Graphene Identify Bacteria

Using a single atom-thick sheet of graphene to track the electronic signals inherent in biological structures, a team led by Boston College researchers has developed a platform to selectively identify deadly strains of bacteria, an advance that could lead to more accurate targeting of infections with appropriate antibiotics, the team reported in the journal Biosensors and Bioelectronics. [28]

Chemists at Texas A&M University are taking a p[h]age from bacteria's playbook in order to beat viruses at their own game and develop new drugs to fight cancer and a host of other human diseases in the process. [27]

Researchers at Western University have developed a new way to deliver the DNA-editing tool CRISPR-Cas9 into microorganisms in the lab, providing a way to efficiently launch a targeted attack on specific bacteria. [26]

The work reflects a growing trend at both the Salk Institute and elsewhere toward integrating computational approaches into biology research. [25]

That's only a smattering of what scientists will be able to examine with the new microscope—an atomic force-Raman microscope, to be exact—now housed in the University of Delaware's Lammot du Pont Laboratory. [24]

The Pt nanoreactor was designed with a controlled core-shell structure and morphology for the visual detection of metabolic biomarkers and direct laser desorption/ionization MS fingerprinting of the native serum. [23]

Nuclear technology companies Phoenix and SHINE Medical Technologies have achieved a new world record for a nuclear fusion reaction in a steady-state system, the strongest of its kind ever produced on Earth. [22]

Bacterial systems are some of the simplest and most effective platforms for the expression of recombinant proteins. [21]

Now, in a new paper published in Nature Structural & Molecular Biology, Mayo researchers have determined how one DNA repair protein gets to the site of DNA damage. [20]

A microscopic thread of DNA evidence in a public genealogy database led California authorities to declare this spring they had caught the Golden State Killer, the rapist and murderer who had eluded authorities for decades. [19]

Researchers at Delft University of Technology, in collaboration with colleagues at the Autonomous University of Madrid, have created an artificial DNA blueprint for the replication of DNA in a cell-like structure. [18]

An LMU team now reveals the inner workings of a molecular motor made of proteins which packs and unpacks DNA. [17]

Chemist Ivan Huc finds the inspiration for his work in the molecular principles that underlie biological systems. [16]

What makes particles self-assemble into complex biological structures? [15]

Scientists from Moscow State University (MSU) working with an international team of researchers have identified the structure of one of the key regions of telomerase—a so-called "cellular immortality" ribonucleoprotein. [14]

Researchers from Tokyo Metropolitan University used a light-sensitive iridium-palladium catalyst to make "sequential" polymers, using visible light to change how building blocks are combined into polymer chains. [13]

Researchers have fused living and non-living cells for the first time in a way that allows them to work together, paving the way for new applications. [12]

UZH researchers have discovered a previously unknown way in which proteins interact with one another and cells organize themselves. [11]

Dr Martin Sweatman from the University of Edinburgh's School of Engineering has discovered a simple physical principle that might explain how life started on Earth. [10]

Nearly 75 years ago, Nobel Prize-winning physicist Erwin Schrödinger wondered if the mysterious world of quantum mechanics played a role in biology. A recent finding by Northwestern University's Prem Kumar adds further evidence that the answer might be yes. [9]

A UNSW Australia-led team of researchers has discovered how algae that survive in very low levels of light are able to switch on and off a weird quantum phenomenon that occurs during photosynthesis. [8]

This paper contains the review of quantum entanglement investigations in living systems, and in the quantum mechanically modeled photoactive prebiotic kernel systems. [7]

The human body is a constant flux of thousands of chemical/biological interactions and processes connecting molecules, cells, organs, and fluids, throughout the brain, body, and nervous system. Up until recently it was thought that all these interactions operated in a linear sequence, passing on information much like a runner passing the baton to the next runner. However, the latest findings in quantum biology and biophysics have discovered that there is in fact a tremendous degree of coherence within all living systems.

The accelerating electrons explain not only the Maxwell Equations and the Special Relativity, but the Heisenberg Uncertainty Relation, the Wave-Particle Duality and the electron's spin also, building the Bridge between the Classical and Quantum Theories.

The Planck Distribution Law of the electromagnetic oscillators explains the electron/proton mass rate and the Weak and Strong Interactions by the diffraction patterns. The Weak Interaction changes the diffraction patterns by moving the electric charge from one side to the other side of the diffraction pattern, which violates the CP and Time reversal symmetry.

The diffraction patterns and the locality of the self-maintaining electromagnetic potential explains also the Quantum Entanglement, giving it as a natural part of the Relativistic Quantum Theory and making possible to understand the Quantum Biology.

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Author: George Rajna

Preface

We define our modeled self-assembled supramolecular photoactive centers, composed of one or more sensitizer molecules, precursors of fatty acids and a number of water molecules, as a photoactive prebiotic kernel system. [7]

The human body is a constant flux of thousands of chemical/biological interactions and processes connecting molecules, cells, organs, and fluids, throughout the brain, body, and nervous system. Up until recently it was thought that all these interactions operated in a linear sequence, passing on information much like a runner passing the baton to the next runner. However, the latest findings in quantum biology and biophysics have discovered that there is in fact a tremendous degree of coherence within all living systems. [5]

Quantum entanglement is a physical phenomenon that occurs when pairs or groups of particles are generated or interact in ways such that the quantum state of each particle cannot be described independently – instead, a quantum state may be given for the system as a whole. [4]

I think that we have a simple bridge between the classical and quantum mechanics by understanding the Heisenberg Uncertainty Relations. It makes clear that the particles are not point like but have a dx and dp uncertainty.

Graphene underpins a new platform to selectively identify deadly strains of bacteria

Using a single atom-thick sheet of graphene to track the electronic signals inherent in biological structures, a team led by Boston College researchers has developed a platform to selectively identify deadly strains of bacteria, an advance that could lead to more accurate targeting of infections with appropriate antibiotics, the team reported in the journal *Biosensors and Bioelectronics*.

The prototype demonstrates the first selective, rapid, and inexpensive electrical detection of the pathogenic bacterial species Staphylococcus aureus and antibiotic resistant Acinetobacter baumannii on a single platform, said Boston College Professor of Physics Kenneth Burch, a lead co-author of the paper.

The rapid increase in antibiotic resistant pathogenic bacteria has become a global threat, in large part because of the over prescription of antibiotics. This is driven largely by the lack of fast, cheap, scalable, and accurate diagnostics, according to co-author and Boston College Associate Professor of Biology Tim van Opijnen.

Particularly crucial is identifying the bacterial species and whether it is resistant to antibiotics, and to do so in a platform which can be easily operated at the majority of points of care. Currently such diagnostics are relatively slow—taking from hours to days—require extensive expertise, and very expensive equipment.

The BC researchers, working with colleagues from Boston University, developed a sensor, known as a graphene field effect transistor (G-FET), that can overcome critical shortcomings of prior detection efforts since it is a highly scalable platform that employs peptides, chains of multiple linked amino acids, which are inexpensive and easy-to-use chemical agents, according to co-author and BC Professor of Chemistry Jianmin Gao.

The team set out to show it could construct a device that can "rapidly detect the presence of specific bacterial strains and species, exploiting the large amount of electric charge on their surface and ability to capture them with synthetic peptides of our own design," said Burch.

The initiative built upon the earlier research of van Opijnen and Gao, who previously found peptides were highly selective, but at that time required expensive fluorescence microscopes for their detection. In addition to Burch, Gao, and van Opijnen, the lead co-authors of the paper included Boston University Assistant Professor of Chemistry Xi Ling.

The team modified existing peptides to allow them to attach to graphene, a single atomic layer of carbon. The peptides were designed to bind to specific bacteria, rejecting all others. In essence, the G-FET is able to monitor the electric charge on the graphene, while exposing it to various biological agents.

Due to the selectivity of the peptides, the researchers were able to pinpoint their attachment to the desired bacterial strain, the team reported in the article "Dielectrophoresis assisted rapid, selective and single cell detection of antibiotic resistant bacteria with G-FETs." By electrically monitoring the resistance and, ultimately, charge on the device, the presence of bacteria attached to graphene could be resolved, even for just a single cell.

To enable greater speed and high sensitivity, an electrical field was placed on the liquid to drive the bacteria to the device, again exploiting the charge on the bacteria, the team reported. This process, known as dielectrocphoresis, had never previously been applied to graphene-based sensors and could potentially open the door to dramatically improving efforts in that field to employ graphene for biosensing, the team reported.

"We were surprised how well the bacteria were electrically guided to the devices," said Burch. "We thought it would somewhat reduce the required time and needed concentration. Instead, it worked so well that the electric field was able to bring needed concentration of bacteria down by a factor of 1000, and reduce the time to detection to five minutes." [28]

Paving the way for new peptide-based therapeutics with novel method of phage display

Chemists at Texas A&M University are taking a p[h]age from bacteria's playbook in order to beat viruses at their own game and develop new drugs to fight cancer and a host of other human diseases in the process.

For decades, scientists have relied on phage display—a technique used to identify novel peptide ligands, or peptides that bind to other proteins or molecules—as a versatile tool in a variety of applications ranging from drug discovery to materials science. A team led by Texas A&M chemist and 2018 Texas A&M Presidential Impact Fellow Dr. Wenshe R. Liu has learned a new trick from an old master, bacteria, successfully harnessing its ability to make short peptides containing noncanonical amino acids (ncAAs) that equip them with special properties, such as enzyme degradation resistance and targeted protein binding capabilities.

Using a clever strategy to "trick" the system so that only viruses containing peptides with ncAAs are capable of reproducing, the Liu research group has found a way to stack the phage display library construction deck, effectively expanding the genetic code of bacteriophages and paving the way for new peptide-based therapeutics. Their findings were published Friday (March 13) in the journal *Nature Communications*.

"Utilizing unnatural amino acids, we greatly expand the utility of phage display for identifying new peptide therapeutics," Liu said.

Phage display is one of several tools that scientist rely on to find new peptides with potential use as drugs to treat diseases, explains 2018 Texas A&M chemistry Ph.D. graduate Dr. Jeffery M. Tharp, a

postdoctoral associate at Yale University and lead author on the team's paper, the third thus far representing his thesis work at Texas A&M. In addition, it is one of the first from the Texas A&M Drug Discovery Laboratory, founded by Liu and fellow Texas A&M chemists in 2018.

"Phage display uses viruses, or phages, to 'fish out' specific peptides from a pool of millions of different peptide variants; however, it is very difficult to use this technique to find peptides containing ncAAs," Tharp added. "In our paper, we developed a new method of phage display that allows for easy retrieval of potential peptide drugs containing diverse ncAAs. In addition, we used our new technique to identify novel peptides containing ncAAs that are very strong inhibitors of sirtuin 2—an enzyme that is involved in regulating human lifespan and is a promising drug target for the treatment of human cancers."

The Liu group collaborated with the Laboratory for Molecular Simulation (LMS), including Texas A&M chemistry Ph.D. candidate and LMS interim manager Andreas Ehnbom and Texas A&M High Performance Research Computing Associate Director Dr. Lisa M. Pérez, who performed the molecular dynamics simulations that enabled the team to understand the selectivity involved for specific peptides.

"The beauty of this work, at least in my mind, is that it crosses multiple disciplines of chemistry—synthetic chemistry, chemical biology and computations," Ehnbom said.

Tharp notes that the founders of phage display were awarded the 2018 Nobel Prize in Chemistry in recognition of the technique's versatility, relative ease of use and effectiveness across myriad disciplines. In combination with the resulting new molecules, he predicts the Liu group's new method will be similarly useful for all applications of phage display.

"This technique allows ncAAs with unique structures to be incorporated into the phage peptides, which can help identify more potent peptide drugs," Tharp added. "In addition, we can include reactive ncAAs into the phage peptides, which can potentially be used to make better materials and drug delivery systems."

Tharp says the team will continue to use their new phage display technique to search for other peptides containing ncAAs that inhibit enzymes related to human disease while continuing to develop other methods that expand its utility. [27]

Researchers unlock potential to use CRISPR to alter the microbiome

Researchers at Western University have developed a new way to deliver the DNA-editing tool CRISPR-Cas9 into microorganisms in the lab, providing a way to efficiently launch a targeted attack on specific bacteria.

Published today in *Nature Communications*, this study opens up the possibility of using CRISPR to alter the makeup of the human microbiome in a way that could be personalized and specific from person

to person. It also presents a potential alternative to traditional antibiotics to kill bacteria like Staphyloccous aureus (Staph A) or Escherichia coli (E. coli).

"One of the major reasons that I am excited about this work is that it has a wide range of possible real-world applications," said Bogumil Karas, Ph.D., Assistant Professor at Western's Schulich School of Medicine & Dentistry. "It has the potential for development of next generation antimicrobial agents that would be effective even for bacteria that are resistant to all known antibiotics. This technology could also be used to help 'good' bacteria produce compounds to treat diseases caused by protein deficiencies."

CRISPR stands for Clustered Regularly Interspaced Short Palindromic Repeats and can be programmed to target specific stretches of genetic code and to edit DNA at precise locations. Researchers use CRISPR to permanently modify genes in living cells and organisms.

