Hypothesis

Rebuilding Quantum Homeostasis

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Posted Date: 16 July 2024

doi: 10.20944/preprints202407.1192.v1

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Rebuilding Quantum Homeostasis

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Abstract: Homeostasis and its interaction with gene expression in the development and maintenance of living systems is discussed in order to formulate a new method to diagnose and treat diseases on this causative level. This includes an inquiry into the unsolved homeostasis problems of: location (where in the cell are calculations performed?), communication (what language used?), identity (set of plans/hierarchy of set points?) and computational (mechanisms used to make necessary adjustments?). As these functions require the processing of vast amounts of information which is communicated at every level of organization including the mechanisms of epigenetics, different computer models are discussed, with examples for each; analog, digital and the possibility of quantum biological. Each one allows certain properties and cell functions to emerge. The difference between functional homeostasis and dysfunctional homeostasis is discussed with strategies to indirectly study them in terms of epigenetic signatures. Hormesis is discussed as a mechanism to reverse the epimutations, leading to a method of treatment to almost any chronic disease. These topics are discussed as being a whole interconnected system.

Keywords: homeostasis; epigenetics; epimutations; hormesis; toxicogenomics; quantum biology; superposition reference image; ultra high dilutions. quantum drug action

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Discussion

Homeostasis involves some of the most interesting unsolved problems in modern biology. Hormones, small molecules and electrical signals can interact with receptors but then within cells the homeostasis information processing at a certain point is not observable, therefore, it is not possible to easily diagnose diseases that originate at this processing level. The mechanisms of homeostasis, when healthy, are able to compare the known value of an endpoint (for example blood pressure) with a known setpoint (the ideal blood pressure stored as a range). It can then produce a reaction to adjust the endpoint. Here are the possible ways in which this system can malfunction leading to disease:

- The information received is incorrect, distorted or incomplete. For example the patient has been infected by a virus but the immune system receives incomplete information about it.
- The homeostasis processing unit can't access the accurate value of the set point.
- The homeostasis processing unit can't complete the plan to adjust the endpoint.

In all of these examples the net result is an endpoint that drifts out of the homeostasis healthy range. In time this can be measured and named as a disease process. For example the body temperature rises over 98.6 (fever), the blood sugar rises (diabetes), the brain hallucinates voices (schizophrenia), undifferentiated cells divide too often (cancer) etc. How can modern tools allow us to directly or indirectly study the exact malfunction in the homeostasis process and correct them?

Defining the Problems

Epigenetics is the study of heritable changes in gene expression that are caused by factors such as DNA methylation rather than by changes in the sequence of base pairs in DNA itself. Optimum patterns of methylation lead to healthy gene expression while methylation patterns that are less than optimal lead to epimutations and disease tendencies [1,2]. Each cell type inherits either robust/optimal epigenetics or fragile/susceptible epigenetics, but what are the mechanisms of homeostasis that maintain correct gene expression in each cell type?

 doi:10.20944/preprints202407.1192.v1

Through control of gene expression and homeostasis, aspects of the epigenome regulate almost every biological process, from cellular differentiation and maintenance of phenotypes to onset of disease and ageing. Epigenetic mechanisms such as DNA methylation, histone tail modifications, chromatin accessibility and changes in DNA architecture are tightly correlated with normal cellular function, while their dysregulation manifests in aberrant gene expression and disease [3].

Life forms, including the organization of methylation patterns are self organizing according to the systems of homeostasis, but how? The analog level explains part of the solution. When one looks at a Swiss watch not only can we appreciate the elegance of the craftsmanship but it can tell us the exact time down to a few seconds of accuracy a day. It can do this because it is an analog computer, the parts are assembled in such a way as to accurately compute the correct time. A well trained watchmaker can open it up and make sense of each piece, its form/material used (steel, glass, jewel etc) and function. The same is true of many cell functions, they are cellular analog computers to an extent. For example, chromatin will arrange itself geographically to optimize correct gene expression. When insulin binds to the receptor on a cell wall, it activates the membrane's computer to allow sugar molecules to enter the cell.

The stoichiometry of cell structures and folded proteins lend themselves to analog functions. Oxygen binds to hemoglobin because the three dimensional structure of the folded protein optimizes this part of the computer to work efficiently so that iron can bind and carry oxygen. It is not difficult to locate and study this level of computing in cells and diagnose obvious mistakes being made. Sickle cell anemia is an example. The proteins are folded incorrectly, so the red blood cells' shapes are abnormal [4]. By analogy if a sprocket is missing on a wheel in the watch, its computer functions break down.

Even at this level, the analog functions only make sense when the whole interconnected system is understood and appreciated. By analogy if one part of a watch is removed and observed in isolation from how it fits into the totality of the functions of the timepiece it has less meaning. Homeostasis needs to configure each set of epigenetic plans for each cell type and continuously adjust these molecular attachments on the DNA accordingly to the needs of that cell and the organism as a whole. The homeostasis mechanism needs to evaluate how many analog molecules it needs to make, where to place them, then collect the data from each one and make sense of this data leading to rational reactions. At a certain point the processing of analog information in cells is not available for examination. Where in each cell and how in each cell is this accomplished? If something goes wrong with homeostasis on this level how can we diagnose and correct it? Have we been able to visualize all the parts and understand how they function?

Cells also generate, collect and process signals, through the nervous system and via small molecules and electrical circuits, this is more like a digital computer. For example when something is touched that is hot, the nervous system sends electrical pain signals to the brain, the brain immediately tells the hand to take itself away from the hot object. We can follow the pain signals to parts of the brain but then a problem presents itself. The location within the cell of where and how the information was analyzed is not revealed. Frustratingly this ‘computer’ which processes analog and digital information is hidden somewhere in cellular tissue, but where exactly and how were the signals processed so accurately?

