Quantum Decoherence and Quantum-Holographic Information Processes: From Biomolecules to Biosystems

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Abstract. Our recently proposed quantum approach to biomolecular recognition processes is hereby additionally supported by biomolecular Resonant Recognition Model and by quantum-chemical theory of biomolecular non-radiative resonant transitions. Previously developed general quantum-decoherence framework for biopolymer conformational changes in very selective ligand-proteins/target-receptors key/lock biomolecular recognition processes (with electron-conformational coupling, giving rise to dynamical modification of many-electron energy-state hypersurface of the cellular quantum-ensemble ligand-proteins/target-receptors biomolecular macroscopic quantum system, with revealed possibility to consider cellular biomolecular recognition as a Hopfield-like quantum-holographic associative neural network) is further extended from nonlocal macroscopic-quantum level of biological cell to nonlocal macroscopic-quantum level of biological organism, based on long-range coherent microwave excitations (as supported by macroscopic quantum-like microwave resonance therapy of the acupuncture system) - which might be of fundamental importance in understanding of underlying macroscopic quantum (quantum-holographic Hopfield-like) control mechanisms of embryogenesis/ontogenesis and morphogenesis, and their backward influence on the expression of genes.

Introduction

Two unresolved issues of the (semi)classically addressed problems in molecular biophysics are unreasonably long time necessary for change of biopolymer conformations and directiveness of selective biomolecular recognition processes - implying their essential quantum nature [1].

The quantum nature of biomolecular conformational transitions can be supported by experimentally observed poorly dimensionally-sensitive dispersion laws (which is generally the case of any internal more or less delocalized quasiparticle excitations in any condensed-state quantum system: electrons, optical phonons, conformomes, etc. [2,3]). On the contrary, (semi)classical kinetic (nonstationary) predictions imply the continuous map/conformation change \( k_i \rightarrow k_f \), which requires a sequence of \( n \) local non-commuting successive elementary transformations (local rotations of characteristic time \( \tau_o \)), with the time necessary for the net transformation much longer than characteristic time necessary for a local rotation \( (\tau_n \sim n\tau_o \gg \tau_o) \) and the frequency of the corresponding global transition much lower than the frequency of a local
rotation \( (f_n \sim 1/n\tau_o \sim f_o/n < f_o) \) - strongly dependent on a degree of polymerization \( n \) (in contradistinction to experiments).

The quantum nature of the process of biomolecular recognition can be supported by high efficacy of the Resonant Recognition Model (RRM) confirmed on more than 1000 proteins from more than 30 functional groups [4] (with numerous potential practical advantages in the fields of molecular biology, biotechnology, medicine, agriculture and nanotechnology) - based on findings that there is a significant correlation between the spectra of the numerical presentation of constitutive elements of primary sequences (amino acids, nucleotides) and their biological activity or interaction in the corresponding biomolecules (proteins, DNAs). The RRM model interprets this linear information by assigning the electron-ion interaction potential (EIIP) value to each constitutive element of the primary sequence thus describing their average energy states of valence electrons [5], with subsequent using of signal analysis methods in FFT transforming this numerical series into single-electron wavenumber/RRM frequency domain and determining the common frequency components as peak frequencies in the multiple cross-spectral function for a group of primary sequences [4]. The presence of peak with significant signal-to-noise ratio in a multiple cross-spectral function of a group of sequences with the same biological function means that all of the analyzed sequences within the group have this single-electron RRM frequency component in common, with the following general conclusions: (i) such a peak exists only for the group of biomolecules with the same sequence; (ii) no significant peak exists for biologically unrelated biomolecules; (iii) peak frequencies are different for different biological function; (iv) ligand-proteins and their biomolecular target-receptors have the same characteristic frequency in common but almost opposite phase - providing also novel theoretical possibilities for protein de novo design with desired functions.