In this way, CRISPR can be programmed to kill bacteria, but until now there wasn't a way to efficiently and specifically target certain bacterial strains.

"Using CRISPR to kill things isn't a new idea because that's what CRISPR does naturally," said David Edgell, Ph.D., Professor at Schulich Medicine & Dentistry. "The problem has always been how you get CRISPR to where you want it to go. Other delivery systems could only go to a few spots, where ours can go anywhere."

The delivery system developed at Western uses bacteria's natural ability to replicate—called bacterial conjugation—to deliver CRISPR to specific bacteria, in order to alter its DNA and kill it.

"Specific delivery of any therapeutic agent, including CRISPR, is usually one of the biggest bottlenecks in development of new treatments. By developing this new delivery system, we created new tools that could help us in the development of more effective therapies in the near future," said Karas.

The team says their delivery system is not only broadly applicable, but it is also more efficient than previous systems.

"We were able to show near complete transfer of the delivery vehicle to another bacterial species under conditions where they are in intimate contact—in a biofilm. This is important because biofilms are the natural state of the majority of bacteria, and being able to transfer DNA under these conditions is typically difficult, but we found a way to make it easy and efficient," said Gregory Gloor, Ph.D., Professor at Schulich Medicine & Dentistry. [26]

Scientists find way to quantify how well cutting-edge microscopy technique works

In 2017, Salk scientists reported that tilting a frozen protein sample as it sat under an electron microscope was an effective approach to acquiring better information about its structure and helping researchers understand a host of diseases ranging from HIV to cancer. Now, they have developed a mathematical framework that underlies some of those initial observations.

Their new study, published in *Progress in Biophysics and Molecular Biology* on September 13, 2019, provides a foundation for quantitatively determining how differences in viewing angles affect the resulting 3-D structures of proteins, and could help other researchers determine the best setup for experiments to improve the imaging technique called cryo-EM.

"This provides a quantitative understanding for why variations in viewing angles affect the quality of resulting 3-D structures of proteins, and where we could do better to improve the data," says Dmitry Lyumkis, a Salk assistant professor of genetics and coauthor of the new work. "These kinds of theoretical frameworks are important to understanding precisely how information is attenuated due to imperfections associated with the imaging experiment, which will lead us to eventually get better structures out of cryo-EM data."

In cryo-EM, or cryogenic electron microscopy, proteins are rapidly frozen in their natural form before being bombarded with electrons. By detecting how the electrons scatter when they hit the sample, researchers can determine the molecular structure of the protein or protein complex. Compared to other imaging methods, it's easier for scientists to prepare proteins for cryo-EM, and the technique can potentially address a broader set of questions in structural biology. However, a long-standing problem in cryo-EM is that proteins tend to stick to the top or bottom of the sample grid that they're prepared on. These select orientations mean that researchers can't always see a protein's structure from every angle. Tilting the sample, Lyumkis and his colleagues found in 2017, helped solve this problem.

"We knew that qualitatively, tilting improved the data in some cases," says Lyumkis. "What we didn't know was exactly the extent to which the structures can be affected by variations in the viewing angle."

Recently, Philip Baldwin, a senior staff researcher at Salk and the paper's coauthor, was examining a set of cryo-EM data collected at different viewing angles when he noticed that such variations affected the overall resolution of the resulting protein structure. After some calculations, he realized that the association between the viewing angle and resolution was generalizable to all cryo-EM experiments.

The new formula lets researchers calculate, for any protein at any tilt angle, a number called the sampling compensation factor, or SCF. The closer the SCF value is to 1, the more complete the protein's structure. If the SCF is 0.5 instead of 1, either the data is incomplete, or researchers must collect data for twice as long to get the same structural resolution. By calculating SCF values ahead of an experiment, scientists can optimize their tilt angle and data collection time.

The new quantitative formulations also helped Lyumkis and Baldwin compute just how incomplete some cryo-EM datasets are. Previously, they might have had to eyeball a set of data and guess whether it was a good or bad approximation of a protein's structure. Now, the SCF can tell them that numerically.

"It's very handy," says Baldwin. "Basically, this formula tells you if you have very bad regions of the protein from which you didn't collect data."

Lyumkis and Baldwin hope that using the formula to assess cryo-EM results—which involves a simple calculation or piece of code—will become standard and help guide experiments and new approaches to cryo-EM. This would lead to faster discoveries in basic biological sciences and in drug development.

The work reflects a growing trend at both the Salk Institute and elsewhere toward integrating computational approaches into biology research. [25]

New microscope with dual capabilities supports multitude of studies

A single strand of DNA. The toxic pollutants in a waft of air. A paint sample from a priceless work of art. Flakes of a Martian meteorite. That's only a smattering of what scientists will be able to examine with the new microscope—an atomic force-Raman microscope, to be exact—now housed in the University of Delaware's Lammot du Pont Laboratory.

"UD is excited to add this important and state-of-the-art new tool to our suite of instruments for examining materials at high resolution," said Charles G. Riordan, vice president for research, scholarship and innovation. "With this capability, UD faculty, students and staff will be able to drive research and education forward in a wide array of fields, from engineering to physical sciences to art conservation."

The new microscope will help researchers go where they couldn't before. Previous scopes just didn't have the super-high resolution and chemistry-uncovering power this one has.

"This microscope will allow scientists to see objects 10,000 times smaller than the diameter of a human hair—plus provide detailed information about both the surface of a material and its chemistry," said Karl Booksh, professor of chemistry and biochemistry and the rallying force behind UD's successful proposal to the National Science Foundation. NSF came through with a $558,228 grant from its Major Research Instrumentation and Chemistry Research Instrumentation programs and the Established Program to Stimulate Competitive Research (EPSCoR). The UD Research Office also helped support the cost of the instrument, which was purchased from Horiba, a leading provider of analytical and scientific measurement systems.

This new tool is a "scientific twofer," combining two microscopes in one. A Raman microscope, named after the late Indian physicist and Nobelist Sir Chandrashekhara Venkata Raman, scans a sample with a laser, interacting with the vibrations of the molecule of interest, scattering the light. These light patterns serve as "fingerprints" for identifying the molecules and for studying their chemical bonds and degree of interactivity with other molecules.

Rachel McCormick (second from left) gives fellow doctoral student Devon Haugh (left) and Wofford College undergrad Savannah Talledo some training in how to use the new microscope, as Prof. Karl Booksh looks on. Credit: University of Delaware

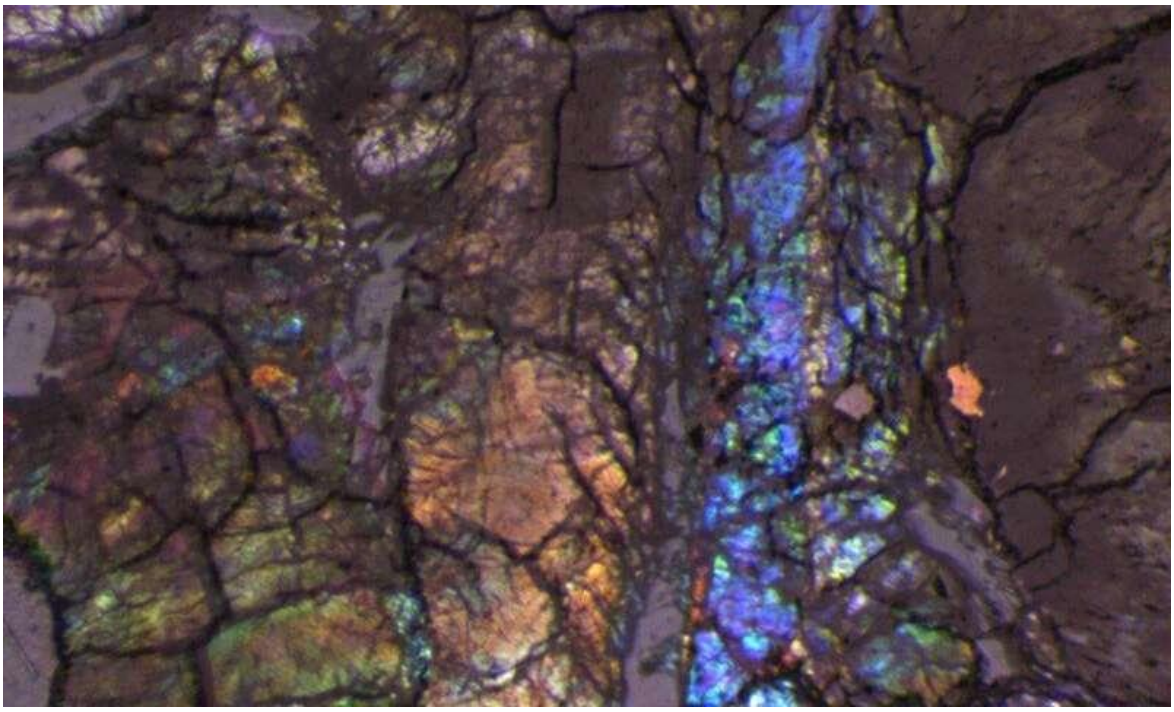
An atomic force microscope scans a sample using a small probe that yields information about the surface, such as its topography, hardness, electrical and thermal properties. This probe, tipped in gold, is nearly "atomically sharp," meaning it is virtually able to detect a single atom.

Combining both techniques within a single microscope delivers a trove of information simultaneously. And that's important for a number of studies across the University and with industry collaborators, as well as partnering institutions such as Winterthur Museum.

Putting the scope to work

During the summer of 2019, doctoral student Devon Haugh and undergraduate Savannah Talledo, a Wofford College student participating in the NSF-funded Science and Engineering Leadership Initiative at UD, used the new microscope to study air pollutants. Tiny gas particles from vehicle exhaust and soot generated from burning coal can fuel climate change and increase the risk of asthma, lung disease, heart disease and other health problems. The microscope helped to determine the acidity of the airborne particles, which influences how quickly they will grow in the atmosphere.

"Understanding acidity can help us improve predictions of how airborne particles affect human health and climate," said Murray Johnson, professor of chemistry and biochemistry, who is leading the project. "In a conventional laboratory, acidity is measured with a pH meter. However, that approach does not work for airborne particles on the sub-micrometer-size scale, hence the need for new measurement approaches such as the Raman microprobe."



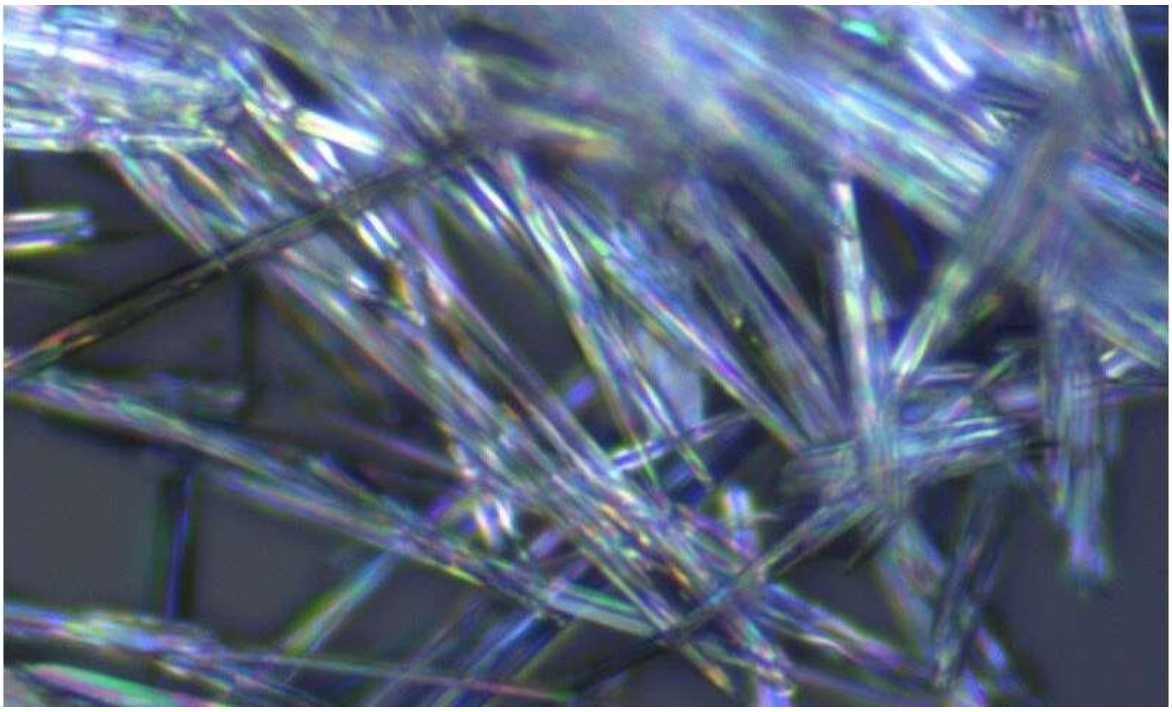
Magnified view of a meteorite specimen from Mars under cross-polarized light. Image taken with UD’s new atomic force-Raman microscope. Credit: University of Delaware

Haugh was glad to have access to the new instrument for her work.

