Condensed-matter science

Five-fold symmetry in liquids

Frans Spaepen

A complete description of the structure of simple liquids is missing from our understanding of matter. But new observations show that liquids contain many configurations with five-fold symmetry.

Understanding the structure of simple liquids is a fundamental, unsolved problem in the mathematical and physical sciences. Attempts to describe liquids as disordered crystals have all failed, and their description as dense gases (fluids) remains too complex. The best approach so far, though far from complete, is to describe liquids as dense packings of tetrahedral (four-sided) building blocks. On page 839 of this issue, Reichert *et al.*[1] report the first direct evidence for such polytetrahedral structures in a monatomic liquid trapped at a solid interface.

A complete picture of the short-range order in a liquid (between nearest neighbours) requires knowledge not only of the number and length of the bonds, but also of their directions. Consider, for example, the two 13-atom clusters shown in Fig. 1a and b. Both consist of 12 atoms surrounding a central one at an equal distance, but the two forms are quite distinct. The cuboctahedral configuration (Fig. 1a), in which the bonds form eight tetrahedra and six half-octahedra (composed of four triangles on a square base), makes up the face-centred cubic packing found in simple crystalline structures. The icosahedral configuration (Fig. 1b) consists of 20 tetrahedra, and is an important building block of the polytetrahedral model for monatomic liquids.

The atomic structure of a liquid changes over space and time, so conventional scattering experiments using X-rays or electrons or neutrons provide only directionally averaged information — specifically the distribution of interatomic distances. Such data already favoured the polytetrahedral model, but Reichert *et al.*[1] provide valuable direct evidence for it. They captured some of the polytetrahedral configurations in liquid lead by aligning them against a crystalline silicon wall. They observed the characteristic five-fold symmetry of the bonds from the scattering of totally internally reflected X-rays, which are sensitive only to the structure of the interface.

Finding a simple structural description of liquids, such as 'periodicity' for crystals or 'sparsity' for gases, is a persistent challenge in condensed-matter science. It is now accepted that a liquid is not a heavily defective crystal or a random assembly of microcrystals, but a well-defined phase in its own right. This was demonstrated most dramatically in the late 1940s by Turnbull[2] when he showed that many simple liquids could be supercooled far below their freezing points without crystallization occurring. This is possible only if the liquid structure is fundamentally different from that of a crystal. That crystals can be substantially superheated later reinforced the idea of a fundamental structural discontinuity between the crystal and liquid states.

Turnbull's observation led Frank[3] to suggest that the structural difference between crystals and liquids arises from liquids having polytetrahedral short-range order. Specifically, he pointed out that, if the interatomic forces act between the centres of the atoms, an icosahedral cluster of 12 atoms surrounding a central one (Fig. 1b) is more stable than a cuboctahedral cluster (Fig. 1a).

The face-centred cubic structure of many crystalline solids (Fig. 1a) maximizes the *long-range* density of closely packed spheres. Polytetrahedral packing can be viewed as an attempt to maximize the *short-range* density of a structure. The densest local configuration that can be created with hard spheres is a tetrahedron. Five tetrahedra can be packed around a common edge (shown in red in Fig. 1c), but they leave a gap of about 7°. Twenty tetrahedra can also be packed around a common point, or vertex, to form an icosahedron, which can also be thought of as 12 interpenetrating five-fold rings.

Five-fold symmetry is incompatible with long-range periodicity, so the polytetrahedral short-range order favours disordered or amorphous structures. The model that has been most successful at explaining scattering data from liquids is Bernal's dense random packing of hard spheres[4,5] and its computational successors[6]. Analysis of the short-range order in these models reveals ubiquitous polytetrahedral packing, in particular five-fold rings.

Moving the gap between the tetrahedra in a five-fold ring (Fig. 1c) requires very little energy. The thermal disorder of a liquid, the ease by which it flows, and the rapidity by which its atoms diffuse can be qualitatively understood by the redistribution of these gaps. The gaps are there because it is impos-

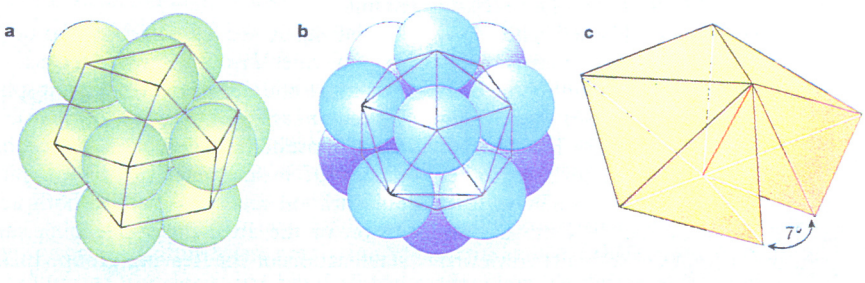

Figure 1 **Structural building blocks. Twelve atoms surrounding a central one can form:** a, **a cuboctahedral arrangement, as in a face-centred cubic crystal; or** b, **an icosahedral arrangement, as found in a liquid.** c, **A ring formed by five tetrahedra sharing an edge, leaving a gap with an angle of 7°. The work of Reichert *et al.*[1] suggests that five-fold symmetry is ubiquitous in the structure of liquids.**

sible to fill space completely with identical regular tetrahedra. These gaps are akin to those left in two dimensions when trying to tile a surface using regular pentagons. In the latter case, the gaps can be closed up by 'curving' the plane into a sphere, in which case twelve pentagons come together to form a regular dodecahedron. Similarly, regular tetrahedra can be made to pack perfectly in a higher-dimensional space — onto the curved three-dimensional surface of a four-dimensional polytope. Mapping this structure into ordinary three-dimensional space requires the systematic introduction of defects (related to the gaps)[6], and the diffraction pattern calculated from such a model is in good agreement with experiment[7,8].

