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The Rules of Variation Expanded, Implications for the Research on Compatible Genomics

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Abstract

The main focus of this article is to present the practical aspect of the code rules of variation and the search for a second set of genomic rules, including comparison of sequences to understand how to preserve compatible organisms in danger of extinction and how to generate biodiversity. Three new rules of variation are introduced: 1) homologous recombination, 2) a healthy fertile offspring, and 3) comparison of compatible genomes. The novel search in the natural world for fully compatible genomes capable of homologous recombination is explored by using examples of human polymorphisms in the LDLRAP1 gene, and by the production of fertile offspring by crossbreeding. Examples of dogs, llamas and finches will be presented by a rational control of: natural crossbreeding of organisms with compatible genomes (something already happening in nature), the current work focuses on the generation of new varieties after a careful plan. This study is presented within the context of biosemiotics, which studies the processing of information, signaling and signs by living systems. I define a group of organisms having compatible genomes as a single theme: the genomic species or population, able to speak the same molecular language through different accents, with each variety within a theme being a different version of the same book. These studies have a molecular, compatible genetics context. Population and ecosystem biosemiotics will be exemplified by a possible genetic damage capable of causing mutations by breaking the rules of variation through the coordinated patterns of atoms present in the 9/11 World Trade Center contaminated dust (U, Ba, La, Ce, Sr, Rb, K, Mn, Mg, etc.), combination that may be able to overload the molecular quality control mechanisms of the human body. I introduce here the balance of codons in the circular genetic code: 2[1(1)+1(3)+1(4)+4(2)]=2[2(2)+3(4)].

Keywords

Compatibility; Genetics; Fertility; Genes; Descendants; Mendel; Bateson; WTC; Strontium

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> "…a detailed understanding of the natural order." b
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> Graeser, Lynn, Schoenheit

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Note: The basic information on the compatible genomes for a fertile offspring and homologous recombination was presented to the 1st and 2nd generation of Medicine and Biology in Puerto Vallarta (C.U.C., U. de G.) and in my AVBRTP first Seminar (Baylor/ Methodist).

[b] Graeser, M. H., Lynn, J. A., Schoenheit, J. W. 2003. Ch. 18. P. 381. The Rejection of Both Scripture and Logic. *In*: One God & One Lord. 3rd ed. *CES*. Indiana. 685 p. URL: http://www.truthortradition.com/book6

Introduction

Since the initial study of population genetics 1 and the discovery of the double helix,2 one of the main concerns has been the compatibility of nucleic acids for organisms to reproduce and multiply.

Working on gene expression, we see that biology is independent of the human attempt to understand life. For example, to build a body we have a body-plan, full of information and meaningful semiosis (sign processing). The external reality is present in nature independently of how we define, describe or classify it. If our view is distant from the objective reality we try to represent, the fruit is going to be null. The closer we are to reality, the more fruitful our work will be.

The existence of organic codes in nature is an issue being currently investigated through the classical method of science, *v.gr.*, with a mechanistic approach of model building.

Kunz wrote: “Regrettably, 140 years after the publication of Darwin’s Origin of Species, we face the grotesque situation that we still do not know what is a species whose origin Darwin wanted to explain. A generally applicable species definition is not available”.3 This article will show that “a generally applicable species definition” is possible through the study of compatible genomics.

We aim to bring novel concepts of theoretical biology into practical use, such as the comparison of nucleotides based on the rotating circular genetic code,4 but also for the preservation of challenged biodiversity through the use of an approach based on compatible genomics, comparing genomes with the goal to produce fertile offspring.

The code rules of biological change relate to the compatible exchange of amino acids based on the circular genetic code: 1) same position in the four quadrants for hydrophobic codons, 2) same or contiguous position in two quadrants for synonymous or related codons, and 3) same quadrant for equivalent codons.4

The circular genetic code exhibits a precise mathematical balance or equilibrium when the triplets within it are grouped by the amino acid they codify: $2[1(1)+1(3)+1(4)+4(2)]=2[2(2)+3(4)]$; the left side represents quadrants one and three while the right side represents quadrants two and four, an aspect to be considered for the design of bioinformatics software based on it (Fig. 1).

The purpose of the current article is to track the genomic rules of variation by seeking reproductive compatibility of higher organisms with molecular genetics as a guide to compare genomes. For example, in the homologous recombination of parental and maternal DNA in the gametes, the comparison has to include a compatible exchange of genomic information at the moment of nuclear fusion of sperm and ovum to complete the number of chromosomes for organisms to be fertile. We need to keep in mind that the recombined chromosomes of each parent have been fixed beforehand when the gametes were produced, delivering directly into the offspring by the parents the recombined genetic information of its four grandparents.