"I care about the health of our environment," she said. "This project allows me to contribute toward better understanding and protecting it."

Experts at Winterthur's Scientific Research and Analysis Lab will focus the microscope on the museum's valuable collections of historic textiles, as well as its Chinese export paintings from the 18th and 19th centuries, according to Jocelyn Alcántara-García, assistant professor and a co-investigator on the grant. In the first half of the 19th century, with the boost in foreign trade due to the opening of ports in China, a large number of Western synthetic chemical pigments were imported to China. Before long, these man-made pigments replaced the mineral and plant pigments that Chinese painters had traditionally used in their artwork, from watercolors to reverse-painted glass. The new microscope will help conservation scientists gain a better understanding of this transitional period.

Alcántara-García said she will use the instrument to understand the fixatives that were used to set the dye in historic textiles, which will help textile conservators and other museum professionals determine degradation mechanisms and potential interventions.



Indomethacin is an anti-inflammatory drug commonly used to treat pain, swelling and stiffness associated with arthritis and bursitis. Image taken with UD's new atomic force-Raman microscope. Credit: University of Delaware

Solving challenges on Earth and Mars

Now, about those meteorites … in a collaboration that began when he joined the UD faculty a decade ago, Booksh is working with Merck senior scientist Joseph P. Smith, who earned his doctorate in analytical chemistry at UD, and with Marietta College professor Frank Smith, who earned his doctorate in geology at UD, to unlock some of the secrets of the planets through clues provided by lunar, Martian and asteroidal meteorites. The samples came to the team on good authority—from NASA's Johnson Space Center and from the Smithsonian.

The team's primary interest is the chemical composition and properties of these rocks, which contain "shock pockets" created from all the fracturing and melting that occurred when they hit the ground. Their chemistry can help reveal the geology and atmospheres of their home planets. Smith said the work also could aid the search for life on Mars in NASA's and the European Space Agency's 2020 rover missions.

"The NASA and ESA rovers both will have, for the first time, Raman spectrometers to help characterize Martian surface materials," Smith said. "As such, our work investigating meteorites may help enhance the search for life on Mars by developing optimal data collection and analysis methodologies."

Booksh and Smith also are working on other intriguing problems right here on Earth—as collaborators on Merck & Co. Inc. and UD project focusing on pharmaceutical applications. The team will investigate polymorphism in drug development—the ability of a solid to exist in two or more crystalline forms, each with vastly different physical and chemical properties. Polymorphs are of

particular concern to the drug industry because one of these forms may be toxic, and more than 50 percent of active pharmaceutical ingredients have more than one polymorph.

"We're hoping to develop the next generation of analytical techniques that will help solve these complex challenges facing the pharmaceutical industry," Smith said. [24]

Scientists improve pancreatic cancer diagnosis with multifunctional platinum nanoreactor

Metabolic analysis involves ongoing biological pathways and can be more distal than proteomic/genomic approaches to in vitro diagnostics (IVD). However, point-of-care (POC) metabolic analysis needs special designed materials to detect target biomarkers of low concentration in complex biosystems.

Scientists from Shanghai Jiao Tong University, University of Surrey and the Dalian Institute of Chemical Physics (DICP) of the Chinese Academy of Sciences (CAS) have developed a multifunctional platinum (Pt) nanoreactor geared towards POC metabolic analysis that performs visual detection and mass spectrometry (MS) fingerprinting simultaneously. Their findings were published in *Matter* on October 2.

The Pt nanoreactor was designed with a controlled core-shell structure and morphology for the visual detection of metabolic biomarkers and direct laser desorption/ionization MS fingerprinting of the native serum. The molecular mechanism of efficient catalytic processes only takes 5 min for visual quantitation of metabolic biomarkers was also investigated. In particular, the platform enabled biopsy-free diagnosis of pancreatic cancer patients with a sensitivity of 84 percent and specificity of 92 percent.

The scientists further identified a potential panel of five biomarkers, which may shed light on progression monitoring in response to therapy.

"It is a minimally invasive, high throughput and fast platform, improving accessibility to disease diagnosis," said Prof. QIAN Kun.

"This development of on-site and on-time diagnostics based on these nanoreactors may enhance the performance of POC devices geared towards personalized medicine and diverse diseases in the near future," Prof. LIU Jian added. [23]

Record breaking fusion reaction could transform medical isotope production

Nuclear technology companies Phoenix and SHINE Medical Technologies have achieved a new world record for a nuclear fusion reaction in a steady-state system, the strongest of its kind ever produced on Earth. The reaction yielded 46 trillion (4.6×10^{13}) neutrons per second,

eclipsing the previous record by nearly 25% and setting a new standard for neutron generator technology.

This breakthrough could prove great news for the field of nuclear medicine. SHINE was founded in 2010 to create a safe, cost-effective and environmentally-friendly technology to produce medical isotopes. And it's using Phoenix's high-flux neutron generators to achieve this.

In particular, the companies aim to resolve the ongoing global supply issues of molybdenum-99 (Mo-99), a radioisotope that decays into the diagnostic imaging agent technetium-99m (Tc-99m). The most prevalent nuclear medicine agent, Tc-99m is employed in tens of millions of medical diagnostic procedures each year, primarily in stress tests to diagnose heart disease or to stage cancer.

Mo-99, however, is currently generated using a handful of ageing nuclear reactors, shutdowns of which have led to serious supply shortages in the past. SHINE plans to replace the nuclear reactor with Phoenix's low-energy, accelerator-based neutron generator.

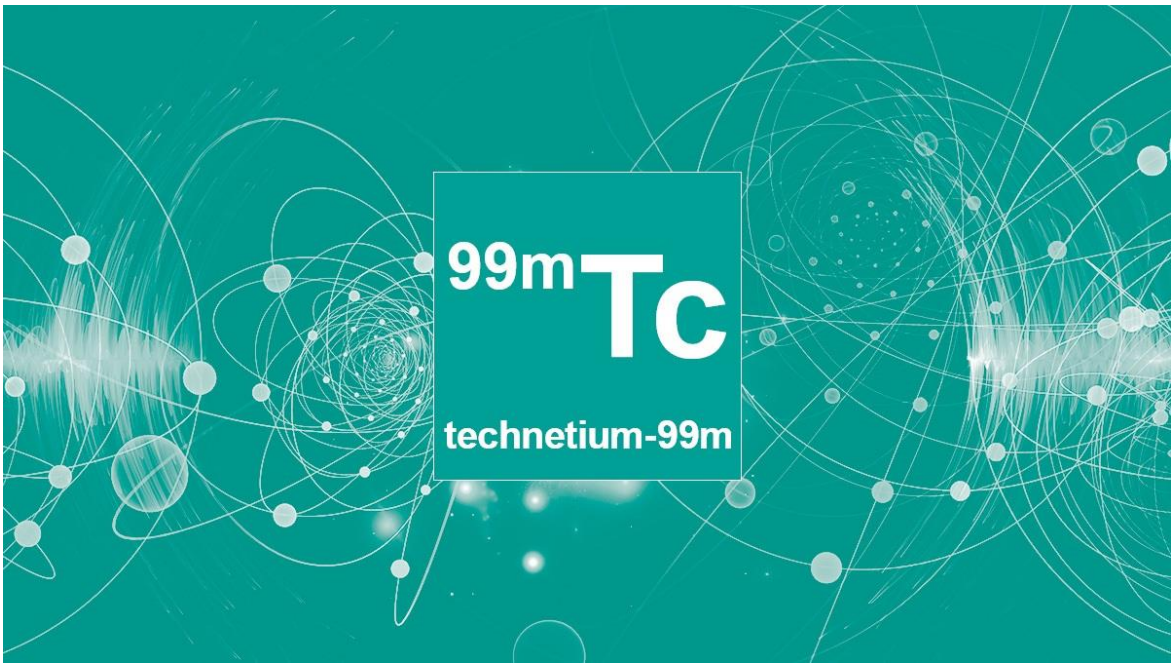
The Phoenix system works by accelerating positively-charged deuterium ions into a target of tritium gas to induce a fusion reaction. This reaction results in the production of high-energy neutrons and helium. These neutrons then pass into a tank and strike their target: low-enriched uranium (LEU) dissolved in an aqueous solution. This causes the uranium nuclei to split and create multiple elements, including Mo-99 and other useful isotopes.

As well as eliminating the need for nuclear reactor facilities, the technology's use of LEU (containing less than 20% U-235) confers a major security advantage. Until recently, most Mo-99 production used targets of weapons-grade highly-enriched uranium (HEU), which contains 20% or more U-235. LEU, however, cannot be used to create nuclear weapons weaponized without highly sophisticated modifications and is thus considered far less of a risk.

Preparing for production

The record-breaking fusion reaction was achieved during a demonstration of Phoenix's third-generation neutron generator, as part of ongoing preparation for full-scale operation of the medical isotope production facility. "The higher neutron yield from the Phoenix system will increase the efficiency of the whole production process," notes Phoenix's president Evan Sengbusch. "Additionally, the demonstration of such a strong neutron source opens the door to other high-flux neutron applications in materials characterization, imaging and fusion energy."

The companies have also performed a 132-hr test run on the neutron generator, which demonstrated more than 99% uptime. These successful tests validate the performance and reliability of the Phoenix neutron generator technology and confirm its status as a "steady-state system" than can operate at high output for long stretches of time. This sets it apart from other high output fusion systems, which have only operated in a pulsed mode over short durations.



Battle of the elements: technetium-99m diagnoses disease then decays away

SHINE anticipates that isotope production will begin in 2021. “Before that, the production facility needs to be built and the target solution needs to be tested,” explains Greg Piefer, SHINE’s CEO and founder, and founder and former CEO of Phoenix. The company began construction of its commercial facility in spring of this year. It will contain eight Mo-99 production units, each with its own Phoenix neutron generator, and once operational will be capable of producing enough isotope to satisfy one-third of global demand.

“The world-record proves the accelerator technology is suitable to produce medical isotopes at the scale required to support a robust business case,” says Piefer. “It is also a stepping stone toward advancing fusion for other, more ambitious applications, including the recycling of nuclear waste and ultimately the creation of cleaner, safer and more abundant energy.” [22]

New technologies for producing medical therapeutic proteins

Bacterial systems are some of the simplest and most effective platforms for the expression of recombinant proteins. They are more cost-effective compared to other methods, and are therefore of great interest not only for Lobachevsky University researchers, but also for manufacturers of therapeutically important drugs.

However, in addition to the target recombinant proteins, cells also produce a large number of endogenous proteins, including SlyD. It is a small protein consisting of three domains. Its C-terminal region is rich in histidine residues, and SlyD therefore exhibits a high affinity for the 2-valent ions and is purified together with the target proteins in the course of metal-affinity chromatography. This

results in the need for additional purification steps, and as a consequence, increases the cost of the technological process for obtaining therapeutic recombinant proteins.

A team of Lobachevsky University researchers under Professor Viktor Novikov, Director of the UNN Center for Molecular Biology and Biomedicine, has obtained a series of E. coli strains deficient in the SlyD/SlyX genes. The strains were engineered using λ-red mediated chromosomal deletion. (Figure 1.)

"The sequence of SlyD/SlyX in the E. coli genome was replaced by a gene responsible for resistance to the antibiotic kanamycin that was flanked on both sides by FRT sites, from where it was later removed by FLP recombinase," Viktor Novikov notes.

Using the example of recombinant bispecific protein MYSTI-2 consisting of two modules that are active centers of antibodies against mouse proteins F4/80 and TNF, the scientists compared the activity of proteins isolated from the original and mutant strains. As a result of the study, it was determined that the removal from the E. coli genome of the SlyD and SlyX genes, which presumably encode chaperones that support the spatial structure of Escherichia coli proteins, does not result in a disruption of recombinant proteins' functional activity.

By obtaining original E. coli strains, the researchers were able to solve the problem of contamination of recombinant proteins and to ensure their successful single-stage purification by metal-affinity chromatography.

"The obtained set of slyD/slyX-deficient strains of E. coli can be used to produce in a pure form a wide range of prokaryotic and eukaryotic proteins, including medical therapeutic proteins. This makes the development and production of new medicinal and preventive biological preparations easier, simpler and cheaper," concludes Viktor Novikov. [21]

Mayo researchers find off/on switch for DNA repair protein

Damage to DNA is a daily occurrence but one that human cells have evolved to manage. Now, in a new paper published in *Nature Structural & Molecular Biology*, Mayo researchers have determined how one DNA repair protein gets to the site of DNA damage. The authors say they hope this discovery research will help identify new therapies for ovarian cancer.

While the human genome is constantly damaged, cells have proteins that detect and repair the damage. One of those proteins is called 53BP1. It is involved in the repair of DNA when both strands break. In the publication, Georges Mer, Ph.D., a Mayo Clinic structural biologist, and his team report on how 53BP1 relocates to chromosomes to do its job.

Dr. Mer explains that, in the absence of DNA damage, 53BP1 is inactive—blocked by a protein called "TIRR." Using a visualization technique called X-ray crystallography, the authors show that TIRR obstructs an area on 53BP1 that 53BP1 uses to bind chromosomes. But what shifts TIRR away from 53BP1, so the repair protein can work?