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The quantum nature of biomolecular transitional processes can be also supported by the theory of non-radiative resonant transitions in mono-molecular and bi-molecular reactions [6], realized through intermediate quantum-coherent superpositions of the externally activated electronic-vibrational states of the participating biomolecules. Within the framework of general quantum-chemical Hamiltonian (including kinetic energies and Coulomb interactions of all biomolecular electrons and nuclei) and Born-Openheimer adiabatic approximation (of separated biomolecular electronic and vibrational degrees of freedom), the (quasi)classical problem of many-electron hypersurface \( E_o(\phi^{(k)}) \), not adiabatically well-defined when traversing between two adjacent local minima, is replaced by better defined problem of two (virtually intersecting) isomeric many-electron hypersurfaces (hyperparaboloids) serving as potential hypersurfaces for two vibrational (isomeric) problems. In this approach, by external perturbation of the isomers, at this very intersection the conditions for electronic-vibrational non-radiative resonant transitions between the two isomers \( (i, f) \) are achieved: these resonance electronic-vibrational states of two isomers are transformed from the corresponding (nonperturbed) products of electronic and vibrational wavefunctions \( (\phi^{(i)}_e \phi^{(i)}_v, \phi^{(f)}_e \phi^{(f)}_v) \) into (perturbed) symmetrized superpositions \( (\phi^{(i)}_e \phi^{(i)}_v \pm \phi^{(f)}_e \phi^{(f)}_v)/\sqrt{2} \), and their (nonperturbed) energies from resonating (equal) superpositions of the ground electronic energies of corresponding minima of many-electron hypersurface and vibrational energies of higher excited states \( (E^{(i)}_e + E^{(i)}_v = E^{(f)}_e + E^{(f)}_v) \) into (perturbed) slightly split energy doublet \( (E^{(i)}_e + E^{(i)}_v + \frac{1}{2}\Delta E, E^{(i)}_e + E^{(i)}_v - \frac{1}{2}\Delta E) \), with \( \Delta E = (E^{(i)}_e + E^{(i)}_v)S^{(i,f)}_{ev} \) (where electronic-vibrational overlap integral between the two resonating isomeric states \( (i, f) \) is \( S^{(i,f)}_{ev} = \int \int \phi^{(f)}_e \phi^{(f)}_v \phi^{(i)}_e \phi^{(i)}_v dV_e dV_v \approx S^{(i,f)}_{v} \), while \( S^{(i,f)}_{ev} \) and \( S^{(i,f)}_{v} \) are corresponding overlap integrals of vibrational and electronic components. In the first approximation, the matrix element
of dipole transition from \( i \)-th to \( f \)-th isomer is given by 
\[
\mu^{(i,f)} \approx \int \int \phi^{(f)}_v \phi^{(f)}_e (\mu_e + \mu_v) \phi^{(i)}_e \phi^{(i)}_v \cdot dV_e dV_v
\]
\( dV_e dV_v \approx \mu^{(i,f)}_v S^{(i,f)}_v + \mu^{(i,f)}_v S^{(i,f)}_e \), where \( \mu_e \) and \( \mu_v \) are corresponding electronic and nuclear components of the operator of total dipole moment. It is obvious that transition between two isomers will be allowed when components of corresponding dipole moments, \( \mu^{(i,f)}_e \) and \( \mu^{(i,f)}_v \), and overlap integrals, \( S^{(i,f)}_v \) and \( S^{(i,f)}_e \), do not vanish!

From the above consideration, it can be concluded that allowed transitions between isomeric states \((i, f)\) are possible only for close states with nonvanishing overlap integrals \( S^{(i,f)}_v \) and \( S^{(i,f)}_e \), or in cascade resonant (vibronic) transitions between close intermediate participating isomeric states.

Also, during these resonant transitions the perturbed biomolecular system is shortly described by quantum-coherent superposition \((\phi^{(i)}_e \phi^{(i)}_v \pm \phi^{(f)}_e \phi^{(f)}_v)/\sqrt{2}\), before its quantum decoherence into final electronic state \( \phi^{(f)}_e \) or into initial electronic state \( \phi^{(i)}_e \) (with subsequent deexcitations into lower vibrational states).

This picture fully approves our previous approach [1] of employing the fundamentals of the quantum decoherence theory, when we were able to reproduce both, existence and stability of the (stationary) ligand-proteins/target-receptors key/lock nonmatching and matching conformations, and the short time scales for the quantum-mechanical processes resulting effectively in (nonstationary) nonmatching-to-matching conformational transitions in selective ligand-proteins/target-receptors key/lock biomolecular recognition processes under external (e.g. compositional/chemical, thermal, optical ...) influences on the cell's complementary cytoplasmatic environment. As these electron-conformational coupling processes give rise to dynamical modification of the many-electron energy-state hypersurface of the cellular quantum-ensemble ligand-proteins/target-receptors biomolecular macroscopic quantum system, this revealed possibility to consider cellular biomolecular recognition as a Hopfield-like quantum-holographic associative neural network.