Biosemiotics can be defined as the biological conversion of physical codes, signals and signs into molecules, pathways and organisms, a promising approach to research the fundamentals of life.

Physical biosemiotics, Pattee’s approach inspired by Michael Polanyi, indicates that physical theory, as applied to biology, consists of laws and boundary conditions often referred to as constraints,5 restraints or boundaries such as the natural limits to biological change, the molecular quality control within cells, and the biological surveillance mechanisms within organisms,6 limiting how much a molecule, a cell, or an organism is capable to change.

Code biosemiotics assumes that at the cellular and molecular level, semiosis is defined by coding, not by interpretation, and its logic predicts that there must be many other organic codes in the living world, a testable hypothesis with clear and important experimental consequences.7

The model of code biosemiotics we are proposing affirms that the research on compatible genomics will help us understand the reproductive fertility among organisms, to produce and to preserve them.

This work attempts: 1) to define compatible genomics as useful in discussions of population variation, 2) to describe the use of compatible genomics in a pro-active production, preservation and reconstruction of biodiversity, and 3) to shape a scientific methodology by which compatible genomics could be studied.

The number of possible organisms or species will be dramatically reduced when we realize that sexual reproduction producing a fertile offspring can take place between variants of the same theme of an organism, even if such variants are currently misclassified as members of different *species* or even *genus*.

Compatible genomics is the search for compatible genomes within the natural world. Compatible genomes are capable to undergo homologous recombination to produce fertile offspring. The repercussions of this are multiple, starting with the preservation of endangered organisms via compatible backcrosses with their abundant relatives. The genomic rules of variation discussed here, reaches not only for the DNA's double helix annealing and recombination, but also for the reproductive or sexual generation of biodiversity.

In ecosystem biosemiotics, I present the possible genetic damage due to the biggest forensics thus far, one of the most extreme environmental hazards known to man to-date. It will be shown how the effects of the elements present in the 9/11 WTC dust are affecting the health of Manhattan's responders and residents. The earlier use of the expression '*Ground Zero*'c in medical journals depicted the extreme damage to all that is human perpetrated in 9/11: "Lots of volunteers but no patients", "**there just wasn't anyone to save**".8 "The flames were still visible, the smoke still billowing out from the rubble, overwhelmingly noxious; huge steel girders had been twisted and bent from the collapse and the heat", "there were no recognizable personal effects - no desks, chairs, computer terminals, doors, or coats. **There was nothing human left**".9

However, under the current normal and natural conditions, through compatible genomics we expect the production of new and abundant biodiversity and the preservation of the life already in existence.

Materials and methods

To search for a second set of rules of variation concerning the genomic compatibility of organisms, to produce fertile offspring through homologous recombination, an internet

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[c] '**Ground Zero**', phrase used by Rehema Ellis in her NBC 9/11 report she started at 11:45 AM on 9/11 on the WTC toxic-dust filled streets of N.Y. [see it in the telling context in which it was aired by Tom Brokaw: http://www.youtube.com/watch?v=hv1fXzJI3E8]

comparison of organisms was done; when available, a comparison of their genes and genomes, both qualitatively and quantitatively, as well as the documented references of fertile offspring resulting from the crossbreeding of specific sets of compatible organisms; providing three examples: dog, llama and finch. The novel field of compatible genomics starts here, and I will present its implications by using a human example with tools already in existence: a quantitative *HapMap* study, widely used by the closest relative of the current compatible genomics approach, the *GWAS* (Genome-wide association study) of genetic epidemiologists. Possible genetic damage will be illustrated by analyzing the patterns of atoms found by the ‘United States Geological Survey’ (*USGS*) in the contaminated 9/11 WTC dust.10, d

Results

Presenting well-known examples in light of compatible genomics will help us understand how to preserve compatible organisms in danger of extinction and how to generate new biodiversity.

Three independent groups of organisms will document the findings: 1) a worldwide domestic animal: the dog; 2) a locally domestic animal from South America: the llama; and 3) the classic example of compatible variation: the Galapagos finches.

