because their neighbours can be described in terms of a few extra interacting nucleons, therefore turning a quantum many-body problem into a few-body problem. Only a handful of doubly magic nuclei are known. On page 53, Taniuchi *et al.*[1] identify the newest member of this elite club: the nickel nucleus ^{78}Ni, which consists of 28 protons and 50 neutrons.

Naturally occurring nickel — used in coins, rechargeable batteries and plumbing fixtures — typically has only 30 neutrons in its nucleus. By comparison, ^{78}Ni is extremely rich in neutrons, which makes it difficult to produce and study. This rare isotope of nickel was first observed[2] in 1995. Apart from its half-life, which was measured[3] in 2005 to be only about 0.1 seconds, little was known about its properties.

Taniuchi and colleagues made and investigated ^{78}Ni by knocking one and two protons out of beams of rare isotopes of copper (^{79}Cu) and zinc (^{80}Zn), respectively. These beams were produced at the Radioactive Isotope Beam Factory in Wako, Japan. Coinciding with the proton-knockout reactions, the authors observed γ-rays that were emitted when ^{78}Ni transitioned from various excited states to the ground state. Key challenges that Taniuchi *et al.* had to contend with included low rates of ^{78}Ni production from the rare-isotope beams and the need to measure a substantial number of associated γ-rays.

The authors detected a strong emission of γ-rays when ^{78}Ni transitioned from an excited state at an energy of 2.6 megaelectronvolts (MeV) to the ground state (Fig. 1). The relatively large energy of this excited state identified ^{78}Ni as a doubly magic nucleus. Taniuchi *et al.* suggest that this excited state is a 2^+ state of ^{78}Ni that is associated with a spherical nucleus — the '2' refers to the intrinsic angular momentum of the nucleus and the '+' indicates that the nucleus has a property known as even parity. This assignment is corroborated by theoretical calculations made by the authors, and by earlier predictions[4,5].

The identification of ^{78}Ni as a doubly magic nucleus provides us with a beachhead from which to explore neutron-rich nuclei in the vicinity of ^{78}Ni. Such exploration is valuable because the synthesis of heavy elements in the Universe proceeds — by means of a nuclear reaction called neutron capture — along pathways that include neutron-rich nuclei that are close to nickel on the Segrè chart. In the neighbourhood of ^{78}Ni, a radioactive process known as β-decay is dominant over neutron capture, which leads to enhanced natural abundances of nuclei that have about 80 nucleons. Taniuchi and colleagues' work will enable nuclear physicists to advance understanding of the neutron-rich nuclei that lie between ^{78}Ni and the next cornerstone on the Segrè chart: the tin nucleus ^{132}Sn, which was shown[6] to be doubly magic in 2010.

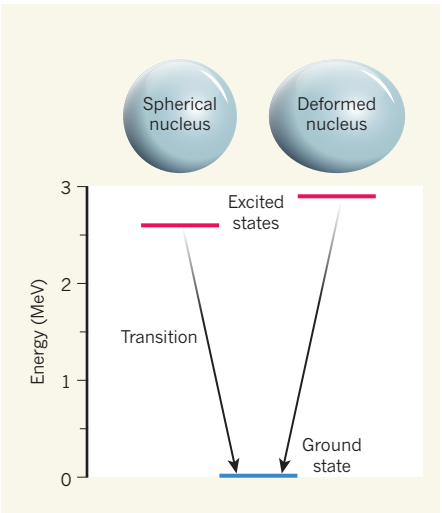

Figure 1 | Properties of the nickel nucleus ^{78}Ni. Taniuchi *et al.*[1] report transitions of ^{78}Ni between excited states and the ground state. An excited state at an energy of 2.6 megaelectronvolts (MeV) suggests that ^{78}Ni is a type of strongly bound nucleus called a 'doubly magic' nucleus. Furthermore, an excited state with an energy of about 2.9 MeV indicates that excited ^{78}Ni can exist with both spherical and deformed shapes.

Among the other transitions observed in their experiment, Taniuchi *et al.* tentatively identified a second 2^+ state at an energy of about 2.9 MeV that corresponds to a deformed nucleus (Fig. 1). This assignment, which is supported by the authors' theoretical calculations, indicates that excited ^{78}Ni has competing spherical and deformed shapes. The results raise further questions. Is there a deformed 0^+ excited state, as predicted by the nuclear-shell model? And why is the spherical 2^+ state seen in only the one-proton knockout reaction and the deformed 2^+ state seen in only the two-proton reaction?

A coexistence of spherical and deformed shapes is rare in general, but not that unusual in neutron-rich nuclei. It will be interesting to see how these structures change and evolve as a few nucleons are added or removed from ^{78}Ni. The competition of the spherical and deformed shapes in ^{78}Ni suggests that nuclei in this region of the Segrè chart — such as neutron-rich isotopes of copper or iron — will be deformed in their ground states. In this sense, ^{78}Ni is a stronghold against deformation in this region. Such a region is called an island of inversion[5,7] because the usual rules about the structure of nuclei, derived from the nuclear-shell model, do not apply.

Investigating and understanding this island of inversion is an exciting yet challenging prospect for nuclear theory and its associated experiments. Deformation sets in when protons and neutrons can occupy spherical shells that are extremely close in energy. In neutron-rich nuclei, the nucleons in the corresponding shells are weakly bound to the nucleus, or even unbound. As a result, accurate modelling is required, for instance, to discover the limits of the nuclear landscape — in other words, to determine the maximum number of neutrons that can be bound together by the strong nuclear force in the isotopes of a given chemical element[8].

For the purposes of theory, it is important to account for nuclear rotation — a collective motion of an entire nucleus. However,