Density of Newly Synthesized Plasma Membrane Proteins in Intracellular Membranes II. Biochemical Studies

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ABSTRACT Using two independent methods, incorporation of radioactive amino-acid and quantitative immunoblotting, we have determined that the rate of synthesis of each of the Semliki Forest virus (SFV) proteins in infected baby hamster kidney (BHK) cells is $1.2 \times 10^5$ copies/cell/min. Given the absolute surface areas of the endoplasmic reticulum and Golgi complex presented in the companion paper (Griffiths, G., G. Warren, P. Quinn, O. Mathieu Costello, and A. Hoppeler, 1984, J. Cell Biol. 98:2133-2141), and the approximate time spent in these organelles during their passage to the plasma membrane (Green I., G. Griffiths, D. Louvard, P. Quinn, and G. Warren 1981, J. Mol. Biol. 152:663-698), the mean density of each viral protein in these organelles can be calculated to be 90 and 750 molecules/$\mu$m$^2$ membrane, respectively. In contrast, we have determined that the density of total endogenous integral membrane proteins in these organelles is $30,000$ molecules/$\mu$m$^2$ so that the spike proteins constitute only 0.28 and 2.3% of total membrane protein in the endoplasmic reticulum and Golgi, respectively. Quantitative immunoblotting was used to give direct estimates of the concentrations of one of the viral membrane protein precursors (E1) in subcellular fractions; these agreed closely with the calculated values. The data are discussed with respect to the sorting of transported proteins from those endogenous to the intracellular membranes.

We have used the two membrane-spanning (spike) glycoproteins (E1 and p62) of Semliki Forest virus (SFV) as probes to follow plasma membrane (PM) proteins from their site of synthesis in the rough endoplasmic reticulum (ER) to the cell surface. During transport they must be separated from the endogenous proteins of the membranes they pass through, and concentrated with respect to the membrane. There are at present no quantitative data available even to define the extent of these processes.

In the accompanying paper, we have introduced the approach for estimating the densities (number of molecules per unit surface area) of the spike proteins of SFV in the ER and Golgi membranes. The absolute surface areas of ER, Golgi, and plasma membrane of an “average” baby hamster kidney (BHK) cell were estimated by stereological procedures. One aim of this paper is to determine the total number of molecules of SFV spike proteins in the membranes of the ER and the Golgi complex of an average infected BHK cell so that their densities can be calculated. The density of spike proteins in mature virions is already known, and direct comparison of the densities at various stages of intracellular transport can therefore be made. For direct measurement of the densities of viral protein in subcellular fractions, it is also necessary to know the total concentration of integral membrane proteins in the membranes of ER, Golgi, and plasma membrane. This is the second aim of this paper.

MATERIALS AND METHODS

Materials, cell culture, viral infection, and labeling of cells were as previously described (14).

Cell Counting: In each experiment, six extra dishes of cells were plated out, grown, and infected in parallel with the experimental cultures. Cell number was determined using a haemocytometer after releasing the cells by incubation with trypsin/EDTA. In some cases, cell number was determined directly by taking random photographs of the cells in situ using a $\times 25$ Zeiss water immersion lens. Cells were counted on the photographically enlarged pictures at a final magnification of $\times 100$. The results from the two methods agreed within 10%.

Quantitative Immunoblotting: Samples of cells or subcellular fractions were prepared for electrophoresis as described (14). Media samples were concentrated by precipitation with trichloroacetic acid (10% wt/vol final con-
centration). After 1 h at 4°C, the precipitates were collected by microcentrifuga-
tion. They were washed twice with ethanol/ether (1:2 vol/vol), then with ether, and allowed to air dry before being dissolved in electrophoresis sample buffer.