Canis

The wolf (*Canis lupus*) is capable of producing fertile offspring with jackals and their variants: common, side-striped, etc. (*Canis aureus*, *Canis adustus*, etc.), with coyotes (*Canis latrans*), Dingoes (*Canis dingo*), New Guinea Singing dogs (*Canis hallstromi*), Ethiopian Wolves (*Canis simensis*), and with all breeds of domestic dogs (*Canis familiaris*), such as the best known dogs and their breeds: Terrier (~35), Hound (~18), Spaniel (~13), Bull (~7), Pointer (~7), Retriever (~6), Mastiff (~5), Shepherd (~5), Sheepdog (~5), Collie (~4), Setter (~4), Pinscher (~4), Schnauzer (~3), Ridgeback (~2), etc., and less known dogs: Xoloitzcuintli, Khala, Inca-Orchid, Dogo, Dogue, Presa-Canario, Ovcharka, Telomian, Podengo, etc., plus new possible varieties of *Canis* in the wild and remote cities, etc.

At least eight *species* and ~>230 breeds e are indeed variations or subspecies of the same and central “theme”: *Canis*.11 All these wolf- or dog-related animals have 78 Chromosomes; however, it is not necessarily the chromosome number what needs to be matched, but the total number of genes and of biologically significant nucleotides (miRNAs in introns, etc.), which is indeed their genomic compatibility.

Llama

The common llama (*Llama glama*) is capable of interbreeding to produce fertile offspring with Guanacos (*Lama guanicoe*), Alpacas (*Lama pacos*) and Vicugnas (*Vicugna vicugna*); four *species* and two *genus* being variations of the same and central “theme”: *Camelids*.

“Interspecific matings are common among New World camelids and the hybrid offspring are fertile. Hence, the classification of the alpaca, llama, guanaco and vicuña as separate species is controversial”.12 Very soon, interbreeding of fertile offspring may be extended to the Camelids of the Old World: the Dromedary and the Bactrian Camels. Fertile offspring also result from crosses between the Bactrian and Dromedary camels.13 New World and

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[d] Table of the 9/11 WTC dust leachate: http://pubs.usgs.gov/of/2001/ofr-01-0429/leach1/WTCleachtable.html [Saved at: http://www.webcitation.org/5wY58KHfV], Table of the 9/11 WTC dust chemistry: http://pubs.usgs.gov/of/2001/ofr-01-0429/chem1/WTCchemistrytable.html [Saved at: http://www.webcitation.org/5wY5dWAb8]

[e] http://www.akc.org/breeds/complete_breed_list.cfm [saved at: http://www.webcitation.org/5wY69REut]

Old World camelids have the same diploid chromosome number (2n=74); there is an ongoing cross-breeding research between them,14,15 (and cloning.16)

The Galapagos Finches

The different types of finches are: Large cactus finch (*Geospiza conirostris*), Large ground finch (*Geospiza magnirostris*), Medium ground finch (*Geospiza fortis*), Cactus finch (*Geospiza scandens*), Sharp-beaked ground finch (*Geospiza difficilis*), Small ground finch (*Geospiza fuliginosa*), Medium tree finch (*Camarhynchus pauper*), Large tree finch (*Camarhynchus psittacula*), Small tree finch (*Camarhynchus parvulus*), Woodpecker finch (*Cactospiza pallida*), Mangrove finch (*Cactospiza heliobates*), Vegetarian tree finch (*Platyspiza crassirostris*) and Warbler finch (*Certhidia olivacea*); 13 *species* and 5 *genus* that may all just be variants of the same "theme": The Finch (*Fringillidae*).

Grzimek's Animal Life Encyclopedia says about finches: "The most common color of the domestic canary is the well-known bright yellow, or "canary yellow," but numerous other color varieties also have been bred. Red-colored canaries owe their origin, and their reddish coloration, to captive interbreeding of the island canary with the black-capped red siskin (*Carduelis atriceps*). Canaries are still a common pet and are prized all over the world as eager songsters. Selective breeding has produced varieties of canaries with distinctly different songs. A variety of other finches also are kept as cage-birds for their song, lively behavior, and/or attractive plumage. Other than the domesticated canary, all finches have some indirect, local economic importance through ecotourism associated with birding".17

Finches have 80 chromosomes (as most birds do) and we read that: "finches **could** and indeed do interbreed and produce fertile offspring; but in the majority they **choose not to**". 18 Worldwide, if genuine finches/canaries are included into these comparisons,[f] then the number encompassed by the common "theme" of 'The Finch' will greatly increase within the same wide tent of one fully compatible population, if we also allow the finches inter-fertility.19

If this dramatic misclassifying of life happens with worldwide domestic and intensely studied animals, what can we expect of the lesser known, extinct or wildest of organisms? [g]

