cells are not color selective, color-coded information is thrown away—because all colors are scrambled together when many lateral geniculate cells converge to create an oriented cortical receptive field. Given the usual economy of sensory coding, the idea of throwing away information is horrifying. That conclusion may be avoided by postulating that the color coding inherent in the retinal output is tapped separately to build color-coded responses in the blob regions. This is the possibility shown, in its extreme form, in the left half of the figure. It is labeled co-coding, because a single ganglion cell carries information both about spatial contrast (by means of the center-surround organization) and about color.

An alternative is to postulate that most retinal ganglion cells are not designed to transmit color information at all (*9*, *10*). In this view, again stated here in extreme form, the fact that most retinal ganglion cells carry color information is a byproduct of evolution's relentless search for high visual acuity. In the primate fovea, ganglion cell acuity reaches the maximum possible: Because one ganglion cell is connected to one cone, acuity is limited only by the size and packing density of the cones. Along the way, the centers of ganglion cell receptive fields incidentally acquire color tuning (because a single cone contains only one pigment). However, that information is not used at the cortical level. Instead, a separate channel uses an independent subtype of retinal ganglion cell to code for color. These project, by means of a specialized region of the lateral geniculate body, to the cortical blob regions (*11*).

A ready candidate for the second pathway exists. The ganglion cells discussed above are the garden variety, making up about 80% of all retinal ganglion cells. Among the remaining 20%, a unique anatomical type coding for blue-yellow opponency has recently been conclusively described (*12*). These cells have nonconcentric receptive fields. They are infrequent and have larger fields than the other retinal ganglion cells. Their responses are chromatically opponent—the receptive field consists of a single region in which the cell is excited by blue light and inhibited by yellow. They seem likely to code color. Among other things, acuity for stimuli that are defined only by their color is low, as would necessarily be true if color is coded by a sparse population of cells.

However, the parallel processing model has its own problems. A red-green analog of the specialized blue-yellow ganglion cell has not yet been found. Furthermore, the anatomical evidence denying chromatically pure surrounds is contradicted by some physiologists (*1*, *13*). If the retina takes the trouble to give retinal ganglion cells chromatically pure surrounds (by some unknown mechanism), it seems unlikely that the information would later be discarded. Disagreements also exist about the types of color coding exhibited by cortical neurons (*9*, *14*).

An encouraging thing about Dacey and co-worker's experiment is that their approach can be applied to most retinal neurons. Once a candidate retinal ganglion cell is identified one can relatively easily accumulate a large sample of cells—and each yields both its physiology and its microanatomy. Together with the results of electron microscopic reconstruction, these studies are giving a completeness and precision to our understanding of the retina's color circuitry never before imaginable. And when the color mechanisms of the retina are sorted out, the central mechanisms may also begin to fall into place.

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Lysosomal Degradation of Ubiquitin-Tagged Receptors

Cytosolic proteins destined for degradation by the proteasome are tagged by the addition of the polypeptide ubiquitin (*1*). Proteins located in the plasma membrane can also be ubiquitinated, but because the proteasome has no access to these proteins it has not been clear whether this ubiquitin tag also signals proteasome degradation. A recent paper by Hicke and Riezman in *Cell* (*2*) now indicates that such ubiquitinated membrane proteins are in fact marked for proteolysis—but in vacuoles, the yeast equivalent of the lysosome, not by the proteasome.

There was some indication that one membrane protein, cystic fibrosis transmembrane conductance regulator (CFTR), might be targeted by its ubiquitination for proteasomal degradation, although how this protein might gain access to the cytosolic degradation machinery was unclear. The cell performs quality control of its secretory and membrane proteins before they leave the endoplasmic reticulum and degrades any that are misfolded or incorrectly assembled. During this process, CFTR is polyubiquitinated and degraded by a proteolytic activity similar to that of the proteasome (*3*).

In their new work, Hicke and Riezman (*2*) have now clarified how a protein that cannot be accessed by the proteasome can nevertheless be degraded as a result of its ubiquitination. Ligand-induced ubiquitination of a receptor—one of the yeast mating pheromone receptors—leads to receptor-ligand complex internalization followed by vacuolar degradation. Ligand binding stimulates α-factor receptor (α-FR) internalization and also stimulates ubiquitination of the α-FR cytoplasmic tail. Mutant yeast cells that lack ubiquitin-conjugating enzymes cannot internalize and degrade the receptor in response to added mating pheromone. Cells expressing a mutant receptor that lacks the ubiquitination site bind pheromone but do not ubiquitinate, internalize, or degrade the receptor-ligand complex efficiently. In cells with protease-deficient vacuoles, ubiquitinated α-FR accumulates in the vacuoles but cannot be efficiently degraded, even though the cells contain functional proteasomes. Conversely, cells with defective proteasomes but intact vacuolar protease activity can degrade the ligand-bound, ubiquitinated, and internalized receptor.

Ubiquitination must now be considered a more universal signal for protein degradation: It can trigger either cytosolic degradation by the proteasome or membrane trafficking to the vacuole, where the degradation of protein also occurs.

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