Condensed-matter physics

Magnetic hopfion rings in new era for topology

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A curious topological structure known as a hopfion ring has been induced in a magnetic material. The first of its kind in 3D, the ring is a tantalizing prospect for several branches of computing development. See p.718

Information is stored on a typical hard disk drive by making the intrinsic angular momentum of the material's electrons — their 'spin' — point uniformly up or down. But complex whirlpool-like arrangements of spins called topological solitons are expected to be more stable at the nanoscale than are those involving parallel spins[1]. Topological solitons crop up in many condensed-matter systems — and they even appear in the motion of proteins and DNA. So far, however, only 2D or quasi-3D topological solitons been observed in real materials. On page 718, Zheng *et al.*[2] report the experimental realization of a complex 3D soliton, known as a hopfion ring, in a magnetic material. The authors' observation and control of this intriguing 'spin texture' could enable a new generation of high-density, energy-efficient computing and memory devices.

To appreciate the importance of complex magnetic spin textures, it's helpful to consider the history of the topological soliton. It was first proposed in 1962 by British physicist Tony Skyrme as the solution to his model for describing nuclear force in an atom[3]. The magnetic analogue of the topological soliton was discovered more than a decade ago[4,5], and affectionately dubbed the skyrmion in Skyrme's honour (Fig. 1a). Topological solitons also form possible solutions for a model of relativistic quantum field theory that includes mathematical terms analogous to those in Skyrme's theory[6]. These solitons behave like knots in the string-like structure of a skyrmion. They are known as hopfions, after the German mathematician Heinz Hopf, who was instrumental in formulating the mathematical theory for describing knot-like structures.

Just as the skyrmion is a magnetic form of the original topological soliton, there have been several proposals to determine whether a magnetic version of the hopfion exists (Fig. 1b). It was predicted to occur in magnetic materials in which neighbouring spins are subject to 'chiral' interactions (those with a specific symmetry known as handedness)[7] and also in chiral magnets characterized by competing interactions between spins[8]. A hopfion-like structure has also been observed in a synthetic magnet consisting of stacks of individual layers composed of iron, cobalt and platinum atoms, respectively[9]. But so far, no robust evidence of a hopfion in a real material has been forthcoming — until now.

Zheng *et al.* observed hopfions in a chiral magnet comprising iron (Fe) and germanium (Ge). Members of the same research group previously showed that strings of skyrmions form in this material[10], so the next step was to try to create hopfions from these skyrmion strings. In the present work, the authors used a carefully designed experimental protocol for reversing the magnetization of a FeGe disk containing one or more skyrmion strings.

> **"The spins of electrons can form whirlpool-like arrangements called topological solitons."**

The technique involved changing the direction of an external magnetic field, which was weak enough that the skyrmion strings remained intact during the switch, but still strong enough to change the magnetization of the material at the edge of the disk. When the field direction was switched back, this edge modulation persisted, and increasing the strength of the field resulted in the appearance of a hopfion ring around the existing skyrmion strings.

The authors are careful to point out that their hopfion rings cannot be classed as isolated hopfions, because they were always accompanied by skyrmion strings. Nonetheless, their direct observation of these rings is an excellent first step towards realization of isolated Hopfions in crystals. Zheng and colleagues' clever 'field-swap' protocol is a promising technique, but there might be other methods for generating and stabilizing these spin textures, as well as better choices of materials and interfaces. There are still open questions about how the hopfions respond to external stimuli, such as electric currents.

The idea that a hopfion ring could be coupled to skyrmion strings is, in itself, a rather intriguing phenomenon that requires further study. Indeed, the authors' direct observation of hopfions in a crystal ushers in an era of 3D topological solitons, with several possible avenues for new technologies. One such direction is topological computing, in which the trajectories of quasiparticles are 'braided' together to perform computational logic operations. It can be imagined that hopfions could interact with other topological structures to create new areas of computing.

Skyrmions are potential candidates for high-density computer storage and energy-efficient switching, and hopfions — as the siblings of skyrmions — could be just as useful. They might also have applications in artificial neural networks. One drawback of using skyrmions in these technologies is that they cannot be moved reliably from one location to another using a magnetic field or an electric current, owing to a phenomenon

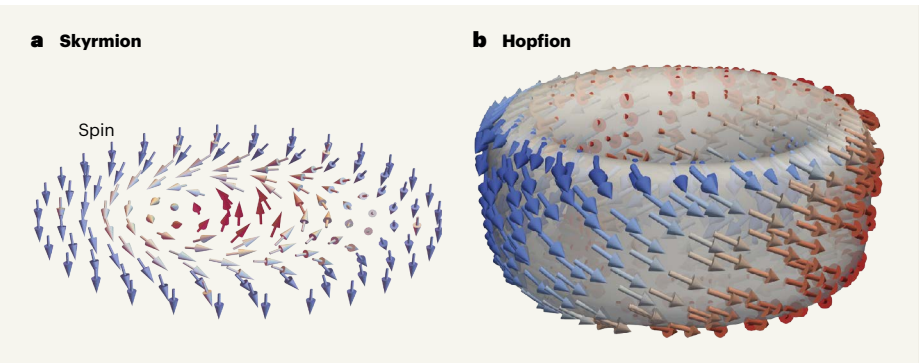

Figure 1 | Magnetic 'spin textures' in 2D and 3D. The spins (intrinsic angular momenta) of electrons can form whirlpool-like arrangements called topological solitons. **a**, Skyrmions are 2D topological solitons that arise in certain magnetic materials. **b**, Zheng *et al.*[2] induced a 3D magnetic topological soliton called a hopfion ring, which resembles a toroid or doughnut. The colour indicates the direction of spins going from positive (red) to negative (blue). This corresponds to red spins pointing up in **a**, and to the right in **b**.

known as the skyrmion Hall effect. This effect is not predicted for hopfions[11], making them potentially ideal for applications. Finally, there is a current push towards 3D electronics, which re-evaluates the idea that information needs to be encoded on a 2D chip. A material that hosts 3D topological solitons, such as those demonstrated by Zheng and colleagues, could have a key role in this endeavour.

