tion, were corrected for absorption and secondary extinction.

The orthorhombic crystals have unit cell dimensions (redetermined), $a = 14.454(5)$ Å, $b = 31.258(10)$ Å, $c = 12.057(5)$ Å. The crystal used for intensity measurements was a flat prism of thickness 0.04 mm, and only 831 of the 2010 independent reflections attainable within $\theta = 28°$ were found to have net intensities higher than three times the standard deviation.

The monoclinic crystals have unit cell dimensions (redetermined), $a = 26.734(8)$ Å, $b = 11.437(4)$ Å, $c = 9.321(4)$ Å, $\beta = 101.97(6)°$. Out of 3397 independent reflections attainable within $\theta = 28°$, 2349 were found to have net intensities higher than three times the standard deviation.

Using anisotropic thermal parameters for all atoms (hydrogen atoms were not included), the least squares refinement converged at conventional R values of 0.043 and 0.032, respectively, for the orthorhombic and the monoclinic crystals.

In both cases two bromine atoms and two ethylenethiourea sulphur atoms are coordinated to tellurium in a distorted square-planar *cis* arrangement. The bromine atoms are situated on twofold axes, and bridge two tellurium atoms. The result is a dinuclear cation of composition $[(etu)_2TeBr_2Te(etu)_2]^{2+}$. In the orthorhombic crystals the tellurium atoms and bromide ions are also situated on twofold axes.

The figure gives views of the cations in the two crystalline forms, with principal bond lengths and angles. The maximum e.s.d. of a bond length given is 0.003 Å.

As seen from the two *cis* S–Te–Br bond angles, the two *trans* S–Te–Br bond angles, and the two Br–Te–Br bond angles, and from the two Te–Br bond lengths, the cation in the monoclinic crystals differs slightly from the higher symmetry of the cation in the orthorhombic crystals.

The $TeBr_2S_2$ groups are nearly planar, the $TeBr_2/TeS_2$ dihedral angles being 4.0° in the orthorhombic form and 3.4° in the monoclinic form.

The average values of the Te–Br and Te–S bond lengths are 3.047 Å and 2.489 Å, compared to 2.994 Å and 2.449 Å for the corresponding bonds in the mononuclear complex *cis*-dibromobis(trimethylenethiourea)tellurium(II), $Te(trtu)_2Br_2$.[3] In the latter complex the Br–Te–Br bond angles are about 12° larger than in the present complex cations. The Te–Te distances are nearly the same in the two dinuclear cations, with an average value of 4.510 Å.

Acknowledgement. We wish to thank Prof. Olav Foss for the crystals, and for his interest.

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Received July 11, 1972.

Exchange of Brain Organelle Proteins with Soluble Cytoplasmic Proteins *in vitro*

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The present evidence suggests that all cellular protein constituents undergo continual synthesis and degradation.[1] The assembly of constituent proteins in intracellular structures and their degradation remain poorly understood.[2] The assembly of bacterial ribosomal proteins appears to be an ordered and co-operative process,[3] but contradictory data have been reported concerning their degradation as to whether they are degraded as a unit [4] or individually.[1] The latter alternative was proposed by an experiment *in vitro* showing a ready exchange of radioactive ribosomal proteins with a nonradioactive supernatant and *vice versa*.[1] Less is known about the exchange of protein in other organelles, although transfer of protein has been described between microsomes and mitochondria *in vitro*.[5] By contrast, the exchange of phospholipids between various structures is well established.[6,7]

This paper reports a consistent exchange of proteins between a supernatant fraction and different organelle fractions incubated

in vitro. The data support the hypothesis of Dice and Schimke[1] that some cellular protein structures are in equilibrium with cytoplasmic proteins. This prompts a mechanism by which organelle proteins may be renewed individually leaving the structure functionally intact. Reassembly of organelle proteins released to the cytoplasm may seriously obscure the interpretation of incorporation data obtained from subcellular structures.

Materials and methods. The experiments were performed with rat brain cortex. To obtain labelled organelles 20 μCi of ^{3}H-leucine (19 Ci/mmol) was injected in a lateral ventricle and the animals were killed 15 min later. At this time close to maximal incorporation of labelled leucine is known to occur in all subcellular fractions of rat brain.[8] Cortices were homogenized in 0.32 M sucrose containing 5 mM $MgCl_2$. Organelles were isolated by sucrose gradient centrifugation according to Gray *et al.*[9] The labelled organelle fractions were separately suspended in 3 ml of a nonlabelled supernatant fraction, and the nonlabelled organelles were accordingly suspended in a labelled supernatant. 1 ml aliquots were incubated at 37° for 30 min. At the end 8 ml of 0.32 M sucrose was added and the tubes were centrifuged at 1000 *g* for the nuclear, 14 000 *g* for the mitochondrial, synaptosomal and myelin, and 100 000 *g* for the microsomal samples for 10, 15, and 45 min, respectively. The supernatants obtained were mixed with an equal volume of 12 % TCA and sedimented to yield the TCA-supernatant containing free leucine and the pellet containing the soluble (cytoplasmic) proteins. The TCA-supernatant was counted in Bray's scintillation fluid; the pellet was washed twice with TCA, once with ethanol, ethanol—chloroform and ethanol—ether, dissolved finally in Soluene-100 and counted in toluene-PPO-POPOP scintillation fluid. The organelle pellets were washed twice with 0.32 M sucrose to remove the attached soluble proteins, precipitated with TCA and washed and prepared for scintillation counting as above. Protein was measured according to Lowry *et al.*[10]