We read: "so far from denying that different species of finches could interbreed, Darwin asserts that "the canary-bird has been crossed with nine distinct species of finches" in chapter IX of the Origin of Species. If he had known about the interbreeding of the Galapagos finches, he might well have cited it as a further illustration of his point." However, in their same paragraph we read: "The very concept of evolution implies that there should not be a single, unambiguous, universally applicable definition of "species" that fits our intuitive notions of what "species" should mean." Then I ask: Isn't that a non-scientific and deliberate way to rhetorically deceive since Darwin? [h] The statement quoted is the absolute opposite of what science should do: **to achieve a detailed understanding of the natural order**. We read: "hybridization has been largely treated as an evolutionary **accident** or statistical **error** in phylogenetic analysis".20

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[f] *v.gr.*, as seen at the link: http://www.avianweb.com/finchspecies.htm [Saved at: http://www.webcitation.org/5wY6gSmqT]

[g] Dinosaurs and their contemporaries included; some of them, previously thought as carnivores are now known as herbivores (see Zanno and Makovicky. 2011. Herbivorous ecomorphology and specialization patterns in theropod dinosaur evolution. *Proc. Natl. Acad. Sci.* 108(1):232–237. [http://www.pnas.org/content/108/1/232, comment by *The Smithsonian* saved at: http://www.webcitation.org/5wahicQzP])

[h] http://skepticwiki.org/index.php/Darwin%27s_Finches [broken] Paragraph saved at http://www.webcitation.org/5wY9hByc3, "I look at the term **species** as one arbitrarily given, for the sake of convenience, to a set of individuals closely resembling each other, and that it does not essentially differ from the term **variety**", Darwin, C., Ch.2. Variation Under Nature, Doubtful Species, last paragraph (13th), *The Origin of Species*, http://tinyurl.com/29j7ppe [Saved at: http://www.webcitation.org/5wZiBYXl5]

We can easily see that the same tool I wish to use to preserve and produce biodiversity has been considered as an ‘*accident*’ or an ‘*error*’ by the current evolutionary paradigm; even when Grant declared, referring to the reversible changes observed on the Galapagos finches: “a microevolutionary change took place”.21 I am able to see that by acutely distinguishing the differences between harmful mutations and natural polymorphisms,4 and by the fact of the obvious and real changes seen at the “micro” scale being clearly distinguished from a philosophically speculative and unseen “macro” context, will help us to discern more clearly the natural world, and to be closer to the compatible genomics I present in this article.

The two selected sequences contain transition substitutions of introns for the low-density lipoprotein receptor adaptor protein 1 (LDLRAP1, *ID*: NG_008932), a gene with nine-exons. These sequences are separated by 1,700 nucleotides: the first polymorphism (rs12096438) is located between exons five and six while the second (rs3856239) between exons seven and eight.

The results are shown below; in bold, italics, and underlined are the dominantly African polymorphisms for each sequence (***C*** and ***A***, respectively). Table 1 presents the percents for the sequences of the groups analyzed. In a thorough genomic sequencing scale, it will be necessary to compress formats or to sub-link genomic segments common of two individuals by using successive capital letters followed by a number while leaving visible the polymorphic nucleotides, in such a way, massive data could be compressed, making easier their comparison. This method of genomic compression is illustrated below, replacing the common sequences with A1, A2 and B1, B2.

rs12096438

GGTGCTTGTGAGGATTAACTGACATC[***C***/T]GAAAGGTTTCTTTCCTCCCGGCTGG

Compressed format:

A1-***C***/T-A2

rs3856239

GGAGGGACCTCACCTGTCGCTTTTCT[***A***/G]CTGAGGCTGTGGGACTCCTGGCATC

Compressed format:

B1-***A***/G-B2

C/T and ***A***/G are two alternate LDLRAP1 nucleotide polymorphisms studied in the human population.

The two polymorphisms for the gene LDLRAP1 predominated in the four populations of African origin, while at the center of the list were Chinese groups flanking Utah residents. At the end of both lists, with the lower percents, we had Mexicans, Gujarati Indians, Japanese and Toscans from Italy.

GWAS, the closest example available related to our compatible genomics is a relatively new method for genomic comparison of thousands of individuals in the search of hereditary diseases.22 *HapMap* 23 compares thousands of human sequences available online in order to track polymorphisms predominant in populations of individuals. What is represented here in a small scale as human diversity for two polymorphisms will be done in compatible genomics for complete genomes.