Homeostasis (totality of set points, an accurate processing of analog and electromagnetic signals) <— — — — — — > Sensors of the internal environment <— — —> External environmental influences <— ---> Homeostasis <—---> Reactions to affect the end points. This is best represented by the following diagram:

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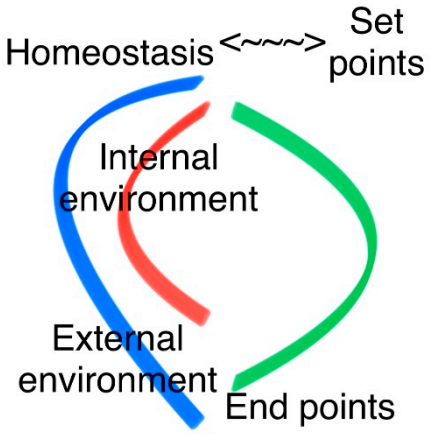

Homeostasis is constantly oscillating around a set-point, monitoring the cellular environment, always ready to reset itself, but also to provide the reference point for change if necessary for survival in an ever-changing environment. Whereas the perspective that homeostasis is static is based on contemporary descriptive biology, the dynamic perspective is best seen in the field of developmental physiology [5],

The fact that we can't get inside of this analog/digital cellular computer to see its 'central processor', its 'resistors', 'memory chips' and 'circuit boards' etc, means that when something goes wrong with it there is no easy fix. We have no homeostasis cure for any chronic disease because we can't find the mistakes being made. We don't know the language used, how the set point information is stored, how the information is processed and then how it is communicated to the DNA to control gene expression, or other organelles within the cells or to the brain. Again without this knowledge, it's not possible to diagnose the causes of diseases that rely on these homeostasis functions.

What about the possibility of quantum biological computers? Increasingly there are reasons to believe quantum biology has a role in cell regulatory dynamics. Classical biology is a product of quantum functions: *In more general terms, we believe that there is a deep understanding to be gained in tackling the emergence of the essentially classical world of biology from its quantized molecular origins* [6].

Most likely all the useful quantum effects survive and are useful in what seems like a biology based only on classical elements.

All living systems are made up of molecules, and fundamentally all molecules are described by quantum mechanics [7]. There is evidence to support the following processes have a quantum explanation: photosynthesis, DNA mutation repair, olfaction, vision, enzymatic activity, mitochondria, molecular solutions in proteins, magnetoreception in bird navigation, ferritin, the conversion of chemical energy into motion and brownian motions in many cellular processes [8–10].

These quantum computations take place within cells, allowing outcomes that can't be explained by classical physics. Lambert et al. said, "*These features go beyond trivial quantum effects and may include harnessing quantum coherence on physiologically important timescales* [11]." Quantum coherences are the quantum rules for each wave function, their mathematical descriptions as they provide the foundation to form atoms, molecules and finally living structures [12].

Quantum mechanics is the fundamental theory that describes the properties of subatomic particles, atoms, molecules, molecular assemblies and possibly beyond. Quantum mechanics operates on the nanometre and sub-nanometre scales and is at the basis of fundamental life processes such as photosynthesis, respiration and vision. In quantum mechanics, all objects have wave-like properties, and when they interact, quantum coherence describes the correlations between the physical quantities describing such objects due to this wave-like nature [13].

The three aspects of quantum field theory as it relates to biology and relevant to this paper are quantum coherence, quantum field theory and superposition/ entanglement.

Quantum coherence as already mentioned is the characteristics of the wave like properties of matter. Each molecule has a unique wave property to create and maintain it, each organelle a combination of unique wave propertiest, each cell type a more complicated wave function etc. The

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description and rules for each wave function maintain each biological structure. Are these quantum properties contributing to the overall functions of homeostasis? Perhaps analog structures within the nucleus can partially explain homeostasis, perhaps a computer model based on electrical signals can partly explain homeostasis? But studies that demonstrate the possibility of quantum homeostasis also could lead to part of the solution.

Superposition and entanglement is the connection of quantum fields in a dimension that is hidden, leading to stored information about that molecule or larger structures such as cells or tissues:

Entanglement, Schrodinger found, is pervasive in quantum physics. When any two subatomic particles collide, they almost always become entangled. When a group of objects forms some larger object, like subatomic particles in an atom or atoms in a molecule, they become entangled. In fact, nearly any interaction between any particles would cause them to become entangled, sharing a single wave function….[14]

If these two ideas are combined then we have cell structures with wave functions/coherence and many wave connections/entanglement. To what extent if any do these entangled quantum structures contribute to homeostasis, maintaining cell structures and whole organisms?

The existence of superposition states in the quantum regime results in uniquely quantum-mechanical properties, which are often counterintuitive. For example, quantum coherence describes the well-defined relationship between the individual states constituting a superposition, and quantum entanglement is a special form of correlation between quantum states. An excellent example is the delocalization of electronic states in photosynthesis that is crucial to explain the speed and efficiency of electronic energy transfer and charge separation at the basis of photosynthesis [13]

Photosynthesis is one example, but we are searching for a comprehensive model where all end-points are continuously being compared to all set points with a mechanism to nudge the end points back to an ideal. This would give homeostasis the capacity to differentiate cells into whole organisms, receive data from every cell structure, perceive the environment and continually make adjustments with predetermined goals. The human body contains about thirty trillion cells [15], (80 billion of which are brain neurons), each cell also contains a minimum of eleven different cell organelles and each cell has to be monitored for a minimum of eleven functions. This means each human is a functional unit with a minimum of 30T x 11T x 11T = 3,630 trillion endpoints and the same number of corresponding setpoints. These are located in every gamete and during cell differentiation every cell with this same number of set points is in contact with the same ones in every other cell. It makes sense to inquire into the possibility of a quantum computer to explain the processing capacity of homeostasis at this level because superposition allows for a field to be nonlocal, in all places at all times and not take up any physical space. It is physically impossible to place an analog or digital computer in every cell with a capacity to process the necessary trillions of computations per second, there just isn't enough room. Also fields by definition are connected to molecules and organelles; this provides a means by which the structures and functions can be communicated to and manipulated by the reference image to perform exact functions.