After electrophoresis on polyacrylamide gels, proteins were transferred to
nitrocellulose filters according to the method of Towbin et al. (32), and modified as described by Burnette (6) and Griffiths et al. (15). Protein was visualized by incubation with antiserum to E1, followed by iodinated protein-A and autoradiography. Quantitation was achieved by excising the radioactive bands with a scalpel and counting them directly in an NE1600 gamma counter. As described by Howe and Hershey (18), counts were linear with added antigen in the range 5–50 ng. In all cases, three standards were run on the gels to allow correction for variations caused by individual incubation conditions.

Subcellular Fractionation: This was performed as described by Renkonen et al. (24) or by Green et al. (14). The two procedures gave similar results for ER and plasma membrane. No Golgi-derived material was obtained using the former method. Washing with sodium carbonate was as described by Howell and Palade (19). The method essentially removes all laminal content of membrane vesicles and most of the peripheral membrane proteins (20). In this paper, we assume that the remaining proteins are integral, either spanning the bilayer or having a portion deeply embedded in it.

Estimation of Phospholipid and Cholesterol: Lipid extraction was performed as described by Bligh and Dyer (4). Total phosphorus was determined by the method of Rouser et al. (28) and cholesterol by the chole-
terol ester-cholesterol oxidase reaction (Boehringer, Mannheim).

Estimation of Protein and Mean Molecular Weight: Total
protein was measured using the Biorad reagent (Biorad Laboratories, München, Federal Republic of Germany) with immunoglobulin standards, or by the micro-Kjeldhal technique, modified as described by Jaenike (21) using ammonium sulphate standards. Results from the two methods agreed within 5%.

Protein molecular weights were determined on 10% SDS-polyacrylamide gels. These were stained with Coomarie Brilliant Blue (SERVA, Heidelberg, Federal Republic of Germany) and photographed with transmitted light using Agfa orthofilm. 35-mm negatives were scanned on an Optronix P-1000 densitometer using a 50-μm band width and the data analyzed by computer (31). Estimation of mean molecular weight of proteins in the sample was from computer calculation of the number of molecules at each data point and assigned a molecular weight by reference to protein standards (Biorad Laboratories) run in a parallel track.

RESULTS

To obtain figures for the total number of viral proteins in the ER and Golgi we have taken advantage of the fact that the approximate time spent in these organelles by the viral membrane proteins can be calculated from published data (14). It is therefore possible to calculate the average number of molecules present from the rate of synthesis of the viral proteins.

Rate of Synthesis of Viral Proteins

Synthetic rates can be estimated in a number of ways and we have used two completely independent methods to pre-
clude significant systematic errors.

MEASUREMENT BY INCORPORATION OF RADIOACTIVE AMINO ACIDS: We have measured the incorporation of [35S]methio-
one into protein by SFV-infected BHK cells, using a con-
stant amount of [35S]methionine and a range of concentra-
tions of unlabeled methionine. Incorporation was allowed to proceed for only 15 min to exclude the possibility of loss of labeled protein from the cells by viral budding. The results are shown in Fig. 1A. Linear regression analysis of the data points using more than 5 μg carrier methionine gave a best fit line of zero slope, indicating that the calculated synthetic rate was independent of the specific activity of the added methionine over this range. The intercept value is 2.59 × 10⁶ molecules of methionine incorporated/cell/min.

As the measured rate of synthesis was unaffected by the specific activity of the labeled methionine used (provided that there was more than 5 μg unlabeled methionine present), it is clear that the estimate of synthetic rate is not distorted by large intracellular pools of unlabeled methionine, nor by the equilibration of external and internal pools being slow in com-
parison with the period of labeling. BHK cells infected with SFV are essentially making only viral proteins. These are made in approximately equimolar amounts from a single mRNA, of which the complete coding sequence is known (13). In this case, then, the extrapolation from moles of methionine incorporated to number of proteins synthesized can be made, and gives a figure of 0.96 × 10⁶ translations of the viral 26S mRNA, per cell, per minute.