The authors theorized that a type of nucleic acid called RNA was responsible for this shift. To test their theory, they engineered a protein that would bind to the 53BP1 repair protein and the RNA molecules released when DNA is damaged. This effort, plus other work detailed in the paper, provides evidence that their idea was sound. The authors report that when DNA damage occurs, RNA molecules produced at that time can bind to TIRR, displacing it from 53BP1 and allowing 53BP1 to swing into action.

"Our study provides a proof-of-principle mechanism for how RNA molecules can trigger the localization of 53BP1 to DNA damage sites," says Dr. Mer. "The TIRR/RNA pair can be seen as an off/on switch that blocks or triggers 53BP1 relocation to DNA damage sites."

Also in the paper, the authors report that displacing TIRR increases sensitivity of cells in cell culture to olaparib, a drug used to treat patients with ovarian cancer.

"Unfortunately, over time cancer cells develop resistance to drugs in this category, called 'PARP inhibitors.' Our work provides a new target, TIRR, for developing therapeutics that would help specifically kill ovarian cancer cells," Dr. Mer says.

Collaborators on this work include the Dana-Farber Cancer Institute and the Wellcome Trust Centre for Human Genetics at the University of Oxford in the U.K. In addition to Dr. Mer, other Mayo Clinic authors are Maria Victoria Botuyan, Ph.D., Gaofeng Cui, Ph.D., James R. Thompson, Ph.D., Benoît Bragantini, Ph.D., and Debiao Zhao, Ph.D.

The authors report no conflict of interest. Funding for this research was provided by the National Institutes of Health, including the Mayo Clinic Ovarian Cancer Specialized Program of Research Excellence, and the U.S. Department of Defense. Additional funding sources are listed in the publication. [20]

Investigators say DNA database can be goldmine for old cases

A microscopic thread of DNA evidence in a public genealogy database led California authorities to declare this spring they had caught the Golden State Killer, the rapist and murderer who had eluded authorities for decades.

Emboldened by that breakthrough, a number of private investigators are spearheading a call for amateur genealogists to help solve other cold cases by contributing their own genetic information to the same public database. They say a larger array of genetic information would widen the pool to find criminals who have eluded capture.

The idea is to get people to transfer profiles compiled by commercial genealogy sites such as Ancestry.com and 23andMe onto the smaller, public open-source database created in 2010, called GEDmatch. The commercial sites require authorities to obtain search warrants for the information; the public site does not.

But the push is running up against privacy concerns.

"When these things start getting used by law enforcement, it's very important that we ensure that to get all of the benefit of that technology we don't end up giving up our rights," said American Civil Liberties Union legal fellow Vera Eidelman.

She argues that when someone uploads their own DNA profile they aren't just adding themselves—they're adding everyone in their family, including dead relatives and those who haven't been born yet. She also said DNA mining could lead to someone's predisposition to mental and health issues being revealed.

"That one click between Ancestry and 23andMe and GEDmatch is actually a huge step in terms of who has access to your information," Eidelman said.

This month, DNA testing service MyHeritage announced that a security breach revealed details about over 92 million accounts. The information did not include genetic data but nonetheless reinforced anxieties.

Nevertheless, the effort is gaining steam with some genetic genealogy experts and investigators.

The shared DNA profiles "could end up being the key to solving one of these cold cases and getting the family closure and getting someone really dangerous off the streets," said CeCe Moore, the head of the genetic genealogy unit at the DNA company Parabon NanoLabs.

She's uploaded her personal genetic information to the public database and wants it to become a larger repository of information for genealogy hobbyists and investigators alike. Separately, Parabon NanoLabs has also uploaded DNA data from 100 unsolved crime scenes in hopes of finding suspects.

Private investigator Jason Jensen holds a Phenotype Report at his office Friday, June 15, 2018, in Salt Lake City. Groups of private investigators in Utah and California have been emboldened by the arrest of the suspected Golden State …more

Genetic genealogy has traditionally been used to map family histories. Labs analyze hundreds of thousands of genetic markers in an individual's DNA, compare them with others and link up families based on similarities. The public database was created to compare family trees and genetic profiles between the commercial sites, which don't cross-reference information.

Its potential as a police tool wasn't broadly known until the April arrest of Golden State Killer suspect Joseph DeAngelo in northern California. Prosecutors allege DeAngelo, a former police officer, is responsible for at least a dozen murders and about 50 rapes in the 1970s and '80s.

But the DNA-assisted hunt that led to his arrest wasn't flawless. It initially led authorities to the wrong man whose relative shared a rare genetic marker with crime-scene evidence. A similar thing happened when authorities used a different public DNA database to investigate a nearly two-decade-old Idaho murder in 2014.

In May, Moore used the public database to help police arrest a 55-year-old Washington man linked to the 1987 killing of a young Canadian couple. She suspects the method will lead to dozens of arrests in similar cold cases.

Courts haven't fully explored legal questions around the technique but are likely to allow it based on current law, said attorney and forensic consultant Bicka Barlow. The theory is that an individual's right to privacy does not extend to material they've abandoned, whether it's DNA or trash.

GEDmatch co-creator Curtis Rogers was initially unaware police used his site to find the suspected Golden State Killer. He's glad it's led to solving crimes but is worried about privacy issues. The site's policy was updated in May and says it can't guarantee how results will be used. Users are allowed to remove their information.

A California-based group of volunteers called the DNA Doe Project has also used the database to identify two bodies that stumped authorities for more than a decade. The group encourages its thousands of online supporters to contribute to the public database.

"It's free, it's like three or four clicks and a couple minutes of your time," said co-founder Margaret Press. "It's altruistic if you have no interest in your own family history; if you did, it's a win-win."

A volunteer group of investigators and attorneys called the Utah Cold Case Coalition has made a similar appeal.

The idea may be particularly appealing in Utah, co-founder Jason Jensen suspects. An interest in genealogy is especially strong in the state, because tenets of The Church of Jesus Christ of Latter-day Saints emphasize the importance of family relationships in the afterlife.

"Arguably that one person can post up their DNA and might potentially break a case that somebody back in Nantucket (Massachusetts) is trying to solve," Jensen said. [19]

Researchers build DNA replication in a model synthetic cell

Researchers at Delft University of Technology, in collaboration with colleagues at the Autonomous University of Madrid, have created an artificial DNA blueprint for the replication of DNA in a cell-like structure. Creating such a complex biological module is an important step towards an even more ambitious goal: building a complete and functioning synthetic cell from the bottom up.

Copying DNA is an essential function of living cells. It allows for cell division and propagation of genetic information to the offspring. The mechanism underlying DNA replication consists of three important steps. First, DNA is transcribed into messenger RNA. Messenger RNA is then translated into proteins—the workhorses of the cell that carry out many of its vital functions. The job of some of these proteins, finally, is to perform the last step in the cycle: the replication (or copying) of DNA. After a cell has replicated its DNA, it can divide into two daughter cells, each containing a copy of the original genetic material.

Closing the cycle

Researchers had already realized all of the separate steps mentioned above. Japanese scientists, for instance, created a minimal, stand-alone system for messenger RNA and protein synthesis by taking the relevant components from *E. coli* and tweaking them. But no one had yet been able to combine this system with autonomous DNA replication. "We wanted to close the cycle and be the first to reconstruct the entire flow of genetic information inside a cell-like structure called a liposome," said group leader Christophe Danelon.

Combining the Japanese system with a module for DNA replication proved difficult. "We tried a few approaches, but none seemed to work convincingly," said Danelon. Then, Ph.D. student Pauline van Nies came up with the idea to use the DNA replication machinery of a virus called Φ29. "Viruses are very intriguing from a molecular biology point of view," said Van Nies. "They are extremely efficient in encoding proteins in a small genome and in robustly replicating their genetic information." In human cells, DNA replication is managed by hundreds of proteins. Φ29 only needs four.

Composing DNA

Many years ago, researchers working at the Autonomous University of Madrid discovered the DNA replication mechanism of the Φ29 virus and managed to isolate it. Van Nies and Danelon worked with these researchers to combine the genes that encode for the replication mechanism with the genetic code that is necessary to operate the Japanese module for transcription and translation.

Van Nies composed a unique DNA blueprint that took into account a number of different factors related to the flow of genetic information, such as a suitable binding site for the ribosome, an element that is essential for the production of proteins.

Combining machinery

A goal that now comes into view is combining the new module that regulates the flow of genetic information with other essential cellular functions such as growth and division. Last year, the Danelon group created a way to synthesize the phospholipids that make up liposomes, such as the ones

the researchers used in this project. The yield of phospholipids was still too small to sustain growth, but Danelon is confident his group can optimize this process.

Cell division may be a tougher nut to crack. In modern cells, it requires a streamlined process in which copied DNA is neatly packed and then evenly distributed towards the poles of the cell. Concurrently, specialized proteins squeeze the mother cell into two daughter cells. Danelon thinks a simple 'budding' mechanism could also do the trick. "I think we can create liposomes that grow until they start budding. If enough DNA is being produced, hopefully enough of these primitive daughter cells will contain the new DNA to sustain a cell population." This may well be how the very first cells self-reproduced, before evolution equipped them with a more elegant and robust solution.

Building a synthetic cell

The mission that ties together all of the fundamental research described above is the construction of a synthetic cell that can grow, divide and sustain itself. Scientists at Delft University of Technology play a leading role in this exciting new research direction that may ultimately lead to intimate understanding of the inner workings of a cell. Research supporting the initiative could lead to advances in biotechnology, health and energy. [18]

Study reveals the inner workings of a molecular motor that packs and unpacks DNA

DNA is tightly packed into the nucleus of a cell. Nevertheless, the cellular machinery needs to constantly access the genomic information. An LMU team now reveals the inner workings of a molecular motor made of proteins which packs and unpacks DNA.

The genomic DNA of higher organisms is compacted in a highly condensed form known as chromatin. The DNA is tightly wound around a myriad of tiny histone spools called nucleosomes. A single human cell, for instance, accommodates in this manner about two meters of DNA. However, genes must be constantly transcribed into messenger RNAs to direct protein synthesis. Moreover, the entire DNA must be replicated before cell division and DNA damage needs to be repaired. Thus, there must be way to actively grant access to the genome.

This is when chromatin remodelers come into play. Chromatin remodelers have an essential role as they are molecular machines: they unpick and unpack segments of the DNA by sliding nucleosome spools back and forth, replacing individual histones, freeing up the DNA for transcription, and finally compacting it again, when the job is done. Since all of this happens in a highly dynamic fashion, chromatin remodelers enable cells to react rapidly to alterations in their environment – and this holds for brewer's yeast as well as for human cells. In mediating gene accessibility, chromatin remodelers are vital for development and cell differentiation; cell types are defined by the sets of genes they express, remodelers help to determine cell identity.

So far, however, very little is known about what remodeling proteins look like and how they go about doing what they do. In molecular terms, functional remodelers are often very large complexes comprising many different protein components, whose coordinated action makes them akin to molecular machines. These features also make it very difficult to determine their detailed structure. But a team led by Professor Karl-Peter Hopfner, who holds a Chair in Structural Molecular Biology at

LMU's Gene Center, has now used cryo-electron microscopy to reconstruct the three-dimensional structure of the nucleosome-sliding remodeler INO80 (which itself consists of 15 subunits) bound to a single nucleosome. "Even with innovative approaches, the best available technology and intensive teamwork, we were always working at the cutting edge," says Dr. Sebastian Eustermann, who worked out the molecular structure of the complex on the basis of electron micrographs of thousands of individual complexes.

By analyzing images of randomly oriented views of the complex formed between INO80 and a nucleosome in the electron micrographs, Hopfner and his team have pieced together its structure at a resolution which has seldom been achieved for a chromatin complex of comparable size. This allowed the researchers to unravel the intricate interaction of the remodeler with its substrate DNA spooled around histones and dissect how the whole machinery works.

From a biochemical point of view, remodelers are responsible for heavy-duty reorganizational tasks. To perform these tasks, they must execute "large-scale conformational changes, which are carried out with astounding precision," says Eustermann. In order to alter the relative positions of nucleosomes, the INO80 complex must first weaken the contacts between the nucleosomal histones and the DNA. A molecular motor which is part of the INO80 complex segmentally detaches the double-stranded DNA from the nucleosome. In doing so, it progressively breaks the contacts that normally keep the DNA tightly wound around the histone particle.

The motor subunit feeds DNA it into the nucleosome. This results in the transient formation of a double-stranded DNA loop that is likely an important intermediate in complex remodeling reactions on the nucleosome. On one hand, the loop exposes some histone proteins that could be replaced by other histones to form a different type of nucleosome. On the other hand, the loop is eventually passed over another subunit and the machine then acts as a ratchet, allowing the nucleosome to "move" on the DNA. Throughout this unpacking process, other subunits in the complex serve to support and stabilize the partially 'denuded' nucleosome itself.

