times larger in the Cu–O plane than perpendicular to it in $YBa_2Cu_3O_7$ (H. Noel, Rennes Univ.). The gradient $-dH_{c2}/dT$ increases with decreasing temperature, and also with increasing applied field from -2 T K^{-1} in low fields (5 T)to -3 T K^{-1} in 20 T (Noel; J.C. Ousset, CNRS, Pont à Mousson) and -4.2 T K^{-1} in 25 T (van Bentum). Superconductivity is often associated with a high degree of magnetic flux exclusion (the Meissner effect). In the new materials the extent of the Meissner effect can be very small (< 4 per cent) in completely superconducting samples with a narrow transition because of the strength of flux pinning when the sample was cooled in a magnetic field (P. Lejay).

Finally, the critical current I_c, at which superconductivity fails, is of great importance in applications of the new materials. Several measurements of I_c in $YBa_2Cu_3O_7$ were reported. Batlogg expects the intrinsic bulk critical current to be much larger (10^6 A cm^{-2}) than the value he has recorded at 77 K, 1,100 A cm^{-2}. R.B. Laibowitz (IBM, Yorktown Heights) has found $I_c \sim 10^6$ A cm^{-2} in thin films at 77 K. Using magnetic hysteresis, values of 10^5 A cm^{-2} at 4.2 K and 1,100 A cm^{-2} at 77 K have been obtained in polycrystalline samples (Lejay), and a value of 750 A cm^{-2} was obtained in a copper-coated wire (H. Yoshimo, Toshiba). □

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Protein structure

One fold among many

Lindsay Sawyer

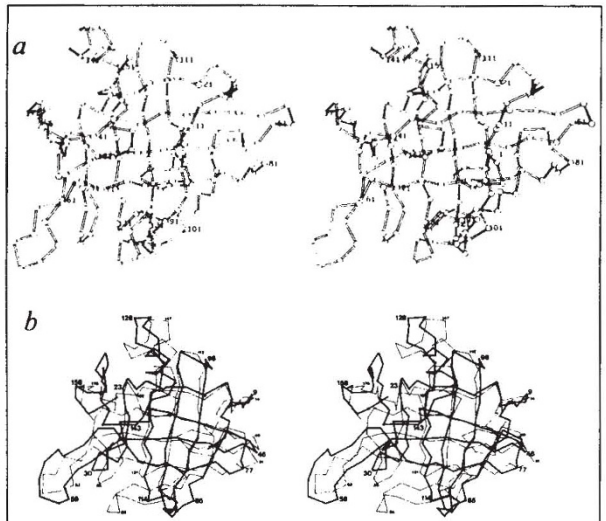
WHAT is the connection between insect camouflage, cow's milk and vitamin A? The anwer is a binding protein, found in the first two and associated with the last. A paper published at the end of last year drew attention to the similarity between the crystal structures of the cow protein β-lactoglobulin (BLG) and plasma retinol-binding protein (RBP), where the striking 'cross-hatching' of the eight strands of anti-parallel β-sheet provides a protective cover for the labile and insoluble retinol (vitamin A) bound in the core of the protein[1]. The particular polypeptide fold, which includes a helix near the carboxyl terminus, is a novel variation of all-β protein. Two independent determinations of the structure of insecticyanin, or bilin-binding protein (BBP), from the butterfly *Pieris brassicae* by Huber and colleagues[2] and from the tobacco hornworm *Manduca sexta* by Holden *et al.*[3], now expand and diversify the family.

The figure shows the backbones of the three structures in the same approximate orientation. The model of Huber and colleagues[2] is incomplete but the authors point out that there is some unexplained electron density in the core of the protein that is likely to be the pigment biliverdin, formed by the breakdown of haem. The structure of Holden *et al.* shows the biliverdin clearly but its horseshoe shape is something of a surprise because, by analogy with retinol in RBP, one might have expected the pocket to be long and thin. The function of the BBP is uncertain, although the colour is important for the camouflage of the insect. But as the ligand is not very soluble at neutral *p*H, this is also consistent with a role as a transporter.

Three diverse proteins sharing a common structure and possibly a similar function, that of transport, may seem little more than a coincidence. Sequence comparisons of the three proteins provide but scant evidence for the similarity of their tertiary structures. In fact, although any pair has around 30 per cent of residues in common, there are less than a dozen residues common to all three. However, these common residues do form a pattern, although less well defined than the template for nucleotide binding[4]: in a protein of mass around 20,000, the sequence -U-X-X-Gly-X-Trp-Y- (U is basic, Y aromatic and X either), occurs near residue 20 and the sequence -Thr-Asp-Tyr-X-X-Y- appears around residue 110. Midway between these two peptides, a disulphide forms a bridge to the carboxyl terminus.

This pattern had already been noticed for BLG and RBP and was extended to include protein HC (or α-1-microglobulin)[5] and α-2u-globulin, a urinary globulin. Two androgen-dependent secretory proteins from the rat epididymis also fit the pattern[6] and apolipoprotein D, which comprises 5 per cent of the high-density lipoprotein involved in lipid transport in serum, has a sequence clearly related to BBP[7]. A protein found in the nasal mucous of the frog *Rana pipiens* also complies[8]. That this protein is somehow involved in transferring odorants to a receptor is a prediction based on its similarity to RBP and one which should hasten the completing of the sequence of bovine odorant-binding protein[9]. Finally, the lobster retinoid-binding protein crustacyanin also seems to be a member (J.B.C. Findlay, personal communication).

Ten distinct proteins so far show the features described and in the four for which DNA sequence information is available the pattern can be extended to include the disposition of intron/exon boundaries, thereby showing a strong evolutionary relationship[10]. The functions of these proteins are mostly unknown, but they all bind small, conjugated molecules that are either sparingly soluble, labile or both. The proteins are all of similar size and, it is reasonable to assume, the same shape. Further, the mammalian ones (at least) all seem to have an associated receptor. Thus, we might expect to find a protein formed into a calyx of eight strands of anti-parallel β-sheet wherever such extracellular transport occurs, whether it is for distribution or acquisition of metabolites, transduction of signals or removal of waste products. What is particularly exciting is that if this basic framework is especially suited to binding small, hydrophobic or fragile molecules, then it should be possible to engineer a transporter for a given molecule by starting from a conveniently cloned and expressed precursor such as β-lactoglobulin or apolipoprotein D. □



a, Stereo view of the bilin-binding protein from *Pieris brassicae*. *b*, Superposition of β-lactoglobulin (thick) and retinol-binding protein (thin) (*a* is Fig. 3*a* from ref. 2; *b* is Fig. 3 from ref. 1).

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