More concretely, the time evolution \( |\phi^{(i)}(t)\rangle_k \) of the quantum-coherent state of the all ligand-proteins/target-receptors key/lock nonmatching and matching conformations \((\phi^{(i)}\)) might be described in Feynman's representation by quantum-holographic Hopfield-like neural network, while the time evolution \( \hat{\rho}_k(t) \) of the classically-reduced stochastic state of the all ligand-proteins/target-receptors key/lock nonmatching and matching conformations might be described by classical Hopfield-like neural network, represented by changes in the shape of the potential hypersurface in the many-electron hypersurface \( E_k(\phi^{(i)}) \) of the cell's ligand-proteins/target-receptors biomolecular macroscopic quantum system - achieved by exciting cell's ligand-proteins/target-receptors biomolecular macroscopic quantum system from initial stationary classically-reduced state \( \hat{\rho}_k = \sum |C_i|^2 |\phi^{(i)}\rangle_k \langle \phi^{(i)}| \) via intermediate nonstationary excitation (during \( T_{\text{ext}} \) quantum-coherent superposition \( |\phi^{(i)}(t)\rangle_k = \sum C_i(t)|\phi^{(i)}\rangle_k \) and nonstationary relaxation (during \( T_{\text{rel}} \) superposition \( |\phi^{(i)}(t)\rangle_k = \sum C_i(t)|\phi^{(i)}\rangle_k \) into subsequent (during nonstationary decoherence transition \( \tau_D \)) final stationary classically-reduced state \( \hat{\rho}^{\infty}_k = \sum |C_i|^2 |\phi^{(i)}\rangle_k \langle \phi^{(i)}| \), with the relative number (concentration) of conformations likely to be different, \( |c_i|^2 \neq |C_i|^2 \). In effect, there has occurred a nonmatching-to-matching conformation change, at least for a sample of molecules in a solution - which is exactly the effect we search for!

Since it is expectable \( T_{\text{ext}} + T_{\text{rel}} >> \tau_D \), the duration of the nonmatching-to-matching conformation nonstationary change in our model is of the order of \( T \approx T_{\text{ext}} + T_{\text{rel}} \) - in obvious contradistinction with the estimates based on the (semi)classical analysis.
In the context of the Resonant Recognition Model mentioned above, the same characteristic single-electron RRM frequency, and almost opposite phase, presumably characterizes not only biomolecular protein and target general function, but also their macroscopic quantum biomolecular recognition/interaction on the level of biological cell - possibly by externally activated (compositionally/chemically, thermally, optically, ...) ligand-proteins/target-receptors (high-energy) RRM quantum-resonantly electron-electron coupling accompanied by $\phi^{(i)}$-annihilation and $\phi^{(f)}$-creation conformones’ quanta in (low-energy vibrational) two-conformational transitions $\phi^{(i)} \to \phi^{(f)}$ (giving rise to (energy-favorable) protein/target many-electron energy-deepening of the final state $\phi^{(f)}$ and ligand-proteins/target-receptors many-electron energy-shallowing of the initial state $\phi^{(i)}$ on the macroscopic quantum level of cell, i.e. to dynamic modification of the many-electron hypersurface $E_e(\phi^{(k)})$ of the cell’s ligand-proteins/target-receptors biomolecular macroscopic quantum system [1], in full analogy with the situation of learning in Hopfield associative neural networks [7] as already revealed in associative-memory-like protein-conformation-recognition [8]).

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The underlying quantum coherent nonlocality mentioned above seems to be even extended on the macroscopic quantum level of biological organism, as supported by macroscopic quantum-like microwave resonance therapy of the acupuncture system [9-11]. In the context of the general quantum-chemical considerations applied above on the level of biomolecular transitions, when extending many-electron system from the level of cell to the level of acupuncture system - it can be concluded that allowed transitions between many-electron acupuncture states $i$ and $f$ are also possible only for close states with nonvanishing overlap integrals $S_{i,f}$, or in cascade resonant transitions between close intermediate participating acupuncture states - presumably based on low-energy long-range coherent microwave Frohlich excitations of strongly polarized molecular subunits in the cell membranes and cytoskeleton proteins [12,13].

Also, during these resonant transitions the perturbed acupuncture system is shortly described by quantum-coherent superposition, before its quantum decoherence into final electronic state $\phi^{(f)}$ or into initial electronic state $\phi^{(i)}$ (with subsequent deexcitation into lower microwave energies).

