

SYMMETRY AND SELF-ORGANIZATION IN PROTEIN

E.Rapis

*Sackler Faculty of Medicine
Tel-Aviv University, Tel-Aviv 64239, ISRAEL
Phone: 03-752-5850, Fax: 972-3-691-8326 (Prof. Oseransky)*

When we look at the forms and structures of living matter, with their wonderful diversity, harmony and beauty, we unwillingly ask ourselves: what is the reason? Who is such extraordinary sculptor of living matter?

Although it is well known that the basis of both the structure and performance of biological systems is protein (*Albert et al.* 1989), it is still a question how protein plays its role. What features of protein give rise to symmetry of self-consistent behaviour of molecular ensembles? How do ordered three-dimensional forms appear (*Kolata* 1986, *Gilbert* 1991, *Richards* 1991, *Siman* 1992)?

As far as we know, up to now there have been no direct experiments on the model system "protein - water" which could enable one to observe visually, on micro- or macroscopic scales, the process of structural formation and self-organization of protein. In this regard our experiments, modeling the simple biological system "protein - water" *in vitro*, make it possible to follow the dynamics of symmetry generation in the process of self-organization of protein thus observing correlation between these two phenomena.

It has been found that on condensing a non-differentiated polymeric protein mass up to a particular critical level, the mass starts to break into fragments due to developing defects reminiscent of dislocation loops or cracks. In the process, separate indivisible structural "blocks" similar to cells are generated.

It is possible to hypothesize that at the critical level of condensation the protein molecules do not gain an ideal crystalline, or long-range-ordered structure. The molecules are most likely to be arranged in a structure with a lot of specific defects which are responsible for an increase in free energy of the system. On condensation when the molecules are brought close together, the number of such defects may considerably grow. It is believed in this case that the free energy of the mass under consideration increases with increasing structural density. When the density and free energy increase, the structural molecular vacancies are most probably aggregated into voids, dislocations or dislocation loops. As discussed by many authors (*Frenkel* 1949, *Geguzin* 1976, and others), the regions of defects form an effective source to disturb the

equilibrium in such molecular systems. It is in these regions that the effects suddenly undergo a catastrophical transformation from one size scale to another, or from one structural level to another. Such a discontinuous change in the non-equilibrium state may produce a qualitative shift in the boundary near-edge region of the protein mass. This can stimulate a diffusive vibrational process with energy and mass transport, *i.e.* with formation of space-and-time dissipative structures, or generation of self-sustained wave vibrations. According to the theory (*Nicolis, Prigogine 1993, Krinsky et al. 1984, Vassiliev et al. 1987*, and others), these wave vibrations order the medium.

We believe in our case that it is the above-mentioned self-sustained wave vibrations that order the protein molecular structure, transforming randomly arranged liquid polymeric chains (primary protein structures) into symmetric three-dimensional, functioning molecules of protein. In the process, protein sequentially changes its primary conformation for the secondary, tertiary and quaternary conformations. It has been established that such behaviour of protein is independent of chemical features of its structure and regular for any solvable protein (haemoglobin, albumen, globulin, crystallin, *etc.*). In addition the sense of the defect is perpetually repeated independently of the kind of protein.

One is inclined to think that it is just the defects that transmit, or "translate" symmetry from the molecular level to the macroscopic scale, since the direction of their slip "is closely related to the molecular crystallographic lattice" (*Geguzin 1976*) of protein.

At first, the homogeneous phase rearranges to a discrete phase with different kinds of symmetry (radial, transverse or helical). The symmetry appearing in a protein substratum under condensation can be related only to molecular or supermolecular orientation in the protein molecular system. At the same time the mechanism of "symmetry transfer" via defects can be related to a system of spatial waves as argued by Prati (*Prati 1994*).

Our experiments have shown that in an open system in non-equilibrium conditions the self-organization process in protein exhibits a specific mechanism providing the equilibrium state. This mechanism is not associated with chemical non-equilibrium as commonly believed (*Nicolis, Prigogine 1990, Hess 1980, Krinsky et al. 1984*, and others). The non-equilibrium state is produced in the boundary structural regions (defects) with no input of energy from the outside for inducing the self-sustained wave vibrations. This is a nonlinear process of protein self-organization.

It is worthwhile to note that the peculiarities of the non-equilibrium mechanism control the character of the self-organization process, because the energy turns out to be confined in-

side one structural block and can not freely transfer as in the Belousov - Zhabotinski reaction. This governs a specific structural configuration of self-organized protein, which consists of morphologically indivisible units, or blocks similar to cells with one helix and one centre being at rest. Such a configuration may be associated with the peculiarities of the self-sustained wave vibrations in a system with geometrical boundaries. The energy is concentrated inside a small volume of a three-dimensional cylindrical block. For this reason the energy "life-time" is extended and the energy dissipation postponed so that the transition phase elongates, providing the possibility of life.

Thus analyzing the self-organization process in the biological system "protein - water" on dehydration, we have observed special non-linear processes in the non-stable transition phase. Our experiments have shown that the system spontaneously generates an algorithmically repeating complicated structure similar to a turbulent structure in various media, for instance, in the case of the Belousov - Zhabotinski chemical reactions, optical phenomena (Prati 1994), and the processes in living organisms. Therefore a helical symmetry develops depending on the peculiarities of the self-sustained wave vibrations in active media. As the helical symmetry inevitably develops in protein, it is thought that protein is an active medium in non-equilibrium conditions, because helical waves represent a fundamental property of active media.

The principal result of this work is as follows: for a protein in the system "protein - water" with no external energy sources appropriate for living systems, we have reliably established a high energetic potential in structural transformations under evaporation of water and condensation. The result has been reproduced in all the experiments. Note that the potential correlates with the protein mass.

Our experiments have shown that nature had brought into existence indeed an exceptionally witty mechanism to gain and concentrate energy seemingly "from nothing". The surprising point is that at the same time the mechanism is sufficient to reproduce biological structural forms. In the system the transmission of information on the form of symmetry therewith occurs. This appears to be possible at standard conditions, for instance, at an ordinary temperature sufficient to evaporate water. Self-organization of protein is closely connected with the developing symmetry, for both the self-organization and symmetry are controlled by physical and chemical properties of biological macropolymeric molecules of protein.

The above presentation is a result of observation of the systems *in vitro* and the related qualitative consideration and characterization. In this connection the most important problem is a quantitative characterization and analysis of the phenomenon revealed experimentally.