The experiments were repeated using [35S]cysteine as the label and very similar results were obtained (Fig. 1B). As with the methionine incorporation, the best line through data points using more than 5 μg unlabeled amino-acid had zero slope. The rate of synthesis, equivalent to 1.09 × 10⁶ copies of each viral protein/cell/min agrees well with the previous estimate.

The rates of synthesis at various times after infection are shown in Fig. 2. From 4 h postinfection, the rate stayed constant for 4 h, and was still 80% of maximum at 14 h. Even at 20 h, when the cells had begun to die, the rate had only dropped by 50%.

MEASUREMENT BY IMMUNOBLOTTING: To quantitate the rate of production of E1, samples were taken from cells and their media at different times after infection. These, together with standard amounts of E1, were run on polyacrylamide
Density of Endogenous Protein in Intracellular Membranes

To provide a reference point for subsequent estimation of E1 abundance in the intracellular membranes of infected cells, it was necessary to establish the density of host cell membrane proteins. If the average molecular weight of the proteins is known, the number of protein molecules can be determined. The area occupied by the associated lipid can be calculated because a molecule of phospholipid is known to occupy 63 Å², and a molecule of cholesterol 35 Å² (8, 11, 22, 33).

Subcellular fractions enriched in ER, Golgi, and plasma membranes were carbonate washed (19) to remove luminal and peripheral proteins. The amounts of lipid and protein found are given in Table I. The mean molecular weight of the proteins in each fraction was calculated from scans of polyacrylamide gels. Each sample was run at several concentrations to allow estimation of each fraction at a loading that was within the range over which protein concentration and optical density on the film negative were linear. Representative scans are shown in Fig. 5. The mean molecular weights

TABLE I

<table>
<thead>
<tr>
<th></th>
<th>ER</th>
<th>Golgi</th>
<th>Plasma membrane</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein</td>
<td>100</td>
<td>100</td>
<td>100</td>
</tr>
<tr>
<td>Mean molecular weight</td>
<td>46</td>
<td>49</td>
<td>51</td>
</tr>
<tr>
<td>Phospholipid</td>
<td>136</td>
<td>130</td>
<td>144</td>
</tr>
<tr>
<td>Cholesterol</td>
<td>9.8</td>
<td>19.9</td>
<td>33.6</td>
</tr>
<tr>
<td>Area occupied by lipid</td>
<td>3.1</td>
<td>3.2</td>
<td>3.9</td>
</tr>
<tr>
<td>Protein density</td>
<td>4.2</td>
<td>3.8</td>
<td>3.0</td>
</tr>
</tbody>
</table>

Units of measure: protein, phospholipid, and cholesterol, micrograms; the area occupied by lipid, microns² × 10⁻⁹ (calculated); and protein density (molecules/micron squared lipid area) × 10⁻⁹.
and the consequent estimates of the density of membrane proteins are given in Table I.

Density of E1 in Intracellular Membranes of Infected Cells

Values for the density of E1 in the rough ER and Golgi membranes of infected cells can be obtained both by calculation from the data obtained from whole cells, and by direct measurement of the protein in isolated subcellular fractions.

CALCULATED DENSITIES: The data given above on the rate of synthesis of E1 can be used, with the knowledge of the time taken for the molecules to pass through each organelle (14) and the morphometric data on the surface area of the organelles in the accompanying paper (16) to calculate the density of E1 in the rough ER and Golgi membranes. This data is summarized in Table II. Clearly the viral protein is very dilute at its site of synthesis, and is concentrated by several orders of magnitude during transport.

