PHYSICS OF STRUCTURAL CHEMISTRY AND BIOMOLECULES WITH THE ATOMIC MODELS OF BSM – SUPERGRAVITATION UNIFIED THEORY

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ABSTRACT

The bond directions between atoms in molecules are important feature in structural chemistry and biomolecules. The proteins have amazing properties of guiding the energy along their long chains and preserving own three-dimensional structure in proper environments. These features cannot obtain satisfactory explanations by the quantum mechanical models of the atoms. A wide range interdisciplinary study, using a different theoretical approach, indicates that the quantum mechanical models do not describe the full physical features of the atoms. Based on an alternative concept about the physical vacuum, the Basic Structures of Matter – Supergravitation Unified Theory (BSM-SG) reveals a non-spherical shape of the elementary particles that build atomic nuclei as fractional 3D structures. The obtained physical models of the atoms exhibit the same energy levels as the quantum mechanical models, while the positions of the electron orbits responsible for chemical bond directions are defined by the nuclear structure. The derived atomic models match quite well the row-column pattern of the Periodic table of Mendeleev. They allow to analyse the physical conditions behind the structural and bond restrictions of the atoms connected in molecules. The existing data base about the atomic structural compositions of the organic and biomolecules provides an excellent opportunity for test and validation of the derived physical models of the atoms. The BSM-SG atomic models allow a new original method for theoretical analysis of complex molecules and biomolecules.

Keywords*: chemical bond directions, Levinthal's paradox, C-value paradox of DNA*

1. Introduction

Despite the huge number of possible configurations of the atoms in the proteins they fold reliably and quickly to their native state. From a point of view of the Quantum mechanical considerations, this effect, known as a Levinthal's paradox, is not explainable. A protein molecule of 2,000 atoms, for example, should possess an astronomical number of degrees of freedom. The observations show that this number is drastically reduced by some strong structural restrictions, such as bond lengths, and restricted angle range of bond connections and rotations. The stable appearance of the secondary and tertiary structures of the proteins indicates also that some additional restrictions take place in a proper environment. All this restrictions could not get satisfactory explanation by the Quantum mechanical models of the atoms. An extensive interdisciplinary study in different fields of physics indicates that the Quantum mechanical models of the atoms are rather mathematical models than physical ones, so they are not able to provide all the physical features that the real atoms possess.

2. Atomic models according to the BSM-SG theory

The Basic Structures of Matter – Supergravitation Unified Theory (BSM-SG), presented elsewhere [1,2,3] allowed derivation of quite different physical models of the atoms, possessing rich physical structures, while characterized by the same energy level of excitation.

The internal structure of the proton and neutron shown in Fig. 1 is revealed by analysis of particle data using the mass equation derived in §3.13.3, Chapter 3 of BSM-SG. The proton core length (LPC) is validated by the Balmer series model (Chapter 7 of BSM-SG) and by vibrational models of simple molecules (Chapter 9 of BSM-SG). The overall shape of the proton is a torus-like structure but twisted like the number 8. The plane projection of the proton shape resembles a Hippoped curve with parameter $a = \sqrt{3}$. The twisting (and folding) direction is strongly defined by

the underlined structures of pion and kaon inside the proton (neutron) envelope. Consequently, all protons (neutrons) involved in atomic nuclei have one and the same handedness of the helical structures they are built of. This defines the twisting (folding) direction of the proton (neutron).

