Ribosomes are distinct assemblies of protein and RNA chains, on which protein biosynthesis occurs in all organisms. Full functional understanding of this process still requires a detailed molecular model. Only active ribosomal particles crystallize. In all cases, particles from dissolved crystals are active even after several months, in contrast to the short lifetime of isolated ribosomes.

The best crystals are of the large (50S) ribosomal subunit. These particles have no internal symmetry and consist of about 32 different proteins and two RNA chains, with total molecular weight of 1.6 x 10^6. The largest crystals are of 50S particles from (I) Halobacterium marismortui (0.6 x 0.6 x 0.1 mm) and (II) Escherichia coli (1.5 x 0.3 x 0.2 mm).

Although fresh crystals of (II) diffract to 5.5 Å, the best crystals are of (I) determined. The mutated L6 x 10^6 particles from (I) halobacterial marismortui (0.6 x 0.6 x 0.1 mm) and of (II) Escherichia coli (1.5 x 0.3 x 0.2 mm). Using synchrotron radiation, cell dimensions of (I): 369 x 680 x 920 Å (P21 x 1 x 1) and of (II): 214 x 300 x 264 (P2221) have been determined.

Although fresh crystals of (II) diffract to 5.5 Å, the high resolution forms are lost after irradiation of 2-3 minutes with synchrotron beam, at -20°C. However, for crystals immersed in an inert hydrocarbon drop, mounted on glass rods and exposed to synchrotron beam for 2-3 days at cryotemperatures (i.e. 85 K), no radiation damage was observed. Thus a full data set could be collected from a single crystal.

A mutant (which lacks protein L11) of (II) was obtained. The mutated 50S subunits crystallize isomorphously with the native particles. Protein L11 from the wild type can be reconstituted into the mutated ribosomes. A heavy atom cluster, undecagold, with diameter of 8.5 Å was used for derivation by soaking and a full data set of this derivative was collected. This cluster was also modified to contain one chemically active group. It, as well as a radioactive mode compound, N-ethylmaleimide, can be covalently attached to 50S particles or to isolated ribosomal proteins through free sulfhydryl groups.

Three-dimensional reconstruction studies performed at 28 Å on ordered arrays of 50S particles from B. stea othermophilus resulted in a model which contains several projecting arms arranged around a cleft, which turns into a tunnel (up to 25 Å diameter, 100-220 Å long). This tunnel may provide the exit path for the nascent polypeptide chain. A similar image reconstruction study performed on 70S ribosomes from the same source at 43 Å resolution, shows clearly the separation between the two subunits and the location at which the protein biosynthesis reaction takes place.

This paper reports an investigation of the structural and thermodynamical modifications induced by γ-irradiation on distearoylphosphatidylcho line liposomes.

γ-Irradiation. Changes were observed in the shape of calorimetric peaks and in the corresponding phase transition temperatures. In particular the appearing of a shoulder was observed at about 20 K. The three phases characteristic of lecithins with identical acyl chains were detected also for the highest value of irradiation dose. The formation of lysolecithin and stearic acid upon phospholipid degradation was observed. The lysolecithin concentration increases as a function of irradiation dose, until a saturation value is reached for a dose of 40 K. These results correlate quite well with...
those obtained for interlayer and interchain distances and for the width of the main phase transition calorimetric peak. At the highest dose (~80 kGy) molecules of cross linked adjacent radicals and other molecular species are also formed. Appreciable differences, with some similarities, were observed in the behaviour of DSPC and DPPC liposomes under γ-irradiation.

For the calculation of the total energy, the following geometrical parameters of this helix model depending on the dihedral angles \( \varphi, \psi \) were calculated:

(i) the length per residue of the helix - \( k = 26 \) Å,
(ii) the angle of winding of the helix - \( \psi \) (deg.),
(iii) the helix diameter \( d = 2.75 \) Å,
(iv) the H-bond angles \( \omega_{n} = \theta_{n} = 120^\circ \) and \( \gamma_{n} = \theta_{n} = 120^\circ \) (n = 3, 4).

The calculated energy surface allows to define a 'low energy pathway' (LEP) in the \( \varphi, \psi \)-plane along which the vibrations of the regular polyglycine helix can take place. The changes of all the geometrical helical parameters (i)-(v) along the LEP enable us to give the following interpretation of the vibration of this helix model. The vibration of the helix can be divided into two regions along the LEP.

In the first region from A \( (\varphi_{A} = -72.0^\circ, \psi_{A} = -17.0^\circ) \)

up to B \( (\varphi_{B} = -71.5^\circ, \psi_{B} = -32.0^\circ) \) on the LEP the helix performs a longitudinal and a torsional vibration.

In the second region from B up to C \( (\varphi_{C} = -33.5^\circ, \psi_{C} = -71.5^\circ) \) on the LEP the helix changes only the stereo orientation of the peptide relative to the helix axis depending on the alteration of \( \varphi, \psi \)-angles (and in this connection, changes of the H-bond geometry). But there is no longitudinal and only a minor torsional vibration in this second region.