As these electron-microwave coupling processes give rise to dynamical modification of the many-electron energy-state hypersurface of the acupuncture macroscopic quantum system, this also reveals possibility to consider acupuncture system as a macroscopic Hopfield-like quantum-holographic associative neural network. This is also supported by necessary conditions for decoherence process, which point out that defining of open quantum system and its (complementary) environment is a simultaneous process - providing also conditions for decoherence process in the context of existence of relative borderline [14]: open quantum system $S$ |(complementary) environment $E$.  

So, we can re-define open quantum system $S$ (to include acupuncture system) and its (complementary) environment $E$. Therefore, by applying quantum decoherence theory, the quantum-coherent state of the acupuncture system $S_i$, $\left| \phi_k \right>_{S_i}$, might be described by superposition of its all possible states $\left| \phi_k \right>$, which after quantum collapsing into classically-reduced state gives rise to stochastic state described by density matrix $\rho_{S_i} = \sum_k |c_k|^2 \left| \phi_k \right> \left< \phi_k \right|_{S_i}$, with probabilities $|c_k|^2$ of the realization of one of the classically decoherent states $\left| \phi_k \right>_{S_i}$ - in quantum measurement-like process upon the initial quantum-coherent state $\left| \phi_k \right>_{S_i}$. The time
evolution $|\phi^k(t)\rangle_{S_k}$ of the quantum-coherent state of the acupuncture system might be described in Feynman's representation by quantum-holographic Hopfield-like neural network, while the time evolution $\tilde{\rho}^{k}_{S_k}(t)$ of the classically-reduced stochastic state of the acupuncture system might be described by classical Hopfield-like neural network, represented by changes in the shape of the potential hypersurface in the acupuncture energy-state space $E_{S_k}(\phi^k)$ - under external stimuli.

The mentioned quantum-holographic picture of cellular biomolecular recognition processes and acupuncture system implies that quantum-holographic hierarchical parts carry information on wholeness, enabling subtle quantum-holographic fractal coupling between different hierarchical biophysical levels - including various acupuncture projection zones and corresponding organs and cells, with underlying macroscopic quantum-informational control mechanisms of embryogenesis/ontogenesis and morphogenesis and their backward influence on the expression of genes [11], starting from the first fertilized cell division which initializes differentiation of the acupuncture system of (electrical synaptic) “gap-junctions” [13,15].

This underlying quantum-coherent nonlocality might be of fundamental importance in understanding macroscopic (quantum) holistic very nature of psychosomatic health and diseases as well [11] - implying also a fuzzy borderline between quantum coherent (nonstationary) and semi-classical decoherent (stationary) manifestations of the acupuncture (as well as any other) macroscopic quantum condensed-state system. On the same line, in the framework of two cognitive modes of consciousness (Hopfield-like quantum-holographic quantum-coherent direct unconscious and classically-reduced indirect conscious ones) [16], conditions of transformations of one mode into another can be considered, with related significant unconscious-contextual psycholinguistic and psychotherapeutic implications [17].

Conclusion

Our previous results [1], describing general quantum-decoherence framework for biopolymer conformational changes in very selective ligand-proteins/target-receptors key/lock biomolecular recognition processes, followed by electron-conformational coupling giving rise to dynamical modification of the many-electron energy-state hypersurface of the cellular quantum-ensemble ligand-proteins/target-receptors biomolecular macroscopic quantum system, revealed possibility to consider cellular biomolecular recognition as a Hopfield-like quantum-holographic associative neural network. The quantum nature of these processes is additionally supported by the biomolecular Resonant Recognition Model (RRM) findings [4] that the same characteristic single-electron RRM frequency, and almost opposite phase, characterize biomolecular ligand-proteins and target-receptors general function, i.e. their biomolecular recognition/interaction; on the other hand, the quantum nature of biomolecular process can be also supported by quantum-chemical theory of non-radiative resonant transitions in mono-molecular and bi-molecular reactions [6], realized through intermediate quantum-coherent superpositions of the externally perturbed electronic-vibrational states of the interacting biomolecules. This underlying macroscopic quantum nonlocality on the level of biological cell seems to be even extended to the macroscopic quantum level of biological organism, based on long-range coherent microwave excitations (as supported by macroscopic quantum-like microwave resonance therapy of the acupuncture system [9-11]) - which might be of fundamental importance in understanding underlying macroscopic quantum (quantum-holographic Hopfield-like) control mechanisms of embryogenesis/ontogenesis and morphogenesis, and their backward influence on the expression of genes, with significant psychosomatic and cognitive macroscopic-quantum-holographic bioinformational implications as well [16,17].
References


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