THE KOBAL COLLECTION

Figure 1 **Tyrone Power tries to work out what has happened to his demand function. (From *That Wonderful Urge*, 20th Century Fox.)**

ently not supported by the data. The latest explanation is the most startling: M. Browning and P. A. Chiappori claim[3] that the *Homo oeconomicus* model is correct: it is just not being taken seriously enough.

They rightly point out that none of the econometric studies conducted to check the Slutsky relations discriminate between individuals and households. However, *Homo oeconomicus* most definitely is single. As soon as two people pool their resources, they will have different utilities. The decision-making process then becomes a bargaining process, and there is no reason to expect that the outcome could be described by a single utility function. In other words, two people will come up with two different rankings for the possible alternatives and will have to find some way to resolve their differences, whereas an individual does not have this problem.

Browning and Chiappori support their argument with data from the Canadian Family Expenditure Survey (FAMEX). Overall, the survey does not support the Slutsky relations. But separating out single females and single males, each batch verifies the Slutsky relations.

The authors then ask themselves about two-person households. As mentioned before, any consumption decision will be the result of bargaining within the household, depending on the relative strengths and weaknesses of each partner (who brings in the money, and who has the strongest character, for example). What can be said about the outcome of such a process? Well, it should be efficient, which means that nothing will be thrown away — we cannot predict how the cake will be split, but we expect that everything will be eaten. This assumption is enough to write down a system of nonlinear partial differential equations which two-person household demand functions have to satisfy (see box). With the right mathematics, these relations can be shown to characterize completely the possible demand functions. And now the happy ending: the FAMEX data for two-person households support the Browning–Chiappori relations, in the same way that the FAMEX data for single people support the Slutsky relations. So the *Homo oeconomicus* model might well be true after all.

Some words about the right mathematics. The equations themselves are horrendous. The right way to handle them is to resort to a theory that was developed a hundred years ago for purely mathematical needs: exterior differential calculus. At that time, mathematicians in France and Germany were trying to construct surfaces with certain geometrical properties, and they were led to very complicated systems of nonlinear partial differential equations. Appropriate methods to solve them were developed over fifty years, and finally codified by Cartan[4]. It is a beautiful piece of mathematics, which has been revived in an unexpected context.

The implications of Browning and Chiappori's work are strange. I can say, "Tell me what you eat, and I will tell you how many you are"; not "Tell me how much you eat, and I will tell you how many you are" — it would come as no surprise that many people eat more than do a few. What I am saying is that, if two households spend the same amount, I will be able to tell how many people there are in the household just by inspecting the consumption pattern. Even more remarkably, I will do this by checking whether a very complicated system of nonlinear partial differential equations is solved or not, using exterior differential calculus — another example of the versatility and power of mathematics. □

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Membrane transport

Green light for Golgi traffic

Hugh R. B. Pelham

When eukaryotic cells secrete proteins, they do so by a circuitous route. The proteins are folded and assembled within a membrane-enclosed organelle, the endoplasmic reticulum (ER), whose membrane and internal contents are specialized for the job. They are then transported to the Golgi apparatus, and from there to the cell surface.

It is widely accepted that the intermediate steps in this process involve the budding and fusion of small vesicles. But the sites at which they form and fuse, and the number of such steps, have remained hotly debated topics. Now, however, in an elegant use of green fluorescent protein (GFP), Presley *et al.*[1] (page 81 of this issue) have answered a major outstanding question about the first step — from ER to Golgi. A few moments of time-lapse video* are enough to resolve an issue that years of microscopy on fixed cells have failed to settle. And the study also poses a new set of questions for the future.