Next, we will see the analysis of patterns resulting from atoms found on the 9/11 WTC toxic dust (Figure 2), transforming into graphics the *USGS* results reported in the two Tables linked in ‘Materials and Methods’, elements analyzed both by leachate and by X-ray fluorescence chemistry.

Several elements were identified by the *USGS* leachate test; its authors indicate that this test "provides an indication of metals that might be **bioavailable** should the dusts be **inhaled**, **ingested**, or discharged into **ecosystems**"; "sub-samples of the leachate were collected and preserved for further analysis".10

Their leachate procedure used "deionized water as the extractant solution rather than the synthetic acid rain used in the EPA 1312 method", and they did "a 5 minute agitation rather than an 18-hour agitation. Hence, it is possible that the concentrations of soluble metals measured with this test would be less" than the actual concentration inhaled by responders and residents.10

The coordinate pattern of atoms found on the 9/11 WTC dust demonstrates that the 9/11 profile of all tested sites for uranium (U) was similar to manganese (Mn) and magnesium (Mg), while the profile for strontium (Sr) was similar to barium (Ba). The profile for rubidium (Rb) was similar to potassium (K).

The correlation coefficients for those atoms are (results higher than 0.8 in bold): ***Leachate***: U and Mn: **0.95**, Mg and Mn: **0.92**, U and Mg: **0.87**, Ba and Sr: 0.76, Rb and K: **0.94**. ***Chemistry***: U and Be: **0.84**, U and Mn: **0.90**, Mg and Mn: 0.46, U and Mg: 0.45, Al and Ti: 0.72, Ba and Sr: **0.98**, Ce and La: **1.00**, Sr and Sb: **0.92**, Fe and As, **0.85**, if we remove the two girder coatings values: Ba and La: **0.89**, Sr and La: **0.90**, Ba and Ce: **0.84**, Sr and Ba: **0.86**, and removing the Mg outlier: Al and Mg: 0.76, Al and Mn: **0.81**.

When comparing the leachate versus the chemistry (respectively), for elements where the highest correlation was achieved by the leachate analysis, we have: U and Mn (**0.95** *vs* **0.90**), Mg and Mn (**0.92** *vs* 0.46), U and Mg (**0.87** vs 0.45), indicating a better suspension/solution for these atoms.

The highest correlation in the chemistry analysis was obtained by Ce and La, **1** = 100%, followed by Ba and Sr (**0.98**), while in the leachate, the highest was U and Mn: **0.95**, followed by Rb and K: **0.94**.

Samples 20 and 36 corresponded to the **indoors**, showing in the leachate a high presence of Sr and K, including the coordinated high presence of their partners Ba and Rb, respectively (left column, Figure 2).

The results also show a similar level indoors and outdoors for the atoms present in the 9/11 toxic dust analyzed by X-ray fluorescence (right column, Figure 2), such as U and Be; Sr and Ba; Mn and Mg; As and Fe; La, Ce and Sb, respectively.

Discussion

A technique to preserve organisms in danger of extinction is presented. Backcrosses with non-endangered members of the same and compatible "theme" can be performed. For example, endangered northern cranes may be preserved by backcrosses with abundant southern cranes, "sandhill cranes will interbreed with whooping cranes in captivity".24

The concept of compatible genomes surpasses phenotypic or behavioral differences and Robertsonian fusions because its comparison goes deeper into the roots of those differences, allowing for the homologous recombination of compatible genetic sequences even if a Robertsonian fusion or its opposite has occurred.

With the novel concept of compatible genomics, the Przewalski's paradox is easily solved: the *Equus przewalskii* has 66 chromosomes and is capable to interbreed with the horse

(*Equus caballus*) that has 64 chromosomes, producing a healthy fertile offspring due to the genomic compatibility and homologous recombination of every significant nucleotide,25 being both members of the same inter-fertile genomic population or theme: ‘The Horse’. Opposite to this, the donkey (*Equus asinus*) has 62 chromosomes and the offspring with the horse (64 chromosomes) is sterile by having 63 chromosomes, an indicator of genomic incompatibility and of a lack of homologous recombination for at least an entire chromosome.

Humanity can also be called a common theme or genomic population with smaller differences but fully compatible genomes. Environment plus immediate or remote choices and circumstances marking the differences we see today between humans and their populations. There is no human ethnicity ‘more evolved’ than another and the same can be said of dogs, llamas and finches. They are just variations of the same theme, some more fit or adapted for specific purposes or environments, but all of them equally valuable.