Background - Non Local Quantum Field Theory

Quantum field theory states that each type of field has unique characteristics and exists at all points of space. This is counterintuitive, we normally think about an object taking up space to the exclusion of other objects using the same exact space. In quantum field theory all the fields are in the same space, but are not necessarily influencing each other. The diagram below lists the fundamental particles (building blocks) of the universe, along with their quantum fields as described by the standard model. David Tong - at the University of Cambridge explains: *There is a field associated with each type of fundamental particle that appears in Nature [8].*

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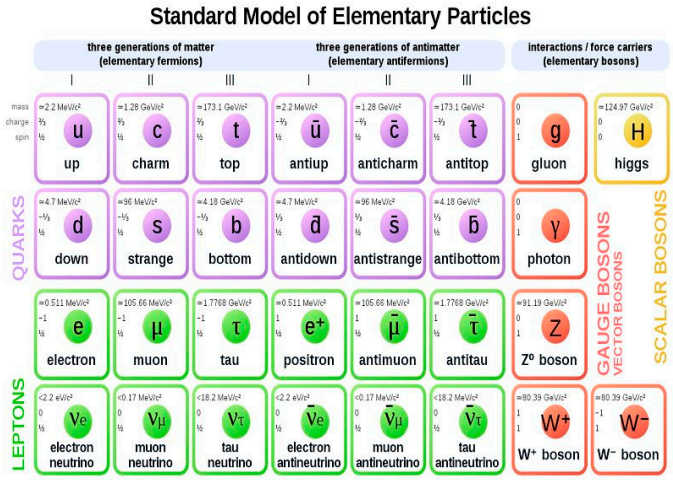
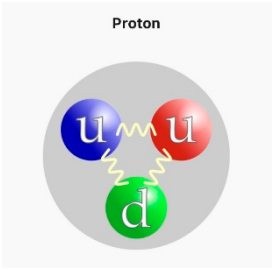
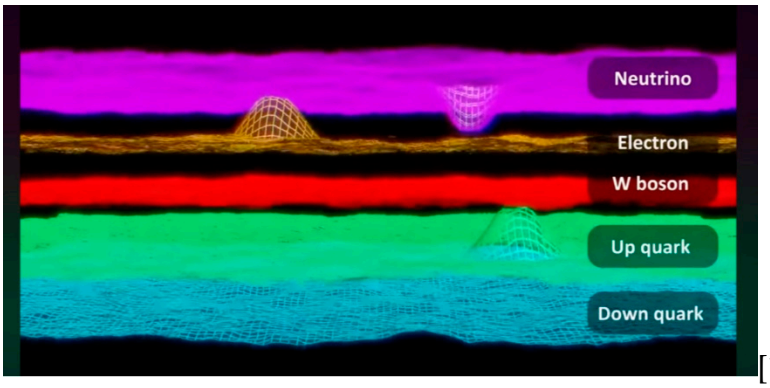


Depending on the number of each type of field, their arrangement and connections between each other, the periodic table of elements can be created. For example a proton is made of an extra two up quark fields and one extra down quark field:



A hydrogen atom is one proton in the proton field and one electron in the electron field. Here is an example of five fields interacting:



[16]

New particles are created depending on how much energy is available in each field:

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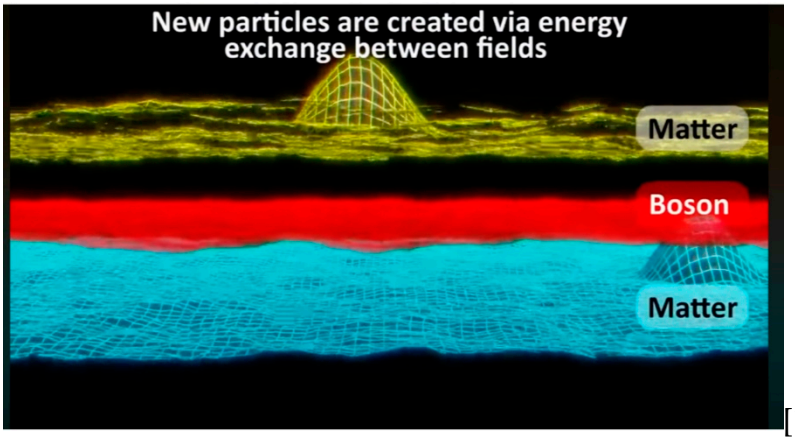

[16]

Carbon - one of the fundamental atoms of life contains 6 protons, six neutrons and 12 electrons. Every part of every living organism is ultimately made up of quantum fields interacting in unique ways.

Each component above in the standard model exists as a field with certain mathematical properties [17]. If enough energy is put into that field a specific type of particle, force or atomic structure will result. The wave function is always in oscillation with the particle function. There is no example in nature where a physical particle can exist without its wave counterpart, because the field is more fundamental, it is there to create and maintain matter. This means by definition complex wave functions exist for each and every biological structure.

Quantum Field Theory and Homeostasis

Is there any usefulness to the fact that in any one organism all the molecules and therefore all the wave structures for each cell structure are in a superposition? In order for quantum homeostasis to make sense as a hypothesis the following would need to be true:

- All the information for each healthy set point of a living organism would need to be contained in this superposition matrix.
- This quantum matrix would need to be able to translate analog, digital and small molecule messenger signals into quantum language and process that information.
- Quantum homeostasis would need to be able to evaluate information, compare information between the end points and set points and come up with an information plan to adjust end points.