DIRECT MEASUREMENT OF E1 IN SUBCELLULAR FRACTIONS: Subcellular fractions were prepared from infected cells, and samples subjected to quantitative immunoblotting as described above. The results are presented in Table III, and are in excellent agreement with the calculated values of E1 densities. Attempts to quantitate the E1 present by direct scanning of Coomassie stained gels were frustrated by overlapping peaks of endogenous protein, although the viral protein could be seen and was clearly more abundant in the Golgi fraction than in the ER. These gels also indicated that the plasma membrane fraction as prepared from infected cells was heavily contaminated with ER; this was supported by the

TABLE II
Calculation of E1 Concentration in Intracellular Membranes

<table>
<thead>
<tr>
<th>Membrane</th>
<th>Surface area</th>
<th>Protein dwell time</th>
<th>No. of E1 mols</th>
<th>Concentration calculated</th>
</tr>
</thead>
<tbody>
<tr>
<td>ER</td>
<td>19,400</td>
<td>15</td>
<td>1.8 x 10^6</td>
<td>93</td>
</tr>
<tr>
<td>Golgi</td>
<td>2,100</td>
<td>15</td>
<td>1.8 x 10^6</td>
<td>860</td>
</tr>
<tr>
<td>PM</td>
<td>3,400</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Virus</td>
<td>0.008</td>
<td></td>
<td>180</td>
<td>22,000</td>
</tr>
</tbody>
</table>

The value used for the rate of synthesis of E1 was 1.2 x 10^5 mols/cell/min.
TABLE III
Concentration of the Viral Protein E1 in Carbonate Washed Subcellular Fractions of Infected BHK Cells, Determined by Quantitative Immunoblotting

<table>
<thead>
<tr>
<th></th>
<th>Total</th>
<th>ER</th>
<th>Golgi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Protein</td>
<td>100</td>
<td>100</td>
<td></td>
</tr>
<tr>
<td>E1</td>
<td>0.19</td>
<td>1.48</td>
<td></td>
</tr>
<tr>
<td>Surface area of associated lipid</td>
<td>3.1</td>
<td>3.2</td>
<td></td>
</tr>
<tr>
<td>Density</td>
<td>70</td>
<td>515</td>
<td></td>
</tr>
<tr>
<td>E1/total protein (%)</td>
<td>0.14</td>
<td>1.14</td>
<td></td>
</tr>
</tbody>
</table>

Units of measure, protein, E1, micrograms; surface area, microns$^2$ x $10^{-10}$ (calculated); density, molecules/micron$^2$ lipid area.

The density of endogenous proteins found in the BHK cell membranes was between thirty and forty thousand molecules/μm$^2$. There are, however, three systematic errors in this estimate, which do not tend to cancel. These are (a) adventitious proteolysis of endogenous membrane protein during the cell fractionation; (b) incomplete removal of peripheral proteins by the carbonate washing procedure; and (c) the contribution the membrane proteins made to the surface area. All would tend to make the estimate high. For the last point, there are cases for which this contribution has been measured; the range of values obtained is from 10–25% of the membrane area in systems as diverse as the erythrocyte ghost (11), Sindbis virus (17), and the retinal rod outer disc (10). The densities found are in good agreement with estimates for other membranes obtained by a variety of techniques (3, 7, 23, 25). It is interesting to compare these figures with an extreme case such as cytochrome c oxidase crystals, which should indicate an upper limit for packing proteins into a lipid bilayer (12). From X-ray and electron microscopic data, the density of “cytochrome oxidase monomers” was determined to be $1.7 \times 10^9/\mu m^2$. This is the value one would expect to obtain by freeze-fracture and counting of intramembrane particles. Each “monomer”, however, consists of 10 polypeptides, of which three are membrane-spanning. The density of integral membrane proteins is therefore $5.1 \times 10^9/\mu m^2$; the other proteins provide a good example of tightly bound, though strictly peripheral proteins. Despite the systematic errors, the correlation with results from other systems suggests that the estimates are reasonably accurate.