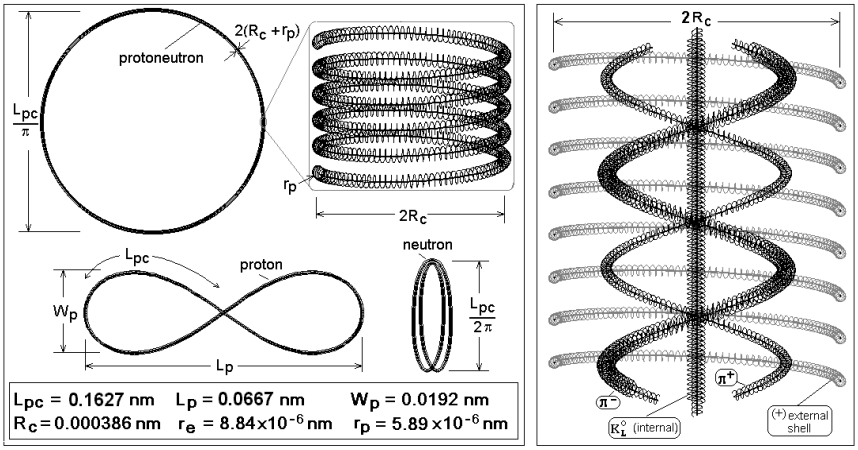
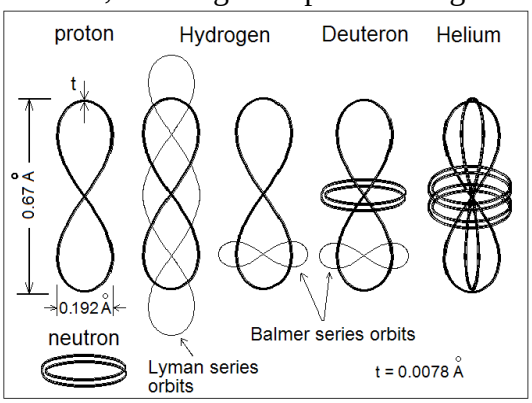


Fig. 1. Overall shape (left side) and internal structures of proton and neutron (right side). The outside helical structure is positive. Inside are 3 helical structures: – a negative pion (+), a positive pion (-) and a central kaon. All helical structures are stable because they are closed tori. If the external positive structure is broken (in particle colliders) the internal pions and kaon are cut and decay.

The question why the shape of the Periodic Table is not a simple square but is so complex has not been answered from the time of Mendeleyev's discovery in 1869. Using the shapes of the proton and neutrons as fractal 3D structures permitted understanding the build-up trend of the atomic nuclei. It was found that the properties of the build-up trend matches perfectly the raw-column pattern of the Periodic table of the elements.

Fig. 2. illustrates the overall shapes of the proton, neutron, Hydrogen (with Balmer and Alpha series orbits), Deuteron and Helium. Fig. 3. illustrates the Z-number build-up trend of stable elements, showing the spatial arrangement of the protons and neutrons in the atomic nuclei.