Results and discussion. Exchange of proteins from labelled organelles to a nonlabelled supernatant is shown in Table 1. During the 30 min incubation all organelle fractions release radioactive proteins in the supernatant. The extent of exchange depends on the organelle studied and on the

Table 1. Exchange of proteins between radioactive organelles and nonradioactive supernatant fraction.

Labelled organelle	Radioactivity in a fraction (cpm/mg protein)		
	Before incubation organelle + supernatant	After incubation organelle	supernatant
Nuclei	885	2110[a]	220
Microsomes	3450	4410	590
Mitochondria	480	1800	45
Myelin	115	1000	20
Synaptosomes	360	1380	45

[a] Protein content of the organelle fractions after incubation (μg): nuclei 280, microsomes 840, mitochondria 110, myelin 20, synaptosomes 210, and supernatant 1000.

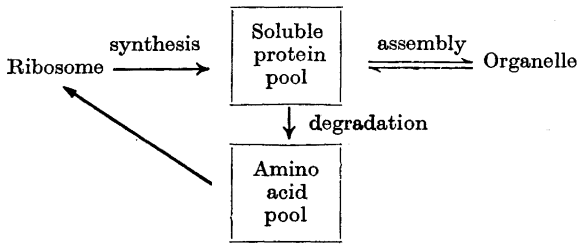

Fig. 1. The proposed scheme for intracellular protein metabolism. The assembled organelle proteins may exchange with the soluble protein to be degraded or to be reassembled in the organelle. The reassembly may seriously obscure data on the turnover of radioactive organelle proteins.

ratio of organelle protein to supernatant protein in an experiment. Myelin with 20 μg of protein has as much radioactive protein in the supernatant as in sedimentable myelin, while microsomes and synaptosomes (840 and 210 μg protein) have exchanged only 20 % of the protein. The recovery of protein-bound radioactivity is 60 % and of protein over 80 %. The disappearance of some labelled protein during the experiment is explained by the thorough washing of the organelle fractions to remove any soluble proteins. Proteolysis as indicated by increasing TCA-soluble radioactivity is observed only in the microsomal and myelin fractions (320 and 80 cpm, respectively).

Uptake of labelled proteins from the supernatant into nonlabelled organelles is shown in Table 2. All fractions take up labelled proteins from the supernatant reaching specific activities of 30 to 45 % (160 % in myelin) of the values quoted in Table 1. The recovery of protein and radioactivity is around 80 %. During the incubation microsomes bind 35 % of the total radioactive proteins in the supernatant. The corresponding proportion is less in other organelles, but soluble organelle proteins obviously make a large fraction of the total cell sap protein.

Table 2. Exchange of proteins between nonradioactive organelles and radioactive supernatant fraction.

Nonlabelled organelle	Radioactivity in a fraction (cpm/mg protein)		
	Before incubation organelle + supernatant	After incubation organelle	supernatant
Nuclei	2310	640[a]	2870
Microsomes	1920	1530	2450
Mitochondria	2400	720	2610
Myelin	3000	1650	2910
Synaptosomes	2220	620	2600

[a] Protein content of the organelle fractions after incubation (μg): nuclei 200, microsomes 990, mitochondria 170, myelin 20, synaptosomes 370, and supernatant 1200.

In this paper we have demonstrated a consistent exchange of labelled proteins between the supernatant fraction and various organelles. Whether the exchanged proteins are capable of restoring functional activity has not been studied, but has been demonstrated for liver ribosomes after a similar experiment.[1] These findings suggest that a proportion of protein constituents in cell structures is readily exchangeable with cytoplasmic proteins and that these proteins turn over individually (Fig. 1). If the scheme of Fig. 1 depicts physiological processes, the possible reassembly of proteins released into cytoplasm is a further complication in analysis of incorporation or turnover data of cellular protein constituents.

This study was supported by The *Sigrid Juselius Foundation* and by *The National Research Council for Medical Sciences*, Finland.

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Received July 3, 1972.