The structure of the complex revealed in the new study sheds new light on the function and mode of action of chromatin remodelers in general. These molecular machines play an essential part in the workings of the cell by maintaining the flexibility of the chromatin, thus enabling the genetic apparatus to respond dynamically to changing metabolic demands. "Our results provide the first well-founded picture of how they do that," says Hopfner. "Moreover, it has recently become clear that remodelers play a central role in tumorigenesis, because they often misregulated in tumor tissue. So structural and mechanistic insights into their functions will be vital for the future development of new therapies for cancer," he adds. [17]

Biomimetic chemistry—DNA mimic outwits viral enzyme

Not only can synthetic molecules mimic the structures of their biological models, they can also take on their functions and may even successfully compete with them, as an artificial DNA sequence designed by Ludwig-Maximilians-Universitaet (LMU) in Munich chemist Ivan Huc now shows.

Chemist Ivan Huc finds the inspiration for his work in the molecular principles that underlie biological systems. As the leader of a research group devoted to biomimetic supramolecular chemistry, he creates 'unnatural' molecules with defined, predetermined shapes that closely resemble the major biological polymers, proteins and DNA found in cells. The backbones of these molecules are referred to as 'foldamers' because, like origami patterns, they adopt predictable shapes and can be easily modified. Having moved to LMU from his previous position at Bordeaux University last summer, Huc has synthesized a helical molecule that mimics surface features of the DNA double helix so closely that bona fide DNA-binding proteins interact with it.

This work is described in a paper published in *Nature Chemistry*. The new study shows that the synthetic compound is capable of inhibiting the activities of several DNA-processing enzymes, including the 'integrase' used by the human immunodeficiency virus (HIV) to insert its genome into that of its host cell. The successful demonstration of the efficacy of the synthetic DNA mimic might lead to a new approach to the treatment of AIDS and other retroviral diseases.

The new paper builds on advances described in two previous publications in *Nature Chemistry* published earlier this year. In the first of these papers, Huc and his colleagues developed a pattern of binding interactions required to enable synthetic molecules to assume stable forms similar to the helical backbones of proteins. In the second, they worked out the conditions required to append their synthetic helix to natural proteins during synthesis by cellular ribosomes. "As always in biology, shape determines function," he explains. In the new study, he introduces a synthetic molecule that folds into a helical structure that mimics surface features of the DNA double helix, and whose precise shape can be altered in a modular fashion by the attachment of various substituents. This enables the experimenter to imitate in detail the shape of natural DNA double helix, in particular the position of negative charges. The imitation is so convincing that it acts as a decoy for two DNA-binding enzymes, including the HIV integrase, which readily bind to it and are essentially inactivated.

However, the crucial question is whether or not the foldamer can effectively compete for the enzymes in the presence of their normal DNA substrate. "If the enzymes still bind to the foldamer under competitive conditions, then the mimic must be a better binder than the natural DNA itself," Huc says. And indeed, the study demonstrates that the HIV integrase binds more strongly to the foldamer than to natural DNA. "Furthermore, although initially designed to resemble DNA, the foldamer owes its most useful and valuable properties to the features that differentiate it from DNA," Huc points out.

Thanks to the modular nature of foldamer design, the structures of these artificial DNA mimics can be readily altered, which enables a broad range of variants to be produced using the same basic platform. In the current study, Huc and his colleagues have focused on enzymes that are generically capable of binding to DNA, irrespective of its base sequence. However, it may also be possible to use the foldamer approach to develop DNA mimics that can block the action of the many important DNA-binding proteins whose functions depend on the recognition of specific nucleotide sequences. [16]

Simulations document self-assembly of proteins and DNA

What makes particles self-assemble into complex biological structures? Often, this phenomenon is due to the competition between forces of attraction and repulsion, produced by electric charges in various sections of the particles. In nature, these phenomena often occur in particles that are suspended in a medium—referred to as colloidal particles—such as proteins, DNA and RNA. To facilitate self-assembly, it is possible to "decorate" various sites on the surface of such particles with different charges, called patches.

In a new study published in *EPJE*, physicists have developed an algorithm to simulate the molecular dynamics of these patchy particles. The findings published by Silvano Ferrari and colleagues from the TU Vienna and the Centre for Computational Materials Science (CMS), Austria, will improve our understanding of what makes self-assembly in biological systems possible.

In this study, the authors model charged patchy particles, which are made up of a rigid body with only two charged patches, located at opposite poles. They then develop the equations governing the dynamics of an ensemble of such colloidal patchy particles.

Based on an existing approach originally developed for molecular particles, their simulation includes additional constraints to guarantee that the electrical charge "decorations" are preserved over time. In this regard, they develop equations for describing the particles' motion; the solutions to these equations describe the trajectories of these colloidal particles. Such molecular dynamics simulations lend themselves to being run in parallel on a huge number of particles.

With these findings, the authors complement the lessons learned from experimental observations of similar particles recently synthesised in the lab. Recent experiments have demonstrated that colloidal particles decorated at two interaction sites display a remarkable propensity for self-organising into highly unusual structures that remain stable over a broad temperature range. [15]

Scientists explore the structure of a key region of longevity protein telomerase

Scientists from Moscow State University (MSU) working with an international team of researchers have identified the structure of one of the key regions of telomerase—a so-called "cellular immortality" ribonucleoprotein. Structural and functional studies on this protein are important for the development of potential anticancer drugs. The results of the study have been published in *Nucleic Acids Research*.

Each cell goes through a DNA replication process before division. This is a precise, fine-tuned process controlled by the coordinated work of a sophisticated enzymatic machinery. However, due to the nature of the copying process, the termini of DNA molecules are left uncopied, and DNA becomes

shorter with each replication. However, no important data is lost in the process, as the termini of DNA molecules (telomeres) consist of thousands of small, repeated regions that do not carry hereditary information. When the reserve of telomere repetitions is exhausted, the cell ceases to divide, and eventually, it can die. Scientists believe that this is the mechanism of cellular aging, which is necessary for the renewal of cells and tissues of the body.

But how do "immortal" strains and stem cells that give life to a huge number of offspring cope with this? This is where the enzyme telomerase comes into play. It can restore telomeric termini of chromosomes and therefore compensate for their shortening during mitosis. The telomerase protein catalytic subunit works together with the RNA molecule, and its short fragment is used as a template to synthesize telomeric repetitions. MSU-based scientists discovered the structure of the telomerase fragment that is in charge of this process.

"Our work is aimed at the structural characterization of the telomerase complex. In a living cell, it includes a catalytic subunit, an RNA molecule, a segment of telomeric DNA, and several auxiliary components. Anomalously low activity of telomerase caused by genetics can result in serious pathogenic conditions (telomeropathy), while its anomalous activation is the reason for the cellular "immortality" of most known cancers. Information on the structure of telomerase and the relationships between its components is necessary for understanding the function and regulation of this enzyme, and in the future, for directed control of its activity," said Elena Rodina, assistant professor of the Department for the Chemistry of Natural Products, Faculty of Chemistry, MSU.

Working with thermotolerant yeast, a model eukaryotic organism, the researchers determined the structure of one of the major domains of the telomerase catalytic subunit (the so-called TEN-domain) and determined which parts of it are responsible for the interaction of the enzyme with the RNA molecule and the synthesized DNA. Based on the experimental data obtained, the scientists constructed a theoretical model of the catalytic core of telomerase.

The activity of the enzyme may be described in a simplified way: Telomerase can be represented as a molecular machine containing an RNA molecule. This machine, with the help of a template part of RNA, binds to the end of a long chain of DNA, and synthesizes a fragment of a new DNA chain along the remaining template fragment. After that, the telomerase machine has to move to the newly synthesized end of the DNA in order to continue to build up the chain. The scientists assume that the TEN-domain allows telomerase to synthesize DNA fragments of strictly defined length, after which the RNA template should be detached from the DNA strand to move closer to its edge. Thus, the TEN domain facilitates the movement of the enzyme to building up a new region, i.e. the next telomeric fragment, and this is how the synthesis cycle is repeated.

In addition, the researchers identified the structural core of the TEN domain that remained unchanged in a variety of organisms, despite all the evolutionary vicissitudes, which indicates the important role of this core in the function of the enzyme. The team also revealed the elements specific for different groups of organisms, which interact with own proteins of individual telomerase complex.

"The data obtained bring us closer to an understanding of the structure, function and regulation of telomerase. In the future, this knowledge can be used to create drugs aimed at regulating telomerase activity—either to increase it (for example, to increase the cell life span in biomaterials for

transplantology) or to reduce (for instance, for immortal cancer cells to lose their immortality)," concludes Elena Rodina. [14]

Custom sequences for polymers using visible light

Researchers from Tokyo Metropolitan University used a light-sensitive iridium-palladium catalyst to make "sequential" polymers, using visible light to change how building blocks are combined into polymer chains. By simply switching the light on or off, they were able to realize different compositions along the polymer chain, allowing precise control over physical properties and material function. This may drastically simplify existing polymer production methods, and help overcome fundamental limits in creating new polymers.

The world is full of long, chain-like molecules known as polymers. Famous examples of "sequential" copolymers, i.e. polymers made of multiple building blocks (or "monomers") arranged in a specific order, include DNA, RNA and proteins; their specific structure imparts the vast range of molecular functionality that underpins biological activity. However, making sequential polymers from scratch is a tricky business. We can design special monomers that assemble in different ways, but the complex syntheses that are required limit their availability, scope and functionality.

To overcome these limits, a team led by Associate Professor Akiko Inagaki from the Department of Chemistry, Tokyo Metropolitan University, applied a light-sensitive catalyst containing iridium and palladium. By switching a light on and off, they were able to control the speed at which two different monomers, styrene and vinyl ether, become part of a polymer chain. When exposed to light, the styrene monomer was found to be incorporated into the copolymer structure much more rapidly than in the dark, resulting in a single copolymer chain with different compositions along its length. Parts that are rich in styrene are more rigid than those rich in vinyl ether; by using different on/off light sequences, they could create polymers with a range of physical properties e.g. different "glass transition" temperatures, above which the polymer becomes softer.

The newly developed process is significantly simpler than existing methods. The team also found that both types of monomer were built into the polymer via a mechanism known as non-radical coordination-insertion; this is a generic mechanism, meaning that this new method might be applied to make polymers using a wide range of catalysts and monomers, with the potential to overcome the limited availability of monomer candidates. [13]

Artificial and biological cells work together as mini chemical factories

Researchers have fused living and non-living cells for the first time in a way that allows them to work together, paving the way for new applications.

The system, created by a team from Imperial College London, encapsulates biological cells within an artificial cell. Using this, researchers can harness the natural ability of biological cells to process chemicals while protecting them from the environment.

This system could lead to applications such as cellular 'batteries' powered by photosynthesis, synthesis of drugs inside the body, and biological sensors that can withstand harsh conditions.

Previous artificial cell design has involved taking parts of biological cell 'machinery' - such as enzymes that support chemical reactions - and putting them into artificial casings. The new study, published today in *Scientific Reports*, goes one step further and encapsulates entire cells in artificial casings.

The artificial cells also contain enzymes that work in concert with the biological cell to produce new chemicals. In the proof-of-concept experiment, the artificial cell systems produced a fluorescent chemical that allowed the researchers to confirm all was working as expected.

Lead researcher Professor Oscar Ces, from the Department of Chemistry at Imperial, said: "Biological cells can perform extremely complex functions, but can be difficult to control when trying to harness one aspect. Artificial cells can be programmed more easily but we cannot yet build in much complexity.

"Our new system bridges the gap between these two approaches by fusing whole biological cells with artificial ones, so that the machinery of both works in concert to produce what we need. This is a paradigm shift in thinking about the way we design artificial cells, which will help accelerate research on applications in healthcare and beyond."

To create the system, the team used microfluidics: directing liquids through small channels. Using water and oil, which do not mix, they were able to make droplets of a defined size that contained the biological cells and enzymes. They then applied an artificial coating to the droplets to provide protection, creating an artificial cell environment.

They tested these artificial cells in a solution high in copper, which is usually highly toxic to biological cells. The team were still able to detect fluorescent chemicals in the majority of the artificial cells, meaning the biological cells were still alive and functioning inside. This ability would be useful in the human body, where the artificial cell casing would protect the foreign biological cellsfrom attack by the body's immune system.

First author of the study Dr Yuval Elani, an EPSRC Research Fellow also from the Department of Chemistry, said: "The system we designed is controllable and customisable. You can create different sizes of artificial cells in a reproducible manner, and there is the potential to add in all kinds of cell machinery, such as chloroplasts for performing photosynthesis or engineered microbes that act as sensors."

To improve the functionality of these artificial cell systems, the next step is to engineer the artificial coating to act more like a biological membrane, but with special functions.

For example, if the membrane could be designed to open and release the chemicals produced within only in response to certain signals, they could be used to deliver drugs to specific areas of the body.

This would be useful for example in cancer treatment to release targeted drugs only at the site of a tumour, reducing side effects.