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Structural biology

Getting to the heart of thick-filament structure

Peter J. Knight

Thick filaments contain the protein myosin that generates the force of every heartbeat. Two studies report how these myosin molecules pack together in thick filaments with other proteins to form a surprisingly complex structure. **See p.853 & p.863**

As you read these words, your beating heart is keeping you alive. No surprise, then, that researchers have sought for decades to understand the structures and mechanisms that underlie how the human heart functions, and to discover what changes in heart disease. The central players that make the heart a pump are the proteins actin and myosin, and these assemble into what are called thin and thick filaments, respectively. Thin filaments have a fairly simple structure that is well understood. Thick filaments are much more complex, and their structure has been difficult to determine. On pages 853 and 863, respectively, Dutta *et al.*[1] and Tamborrini *et al.*[2] report their use of the technique cryo-electron microscopy (cryo-EM) to reveal most of the structure of thick filaments in exquisite detail. These results reveal a structure that no one had predicted and that opens the door to a new world of experiment and understanding.

The structure of thick filaments of vertebrate cardiac and skeletal muscle was outlined 60 years ago[3]. Myosin comprises two pear-shaped 'heads' attached to a tail that measures approximately 1,600 by 20 ångströms. The tails of many myosin molecules bundle together like a sheaf of sticks to form the backbone of each filament — with the heads protruding from the surface, where they can reach out to make force-generating interactions with neighbouring thin filaments. All the tails point towards the midpoint of the filament, and the heads are present all the way from both tips of the filament to a bare zone in the centre, where tails of opposite polarity overlap (Fig. 1).

Thick filaments from the cardiac and skeletal muscle of all vertebrates have indistinguishable dimensions and minor variations in composition. Each is assembled with great precision, and has 294 myosin molecules[4,5]. These are precisely positioned in the filament: groups, termed crowns, consisting of the six heads of three myosin molecules, lie on the filament surface at intervals of approximately 143 Å along each half of the filament and are arranged in a quasi-helical way that repeats every third crown (corresponding to 430 Å). One consequence of this is that 33 tails pack together at most points along the filament backbone. Visualizing the paths taken by individual tails in this array has been an insurmountable task.

Hopes for solving thick-filament structure were first raised in 2005, when cryo-EM was used to determine the structure and arrangement of the myosin heads for thick filaments from a tarantula spider[6]. Since then, there has been a revolution in the capabilities of the associated hardware and software. This enabled researchers in 2016 to determine the arrangement of tails in thick filaments from a giant water bug, *Lethocerus*[7]. It shows that the tails are packed together in a crystalline way — an arrangement similar to one that had been proposed in 1973 (ref. 8). Crucially, however, these invertebrate filaments are perfectly helical rather than quasi-helical, with an exact repeat every 143 Å. The reason that thick filaments in vertebrates are not absolutely helical could be that two proteins found in vertebrates — titin and MyBP-C — are absent in invertebrates. But how these proteins might affect the arrangement of myosin was unknown.

Each titin molecule is a long, thin thread. In the contractile organelle of muscle formed by arrays of overlapping thin and thick filaments (called a myofibril), part of a titin molecule lies along one half of a thick filament, and the rest elastically anchors the thick filament in the myofibril to prevent disorder of the arrays during contraction (Fig. 1). The thick-filament region of titin consists mostly of units that each comprise roughly 100 amino-acid residues; these are predicted to fold into two kinds of globular domain, each 40 Å wide. In much of the filament, these two types of domain create a pattern that repeats every 11 domains, forming a 'super-repeat' that could correspond to the repeat in the filament that occurs every 430 Å. Titin has therefore long been suggested to act as a 'molecular ruler' that modulates the arrangement of myosin, and is thereby responsible for the remarkable precision of thick-filament structure[9].

Cardiac MyBP-C (cMyBP-C) comprises a string of 11 of the same two kinds of 40 Å domains as titin, and is located at intervals of 430 Å along the filament in the region where titin has its 11-domain super-repeat. As well as binding to the thick-filament backbone, cMyBP-C's amino-terminal end binds to thin filaments, and is subject to modification through a process termed phosphorylation that correlates with altered contraction in the heart. Also, cMyBP-C is the site of approximately 40% of a type of genetic change (point mutations) that is known to cause the heart condition hypertrophic cardiomyopathy[10]. There is thus intense interest in cMyBP-C's role in thick-filament structure and activity.

The two groups of researchers used complementary cryo-EM methods to arrive at satisfyingly consistent reports about filament structure. Dutta *et al.* purified thick filaments from human hearts, examining the specimens under conditions that correspond to the relaxation phase of the cardiac cycle, and determined the structure of the 430 Å repeat, reaching an overall resolution level of 6.0 Å. Tamborrini *et al.* used myofibrils from mouse hearts to prepare arrays of thin and thick filaments in a near-natural relaxed state. They then used tomographic methods[11] to determine the structure, reaching a resolution of 8 Å for the thin filaments and 18 Å for the thick filaments. Although this is a lower resolution than that reported by Dutta *et al.*, the tomographic