High-temperature superconductivity

Stripes defeat the Fermi liquid

J. Zaanen

Some 50 years ago, profound insights were obtained into the nature of the metallic and superconducting states of electrons in solids. According to Fermi-liquid theory, electrons in ordinary metals can be viewed as a non-interacting electron gas. Then, as their temperature is lowered, the electrons form Cooper pairs that are responsible for superconductivity in the Bardeen–Cooper–Schrieffer (BCS) theory. On pages 729 and 736 of this issue, Mook *et al.*[1] and Sharma *et al.*[2] announce the results of two independent experiments showing that the conventional theories of metals and superconductors are no longer universally valid. At the same time, both works are inspired by and add further credibility to an alternative picture of electrons in solids known as 'dynamical stripes'.

The first hints of a challenge to the established paradigm came with the discovery of the high-temperature superconductors in 1987. Soon after their arrival, suspicions arose that something completely different was going on in these copper oxide superconductors[3]. But the conventional theories proved flexible and were defended quite successfully. Mook *et al.*[1] and Sharma *et al.*[2] have now used different experimental probes (neutron scattering and ion channelling) aimed at dissimilar properties of the copper oxides (spin and ion-lattice fluctuations) to disqualify, once and for all, these theories as an explanation for high-temperature superconductivity.

The state of electrons in normal metals should be understood as an extreme expression of the perpetual motions of quantum physics. In Fermi-liquid theory, the metallic state of matter corresponds to a quantum gas of 'quasiparticles', which are like electrons in every way except that they no longer interact. The quasiparticles are fermions and have to obey the Pauli exclusion principle, which forbids any two fermions from being in the same state. This forces the electrons into states of high quantum kinetic energy and, remarkably, the fierce quantum motions wash away completely the inter-actions between electrons. Conventional superconductivity is a sibling of this state. In the presence of any residual attractive interaction the quasiparticles form pairs and, because these Cooper pairs are bosons (and so are not constrained by the Pauli principle), they immediately condense into a BCS superconductor.

These quantum gases are very simple and rather featureless. The spin and lattice fluctuations in the copper oxides seen by Mook *et al.* and Sharma *et al.* reflect a complexity of behaviour in the electron system that cannot be attributed to any gas, even a quantum gas of quasiparticles. A high degree of cooperativity is needed to explain these diverse

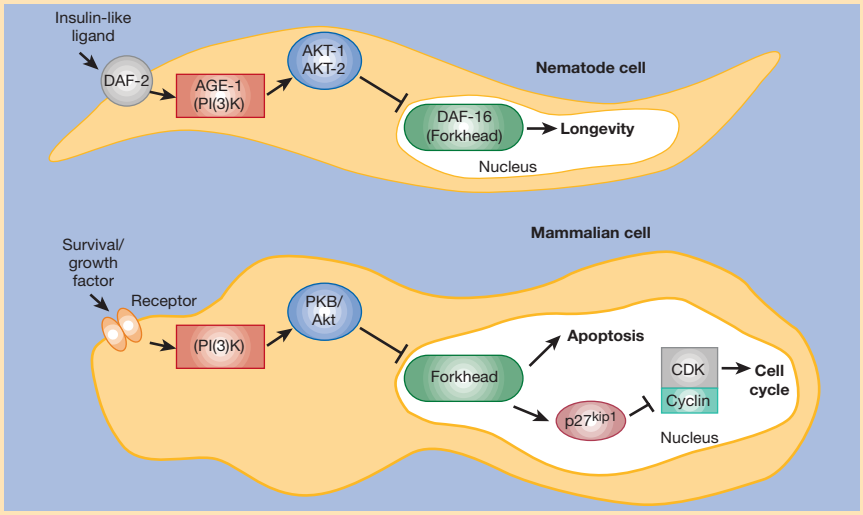
Signal transduction

An arresting tale

The external differences between species belie the fact that many of their genes, proteins and intracellular signalling pathways are very similar. So, for example, we can learn much about ourselves from studying such experimentally useful animals as the nematode *Caenorhabditis elegans*. Elsewhere in this issue (*Nature* **404,** 782–787; 2000), however, René H. Medema and colleagues turn the tables. They describe a new branch of a signalling pathway in mammalian cells that may also offer insight into an important developmental state in *C. elegans*.