The density of E1 in the intracellular membranes is extremely low, constituting only 0.14% of the endogenous ER protein. Since the other viral spike protein, p62, is present in an equimolar amount, the total plasma membrane protein precursor in the ER is 0.28% of the endogenous protein. What limits this density is unclear, but it is reasonable that, as suggested by Rothman (26), the levels of non-ER proteins should be kept low to prevent the ER assuming the characteristics of other compartments. There has been one previous estimate of the density of plasma membrane precursor proteins in the ER (26). A value of 0.01% of that found in the plasma membrane was obtained using data from liver. Our data, obtained by direct measurement as well as calculation, give a figure 28-fold higher. The difference may simply reflect the much larger amount of ER and longer turnover time of plasma membrane proteins in hepatocytes. It should be noted here that the close agreement between the calculated and measured densities of E1 in the ER and Golgi membranes is in itself good evidence that most, if not all, of the membrane measured as ER or Golgi in the morphometric study is involved in the synthesis and transport of viral membrane proteins, and that the isolated membrane fractions are representative of those compartments.

The viral protein is concentrated some 240-fold, from a density of $0.9 \times 10^4$ molecules/μm$^2$ in the ER, to $2.2 \times 10^4$ molecules/μm$^2$ in virus particles. A 9-fold concentration is found after transfer from the ER to the Golgi complex. These experiments, of course, provide only an average figure and any concentration gradient across the Golgi stack would not be observed. However, the available immunocytochemical data (e.g., 14, 15) show no such gradient, which suggests that concentration steps occur during transport to and from not within the Golgi stack. If the transfer steps from Golgi to plasma membrane, and from plasma membrane to virus result in concentration of the same order of magnitude as that seen upon transfer from ER to Golgi, they would be more than sufficient to explain the densities observed. Data for the concentration that can be achieved at a single step are available only for the plasma membrane, where receptors are concentrated into coated pits. The best documented is the low-density lipoprotein receptor, which can be concentrated at least 100-fold in the plane of the membrane (1). The evidence that coated vesicles are involved in intracellular transport (27) makes it plausible that a mechanism of comparable selectivity is operating during transport from the ER and from the Golgi complex. The potential for concentration at just these two steps is clearly much higher than required.

It is not sufficient, however, to simply concentrate the proteins to be transported: they must also be purified from the endogenous proteins of the intracellular membranes that would otherwise necessarily contaminate them. Coated pits can not only concentrate selected proteins, but can also exclude others (5). The extent of exclusion, taking the raw data is between 10 and 100-fold. The data, obtained by immunoferritin binding to excluded antigens showed that labeling of coated pits was comparable with background labeling and the estimate is therefore a minimum figure. The product of the concentration and exclusion factors, $10^3 \times 10^4$, fold, is the purification obtainable in a single step. It can also be argued that for vesicular traffic to occur but leave the membrane compartments in balance, an equal and opposite...
traffic of vesicles is required, which returns material to the original donor membrane. This provides a further opportunity to collect any proteins that might have been transported in error; the purification achievable by a single such cycle would be in the range of $10^5$ to $10^6$-fold. These figures imply that selection of proteins to be transported would, in a single step, result in contamination by endogenous proteins of, at most, 25%: a complete vesicle shuttle cycle would lower this to <0.03%, though it must be noted that the data for concentration and exclusion apply to the plasma membrane. Whether intracellular selection mechanisms are equally efficient, and what level of contamination is acceptable to the cells are not yet known. The possible need for more than one purification step was first noted by Rothman (26), who proposed that purification would be best achieved by reselection from a partially purified pool of protein in a process analogous to fractional distillation. However, given that two steps are sufficient for purification, and that our results are generally applicable, purification could be achieved by a single vesicle shuttle cycle between two compartments, and would not require a stack of Golgi cisternae. We would like to thank Gerrit van Meer for extensive help with the cholesterol and phospholipid determinations, Keith Stanley for help with the computer analysis of gel scans, and Ruth Giovanelli for expert technical assistance. Brian Burke, Steve Fuller, and Karen Miller kindly and critically read the manuscript, which was typed by Annie Steiner.

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REFERENCES