Because science is based on the verification of theories, this theory needs studies to prove it. It is interesting that cells act as if this theory was true. They seem to process information through a homeostasis filter that can accomplish these goals continuously. Every cell acts as if it has a reference image for all its end points. If this was the basis for how homeostasis works, then here are the advantages of such a system:

- Every epigenetic pattern, protein, cell structure, organelle function, type of cell, tissue system and the overall anatomy and physiology or an organism would be able to see itself as a part of and retain its identity, as a part of the completed quantum reference image (set of plans) - know its structure, place and function in this integrated superposition matrix.
- This quantum matrix would allow for an interconnected system in a two way communication with every cell structure and function.
- It would conserve space as it could be present everywhere at all times, but take up no physical space.
- It could be positioned/available to filter all information through itself almost instantaneously, all the information from within and from the environment.
- As a result it could also react almost instantaneously to this information to maintain homeostasis. Imagine sending information through a quantum computer, the reactions are

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almost instantaneous, this is what we observe. If only slow moving molecules were the messengers in homeostasis, then imagine mail being sent via a sailing ship.

– This model can more easily explain developmental biology and cell differentiation. The set of plans is in every cell of the whole organism and contained in every gamete. An organism can only develop and make a copy of itself according to this plan that exists in a quantum matrix.

Because this is what cells and organisms seem to do, it should be tested as one of many theories that tries to explain homeostasis.

Possible Theories of Homeostasis

Analog - it only explains some functions of homeostasis and breaks down as a complete observable system within cells.

Digital and chemical homeostasis - Also offers a partial explanation, no digital set points have been found stored in any cell organelle. It is difficult to explain developmental biology with this model because what digital mechanisms control the epigenetic patterns for each cell? We can measure the results; epigenetic patterns being unique in each cell type, but not how this was accomplished.

Quantum Homeostasis - the ability of cells to receive analog, digital, chemical and quantum information/signals and process this information by comparing it to a totality of quantum set points - a quantum reference image. Use of quantum language to communicate, process information and react by building and repairing any cell structure - end point.

Homeostasis is conventionally thought of merely as a synchronic (same time) servo-mechanism that maintains the status quo for organismal physiology. However, when seen from the perspective of developmental physiology, homeostasis is a robust, dynamic, intergenerational, diachronic (across-time) mechanism for the maintenance, perpetuation and modification of physiologic structure and function [5].

Functional Resilient and Dysfunctional Diseased Homeostasis

Functional homeostasis means stress can be applied to any endpoint and it becomes stronger - because the mechanisms of homeostasis are extremely robust. Any endpoint when healthy can display resilience and adapt to any given stress, a toxin or environmental change. The limit of resilience is usually about 130 to 160% beyond the normal control. For example if a healthy athlete can lift 80 Lbs then when more weight is gradually introduced over a few months of training many athletes can achieve lifting a weight of 104 to 128 Lbs.

If an individual has functional homeostasis in all areas, for all endpoints, then the stress has to be over 160% to cause any symptoms. These are the people who can smoke a certain amount, consume sugar and alcohol in excess at times, don't exercise on a regular basis, are exposed to various toxins in moderate amounts and proceed to live without any chronic diseases into their late 80's or beyond.

This can be graphed: Stress increases on the X axis. Resilience increases on the Y axis. Below the X axis symptoms result. The curved yellow line has a more robust value for a given function of homeostasis. The green line has a slightly susceptible homeostasis functional ability to tolerate a certain stress. The red line depicts a homeostasis function that is very susceptible to a particular stress, it is easily overwhelmed and symptoms are easily produced.

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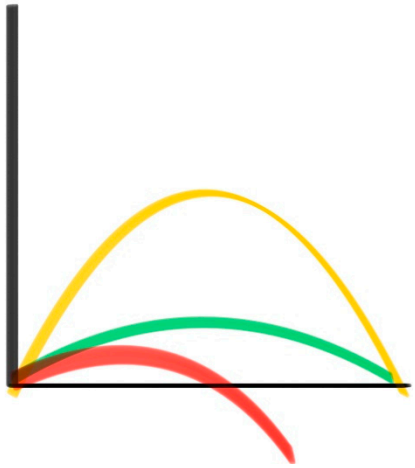

Dysfunctional homeostasis is the opposite of resilient homeostasis. Within most individuals there are one or more deficiencies in homeostasis, creating specific sensitivities to various stresses and leading to pathologies that can be named. The homeostasis in certain areas is very fragile; such as a few pollen grains leading to hay fever, eating gluten leading to abdominal pain, drinking a small amount of alcohol leading to headaches, and eating sweets resulting in adult onset diabetes. For every person with a chronic disease there are stresses which those persons can not tolerate, even in small amounts. This is the opposite of resilience, it is homeostasis that is decompensated and dysfunctional.

Dysfunctional homeostasis affects epigenetic markers, affecting gene expression, leading to abnormal cell functions, leading to a disease susceptibility. It is not moderate stresses that causes diseases, it is the ever more fragile and deepening susceptibility. Moderate stresses can easily be tolerated by those with a fully functioning homeostasis profile. In fact they can make individuals stronger.

When one or more of the systems of homeostasis becomes dysfunctional, how can it be diagnosed? In this model we are assuming these dysfunctions of homeostasis are originating on a quantum level.

Most likely there will never be a tool to directly study the pathways, connections and hierarchies of quantum homeostasis within an organism. As soon as a quantum state is measured it collapses the wave function and it changes its properties to the next level of manifestation, that being a particle or degraded energy signal. At best, trying to test quantum properties directly would only reveal one small part of homeostasis at this level, by analogy, one word from say a Shakespeare play. We need a system of analysis to reveal the whole play, the story of each character (physical markers of the disease process) and quality of the language (qualities of the disease process). If we can't study it directly, what reliable tools are left to study the language of quantum homeostasis - especially the dysfunctional patterns?