Genomic compatibility is a better reproductive indicator to produce a fertile offspring than the one based on preferences or behavior. We read that: “the barrier to interbreeding set up by morphological and **song** differences is not impermeable but leaks”.26 To equate such statement to well known organisms, think of it as talking about breeds of dogs (“*the barrier to interbreeding set up by morphological and **bark** differences is not impermeable but leaks*”), or of humans (“*the barrier to interbreeding set up by morphological and **language** differences is not impermeable but leaks*”). Can you imagine what could have happened if each breed of dogs were classified as a different ‘species’? It may have occurred what we see today in the misclassified wild relatives of the dog, fully genetically compatible among themselves. The same ‘misclassifying’ is seen in many other wild organisms like finches, llamas, etc. (Fig. 3a).

In all instances, the number of unique “themes” will be reduced to a pair (two) per theme (male and female) for any organism and its genomic population, having each theme the enormous potential to produce all the rest of compatible varieties or subspecies known or unknown (Fig. 3a).

How will such information hold within the context of compatible genomics? For starters, the “origin of species” will be circumscribed to the realistic and practical “origin of varieties” while studies on “speciation” will be considered for what they really are: studies on a compatible “variation” within a common Theme.

Similar to humans, the canaries and finches,27 warblers,28 and sparrows,29 can indeed learn the songs of other varieties within their own compatible Theme. Polymorphisms can experience non-random reversible changes if conditions return to the previous in few generations 21,30,31 by a process barely understood.32,33,34

If “*the barrier to interbreeding leaks*”,26 it certainly is a very weak “*barrier*”. Whenever you read of such “*barriers*” as attributed to wild and living organisms always think in terms of humanity to evaluate them. The Pigmy is as human as the Inuit, even if it is highly possible that no one has ever seen a marriage between them. You may as well read, having such human context in mind, the next statements: “differences in both **song** and morphology can act as pre-mating barriers to interbreeding”, “when species are very different in **size** they do not interbreed”, “**harassment** is another reason why interbreeding does not occur”, “a barrier to interbreeding can be strengthened in the non-breeding season as a result of **ecological factors**”.26 The bottom line is that preferences and phenotypic differences vanish when comparing organisms on the basis of compatible genomes. The concept of compatible genomics presented in this article goes beyond and surpasses any reproductive and isolationist “*barrier*”, which are mostly based on phenotypes and behavior.

The same exercise done here can indeed be done for any living organism, *v.gr.*, monkeys: "*Cercopithecus* monkeys, you'd be hard-pressed to identify different species from their bones"; "a cautionary tale of a different sort comes from two species of baboon, *Papio anubis* and *Papio hamadryas*, which live in overlapping territories in Ethiopia. "These species interbreed quite freely," says Clifford Jolly of *NYU*. "The offspring, which are fertile, are intermediate in anatomy and behavior between the parental species", they "breed and produce fertile hybrids";35 gene exchange is also possible between "macaque groups such as *M. irus* and *M. speciosa*, or *M. irus* and *M. nemestrina*, in their zones of geographic overlap", "*M. nemestrina* and *M. assainensis* may intergrade to constitute an enlarged species", "a not uncommon view among students of the primates is that *M. assainensis* (along with *M. cyclopis*) is closely allied to *M. mulatta*".36

And more extreme, what could have happened if every different ethnic group of humans were misclassified in such a pernicious or careless way as the Galapagos' Finches were?

The examples are so numerous that the list may just go on and on. It will suffice to say that the currently over-inflated number of species as well as the deliberately ambiguous definition of 'species' is hampering a detailed understanding of the natural order, while preventing the take of practical measures to help endangered organisms with the aid of their abundant compatible relatives.

"We design animal bodies according to our taste", "purposefully plan the life spans of our livestock";37 and now we can improve the generation of new biodiversity through the study of compatible genomics.

If we allow the experience of the breeders to be included in our knowledge of nature,38 we may be able to appreciate the importance of genomic compatibility far above phenotypes and behavior.

William Bateson's statement has been on hold for more than a hundred years due to the current conceptual constraints. Bateson wrote: "In these pages I have only touched the edge of that new country which is stretching out before us, whence in ten years' time we shall look back on the present days of our captivity. Soon every science that deals with animals and plants will be teeming with discovery, made possible by Mendel's work. The breeder, whether of plants or of animals, no longer trudging in the old paths of tradition, will be second only to the chemist in resource and in foresight. Each conception of life in which heredity bears a part - and which of them is exempt? - must change before the coming rush of facts".39 Bateson was considering the generation of new biodiversity through the use of the newly discovered knowledge of genetics, goal that seems stronger now with our proposal of compatible genomics.