While a system like that may be a way off yet, the team say this is a promising leap in the right direction. The work is the first example of fusing living and non-living components to emerge from Imperial and King's College's new FABRICELL centre for artificial cell science. [12]

New interaction mechanism of proteins discovered

UZH researchers have discovered a previously unknown way in which proteins interact with one another and cells organize themselves. This new mechanism involves two fully unstructured proteins forming an ultra-high-affinity complex due to their opposite net charge. Proteins usually bind one another as a result of perfectly matching shapes in their three-dimensional structures.

Proteins are among the most important biomolecules and are the key mediators of molecular communication between and within cells. For two proteins to bind, specific regions of their three-dimensional structures have to match one another exactly, as a key fits into a lock. The structure of proteins is extremely important for their functioning and for triggering the required responses in cells. Now, researchers at the University of Zurich, together with colleagues from Denmark and the U.S., have discovered that unstructured proteins can also have ultra-high-affinity interactions.

One of these proteins is histone H1, which, as a component of chromatin, is responsible for DNA packaging. Its binding partner, prothymosin α, acts as a kind of shuttle that deposits and removes the histone from the DNA. This process determines whether or not genes in specific parts of the DNA can be read. Both proteins are involved in several regulatory processes in the body, such as cell division and proliferation, and therefore also play a role when it comes to a number of diseases, including cancer. Ben Schuler, professor at the Department of Biochemistry at UZH and head of the research project published in *Nature*, says, "The interesting thing about these proteins is that they're completely unstructured—like boiled noodles in water." How such disordered proteins should be able to interact according to the key/lock principle had puzzled the team of researchers.

Notably, the two proteins bind to one another much more strongly than the average protein partners. The research team used single-molecule fluorescence and nuclear magnetic resonance spectroscopy to determine the arrangement of the proteins. Observed in isolation, they show extended unstructured protein chains. The chains become more compact as soon as both binding partners come together and form a complex. The strong interaction is caused by the strong electrostatic attraction, since histone H1 is highly positively charged while prothymosin α is highly negatively charged. Even more surprising was the discovery that the protein complex was also fully unstructured, as several analyses confirmed.

To investigate the shape of the protein complex, the researchers labeled both proteins with fluorescent probes, which they then added to selected sites on the proteins. Together with computer simulations, this molecular map yielded the following results: Histone 1 interacts with prothymosin α preferably in its central region, which is the region with the highest charge density. Moreover, it

emerged that the complex is highly dynamic: The proteins' position in the complex changes extremely quickly—in a matter of approx. 100 nanoseconds.

The interaction behavior is likely to be fairly common. Cells have many proteins that contain highly charged sequences and may be able to form such protein complexes. There are hundreds of such proteins in the human body alone. "It's likely that the interaction between disordered, highly charged proteins is a basic mechanism for how cells function and organize themselves," concludes Ben Schuler. According to the biophysicist, textbooks will need revision to account for this new way of binding. The discovery is also relevant for developing new therapies, since unstructured proteins are largely unresponsive to traditional drugs, which bind to specific structures on the protein surface. [11]

Particles in charged solution form clusters that reproduce

Dr Martin Sweatman from the University of Edinburgh's School of Engineering has discovered a simple physical principle that might explain how life started on Earth.
He has shown that particles that become charged in solution, like many biological molecules, can form giant clusters that can reproduce. Reproduction is shown to be driven by simple physics—a balance of forces between short-range attraction and long-range repulsion. Once cluster reproduction begins, he suggests chemical evolution of clusters could follow, leading eventually to life.

Many biological molecules, like DNA and proteins, might show this behaviour. Even the building blocks of life, amino acids and nucleobases, might show this behaviour. Reproduction in modern cells might even be driven by this simple physical mechanism, i.e. chemistry is not so important.

Dr Sweatman's research uses theoretical methods and computer simulations of simple particles. They clearly show giant clusters of molecules with the right balance of forces can reproduce. No chemistry is involved. However, these theoretical predictions have yet to be confirmed by experiment.

Dr Sweatman said, "Although it will be difficult to see this behaviour for solutions of small biomolecules, it should be possible to confirm this behaviour experimentally with much larger particles that can be seen under a microscope, like charged colloids.

"If this behaviour is confirmed, then we take another step towards Darwin's idea of life beginning in a warm little pond. A simple evaporation and condensation cycle in a pond might be sufficient to drive cluster reproduction initially. Survival of the fittest clusters of chemicals might then eventually lead to life."

The research has been published in the international journal *Molecular Physics*.

Experiment demonstrates quantum mechanical effects from biological systems

Nearly 75 years ago, Nobel Prize-winning physicist Erwin Schrödinger wondered if the mysterious world of quantum mechanics played a role in biology. A recent finding by Northwestern University's Prem Kumar adds further evidence that the answer might be yes.

Kumar and his team have, for the first time, created quantum entanglement from a biological system. This finding could advance scientists' fundamental understanding of biology and potentially open doors to exploit biological tools to enable new functions by harnessing quantum mechanics.

"Can we apply quantum tools to learn about biology?" said Kumar, professor of electrical engineering and computer science in Northwestern's McCormick School of Engineering and of physics and astronomy in the Weinberg College of Arts and Sciences. "People have asked this question for many, many years—dating back to the dawn of quantum mechanics. The reason we are interested in these new quantum states is because they allow applications that are otherwise impossible."

Partially supported by the Defense Advanced Research Projects Agency, the research was published Dec. 5 in *Nature Communications*.

Quantum entanglement is one of quantum mechanics' most mystifying phenomena. When two particles—such as atoms, photons, or electrons—are entangled, they experience an inexplicable link that is maintained even if the particles are on opposite sides of the universe. While entangled, the particles' behavior is tied one another. If one particle is found spinning in one direction, for example, then the other particle instantaneously changes its spin in a corresponding manner dictated by the entanglement. Researchers, including Kumar, have been interested in harnessing quantum entanglement for several applications, including quantum communications. Because the particles can communicate without wires or cables, they could be used to send secure messages or help build an extremely fast "quantum Internet."

"Researchers have been trying to entangle a larger and larger set of atoms or photons to develop substrates on which to design and build a quantum machine," Kumar said. "My laboratory is asking if we can build these machines on a biological substrate."

In the study, Kumar's team used green fluorescent proteins, which are responsible for bioluminescence and commonly used in biomedical research. The team attempted to entangle the photons generated from the fluorescing molecules within the algae's barrel-shaped protein structure by exposing them to spontaneous four-wave mixing, a process in which multiple wavelengths interact with one another to produce new wavelengths.

Through a series of these experiments, Kumar and his team successfully demonstrated a type of entanglement, called polarization entanglement, between photon pairs. The same feature used to make glasses for viewing 3D movies, polarization is the orientation of oscillations in light waves. A wave can oscillate vertically, horizontally, or at different angles. In Kumar's entangled pairs, the photons' polarizations are entangled, meaning that the oscillation directions of light waves are

linked. Kumar also noticed that the barrel-shaped structure surrounding the fluorescing molecules protected the entanglement from being disrupted.

"When I measured the vertical polarization of one particle, we knew it would be the same in the other," he said. "If we measured the horizontal polarization of one particle, we could predict the horizontal polarization in the other particle. We created an entangled state that correlated in all possibilities simultaneously."

Now that they have demonstrated that it's possible to create quantum entanglement from biological particles, next Kumar and his team plan to make a biological substrate of entangled particles, which could be used to build a quantum machine. Then, they will seek to understand if a biological substrate works more efficiently than a synthetic one. [9]

Quantum biology: Algae evolved to switch quantum coherence on and off

A UNSW Australia-led team of researchers has discovered how algae that survive in very low levels of light are able to switch on and off a weird quantum phenomenon that occurs during photosynthesis.

The function in the algae of this quantum effect, known as coherence, remains a mystery, but it is thought it could help them harvest energy from the sun much more efficiently. Working out its role in a living organism could lead to technological advances, such as better organic solar cells and quantum-based electronic devices.

The research is published in the journal Proceedings of the National Academy of Sciences.

It is part of an emerging field called quantum biology, in which evidence is growing that quantum phenomena are operating in nature, not just the laboratory, and may even account for how birds can navigate using the earth's magnetic field.

"We studied tiny single-celled algae called cryptophytes that thrive in the bottom of pools of water, or under thick ice, where very little light reaches them," says senior author, Professor Paul Curmi, of the UNSW School of Physics.

"Most cryptophytes have a light-harvesting system where quantum coherence is present. But we have found a class of cryptophytes where it is switched off because of a genetic mutation that alters the shape of a light-harvesting protein.

"This is a very exciting find. It means we will be able to uncover the role of quantum coherence in photosynthesis by comparing organisms with the two different types of proteins."

In the weird world of quantum physics, a system that is coherent – with all quantum waves in step with each other – can exist in many different states simultaneously, an effect known as superposition. This phenomenon is usually only observed under tightly controlled laboratory conditions.

So the team, which includes Professor Gregory Scholes from the University of Toronto in Canada, was surprised to discover in 2010 that the transfer of energy between molecules in the light harvesting systems from two different cryptophyte species was coherent.

The same effect has been found in green sulphur bacteria that also survive in very low light levels.

"The assumption is that this could increase the efficiency of photosynthesis, allowing the algae and bacteria to exist on almost no light," says Professor Curmi.

"Once a light-harvesting protein has captured sunlight, it needs to get that trapped energy to the reaction centre in the cell as quickly as possible, where the energy is converted into chemical energy for the organism.

"It was assumed the energy gets to the reaction centre in a random fashion, like a drunk staggering home. But quantum coherence would allow the energy to test every possible pathway simultaneously before travelling via the quickest route."

In the new study, the team used x-ray crystallography to work out the crystal structure of the lightharvesting complexes from three different species of cryptophytes.

They found that in two species a genetic mutation has led to the insertion of an extra amino acid that changes the structure of the protein complex, disrupting coherence.

"This shows cryptophytes have evolved an elegant but powerful genetic switch to control coherence and change the mechanisms used for light harvesting," says Professor Curmi.

The next step will be to compare the biology of different cryptophytes, such as whether they inhabit different environmental niches, to work out whether the quantum coherence effect is assisting their survival. [8]

Photoactive Prebiotic Systems

We propose that life first emerged in the form of such minimal photoactive prebiotic kernel systems and later in the process of evolution these photoactive prebiotic kernel systems would have produced fatty acids and covered themselves with fatty acid envelopes to become the minimal cells of the Fatty Acid World. Specifically, we model self-assembling of photoactive prebiotic systems with observed quantum entanglement phenomena. We address the idea that quantum entanglement was important in the first stages of origins of life and evolution of the biospheres because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states, leading to faster growth and self-replication of minimal living cells. The quantum mechanically modeled possibility of synthesizing artificial selfreproducing quantum entangled prebiotic kernel systems and minimal cells also impacts the possibility of the most probable path of emergence of photocells on the Earth or elsewhere. We also examine the quantum entangled logic gates discovered in the modeled systems composed of two prebiotic kernels. Such logic gates may have application in the destruction of cancer cells or becoming building blocks of new forms of artificial cells including magnetically active ones.

Significance Statement

Our investigated self-assembly of molecules towards supramolecular bioorganic and minimal cellular systems depends on the quantum mechanics laws which induce hydrogen and Van der Waals bindings (Tamulis A, Grigalavicius, M, Orig Life Evol Biosph 41:51-71, 2011).

In the work presented here, quantum entanglement takes the form of a quantum superposition of the active components in synthesized self-assembling and self-replicating living systems. When a quantum calculation of an entangled system is made that causes one photoactive biomolecule of such a pair to take on a definite value (e.g., electron density transfer or electron spin density transfer), the other member of this entangled pair will be found to have taken the appropriately correlated value (e.g., electron density transfer or electron spin density transfer). In our simulations, the separation distance of supramolecular bio systems changes took place during geometry optimization procedures, which mimic real-world intermolecular interaction processes.