Exit from the ER has long been a model of vesicular transport[2]. Electron microscopic images show, adjacent to the stacked cisternae of the Golgi complex, regions of the ER membrane that bud off to form vesicles (Fig. 1, overleaf). These vesicles then seem to fuse with a tubular network at the *cis* face of the Golgi apparatus, which is often referred to as the *cis*-Golgi network. Vesicles are formed from the ER by the action of the COPII (coat protein II) complex[3], and they incorporate vesicle-targeting molecules (known as v-SNAREs). These proteins interact with corresponding t-SNAREs, which are present on the target membranes of the *cis*-Golgi network[4,5].

However, there is a twist. Proteins do not leave the ER only near to Golgi membranes — they emerge at sites that are distributed apparently at random, all over the cell. These sites are marked by little groups of vesicles and tubules[2,6] (vesicular–tubular clusters, or VTCs), which have been extensively studied by electron microscopy. The relationship between these peripheral VTCs and the *cis*-Golgi network has been puzzling. They contain similar marker proteins, and both are sites at which escaped

*The video is at http://dir.nichd.nih.gov/CBMB/pbllabob.html

resident proteins from the ER can be retrieved in vesicles that are coated with COPI proteins[6,7]. But do secretory proteins pass through both the VTCs and the *cis*-Golgi network? If so, are there several vesicular steps, each with its own budding and targeting machinery? One view has been that the VTCs move along microtubules to the Golgi region, and join the tubular network there[8]. Another is that a second round of vesicle transport, mediated by COPI, carries cargo to the *cis*-Golgi network[9].

It now turns out that the VTCs move. Presley *et al.*[1] fused GFP to the cytoplasmic tail of the ts045 mutant form of vesicular stomatitis virus glycoprotein, which is a favourite marker for transport studies. At high temperature this protein fails to fold correctly and it remains in the ER. On shift down to 32 °C, however, it rapidly exits, and a wave of traffic through the secretory pathway can be followed.

Luckily, the addition of GFP has very little effect on the transport of the viral glycoprotein, so the authors could directly watch the secretory process. They found that individual dots corresponding to peripheral VTCs formed, then moved along microtubules to the Golgi apparatus where they seemed to fuse into larger structures (Fig. 2). The moving elements were elongated and clearly larger than vesicles. Most surprising, perhaps, was the observation that once a VTC had left an exit point on the ER, that particular point was seldom — if ever — used again. Instead, new structures formed spontaneously, at apparently random locations.

Why is this result important? Not only does it dramatically show the role of the peripheral VTCs, but it also raises some fascinating questions. For example, what triggers the burst of active budding that forms the elements, and why does it cease equally suddenly? How can a structure that is derived entirely from the ER behave so differently just

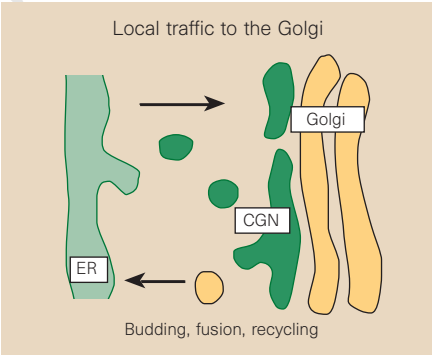

Figure 1 **In an elegant study using green fluorescent protein, Presley *et al.*[1] have been able to observe directly the transport of proteins between the endoplasmic reticulum (ER) and the tubular network at the *cis* face of the Golgi apparatus (the *cis*-Golgi network, CGN). Over short distances, secreted proteins bud off in vesicles, which dock and fuse with the *cis*-Golgi network.**

