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Molecular gyroscope as a likely target for weak electromagnetic fields in biological systems

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Introduction

The mechanism based on the interference of ion quantum states within the protein cavity predicts variety of complicated dependences of biological responses on electromagnetic field parameters [1–5]. In many cases they match nicely experimental observations. However, the mechanism relies on the serious physical postulate, that the thermalization time of an ion inside the cavity exceeds its lifetime, i.e. the time of an ion stay within the cavity before escape. It is reasonable therefore to use conservation lows of a rotational dynamics in order to overcome that difficulty. The close interrelation of rotations and magnetic fields regarding magnetic field effects in biology was studied first in [4–5]. Here, another aspect of such a relation is developed.

Results

Consider a dipole molecular group that are attached within the cavity to its walls in two points, i.e. by two covalent bonds, thus forming a group that may rotate inside the cavity without direct contacts with walls. Such a construction is referred to as the gyroscope. In the case, it is a molecular gyroscope. Of importance is the fact that thermal oscillations of the gyroscope's seats make only zero torque about the axis of rotation. This leads to just relatively slow thermalization of a gyroscopic degree of freedom. Relaxation is due to dipole electromagnetic radiation and long-range van der Waals interaction with thermalizing walls, the latter being highly predominant factor. As far as the interaction potential, the Lennard-Jones potential, decreases as $1/r^6$ and walls' inner surface grows as r^2, the overall van der Waals contribution falls directly with $1/r^4$. That is, relaxation quickly diminishes with the cavity size to grow. Usually, relaxation time is inversely proportional with the energy exchange, being about 10^{-10} s at 1 Angstrom scale. Consequently, e.g. at 100 Angstrom cavity radius the relaxation time will be 0.01 s in order of magnitude. This is enough for the ion interference mechanism to display itself [4]. Probably, such roomy cavities are formed by ensembles of a few protein globules, between them. For example, amino acid molecules might be built in such cavities, organizing two chemical bonds at distant ends of the molecule, third polar group being free to interact chemically with a special active site on the inner wall surface. Such a molecule as a whole rotational dynamic unit features by a single degree of freedom, polar angle φ, that makes it easy to analyze its behavior in a magnetic field. Hamiltonian of the system in a magnetic field $H(t)\|z$ in line with the axis of rotation has the form

$$H=\frac{L^2}{2I}-\omega(t)L,\ \omega=\frac{QH}{2Ic},\ I=\sum_i M_i r_i^2\sin^2\theta_i,\ Q=\sum_i q_i r_i^2\sin^2\theta_i,\ L=-i\hbar\frac{\partial}{\partial\varphi}.$$

Here I and Q are moment of inertia and "charge moment of inertia", L is the angular momentum operator, and M_i, q_i, r_i, θ_i are mass, charge, and spherical coordinates of an i-th atom of the molecule. We suggest that "freezing" of the angular distribution of the

probability density of the rotating group results in a conformational change inside proteins that in turn activates them to modulate biochemical processes. Using the method [1], the "magnetic" part of the relative probability of such a change may be found. It determines both frequency and amplitude dependences of the probability of a biological effect in a magnetic field $H_{DC}+H_{AC}\cos(\Omega t)$. Predicted frequency and amplitude spectra have essentially the same form as in the case of the ion interference in protein cavity [1]:

$$f'_{max}=\frac{m}{n},\quad P(h')\propto J_n^2\left(m\frac{h'}{f'}\right),\quad f'=\frac{\Omega}{\Omega_r},\quad h'=\frac{H_{AC}}{H_{DC}},\quad \Omega_r\equiv\frac{QH_{DC}}{Ic},$$

where P is the probability of an effect, J_n is the first kind Bessel function of the n-th order, n and m are small integers. Frequency peaks' relative intensities depend on the populations of energy levels with different rotational quantum numbers. Interference of the molecular gyroscope differs from that of ions in that that peak frequencies are defined with respect to the rotatory frequency Ω_r, which is a rotational equivalent of the cyclotron frequency. So, positions of frequency peaks may differ from the cyclotron series. The model also provides 'windowed" spectra of sensitivity to electromagnetic fields in the microwave range.

Conclusions

Today, the model is a unique one to fix the known kT-problem in magnetobiology. The only postulate it relies on is an existence of more-or-less freely rotating molecular groups inside macromolecular cavities. Unfortunately, rotating groups cannot be detected by usual x-ray methods, so their existence remains under the question until proper indirect methods are developed. Beside amino acids within protein cavities, probably, the Watson-Crick base pairs adenine-thymine and guanine-cytosine, which bond DNA strands into the double-helix, might form the molecular gyroscopes within the scope of activity of some enzymes like the topoisomerase that removes supercoils from DNA thus making base pairs free of inter-base hydrogen bonds and making them to rotate freely for a time. It is interesting to note that combining the "immunity" of the molecular gyroscope to thermal environmental disturbances with individual molecular rotations [4] we obtain a possibility, however just hypothetical, to explain biological effects [6] of superweak magnetic fields of order of nano and picoTesla.

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