If we zoom-in, we can think of an organism's common 'theme' or genomic population as a planetary orbit (Fig. 3b), with each possible variety within it as a different **dot** or position within such orbit. Compatible varieties and their corresponding genomes are one molecular language spoken through different accents, being each variety a different version of the same book.

Here, a variety within one orbit never jumps to engrain itself into another orbit, being each orbit the Mendel's limit, which he was searching when he declared in his conclusion that "species are fixed i with limits beyond which they cannot change".40

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[i] *Fixed* = "*fest*" (German), 'definite limits to how species may be transformed through cross-breeding.' [Taken from: http://www.mendelweb.org/MWgloss.html#fixed, saved at: http://www.webcitation.org/5y2nUFd3R]

As new varieties are generated, each orbit expands like an ideal gas balloon, demonstrating that here there is no end to the possibilities of **variation within a theme**, even when a clear boundary is formed by each specific orbit. The boundaries of common themes are studied by the molecular quality control mechanisms dwelling within each cell and organism.

Current economical and technological constraints delay the progress for the novel research on ‘compatible genomics’ which among other things will be in need of: 1) the full sequencing of the genome for each individual organism under consideration, 2) to compare one genome with another fully sequenced genome that we had previously hypothesized as compatible. Furthermore, a serious methodological concern is the current contamination of thousands of sequences in the *Genbank* due to the current technologies; for example, we have contaminants forming tandems or partial tandems in palindromes derived from the *ZAP* adaptor 41›42›43 and many other sequence contaminants that escape to be removed by the current filtering tools (Table 2), still being the human eye the best filter available, even if slower than a computer.

Another concern to be mentioned here is the standard decry of a naturally occurring and compatible interbreeding in nature by assuming beforehand that current biodiversity can be lost forever, such as when differently colored schools of cichlids converge in natural lakes and interbreed giving rise to an non-attractive ‘grey cichlid’, an aspect to be seriously considered in any crossbreeding program.

One reviewer expressed his concern that by changing the specific features of subspecies, such as behavior, appearance, etc., we may produce new organisms with “potentially new relationships to the environment and with unexpected ecological consequences”, fearing that new subspecies may compete with original subspecies to finally endanger the populations of natural subspecies. “No kind of rational taming would give us a sufficient guarantee”, he concluded. To exacerbate the scene, we can include the dangers of a stronger invasive organism interbreeding with milder natives (*v.gr.*, the African bee in America and its Africanized offspring). However, we may be able to direct the generation of new biodiversity by the use of an extremely careful crossbreeding system. With optimism we can rationally ‘tame’ and control a compatible interbreeding already happening in nature; *v.gr.*, we can **learn the genes for the color** of feathers and **bring back into existence** organisms such as the Mauritius Blue Pigeon (*Alectroenas nitidissima*), the American Passenger Pigeon (*Ectopistes migratorius*), the Ryukyu Wood Pigeon (*Columba jouyi*) and many others already extinct but with numerous genetically compatible relatives alive today. Instead of losing biodiversity, by tackling the hard issue of genetic compatibility, we could be able to do just the opposite.

At the organism and ecosystem level, a model of interpretive biosemiotics 44 assumes that semiosis is defined through a dual interpretation by the individual of: ***1***) An ‘external reference’ made by objects and the surrounding reality or “semiotic niche”,45 and ***2***) An ‘internal sense’ constituted by the brain and the specifics captured by its five senses, ***3***) being the reason of the individual itself the ‘third’ factor.

Prompted by another reviewer, the rest of this discussion will be devoted to the study on how to prevent the possible expression of hereditary diseases among the population exposed on 9/11 to the WTC contaminated dust, both first responders and Manhattan residents.

The current and deep-rooted twofold partition in science and other scholarly disciplines is between facts and values, between descriptive and normative aspects of reality; we can even recognize the existence of the implicit and the explicit self.37

Ecosystem biosemiotics as applied to the human population will be defined as the twofold modifying interaction of a group of organisms (society) and their environment (nature), with both sides being mutually affected. Lynn Margulis (2010) presented an example,[46] here interpreted as political and atmospheric.