The story starts with humanity's fascination with extending life. For this reason, long-lived mutants of organisms such as *C. elegans* have received a lot of attention. By identifying the genes mutated in such organisms, we can get some idea about the proteins and signalling pathways involved in longevity. One pathway involves a cascade of enzymes known as kinases, culminating in the regulation of DAF-16 — a transcription factor of the so-called Forkhead family (see diagram). This pathway also regulates the developmentally arrested nematode larval state known as 'dauer', which occurs as a result of crowding and starvation.

At the cellular level, it is possible that, for a cell to stay alive, its death (by 'apoptosis') must be actively suppressed. In mammals, a pathway that represses apoptosis contains counterparts of many proteins from the nematode longevity pathway (see diagram; proteins that are conserved in the two pathways are shown in the same colours). This 'survival' pathway also ends with inhibition of members of the Forkhead family, resulting in repression of genes of the death machine.



Medema *et al.* now show that this signalling pathway has another, possibly more important, function: it puts a brake on the cell-division cycle. The authors find that signalling progresses along the now familiar enzymatic cascade, up to the point at which Forkhead proteins are regulated. Then, the pathway forks. One line leads to suppression of cell death, while the other leads to cell-cycle arrest — the key molecular effect here being an increase in levels of the protein $p27^{kip1}$. This appears to occur through increased expression of the gene encoding $p27^{kip1}$, rather than through stabilization of the $p27^{kip1}$ protein.

$p27^{kip1}$ is a well known molecule: it inhibits the activity of important regulators of the cell cycle, called cyclin/cyclin-dependent kinase (CDK) complexes. Increased $p27^{kip1}$ levels would be expected to lead to cell-cycle arrest in the period before DNA replication occurs. Such a block is exactly what Medema *et al.* find when they activate Forkhead proteins in mammalian cells.

This new prong of a known signalling pathway may provide an explanation for the proposed role of defects in this pathway in cancer — a condition that is essentially characterized by the undermining of the finely tuned molecular network that ensures controlled cell division and finite cellular lifespan. This story may also have come full circle in explaining why, in nematodes, this pathway blocks larval development.

Bernd Pulverer

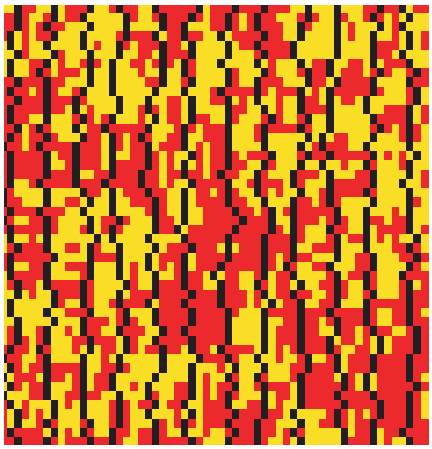


Figure 1 **A snapshot of stripes in action. Fluctuating quantum stripes (lines of black dots) are shown moving through a quantum antiferromagnet (red/yellow background) from an imaginary time slice of a quantum Monte Carlo simulation. In the classical limit the background would be, say, uniformly red, corresponding to a simple antiferromagnet. Here the yellow patches represent spin fluctuations. The first conclusive evidence for the existence of stripes in high-temperature superconductors is given by Mook *et al.*[1] and Sharma *et al.*[2]. A consequence of this work is that the conventional picture of ordinary metals and superconductors can no longer explain high-temperature superconductivity. (Unpublished figure, O. Y. Osman, J. Tworzydlo and J. Zaanen.)**

observations, and the best interpretations are found in the new theory of dynamical stripes. This increasingly popular theory refers to a state that is radically different from a Fermi liquid. In stripes, the electrons have been incorporated in complex, quantum fluctuating patterns and, although much is unclear, many now believe that superconductivity and stripes have a deep and profound relationship.