Each individual substance leaves the same quantum imprint in a given organism and the same epigenetic signature. We know this because in toxicology, the biomarkers and epigenetic signatures are consistent over many models and end points studied [18]. Toxic substances break, bend or exaggerate quantum connections according to their exact character, configuration and quantum strength. It is best to think of this property as a unique thumb print with a variable loudness of frequency. There are three ways to increase the loudness/toxicity of a quantum substance; increase the dose size — more atoms, repeat the dose more often and or turn up the intensity or loudness of the quantum field (This is the subject of another paper. Quantum loudness can be a function of the intensity of a frequency, its toxicity and how often repeated). All or one can lead to toxicity depending on how they are combined. We can measure this toxicity in terms of symptoms or in terms of biological markers. The toxicity can also be measured as qualitative stories, ones that have themes and characteristics. For example, cutting onions creates burning and watery eyes. This means, the signal caused by the sulfur in the onion vapor is enough to create a temporary disturbance and overwhelm the physical and quantum matrix of the conjunctiva leading to a sensation of burning and watery eyes. We can't see exactly where and how the quantum computers in those cells were affected

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but at least we have one piece of valuable and accurate and repeatable information, the reaction is the same for everyone. Including a binary imprint, called an epigenetic signature for each toxin. Each toxin affects homeostasis in such a way as to pathologically turn certain genes in and others off. Lead and many other toxins can now be defined by their epigenetic signatures [19]. The goal is to know this exact epigenetic signature for every substance, if we know this, then in theory we know the epigenetic signature of potentially every disease process. This requires more explanation:

Every substance sent into the matrix of the human quantum computer, produces a unique epigenetic signature. It is a combination of the effect on and the reaction to that substance. Eyes burn and water from onions, epicac causes vomiting, pepper causes sneezing, salt creates excessive thirst etc. Every substance in a large dose produces a picture of toxicity but also an epigenetic signature.

We can't see or directly measure the inner mechanisms of quantum computers in living organisms but if we send in a known substance then very precise effects are echoed back. If enough are sent in, we have a precise map of all the possible ways that the quantum human computer can break, the same list as all possible diseases. Each disease process is also an assault on the human quantum computer, each one stressing it in a very particular manner. By analogy a surveillance plane, sending radar signals onto the topography of the Earth, even when densely forested, can eventually give us clues about past civilizations, such as old building sites and road patterns. Life forms echo back information from toxins, except in this case we have the symptoms of the toxin, (burning eyes) therefore a complete description of a unique disease process in terms of symptoms (such as hay fever) and the epigenetic code for that substance.

There are a finite number of ways the human quantum computer can break, just as any computer has vulnerable components. There is not any difference between the quantum epigenetic code produced by a toxin A, or an organic disease B, that developed and broke the same homeostasis functions. In one case it could be an environmental cause mixed with a genetic susceptibility that matches exactly toxin A, because they can break exactly the same homeostasis functions. This concept is crucial to the parts of the clock in this model. Imagine a patient with hay fever, her eyes are watery and burning because of pollen and a genetic susceptibility to that illness. The eyes are constantly burning as if they had been exposed to onions. But she was not exposed to onions, she has a specific type of hay fever, triggered by a certain combination of pollens. The pollen happens to damage exactly the same homeostasis functions, distort the same epigenetic patterns, activate the same susceptibility and produce the same symptoms as can be created by cutting onions. This is an extremely helpful concept. If the reaction to two different stresses, one a toxin and one a disease process, are identical then the same quantum connections are broken in the same way. We can therefore categorize diseases in this way, by the substance that can cause that same disease process. Every substance can therefore be defined by its unique imprint on the quantum computer by its binary code called an epigenetic signature — also called toxicogenomics. Every person with an individual disease process can also then be named by the substance that can cause that susceptibility. Every substance in a large enough dose becomes toxic and can be defined by this method, its epigenetic signature. Every substance is a character in a Shakespeare play - metaphorically and literally.

There are many databases that collect the epigenetic codes for toxins. ToxSign [20] has accumulated over 8,000 epigenetic signatures [21]. The data stored in TOXRIC contains 113,372 compounds [22].

The significance of this is that every toxicology signature is defining a possible disease from its homeostasis and epigenetic origins through many measurable markers along pathways that culminate in objective and subjective symptoms, finally affecting the phenotype. The benefit we have is that the epigenetic signature of a toxin can be compared to the epigenetic signature of a disease process in an individual. If they are the same, the name of the toxin is the best name for the disease, and **hormesis** tells us that if that toxin is used in a small dose it will always be a stimulant, the name of the toxin also becomes the cure. A stimulant to correct homeostasis and reverse the epimutation(s) and the disease process. What is hormesis?

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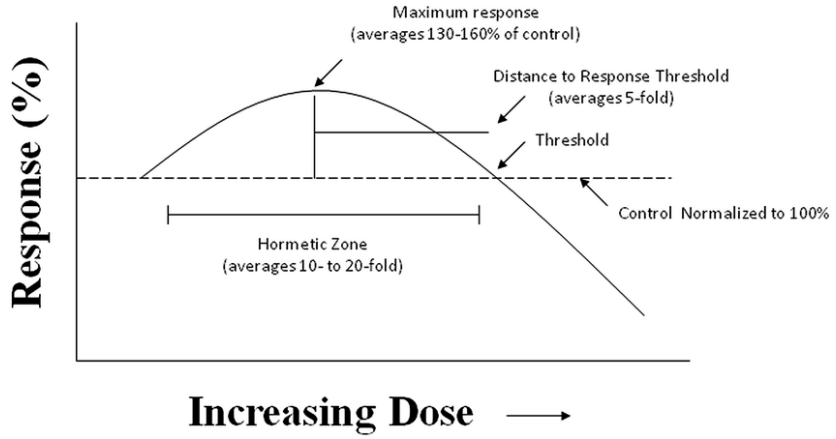
Hormesis

Hormesis is a term used by toxicologists to refer to a biphasic dose response to an environmental agent characterized by a low dose stimulation or beneficial effect and a high dose inhibitory or toxic effect. In the fields of biology and medicine hormesis is defined as an adaptive response of cells and organisms to a moderate (usually intermittent) stress [23].