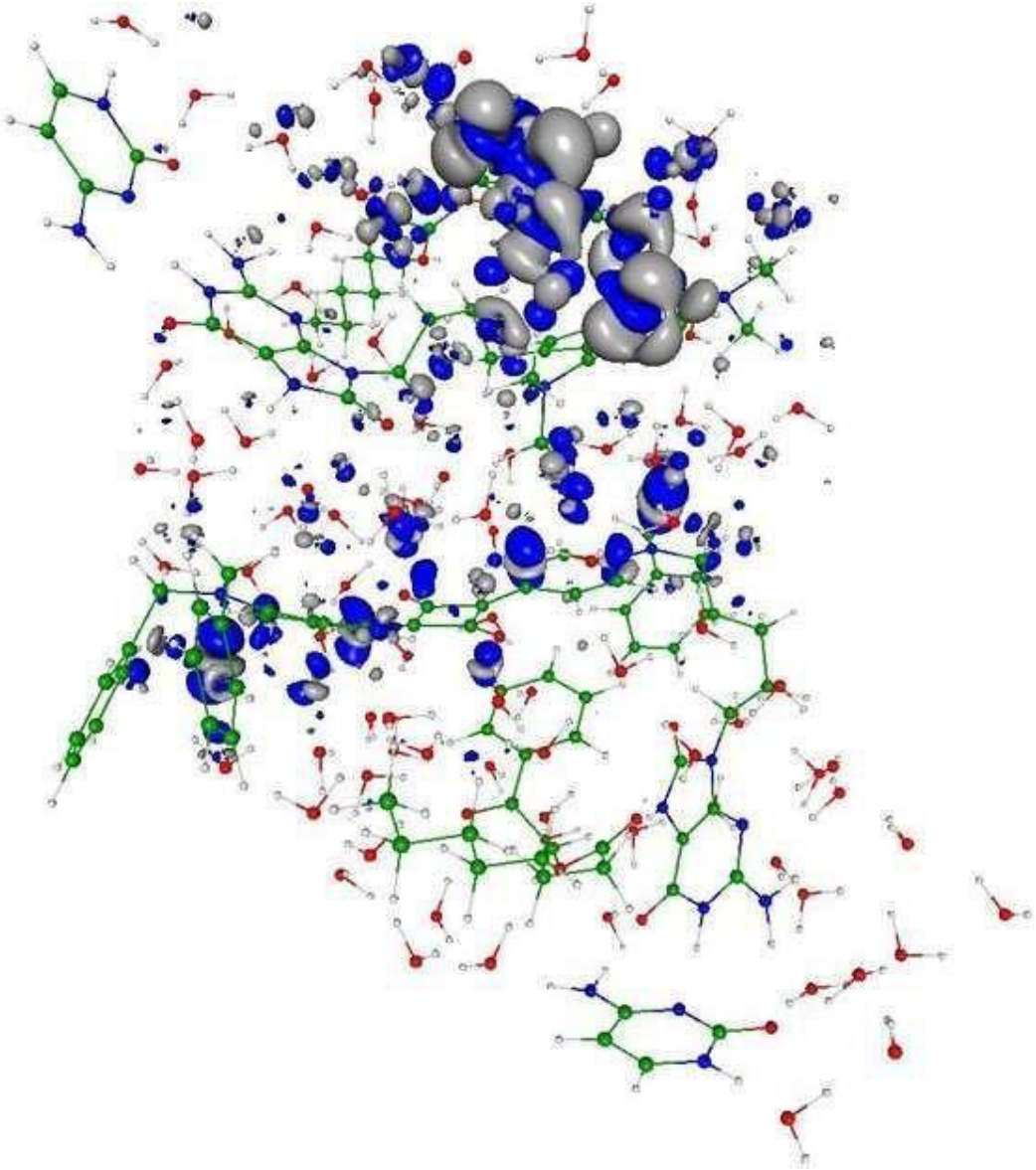
Our discovered phenomenon of the quantum entanglement in the prebiotic systems enhance the photosynthesis in the proposed systems because simultaneously excite two prebiotic kernels in the system by appearance of two additional quantum entangled excited states (Tamulis A, Grigalavicius M, Baltrusaitis J, Orig Life Evol Biosph 43:49-66, 2013; Tamulis A, Grigalavicius M, Krisciukaitis S (2014) , J Comput Theor Nanos, 11, 1597-1608, 2014; Tamulis A, Grigalavicius M, 8:117-140, 2014.). We can propose that quantum entanglement enhanced the emergence of photosynthetic prebiotic kernels and accelerated the evolution of photosynthetic life because of additional absorbed light energy, leading to faster growth and self-replication of minimal living cells.

We can state that: Livings are self-assembled and self-replicating wet and warm stochastically moving supramolecular systems where quantum entanglement can be continuously generated and destroyed by non-equilibrium effects in an environment where no static entanglement exists; quantum entanglement involve the biomolecule inside one living or between other neighboring livings.

This warm quantum coherence is basic for the explanation of DNA stability and for the understanding of brain magnetic orientation during migration in more than 50 species of birds, fishes and insects. Exists experimental evidence for quantum-coherent is used for more efficient light-harvesting in plant photosynthesis. Quantum entanglement exists in supramolecules determining the sense of smell and in the brain neurons microtubules due to quantum vibrations.

In the work presented here, we started to design and quantum mechanical investigations of the molecular logical devices which are useful for construction of nano medicine biorobots against the molecular diseases such a cancer tumors, and against the new kinds of synthesized microorganisms and nano guns.

Figure legend



You can see in the enclosed figure the quantum entanglement phenomenon in the closely selfassembled two synthesized protocell system due to the photo excited electron charge transfer from one protocell to another that leads to closer self-assembly and exchange of energy and information.

Visualization of the electron charge tunneling associated with the 6th (467.3 nm) excited state. The transition is mainly from squarine molecule of the first protocell situated in the bottom of this bi cellular system to precursor of fatty acid (pFA) molecule of the second subsystem (in the top) and little from the 1,4-bis(N,N-dimethylamino)naphthalene molecule (in the top-right) to the same pFA molecule of the second subsystem (in the top). The electron cloud hole is indicated by the dark blue color while the transferred electron cloud location is designated by the gray color.

As a result, these nonlinear quantum interactions compressed the overall molecular system resulting in a smaller gap between the HOMO and LUMO electron energy levels which allows

enhanced tunneling of photo excited electrons from the sensitizer squarine and (1,4bis(N,Ndimethylamino)naphthalene) to the pFA molecule resulting in its cleavage. The new fatty acid joins the existing minimal cell thus increasing it in size. After reaching some critical size, the minimal cell should divide (i.e. self-replicate) into two separate smaller minimal cells. [7]

Quantum Biology

Researchers have long suspected that something unusual is afoot in photosynthesis. Particles of light called photons, streaming down from the Sun; arrive randomly at the chlorophyll molecules and other light-absorbing 'antenna' pigments that cluster inside the cells of every leaf, and within every photosynthetic bacterium. But once the photons' energy is deposited, it doesn't stay random. Somehow, it gets channeled into a steady flow towards the cell's photosynthetic reaction centre, which can then use it at maximum efficiency to convert carbon dioxide into sugars. Quantum coherence in photosynthesis seems to be beneficial to the organisms using it. But did their ability to exploit quantum effects evolve through natural selection? Or is quantum coherence just an accidental side effect of the way certain molecules are structured? [6]

Quantum Consciousness

Extensive scientific investigation has found that a form of quantum coherence operates within living biological systems through what is known as biological excitations and biophoton emission. What this means is that metabolic energy is stored as a form of electromechanical and electromagnetic excitations. These coherent excitations are considered responsible for generating and maintaining long-range order via the transformation of energy and very weak electromagnetic signals. After nearly twenty years of experimental research, Fritz-Albert Popp put forward the hypothesis that biophotons are emitted from a coherent electrodynamics field within the living system.

What this means is that each living cell is giving off, or resonating, a biophoton field of coherent energy. If each cell is emitting this field, then the whole living system is, in effect, a resonating field-a ubiquitous nonlocal field. And since biophotons are the entities through which the living system communicates, there is near-instantaneous intercommunication throughout. And this, claims Popp, is the basis for coherent biological organization -- referred to as quantum coherence. This discovery led Popp to state that the capacity for evolution rests not on aggressive struggle and rivalry but on the capacity for communication and cooperation. In this sense the built-in capacity for species evolution is not based on the individual but rather living systems that are interlinked within a coherent whole: Living systems are thus neither the subjects alone, nor objects isolated, but both subjects and objects in a mutually communicating universe of meaning. . . . Just as the cells in an organism take on different tasks for the whole, different populations enfold information not only for themselves, but for all other organisms, expanding the consciousness of the whole, while at the same time becoming more and more aware of this collective consciousness.

Biophysicist Mae-Wan Ho describes how the living organism, including the human body, is coordinated throughout and is "coherent beyond our wildest dreams." It appears that every part of our body is "in communication with every other part through a dynamic, tunable, responsive, liquid crystalline medium that pervades the whole body, from organs and tissues to the interior of every cell."

What this tells us is that the medium of our bodies is a form of liquid crystal, an ideal transmitter of communication, resonance, and coherence. These relatively new developments in biophysics have discovered that all biological organisms are constituted of a liquid crystalline medium. Further, DNA is a liquid-crystal, lattice-type structure (which some refer to as a liquid crystal gel), whereby body cells are involved in a holographic instantaneous communication via the emitting of biophotons (a source based on light). This implies that all living biological organisms continuously emit radiations of light that form a field of coherence and communication. Moreover, biophysics has discovered that living organisms are permeated by quantum wave forms. [5]

Creating quantum technology

Another area of potential application is in quantum computing. The long-standing goal of the physicists and engineers working in this area is to manipulate data encoded in quantum bits (qubits) of information, such as the spin-up and spin-down states of an electron or of an atomic nucleus. Qubits can exist in both states at once, thus permitting the simultaneous exploration of all possible answers to the computation that they encode. In principle, this would give quantum computers the power to find the best solution far more quickly than today’s computers can — but only if the qubits can maintain their coherence, without the noise of the surrounding environment, such as the jostling of neighboring atoms, destroying the synchrony of the waves. [6]

Quantum Entanglement

Measurements of physical properties such as position, momentum, spin, polarization, etc. performed on entangled particles are found to be appropriately correlated. For example, if a pair of particles is generated in such a way that their total spin is known to be zero, and one particle is found to have clockwise spin on a certain axis, then the spin of the other particle, measured on the same axis, will be found to be counterclockwise. Because of the nature of quantum measurement, however, this behavior gives rise to effects that can appear paradoxical: any measurement of a property of a particle can be seen as acting on that particle (e.g. by collapsing a number of superimposed states); and in the case of entangled particles, such action must be on the entangled system as a whole. It thus appears that one particle of an entangled pair "knows" what measurement has been performed on the other, and with what outcome, even though there is no known means for such information to be communicated between the particles, which at the time of measurement may be separated by arbitrarily large distances. [4]

The Bridge

The accelerating electrons explain not only the Maxwell Equations and the Special Relativity, but the Heisenberg Uncertainty Relation, the wave particle duality and the electron's spin also, building the bridge between the Classical and Quantum Theories. [1]

Accelerating charges

The moving charges are self maintain the electromagnetic field locally, causing their movement and this is the result of their acceleration under the force of this field. In the classical physics the charges will distributed along the electric current so that the electric potential lowering along the current, by linearly increasing the way they take every next time period because this accelerated motion. The same thing happens on the atomic scale giving a dp impulse difference and a dx way difference between the different part of the not point like particles.

Relativistic effect

Another bridge between the classical and quantum mechanics in the realm of relativity is that the charge distribution is lowering in the reference frame of the accelerating charges linearly: $ds/dt = at$ (time coordinate), but in the reference frame of the current it is parabolic: $s = a/2\ t^2$ (geometric coordinate).

Heisenberg Uncertainty Relation

In the atomic scale the Heisenberg uncertainty relation gives the same result, since the moving electron in the atom accelerating in the electric field of the proton, causing a charge distribution on delta x position difference and with a delta p momentum difference such a way that they product is about the half Planck reduced constant. For the proton this delta x much less in the nucleon, than in the orbit of the electron in the atom, the delta p is much higher because of the greater proton mass.

This means that the electron and proton are not point like particles, but has a real charge distribution.

Wave – Particle Duality

The accelerating electrons explains the wave – particle duality of the electrons and photons, since the elementary charges are distributed on delta x position with delta p impulse and creating a wave packet of the electron. The photon gives the electromagnetic particle of the mediating force of the electrons electromagnetic field with the same distribution of wavelengths.

Atomic model

The constantly accelerating electron in the Hydrogen atom is moving on the equipotential line of the proton and it's kinetic and potential energy will be constant. Its energy will change only when it

is changing its way to another equipotential line with another value of potential energy or getting free with enough kinetic energy. This means that the Rutherford-Bohr atomic model is right and only that changing acceleration of the electric charge causes radiation, not the steady acceleration. The steady acceleration of the charges only creates a centric parabolic steady electric field around the charge, the magnetic field. This gives the magnetic moment of the atoms, summing up the proton and electron magnetic moments caused by their circular motions and spins.

The Relativistic Bridge

Commonly accepted idea that the relativistic effect on the particle physics it is the fermions' spin - another unresolved problem in the classical concepts. If the electric charges can move only with accelerated motions in the self maintaining electromagnetic field, once upon a time they would reach the velocity of the electromagnetic field. The resolution of this problem is the spinning particle, constantly accelerating and not reaching the velocity of light because the acceleration is radial. One origin of the Quantum Physics is the Planck Distribution Law of the electromagnetic oscillators, giving equal intensity for 2 different wavelengths on any temperature. Any of these two wavelengths will give equal intensity diffraction patterns, building different asymmetric constructions, for example proton - electron structures (atoms), molecules, etc. Since the particles are centers of diffraction patterns they also have particle – wave duality as the electromagnetic waves have. [2]

The weak interaction

The weak interaction transforms an electric charge in the diffraction pattern from one side to the other side, causing an electric dipole momentum change, which violates the CP and time reversal symmetry. The Electroweak Interaction shows that the Weak Interaction is basically electromagnetic in nature. The arrow of time shows the entropy grows by changing the temperature dependent diffraction patterns of the electromagnetic oscillators.

Another important issue of the quark model is when one quark changes its flavor such that a linear oscillation transforms into plane oscillation or vice versa, changing the charge value with 1 or -1. This kind of change in the oscillation mode requires not only parity change, but also charge and time changes (CPT symmetry) resulting a right handed anti-neutrino or a left handed neutrino.