Owing to a spectacular series of discoveries in the past few years (see ref. 4 for a review), there now exists some understanding of the counterintuitive nature of this 'complex quantum matter'. In many-body systems (so-called quantum fields), quantum effects might turn out to be relatively modest at short-length scales, but increasingly important over larger distances. This is unlike few-body systems, where quantum mechanics invariably dominates at the shortest distances. Earlier neutron-scattering experiments[5] suggested that this general field-theory mechanism was also at work in the copper oxide superconductors[6]. Because the long-wavelength quantum fluctuations involve small energy scales, one expects to easily suppress these, driving the state to its classical limit. Tranquada and co-workers[7] accomplished this feat in 1995, and their frozen version of stripes allowed experimentalists to have a closer look at the nature of this complex electronic matter.

The static state of stripes is highly unusual (Fig. 1). It consists of antiferromagnetic (and presumably insulating) domains about a nanometre in width, separated by domain walls on which the charge carriers reside. In the static phase these domain walls, or stripes, condense in a regular pattern. Such phases were actually predicted theoretically[8,9] (triggering the experimental search), and the current consensus is that they arise from competition between quantum kinetic energy and electron–electron interactions on the microscopic scale.

How can we understand dynamical (as opposed to static) stripes? This is the state associated with superconductivity, in which the system of stripes is disordered by long-wavelength quantum fluctuations. Figure 1 illustrates a popular view. It gives a snapshot at a fixed (imaginary) time from a quantum Monte Carlo calculation, and the overall quantum state should be viewed as a sequence of many of these pictures, in which the irregular features vary according to the quantum fluctuations. Yellow and red indicate opposite orientations of the stripe antiferromagnet: the background would be uniformly red in the classical limit. Although the stripes are still intact (lines of black dots), they undergo vigorous quantum motions. In fact, several theoretical groups are studying these stripe fluctuations in terms of simple string theories[10].

The superconductivity community takes such pictures increasingly seriously, if only because of their effectiveness in guiding the experimental work. This does not mean that the problem of high-temperature superconductivity is solved. Over long distances the quantum fluctuations get truly out of hand, destroying the semiclassical picture presented above. Remarkably, in this regime there are similarities with a BCS superconductor, although these might not be as straightforward as some defenders of the conventional model want to believe. At the moment the relationship between stripes at short distances and BCS-like behaviour at large distances is an enigma. But I am an optimist and I take this mystery as prime evidence that there will be a glorious theory of physics waiting at the end of the journey. ■

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Functional genomics

Recognizing DNA in the library

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The transcription of DNA into RNA requires a battery of proteins, the precise complement of which depends on the circumstances. One group of such proteins is the basic helix–loop–helix (bHLH) family of DNA-binding transcription factors. So far, over 250 of these bHLH factors have been characterized; they regulate gene expression in various processes such as muscle development, circadian rhythms and cell growth[1]. In a paper in *Chemistry and Biology*[2], Winston and Gottesfeld use a novel combinatorial approach to provide new information about the bHLH DNA-binding equipment. Importantly, this approach can be easily adapted for high-throughput studies of structure–function relationships for any protein.

Basic helix–loop–helix transcription factors were first identified by Baltimore and co-workers[3] over ten years ago. The conserved amino acids in the bHLH family are present in two α-helices (helix 1 and helix 2, respectively), which are separated by a loop region of variable length and amino-acid composition[4,5]. The bHLH domain of several transcription factors is necessary and sufficient for the required dimerization of the protein, and subsequent recognition of six specific nucleotides in the target DNA sequence. Residues in the amino terminus of helix 1 provide sequence-specific DNA recognition, whereas dimerization is largely mediated by helix 2 and the carboxy terminus of helix 1 (Fig. 1, overleaf).

What Winston and Gottesfeld[2] have done is to use a combinatorial strategy to look at the role of the loop region in a *Drosophila* bHLH factor, Deadpan, in sequence-specific DNA recognition. Using solid-phase peptide synthesis methods and high-resolution mass spectrometry, they have determined the minimal loop requirements necessary to retain full DNA-binding activity. Furthermore, they have identified a loop residue that has a key part in binding DNA through elements that lie outside the core-DNA recognition sequence.

The studies of Winston and Gottesfeld involved parallel approaches to generate