In the above graph the small dose stimulates an endpoint such as longevity or muscle strength (it could be any endpoint) - but as the dose is increased or repeated too often the response falls below the normal range and becomes toxic.

Hormesis studies have tested tens of thousands of substances to prove this concept [24–26]. Hormesis has two applications. Making areas that are healthy stronger and secondly, reactivating areas that are not functional; areas of disease, where there are deficiencies of homeostasis, to restore them (This second application was the life work of Samuel Hahnemann and subsequent development of homeopathy).

In order to diagnose and treat chronic diseases this second use of hormesis is relevant to this discussion:

Hormesis Mechanism of Action — Small Dose Stimulation

There are always two drug reactions when any drug is given - primary and secondary drug action. One or the other will be stronger depending on the dose size and dose repetition.

— **Primary Drug Action**: The immediate effect of a drug to push certain reactions in a certain direction. The drug has to be in a large enough dose to temporarily override homeostasis. Homeostasis will always oppose the primary drug action, leading to drug resistance, a function of secondary drug action. Examples are the toxic effects of lead, cadmium and arsenic.

— **Secondary Drug Action**: These reactions are exactly opposite to the primary drug action. They are a function of homeostasis. The dose has to be small enough to create a net opposite effect. These reactions are always adaptive, they work in the same direction as homeostasis. For example a small dose of lead will increase the functions of homeostasis in certain areas, these extra string functions could be useful to prevent an illness.

The above hormesis graph shows the net effect of these two drug actions. But perhaps it is more clear if both actions are depicted. See graph below. The X axis is dose size, the Y axis dose effect, either a stimulus or toxic. The red line is the primary drug action. The blue line is the counter secondary drug reaction. At small doses there is a net secondary drug action, at large doses there is a net primary drug action.

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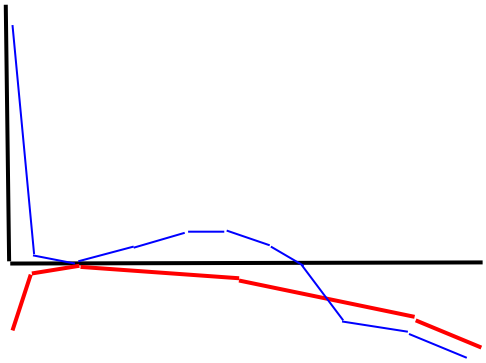

The Hormetic Zone

The drug reaction in this zone strengthens homeostasis, it's unconditional, the organism has no choice but to create an exact opposite effect that is able to overcome the primary drug action. This is a big advantage because diseases are caused by deficits in homeostasis self regulation, leading to epimutations. To cure any chronic disease one has to activate the exact quantum connections with a drug that has the correct secondary or opposite action to that of the disease process. A regained greater strength in quantum self regulation - homeostasis, leads to a healthier epigenome and later to healthier structures and functions on the tissue level. The diagnosis of the exact substance needed for each patient is what is most difficult but the toxicogenomic study described below, can prove a method to determine this. Eventually determining the epigenetic signature of every substance and therefore the cure of every disease that was caused by a lack of homeostasis.

What is Hormesis: When life began, the ability to react against stress was essential in order to develop a strategy to survive, the quantum properties of communication, storage of a reference image, and how dead atoms could be animated into living organelles and cell membranes all most likely developed incrementally together. The ability to make micro adaptations, equal and opposite to the stress, also came into being out of necessity to preserve resources and fix errors immediately. Random mutations allow for the possibility of new proteins, but day to day each organism needs to be able to make small changes, to cope with an ever challenging environment and cope with stresses that can cause diseases. Without these coping mechanisms fully intact, individuals and species would have gone extinct more quickly, because the environment was always changing and new pathogens needed to be dealt with. What is the takeaway when all this information is put together?

— Toxins produce incredibly precise outcomes, we can use them to epigenetically map all disease possibilities.

— There is a self correcting mechanism in all living systems, it requires the use of a small dose to activate it. The smaller the quantum doses, the louder the quantum properties and the stronger the response back (It is not surprising that quantum fields have a loudness or variability of intensity).

— The exact reciprocal is needed to stimulate a curative response. For every toxin at the correct dose, there is an equal and opposite reaction.

— A database of every toxin is needed to implement this strategy. Each patient can then be tested to determine their epimutations, a match can then be found of a toxin that produces that same epimutation. Through the principle of hormesis, this toxin in a small dose will correct the patient's epimutations.

Mechanisms of Quantum Biology

As a thought experiment, imagine quantum properties that get stronger if a stress is applied to them. This is perhaps one of the basic mechanisms of life. When an organism is sick; are the connections between fields tight and correctly aligned or loose and easily falling apart, allowing for faulty connections? Is homeostasis able to communicate with the reference image correctly? Are the pathways of communication and connections all tuned like an orchestra and able to play with the correct intensity? All living things have a strong intention to survive, to live a long life, to accomplish

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things, this ability is inextricably connected to these abilities. If not then homeostasis begins to break down, the epigenome changes and symptoms can start to develop. There is an advantage in thinking about life and biology in this way, and how the human quantum computers are affected by environmental influences - because it is a comprehensive model, with a solution regarding how to affect the causes of diseases.