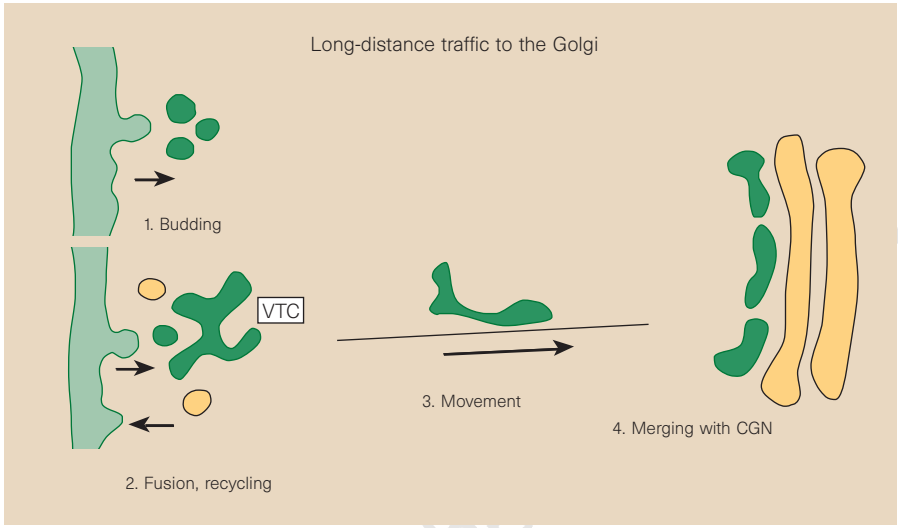

Figure 2 **Proteins can also be transported from the ER to the Golgi over long distances, from sites that are randomly distributed around the cell. These sites are marked by groups of vesicles and tubules called vesicular–tubular clusters (VTCs). These VTCs, containing the secreted proteins, travel along microtubules to the Golgi apparatus, where they fuse with the *cis*-Golgi network. This is the first time that such transport has been directly observed, and the new study resolves the debate as to the function of the VTCs.**

moments later — sorting out ER proteins, budding COPI vesicles and moving along microtubules in the opposite direction to ER membranes? Protein sorting during the budding step must ultimately be responsible for this change in character which may, perhaps, be initiated by the separation of ion pumps from counterbalancing channels, or of some lipid-modifying enzymes from others.

If these thoughts sound familiar, it is because the dynamics of the ER-to-Golgi step are strikingly similar to one view of endocytosis. Here, endocytic vesicles fuse to form early endosomes. Some proteins are then recycled to the cell surface while the remaining structures move to the Golgi region (for discussion see ref. 10). Similar mechanistic problems exist in each case.

A further implication of the work by Presley *et al.*[1] is that the v- and t-SNAREs, which are thought to mark vesicles and their targets[4], respectively, have less distinct functions than has been assumed. The *de novo* formation of VTCs implies that ER-derived vesicles fuse with one another. Fusion is likely to be driven by t-SNARE/v-SNARE interactions and, indeed, the 'early-Golgi' t-SNARE syntaxin 5 is found in VTCs (J. Stinchcombe and C. Hopkins, personal communication), which it must reach by recycling through the ER. So the initial fusion step in the secretory pathway (as in the endocytic pathway) may be between equivalent membranes that bear both t- and v-SNAREs. There is a precedent for this event in the homotypic fusion of yeast vacuoles[11].

The spontaneous generation of membranes resembling the *cis*-Golgi network from the ER is, for those who have seen the movie, a startling and unforgettable sight. It bears on another controversy, concerning the mechanism by which proteins pass through the stacked cisternae of the Golgi complex[6,12]. One model, derived from electron microscopic studies, invokes cisternal maturation. This requires the continuous generation of new, cargo-carrying cisternae which, as they pass through the Golgi stack, are modified by vesicle-mediated delivery and removal of components. They will eventually be converted into post-Golgi carriers.

The events seen by Presley *et al.*[1] could plausibly be interpreted as being the first step in this process. However, they do not rule out the alternative possibility — that cisternae have a stable existence, and that cargo is carried between them in vesicles. The delivery of VTCs to the *cis*-Golgi network would then do no more than compensate for the loss of membrane in vesicular form. Unfortunately, light microscopy cannot achieve a sufficiently high resolution to allow a distinction between vesicular and cisternal transport within the Golgi stack to be made, and the debate will continue. Spectacular though it is, GFP technology has its limits. □

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