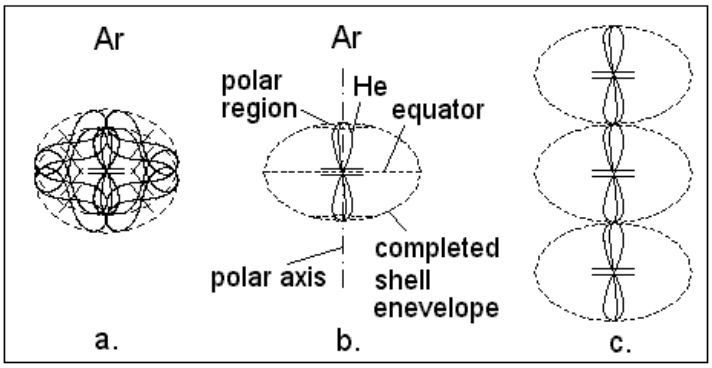


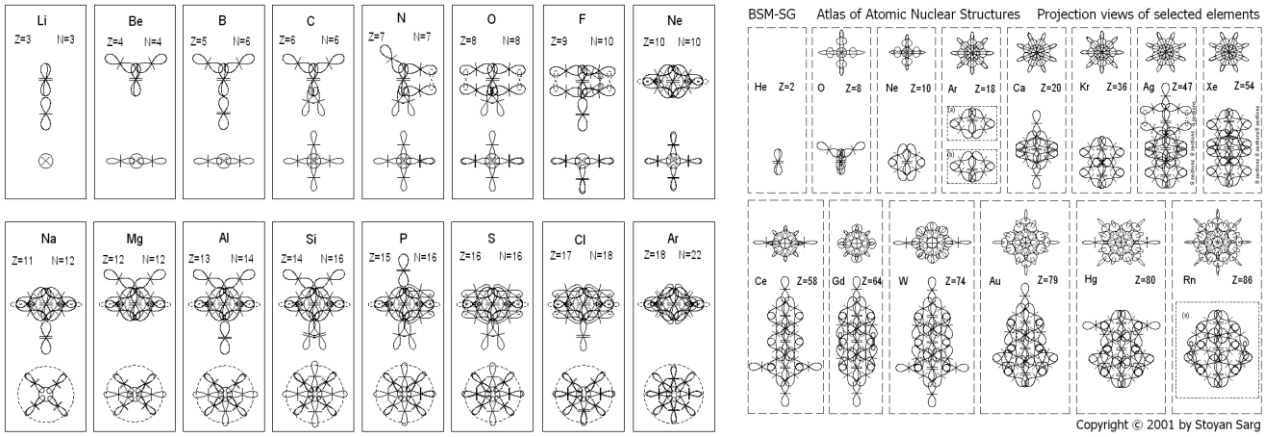
Fig. 2. Overall shapes of the proton, neutron, Hydrogen (with Balmer and Alpha series orbits), Deuteron and Helium. The calculated dimensions are in Angstrom units (1A = $1x10^{-10}$ (m)

Fig. 3. Z-number build-up trend of stable elements showing the spatial arrangement of the protons and neutrons in the atomic nuclei. a. – Polar axis section of Argon nucleus, b. – simplified drawing of Ar nucleus, c. - a chain structure in heavier elements.

It is known that the single neutron is not stable and decays to a proton. The reason is that the locked electrical charge cannot be held in proximity the core structure for a long time. It is unlocked

when the folded torus is unfolded to the shape of proton. The neutron however is stable when over the proton, forming in such way a deuteron and helium nuclei, as shown in Fig. 2.

Fig. 4.a. shows polar view and section of the nuclear structures of the elements from two rows of the Periodic table. The principal and secondary valences are clearly identifiable from the nuclear structures. Fig. 4.b. shows the polar view and section of some selected atomic nuclei.