Quantum Drugs

If a quantum dose, (doses smaller than 10 to the minus 24) of a substance, (ultra high dilutions), is exposed to an organism with insufficient specific homeostasis, with the same exact epigenetic code as the disease, then that epimutation will be reversed to the opposite, back to health. Here is some evidence to support this assertion: Ultra-high dilutions have been found to affect gene expression in a number of recent studies [28–35]. If this concept is combined with the implications of hormesis studies then a safe, non-invasive diagnostic technique and reliable system of gene therapy can be developed for acute and chronic diseases. I realize this is controversial, doses this small are not considered biologically active. But if one was to read all these studies in references 28 to 35, the evidence is compelling. Ultra high dilutions can easily affect gene expression. Carl Sagan said it best:

The suppression of uncomfortable ideas may be common in religion or in politics, but it is not the path to knowledge, and there's no place for it in the endeavor of science.

Here is an example of this evidence from one of these studie:

As compared to placebo, the AM-30C- <a dilution of ten to the minus 60> treated bacteria showed less DNA damage and oxidative stress as manifested by a decrease in ROS generation, and an increase in SOD, CAT and GSH activities. AM-30C also up-regulated the expression of repair genes as compared to the control. CONCLUSION: AM-30C helped repair the DNA damage through up-regulation of repair genes and also ameliorated the oxidative stress through the reduction of ROS generation and suitable modulation of anti-oxidative stress enzymes [36].

Summary of Expected Findings - A Proof of Concept Study

If we put all these concepts together a useful method becomes available to diagnose the human quantum computer and repair it. Toxicology can now give us the epigenetic code for any substance. Each substance tells us a code for a possible vulnerability of the quantum human computer and the possible diseases. Here are the expected results if this theory was tested for Sulfur. The toxin does not have to be Sulfur, it could be any substance. The first step is to give that toxin to healthy individuals to cause at least two or three stable epimutations in 80 to 90% of the cells for at least one month after the toxin is no longer administered to the cells.

Here are the two possible reactions:

Primary Action Dominates — the primary toxic action is stronger than homeostasis, one or more or the quantum homeostasis functions are broken. The epimutation is clearly expressed in two genes.

Secondary Action Predominates — The homeostasis functions are made stronger, they resist the effect of the toxic dose and less epimutations appear in the same two genes. The secondary action can also be used later to reverse the same epimutations.

Study Design

Collaboration with a lab that is already doing toxicogenomics research.

Equipment –Illumina's Infinium Methylation Array technology. Infinium EPIC Array v2.

Cell cultures: Peripheral blood cells from at least twenty healthy adults between the ages of 30 and 60 who have no chronic symptoms, a healthy family history and are not on any medications, non smokers and no alcohol consumed for one week prior to collection. They are divided into several groups and given different doses of sulfur at different intervals [37]. The study is over an eight week period. Day one to day fifty six.

Placebo Group

Test cells every three days for thirty days. Note that there are no extreme epimutations.

Cohorts

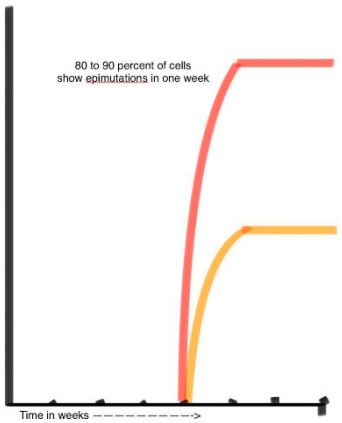
 doi:10.20944/preprints202407.1192.v1

Schedule 1. Sulfur — (1 mM)[38] Create a new epimutation pattern: repeat this once a day for seven days starting on day thirty. A dose that is toxic enough to the cell culture to create a stable epimutations in two genes in 80 to 90% of the cells after seven days and persist in that range for the next 21 days, but not toxic enough to kill the cells [37]. Samples are taken every three days to determine the number of cells displaying the gene mutations. Take samples every three days for a total of 28 days.

Schedule 2. Sulfur — (0.5 mM) repeated one time a day for seven days starting on day thirty. The toxic signature should show up in about 30 to 40% of the same two genes after seven days and persist in that range for the next 21 days. Samples are taken every three days to determine the number of cells displaying the gene mutations.

These two schedules have to be done first in order to determine the baseline of the study. The dosage may need to be adjusted to reach the optimum percentage of mutations - 80 to 90% of cells in Schedule 1 and 30 to 40% of cells in Schedule 2.

Here is the expected result:



Schedule 3. No sulfur — Placebo - distilled water and same percent alcohol as in Schedule 1 for seven days. Start on day one, continue for fifty six days. Expected results: No epimutations noticed in the two genes over the fifty six days. Samples are taken every three days.

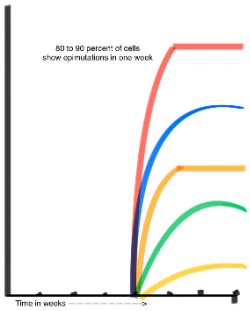
Schedule 4. Sulfur — .000,000,000,000,1 mM - quantum dose 0f 6C, meaning that the quantum properties of the sulfur are predominant and interacting with the quantum properties of the cells. Repeated three times a day for 28 days. On day 30, Schedule 1 is introduced for a week. The toxic signature should be delayed and show up in fewer cells. It should prevent the epimutations from forming when the large toxic dose is given on day 30 and recover more quickly in more of the cells during the last 21 days compared to Schedule 1. The samples are taken every three days for the entire 56 days.