The right handed anti-neutrino and the left handed neutrino exist only because changing back the quark flavor could happen only in reverse, because they are different geometrical constructions, the u is 2 dimensional and positively charged and the d is 1 dimensional and negatively charged. It needs also a time reversal, because anti particle (anti neutrino) is involved.

The neutrino is a 1/2spin creator particle to make equal the spins of the weak interaction, for example neutron decay to 2 fermions, every particle is fermions with ½ spin. The weak interaction changes the entropy since more or less particles will give more or less freedom of movement. The entropy change is a result of temperature change and breaks the equality of oscillator diffraction

intensity of the Maxwell–Boltzmann statistics. This way it changes the time coordinate measure and makes possible a different time dilation as of the special relativity.

The limit of the velocity of particles as the speed of light appropriate only for electrical charged particles, since the accelerated charges are self maintaining locally the accelerating electric force. The neutrinos are CP symmetry breaking particles compensated by time in the CPT symmetry, that is the time coordinate not works as in the electromagnetic interactions, consequently the speed of neutrinos is not limited by the speed of light.

The weak interaction T-asymmetry is in conjunction with the T-asymmetry of the second law of thermodynamics, meaning that locally lowering entropy (on extremely high temperature) causes the
weak interaction, for example the Hydrogen fusion.

Probably because it is a spin creating movement changing linear oscillation to 2 dimensional oscillation by changing d to u quark and creating anti neutrino going back in time relative to the proton and electron created from the neutron, it seems that the anti neutrino fastest then the velocity of the photons created also in this weak interaction?

A quark flavor changing shows that it is a reflection changes movement and the CP- and T-symmetry breaking!!! This flavor changing oscillation could prove that it could be also on higher level such as atoms, molecules, probably big biological significant molecules and responsible on the aging of the life.

Important to mention that the weak interaction is always contains particles and antiparticles, where the neutrinos (antineutrinos) present the opposite side. It means by Feynman's interpretation that these particles present the backward time and probably because this they seem to move faster than the speed of light in the reference frame of the other side.

Finally since the weak interaction is an electric dipole change with ½ spin creating; it is limited by the velocity of the electromagnetic wave, so the neutrino's velocity cannot exceed the velocity of light.

The General Weak Interaction

The Weak Interactions T-asymmetry is in conjunction with the T-asymmetry of the Second Law of Thermodynamics, meaning that locally lowering entropy (on extremely high temperature) causes for example the Hydrogen fusion. The arrow of time by the Second Law of Thermodynamics shows the increasing entropy and decreasing information by the Weak Interaction, changing the temperature dependent diffraction patterns. A good example of this is the neutron decay, creating more particles with less known information about them.
The neutrino oscillation of the Weak Interaction shows that it is a general electric dipole change and it is possible to any other temperature dependent entropy and information changing diffraction pattern of atoms, molecules and even complicated biological living structures. We can generalize the weak interaction on all of the decaying matter constructions, even on the biological too. This gives the limited lifetime for the biological constructions also by the arrow of

time. There should be a new research space of the Quantum Information Science the 'general neutrino oscillation' for the greater then subatomic matter structures as an electric dipole change.

There is also connection between statistical physics and evolutionary biology, since the arrow of time is working in the biological evolution also.
The Fluctuation Theorem says that there is a probability that entropy will flow in a direction opposite to that dictated by the Second Law of Thermodynamics. In this case the Information is growing that is the matter formulas are emerging from the chaos. So the Weak Interaction has two directions, samples for one direction is the Neutron decay, and Hydrogen fusion is the opposite direction.

Fermions and Bosons

The fermions are the diffraction patterns of the bosons such a way that they are both sides of the same thing.

Van Der Waals force

Named after the Dutch scientist Johannes Diderik van der Waals – who first proposed it in 1873 to explain the behaviour of gases – it is a very weak force that only becomes relevant when atoms and molecules are very close together. Fluctuations in the electronic cloud of an atom mean that it will have an instantaneous dipole moment. This can induce a dipole moment in a nearby atom, the result being an attractive dipole–dipole interaction.

Electromagnetic inertia and mass

Electromagnetic Induction

Since the magnetic induction creates a negative electric field as a result of the changing acceleration, it works as an electromagnetic inertia, causing an electromagnetic mass. [1]

Relativistic change of mass

The increasing mass of the electric charges the result of the increasing inductive electric force acting against the accelerating force. The decreasing mass of the decreasing acceleration is the result of the inductive electric force acting against the decreasing force. This is the relativistic mass change explanation, especially importantly explaining the mass reduction in case of velocity decrease.

The frequency dependence of mass

Since $E = h\nu$ and $E = mc^2$, $m = h\nu / c^2$ that is the m depends only on the ν frequency. It means that the mass of the proton and electron are electromagnetic and the result of the electromagnetic induction, caused by the changing acceleration of the spinning and moving charge! It could be that the m_o inertial mass is the result of the spin, since this is the only accelerating motion of the electric charge. Since the accelerating motion has different frequency for the electron in the atom

and the proton, they masses are different, also as the wavelengths on both sides of the diffraction pattern, giving equal intensity of radiation.

Electron – Proton mass rate

The Planck distribution law explains the different frequencies of the proton and electron, giving equal intensity to different lambda wavelengths! Also since the particles are diffraction patterns they have some closeness to each other – can be seen as a gravitational force. [2]

There is an asymmetry between the mass of the electric charges, for example proton and electron, can understood by the asymmetrical Planck Distribution Law. This temperature dependent energy distribution is asymmetric around the maximum intensity, where the annihilation of matter and antimatter is a high probability event. The asymmetric sides are creating different frequencies of electromagnetic radiations being in the same intensity level and compensating each other. One of these compensating ratios is the electron – proton mass ratio. The lower energy side has no compensating intensity level, it is the dark energy and the corresponding matter is the dark matter.

Gravity from the point of view of quantum physics

The Gravitational force

The gravitational attractive force is basically a magnetic force.

The same electric charges can attract one another by the magnetic force if they are moving parallel in the same direction. Since the electrically neutral matter is composed of negative and positive charges they need 2 photons to mediate this attractive force, one per charges. The Bing Bang caused parallel moving of the matter gives this magnetic force, experienced as gravitational force.

Since graviton is a tensor field, it has spin = 2, could be 2 photons with spin = 1 together.

You can think about photons as virtual electron – positron pairs, obtaining the necessary virtual mass for gravity.

The mass as seen before a result of the diffraction, for example the proton – electron mass rate Mp=1840 Me. In order to move one of these diffraction maximum (electron or proton) we need to intervene into the diffraction pattern with a force appropriate to the intensity of this diffraction maximum, means its intensity or mass.

The Big Bang caused acceleration created radial currents of the matter, and since the matter is composed of negative and positive charges, these currents are creating magnetic field and attracting forces between the parallel moving electric currents. This is the gravitational force experienced by the matter, and also the mass is result of the electromagnetic forces between the charged particles. The positive and negative charged currents attracts each other or by the magnetic forces or by the much stronger electrostatic forces!?

The gravitational force attracting the matter, causing concentration of the matter in a small space and leaving much space with low matter concentration: dark matter and energy.
There is an asymmetry between the mass of the electric charges, for example proton and electron, can understood by the asymmetrical Planck Distribution Law. This temperature dependent energy

distribution is asymmetric around the maximum intensity, where the annihilation of matter and antimatter is a high probability event. The asymmetric sides are creating different frequencies of electromagnetic radiations being in the same intensity level and compensating each other. One of these compensating ratios is the electron – proton mass ratio. The lower energy side has no compensating intensity level, it is the dark energy and the corresponding matter is the dark matter.

The Higgs boson

By March 2013, the particle had been proven to behave, interact and decay in many of the expected ways predicted by the Standard Model, and was also tentatively confirmed to have + parity and zero spin, two fundamental criteria of a Higgs boson, making it also the first known scalar particle to be discovered in nature, although a number of other properties were not fully proven and some partial results do not yet precisely match those expected; in some cases data is also still awaited or being analyzed.

Since the Higgs boson is necessary to the W and Z bosons, the dipole change of the Weak interaction and the change in the magnetic effect caused gravitation must be conducted. The Wien law is also important to explain the Weak interaction, since it describes the T_{max} change and the diffraction patterns change. [2]

Higgs mechanism and Quantum Gravity

The magnetic induction creates a negative electric field, causing an electromagnetic inertia. Probably it is the mysterious Higgs field giving mass to the charged particles? We can think about the photon as an electron-positron pair, they have mass. The neutral particles are built from negative and positive charges, for example the neutron, decaying to proton and electron. The wave – particle duality makes sure that the particles are oscillating and creating magnetic induction as an inertial mass, explaining also the relativistic mass change. Higher frequency creates stronger magnetic induction, smaller frequency results lesser magnetic induction. It seems to me that the magnetic induction is the secret of the Higgs field.

In particle physics, the Higgs mechanism is a kind of mass generation mechanism, a process that gives mass to elementary particles. According to this theory, particles gain mass by interacting with the Higgs field that permeates all space. More precisely, the Higgs mechanism endows gauge bosons in a gauge theory with mass through absorption of Nambu–Goldstone bosons arising in spontaneous symmetry breaking.

The simplest implementation of the mechanism adds an extra Higgs field to the gauge theory. The spontaneous symmetry breaking of the underlying local symmetry triggers conversion of components of this Higgs field to Goldstone bosons which interact with (at least some of) the other fields in the theory, so as to produce mass terms for (at least some of) the gauge bosons. This mechanism may also leave behind elementary scalar (spin-0) particles, known as Higgs bosons.

In the Standard Model, the phrase "Higgs mechanism" refers specifically to the generation of masses for the $W^{\pm}$, and Z weak gauge bosons through electroweak symmetry breaking. The Large Hadron Collider at CERN announced results consistent with the Higgs particle on July 4, 2012 but stressed that further testing is needed to confirm the Standard Model.

What is the Spin?

So we know already that the new particle has spin zero or spin two and we could tell which one if we could detect the polarizations of the photons produced. Unfortunately this is difficult and neither ATLAS nor CMS are able to measure polarizations. The only direct and sure way to confirm that the particle is indeed a scalar is to plot the angular distribution of the photons in the rest frame of the centre of mass. A spin zero particles like the Higgs carries no directional information away from the original collision so the distribution will be even in all directions. This test will be possible when a much larger number of events have been observed. In the mean time we can settle for less certain indirect indicators.

The Graviton

In physics, the graviton is a hypothetical elementary particle that mediates the force of gravitation in the framework of quantum field theory. If it exists, the graviton is expected to be massless (because the gravitational force appears to have unlimited range) and must be a spin-2 boson. The spin follows from the fact that the source of gravitation is the stress-energy tensor, a second-rank tensor (compared to electromagnetism's spin-1 photon, the source of which is the four-current, a first-rank tensor). Additionally, it can be shown that any massless spin-2 field would give rise to a force indistinguishable from gravitation, because a massless spin-2 field must couple to (interact with) the stress-energy tensor in the same way that the gravitational field does. This result suggests that, if a massless spin-2 particle is discovered, it must be the graviton, so that the only experimental verification needed for the graviton may simply be the discovery of a massless spin-2 particle. [3]

Conclusions

Exists experimental evidence for quantum-coherent is used for more efficient light-harvesting in plant photosynthesis. Quantum entanglement exists in supramolecules determining the sense of smell and in the brain neurons microtubules due to quantum vibrations.

In the work presented here, we started to design and quantum mechanical investigations of the molecular logical devices which are useful for construction of nano medicine biorobots against the molecular diseases such a cancer tumors, and against the new kinds of synthesized microorganisms and nano guns. [7]

One of the most important conclusions is that the electric charges are moving in an accelerated way and even if their velocity is constant, they have an intrinsic acceleration anyway, the so called spin, since they need at least an intrinsic acceleration to make possible they movement . The accelerated charges self-maintaining potential shows the locality of the relativity, working on the quantum level also. [1]

The bridge between the classical and quantum theory is based on this intrinsic acceleration of the spin, explaining also the Heisenberg Uncertainty Principle. The particle – wave duality of the electric charges and the photon makes certain that they are both sides of the same thing. The

Secret of Quantum Entanglement that the particles are diffraction patterns of the

electromagnetic waves and this way their quantum states every time is the result of the quantum state of the intermediate electromagnetic waves. [2]
These relatively new developments in biophysics have discovered that all biological organisms are constituted of a liquid crystalline medium. Further, DNA is a liquid-crystal, lattice-type structure (which some refer to as a liquid crystal gel), whereby body cells are involved in a holographic instantaneous communication via the emitting of biophotons (a source based on light). This implies that all living biological organisms continuously emit radiations of light that form a field of coherence and communication. Moreover, biophysics has discovered that living organisms are permeated by quantum wave forms. [5]
Basing the gravitational force on the accelerating Universe caused magnetic force and the Planck Distribution Law of the electromagnetic waves caused diffraction gives us the basis to build a Unified Theory of the physical interactions also.

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