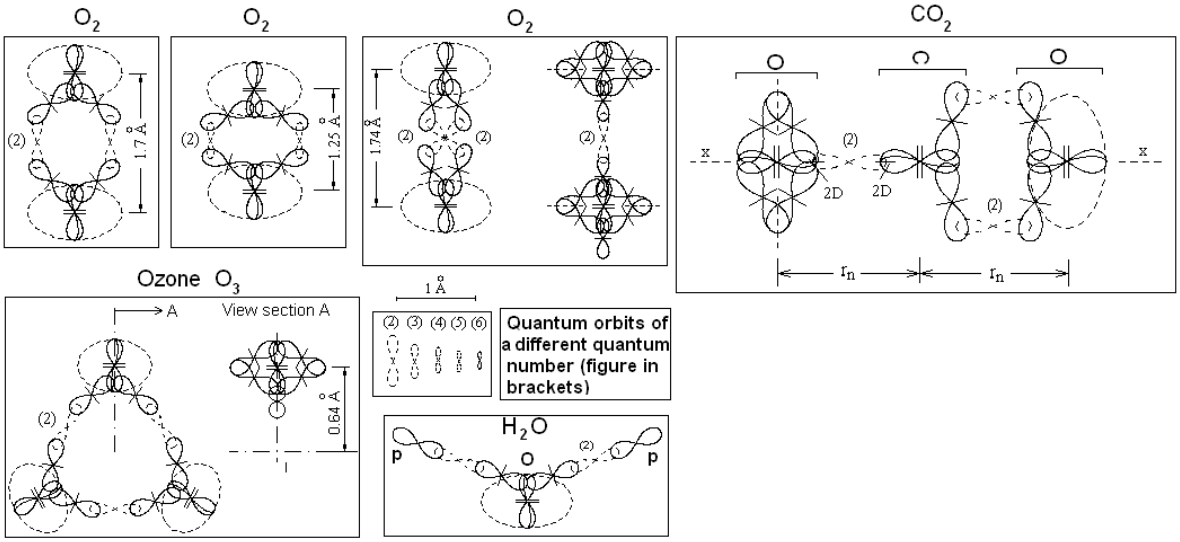


a. b.

Fig. 4. a.- Polar view and section of two rows of Periodic table; b – polar section and view of some selected atomic nuclei [4].

3. Application of the BSM-SG atomic models for revealing the fine structure of the molecules and nanotechnology

Fig, 5. illustrates some simple molecules using the BSM-SG atomic models. The theoretically estimated bonds distances and directions match the experimental data.



Fig, 5. Simple diatomic and thriatomic molecules using the BSM-SG atomic models.

Fig. 6 illustrates the shape of the molecule of aspirin by the current models of structural chemistry and by using the BSM-SG models

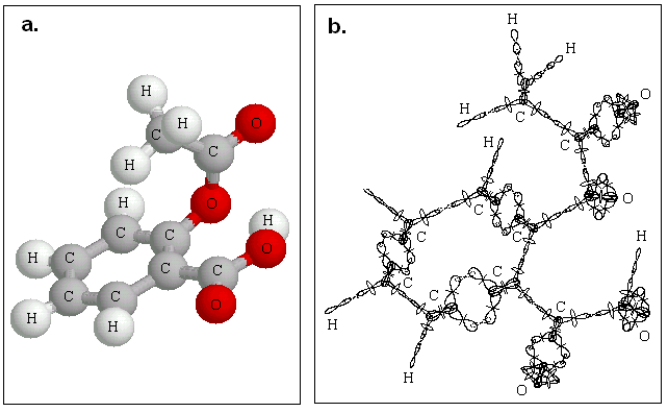


Fig. 6. Shape of aspirin molecule. A. by current model, b. by BSM-SG atomic models

The signature of spatial 3D structure of carbon atoms is identifiable by high resolution microscopy. This is illustrated by fig. 7.

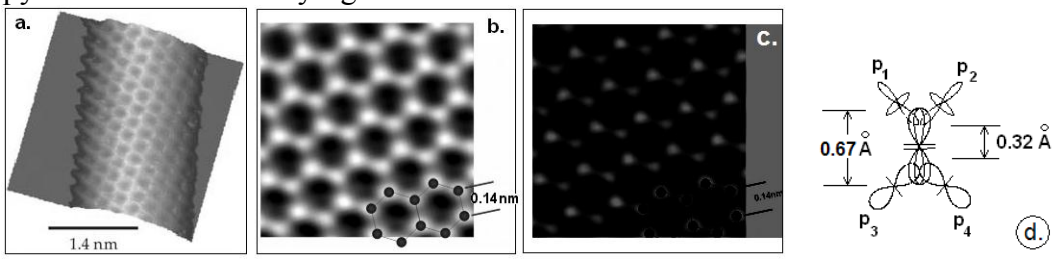


Fig. 7. a. Single-wall nanotube (Courtesy of A. Javey et al.) [5], (public domain); b. Single wall Carbon sheet with TEAM microscope [6], (public domain); c. Processed image by brightness adjustment; d. Sketch of the carbon nucleus (p3 and p4 are aligned with the drawing plane, while p1, p2 are in a perpendicular plane).