Schedule 5. Sulfur — 1/10-60 mM - quantum dose of 30C, meaning that the quantum properties of the sulfur are predominant and interacting with the quantum properties of the cells. Repeated once a week for 28 days. On day 30, Schedule 1 is implemented for a week. The toxic signature should be delayed further than Schedule 4 and show up in fewer cells. The secondary action of the sulfur will predominate. There should be almost no epimutations forming and the ones that form should reverse during the last 21 days. The samples are taken every three days for 56 days. In theory a very few epimutations could remain unaffected by the antidote because the toxicity of the sulfur joined with a few established susceptibilities in the cells and formed a new susceptibility. This does not refute the overall hypothesis.

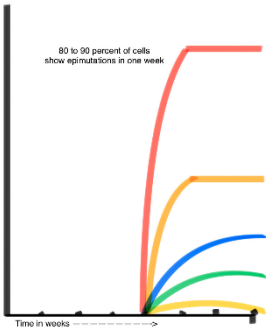
Schedule 6. Sulfur — 1/10-400 mM - quantum dose of 200c, meaning that the quantum properties of the sulfur are predominant and interacting with the quantum properties of the cells. Repeated once every two weeks for 42 days - 4 doses. On day 30, schedule 1 is implemented for a week. The toxic signature should be delayed further than Schedule 5 and show up in fewer genes. The secondary action of the sulfur will predominate. There should be almost no epimutations forming and the ones that do form should almost all reverse after day 35.

 doi:10.20944/preprints202407.1192.v1

Expected results: The effect of the primers at three different levels of concentration, blue, green and yellow - in this case the higher concentration of toxin was added after one month.



Here is the graph for the primer groups when the 50 percent concentrated toxin was added after one month. This would be an added on protocol:



After thirty five days, split Schedule 1 cells into 4 groups - Schedule A7, A8, A9 and A10.

Schedule A7 - This is the original group of cells given sulfur (1 mM). Nothing is given to this group for the next 21 days. Samples are taken every three days. The epimutations should persist in the range of 80 to 90% of the cells.

Schedule A8 - This is a subgroup Schedule 1, but now on day 36 the Sulfur 6c is given again three times a day for one week. The samples are collected every three days for 21 days.

Schedule A9 - This is a subgroup of Schedule 1, but now on day 36 the Sulfur 30c is given to the cells once a week for 21 days.

Schedule A10 - This is a subgroup of Schedule 1, but now on day 36 the Sulfur 200c is given to the cells one time every two weeks for the remaining 21 days. Two doses.

After thirty five days, split Schedule 2 cells into 4 groups, Schedule B11, B12, B13 and B14.

Schedule B11 - This is the original group of cells given sulfur (.5 mM). Nothing is given to this group for the next 21 days. Samples are taken every three days. The epimutations should persist in the range of 40 to 50% of the cells.

Schedule B12 - This is a subgroup Schedule 2, but now on day 36 the Sulfur 6c is given again three times a day for one week. The samples are collected every three days for 21 days.

Schedule B13 - This is a subgroup of Schedule 2, but now on day 36 the Sulfur 30c is given to the cells once a week for 21 days.

Schedule B1480 - This is a subgroup of Schedule 2, but now on day 36 the Sulfur 200c is given to the cells one time every two weeks for the remaining 21 days. Two doses.

Expected effect of 6c- Blue, 30C - Green and 200c - Yellow applied on day 29. The 200c is able to prevent the greatest percentage of epimutations and reverse the greatest percentage of epimutations. The 30c is the next strongest and finally the 6c is the weakest preventer of epimutation and weakest antidote.

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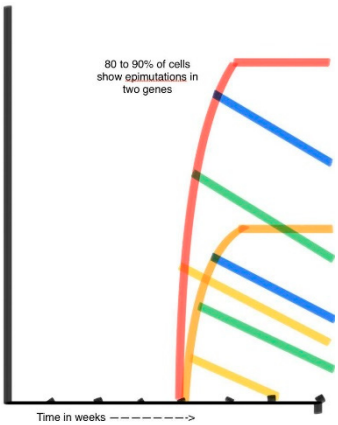

Red Line: Sulfur as a toxin, Schedule 1. - Primary drug action predominates.
Orange Line: Sulfur at a less toxic dose, Schedule 2. Primary drug action predominates.
Blue Line: Sulfur 6c. Secondary drug action provides an influence.
Green Line: Sulfur 12c. Secondary drug action provides an influence.
Yellow Line: Sulfur 200c. Secondary drug action provides an influence.

Conclusion

This is a theory worth considering and testing for its validity because the cause and cure of most chronic diseases has not been realized. Most likely the functions of homeostasis originate with what we can best describe as a quantum computer. When homeostasis is restored the epimutations will resolve. We can learn the epigenetic codes for each drug/toxin. The codes for each toxin tell us what medicine to give to restore quantum homeostasis for each patient.

Implications

If the toxicogenomic signature (thumb prints) of 10,000 substances are known, then 10,000 disease processes are known and the antidote is also known. If a patient with a chronic disease has one of these signatures then the treatment for that chronic disease is known. In this way any and all epigenetic chronic diseases could be diagnosed and treated according to an understanding of the secondary action drugs that affect the human quantum computer. Ideally, all known substances eventually would be in the database.

The language of the human quantum computer can respond to the quantum properties of all known substances. In the above study Sulfur was used in a quantum dose to prevent and reverse the epimutations caused by Sulfur. In this way we can learn the effect of each substance. Quantum doses all follow the same rules, they are written in our favor, because of the laws of secondary drug action. The language of the universe is written in quantum formulas. Living systems all follow the same laws of nature, there is no dividing line between the non living chemistry and living chemistry — why and how could the laws suddenly change? In this case we need to use the resources available to us by following these quantum principles. It's just a matter of what signal is needed and how loud it needs to be, nature will do the rest. Quantum structures are continually creating themselves into more complex physical structures, but at times in living systems that are suffering from a disease, they need a clear signal to create coherence and rebuild their connections. We all at some point in life need self healing that reaches a renewal from the source.

Conflict of interest: The author declares no conflict of interest

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