The experiment by Reichert *et al.*[1] suggests that studying polytetrahedral structures and their defects is a promising route towards understanding the structure of liquids. But much remains to be done. The polytetrahedral polytope used in theoretical studies contains only 120 atoms — only a small part of the bulk liquid. We would also like to be able to use the defects to enumerate all possible configurations of the liquid, and hence to calculate its entropy and other thermodynamic properties. A detailed picture is needed of how the defects allow the local shear that causes viscous flow, or how they affect atomic diffusion.

And last but not least, the solid–liquid interface, of the type studied here, remains poorly understood. The interface between a crystal and its own melt controls both the nucleation and the growth of crystals — important for all industrial solidification processes, as well as for glass formation. Lack of knowledge about this interface is the largest bottleneck in quantitative modelling of solidification processes[9]. The polytetrahedral approach has been used to create structural models for the crystal–melt interface, and to estimate its thermodynamic properties. The X-ray technique developed by Reichert *et al.*[1] is a useful tool for the direct structural investigation of a variety of crystal–melt interfaces. ■

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RNA splicing

The case for an RNA enzyme

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New evidence suggests that RNA splicing, the removal of non-coding parts of a messenger RNA, is catalysed by an RNA component of the splicing machinery. This component binds a crucial metal ion.

Most messenger RNAs encoded by nuclear genes are synthesized as precursor RNA molecules, in which coding sequences (exons) are interrupted by intervening sequences (introns). For the mRNA to become functional — capable of being translated into protein — the introns must be excised and the exons precisely joined together. The 'splicing' reaction is achieved by the spliceosome, a massive complex consisting of five RNAs and more than 50 proteins. Parallels between the splicing of precursor mRNAs in the nucleus and the self-splicing of introns in some other organelles have fuelled speculation that catalysis within the spliceosome is performed by its RNA constituents (reviewed in refs 1, 2). Proof of this hypothesis would have fundamental implications for our understanding of the evolutionary origin of introns and the machinery that removes them.

On page 881 of this issue[3], Yean and colleagues show that one spliceosomal RNA component — the U6 small nuclear (sn) RNA — specifically binds a divalent metal ion that is required for catalysis of the first step of splicing. It was already known that the spliceosome is a metal-dependent enzyme[4], so the new results substantially strengthen the case for RNA-based catalysis in splicing.

Splicing is accomplished in two steps, each of which involves a transesterification reaction — the replacement of one phosphodiester linkage with another (Fig. 1a). In RNA, phosphodiester linkages connect one nucleotide to another. Catalysis of transesterification reactions requires both activation of the attacking 'nucleophile' and stabilization of the 'leaving group'. In the first step of splicing, the 2′ hydroxyl group of the so-called branch-point adenosine nucleotide (within the intron) is the nucleophile, and the 3′ oxygen of the phosphodiester linkage at the 5′ splice site (where the 5′ exon joins the intron) is the leaving group. Studies of self-splicing introns have shown that RNA can catalyse transesterification reactions by a mechanism in which metal ions that interact with specific atoms in the RNA activate the attacking nucleophile and stabilize the leaving group (reviewed in ref. 5). But in the context of the spliceosome, it is extremely difficult to distinguish between the relative contributions of RNA co-factors and proteins, both of which are essential (see, for example, ref. 6).

Unlike the cellular protein-translating machinery — the ribosome — the spliceosome is assembled anew on each substrate. Five snRNAs — U1, U2, U4/U6 and U5 — are required for intron recognition and spliceosome assembly. Following initial assembly, a complex series of conformational changes ensues such that the U1 and U4 snRNAs are released before catalysis occurs. So, only U2, U5 and U6 snRNAs could potentially participate in the chemical reactions of splicing.

Of these, U6 has consistently emerged as the best candidate to have a direct role in catalysis. Analyses in a variety of systems have revealed that U6 snRNA must act at or near the active site of the spliceosome. Furthermore, U6 is exceptionally sensitive to mutation and modification. Experiments done several years ago showed that replacing a single oxygen atom with a sulphur atom at a specific phosphodiester linkage within the U6 backbone completely blocked splicing (reviewed in ref. 1). Although it is remarkable that such a subtle alteration could have such a dramatic consequence in the context of a huge, multicomponent complex, the mechanistic basis for this effect could not be established.

Yean *et al.*[3] have now looked further at the role of the phosphodiester backbone of U6 and, importantly, their results are amenable to mechanistic interpretation. Each phosphodiester linkage contains two distinguishable 'non-bridging' oxygen molecules, designated R_P and S_P (Fig. 1b). Previous work had established that U6 is inactivated by replacing the R_P oxygen at a specific phosphodiester bond with sulphur. Yean *et al.* show that substituting the S_P oxygen with sulphur at the same position in U6 is equally inhibitory. One well-documented consequence of such substitutions is that they alter the ability of phosphate groups to interact specifically with magnesium ions. So the failure of the U6 snRNA to function might have resulted from its inability to bind a critical metal ion.

To test this possibility, Yean *et al.* determined whether sulphur-substituted U6 could function in the presence of manganese. This metal can, in many cases, fulfil the function of magnesium — but, unlike magnesium, it can interact with sulphur. Remarkably, the function of U6 in which the S_P oxygen was replaced by sulphur was restored when reaction mixtures were