4. Application of the BSM-SG atomic models in biomolecules. Energy storage mechanism of atomic ring structure.

It is known from the Grotrian diagrams of the atomic spectra that only the atoms from the first column of the periodic table (having a single electron in the external shell) behave as the hydrogen atoms. In other columns with more than one electron, the bottom energy level is displaced up. With the BSM-SG atomic models it was revealed this is a result of a specific energy saving mechanism: a fraction of the energy of the excited electron is transferred to the energy of other electron. This is a transitional process taking place only at some beginning, which is difficult to observe. BSM-SG reveals that a similar effect takes place in some ring atomic structures. Then some excited states doe not lead to immediately emission of a photon but the energy is rotated in the ring. This is a specific energy storage mechanism, which is very important for the biomolecules.

There is a huge abundance of atomic rings in the DNA, as shown in Fig. 8.

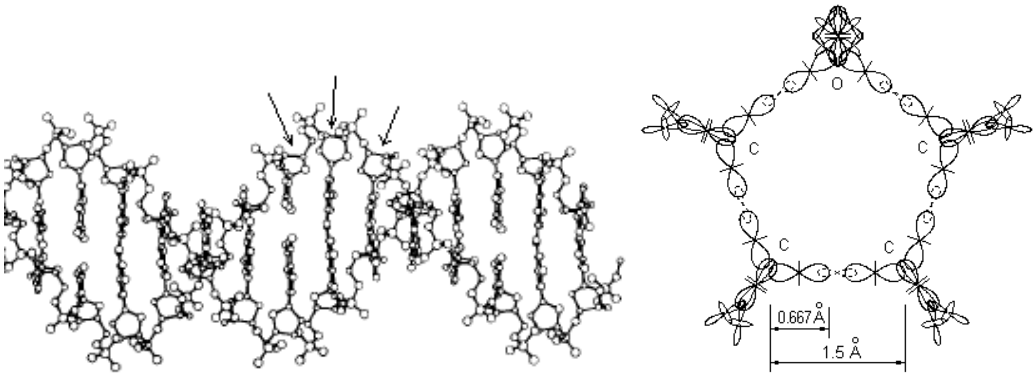


Fig. 8. Ring atomic structures in DNA strands.

Fig. 9. illustrates the two types of hydrogen bonds in the DNA.

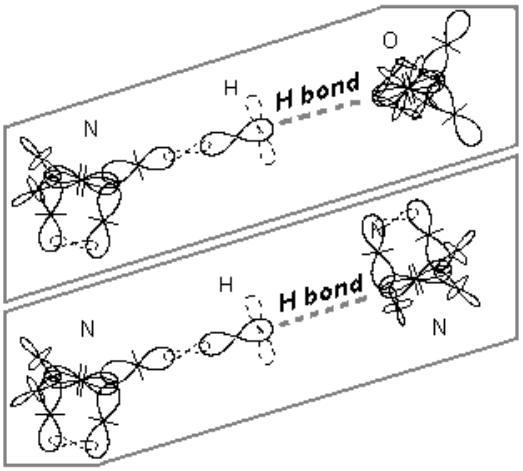


Fig. 9. Two types of hydrogen bonds in DNA: NHO and NHN.

The analysis of the DNA molecule in BSM-SG leads to the conclusion that the energy storage mechanism plays an important role for intermolecular communication between the DNA molecules in different cells of the organism. The accumulated energy in the ring structure can be released by a signal in the DNA strand. The released consequence causes an avalanche release of energy, causing a formation of entangled photons that have increase penetration capability. At the same time this consequence carries the genetic information encoded by the cordons. Many repeatable codon sequences, which do not carry genetic information, serve as synchronization of the intercommunication. This is the BSM-SG explanation of the enigmatic C-value paradox. A detailed analysis and explanation is provided in Chapter 11 of BSM-SG and in on-line publication [7], where it is shown that the theoretical explanation matches the observational data [8,9,10]. In the same chapter and article, a hypothesis about the decoding process in some of the complexes amynoacyle-tRNA synthetases - tRNA is also presented.

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