MATERIALS SCIENCE

Let assemblies bloom

In nature, complexity and order can often result from self-assembly — the spontaneous and reversible aggregation of the components of a disordered system into an ordered one. But so far, researchers have mainly studied systems of one or two components, whereas nature can mix many more — as is the case, for example, with the assembly of ribosomes, the protein-synthesizing organelles in cells. On page 999 of this issue, Erb *et al.* show that man-made multi-component systems can assemble under the action of a magnetic field (R. M. Erb *et al.* *Nature* **457**, 999–1002; 2009).

Self-assembly processes are usually driven by intermolecular forces, including hydrophobicity and the formation of hydrogen bonds, as opposed to the more-stable covalent forces. But external effects such as electrical and magnetic forces can also lend a hand. The components

of such a system can range from metallic nanoparticles to biopolymers and macroscopic objects.

The system studied by Erb and colleagues is a ferrofluid — a mixture of water and magnetic nanoparticles — to which larger, micrometre-sized colloidal particles of different kinds are added. When the fluid is subjected to a magnetic field, the particles can align their magnetic dipoles either with or opposite to the field depending on their magnetic properties with respect to the ferrofluid. When further magnetic nanoparticles are added, what might previously have behaved as a paramagnetic colloidal particle (one that aligns with the field) can become a diamagnetic one (aligning opposite to the field), and vice versa. Such changes cause the particles to assemble into diverse structures.

The type of structure that forms

depends on the size and magnetic properties of the components. Thus, the geometries of the assemblies can feature clusters of smaller particles at the poles of a larger central particle or at its equator (pictured), or even more complex, flower-shaped arrangements.

Erb *et al.* show that these

structures have a remarkably uniform shape, and that they do not aggregate among themselves because their large, central paramagnetic particles repel each other. And they can be made to persist even after the field has been turned off. To do this, their components are made to stick to each other by attaching two kinds of molecule to them that act like Velcro once they are in close proximity. Thus, when the magnetic field is turned off and the structures are dried, they don't fall apart and can be studied individually.

In the future, the use of a larger number of smaller and differently shaped

components may help our understanding of complex assemblies to blossom, together with our ability to make them. A possible outcome could be the development of materials with tailored optical properties that would be useful for making biosensors.

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MOLECULAR BIOLOGY

The long and short of RNAs

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The known world of RNA is expanding faster than that of any other cellular building block. The latest additions are types of long and short non-coding RNAs formed by bidirectional transcription and unusual processing.

The relationship between DNA, RNA and protein is no longer as simple as we once thought — that specific genomic sequences are transcribed into messenger RNAs, which are then translated into proteins. In recent years, a flurry of studies has reported the existence of a large and growing family of non-protein-coding RNAs (ncRNAs), describing the different mechanisms of their transcription and their role in regulating gene expression. Six remarkable papers^{1–6}, including three in this issue^{1–3}, form the latest additions to the list of studies.

Reports of the identification of ncRNAs were initially met with scepticism because of the inherent instability of these single-stranded molecules: RNA is prone to chemical degradation and enzymatic cleavage, as well as to incomplete conversion back to DNA. Sporadic identification of ncRNAs in the past has therefore often been dismissed as one of

these artefacts. High-throughput genomics approaches, however, have begun to chart consistent patterns that are unlikely to be artefacts, and reveal several specific mechanisms for ncRNA biogenesis and processing.

The mechanisms by which ncRNAs are generated seem to be similar to those that operate during mRNA transcription and processing. Normally, the enzyme RNA polymerase II (Pol II) binds to the promoter sequence of a given gene to generate mRNA from the downstream genomic region. In a few cases, the 5' ends of genes on opposite DNA strands are located close together and so share the same promoter, which — when bound to Pol II — bidirectionally triggers their transcription^{7,8}. These mRNAs, which are generally long, are also often translated into proteins. The latest studies report the widespread existence of ncRNAs in yeast^{2,3} and mammalian cells^{1,4,5}, and show that these sequences originate from

known promoters and can also be transcribed in the opposite orientation to known genes.

Promoter-mediated transcription is not the only property that ncRNAs share with mRNA. Soon after transcription begins, a structure called a cap is added to the 5' end of the RNAs transcribed by Pol II (ref. 9); this structure is required for RNA stability and protein translation. Researchers of the Affymetrix/Cold Spring Harbor Laboratory ENCODE Transcriptome Project¹ (page 1028) show that ncRNAs are also 'capped', but — as discussed below — in some circumstances this process seems to occur even independently of transcription.

In the yeast *Saccharomyces cerevisiae*, only a few RNA sequences, called cryptic unstable transcripts (CUTs), had previously been identified. Xu *et al.*² (page 1033) and Neil *et al.*³ (page 1038) now show that these sequences form a main class of Pol-II-transcribed long ncRNAs, which are degraded soon after synthesis by an RNA surveillance pathway. By preventing degradation of CUTs experimentally, the authors show that these ncRNAs are a consistent part of the cell's total pool of transcripts, being transcribed from promoter regions in both directions. In fact, the authors find that at least a third of all genes are transcribed into either CUTs or another, more stable class of long ncRNAs called SUTs (for stable unannotated transcripts) (Fig. 1a). Until now, the only