Carbon nanotubes were recently found inside the lungs of first responders to the World Trade Center 9/11 disaster.[47] Babcock (2002) edited a nanotechnology review that included carbon nanotubes.[48]

An assumption that can be made is that inside the bodies, lungs and circulatory systems[49] of at least the **300,000** New York City residents who lived in the vicinity of the Twin Towers,[50,51] whose number could be much higher,[52] and inside the more than **50,000** first responders that wore little or no protective gear,[j] are present multiple particles/microspheres (iron, glass, silicon, lead, etc.) produced at the fall of the WTC and present in the 9/11 toxic dust,[53] together to many other highly toxic particles, compounds and atoms.[54,55,56,57,58]

On 9/11 there was a deliberate toning-down of the results, *v.gr.*, the extremely alkaline or caustic nature of the 9/11 WTC dust, its highly basic pH (**12.4**),[59] its high concentration of asbestos (**3.3%**),[60] the extremely high presence of strontium, Sr (**1.7 mg/L** as the maximum indoors), etc. (See footnotes l and o).

We read that “for nuclear decay reactions, the sum of all mass and atomic numbers in the products must equal the same sum of these numbers in the reactants”;[61] that “every element has at least one unstable or radioactive isotope, but most have several”,[62] and that there is “asymmetric fission in proton-rich nuclei”.[63]

Strontium[64,65] was found in sediment cores pulled from the Hudson River near the World Trade Center a month after September 11, 2001; the top 3 cm of silt contained layers with **unnaturally high concentrations of metal-rich ash** that included “copper, **strontium**, and zinc”.[66] The leachate suspension/solution of the 9/11 dust had Sr at a high average level of **1.1 mg/L** while in the dry dust analyzed by chemical X-ray fluorescence its level was 726.6 ppm,[10] exhibiting in both cases a coordinated pattern with Barium[67] for all tested locations, as if being originated at the same time and by the same mechanisms.

As seen in the results, if we add the atomic numbers of the elements expressing a similar pattern (Figures 2 and 4) from the 9/11 dust leachate, we find that the sum of magnesium (Mg = 12) and manganese (Mn = 25) equals the atomic number of rubidium (Rb = 37).

If we then sum Rb (37) and potassium (K = 19), we obtain the atomic number of barium (Ba = 56).

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[j] “Following 9/11, it is estimated that as many as **50,000** at Ground Zero wore little or no protective gear”, http://www.webcitation.org/5wY7sF09M, http://www.wtcemergencyworkers.com “of the estimated 60,000 to 70,000 emergency responders” (Wu et al. 2010). Also see: Ryan, K. 2011. Energetic Materials as a Potential Cause of the 9/11 First Responder Illnesses. *Foreign Policy Journal* [Online: http://www.webcitation.org/5wY7sF09M, http://www.webcitation.org/5wZoR2t4a, http://www.webcitation.org/5wZTaeFRO]

[l] http://www.webcitation.org/5wYA07Vmt; Toxic dust: http://www.youtube.com/watch?v=UsoLm66lEUQ; Tampering the results: http://www.youtube.com/watch?v=rXCQ3KIt-ro See also: http://www.webcitation.org/5y2Yyw2RY, http://www.webcitation.org/5y2ZF2AJb, http://www.webcitation.org/5y2ZUDR0f (“*the number of seriously ill New Yorkers could climb to 300,000 in the near future*”, Oct. 2007), http://www.webcitation.org/5y2ZeTi0i, http://www.webcitation.org/5y2ZmczVg, http://www.webcitation.org/5y2ZwdOSh, http://www.webcitation.org/5y3yvTtua

[o] Cahill called the products of this stage of the 9/11 destruction “the miserable “brutal” materials of the smolder phase, with its disastrous and continuing health impacts. These will inevitably include ischemic heart disease deaths in a few years”; he talked about “the now accepted lethality of the fuming smolder phase” (03/23/2007 to Jenkins, 2007).[59] The 9/11 WTC extreme heat was “shown by the melting of metals”[57]: http://www.youtube.com/watch?v=hWHvnprvSbc, http://www.youtube.com/watch?v=1WWAnCd_6lg

If we sum Ba (56) and strontium (Sr = 38) we obtain the atomic number of plutonium (***Pu*** = 94).

In the 9/11 WTC chemical analysis, Ba and Sr were present in astronomical concentrations of 400 ppm to over 3,000 ppm, varying from place to place in lockstep according to the known nuclear relationships.

Cahill declared: “It may take years before these effects show up, just like with **radiation**”; 50,[k] in the 9/11 powder Cahill found the highest levels of very fine particles when compared to over 7,000 measurements done worldwide.[l] In the 9/11 WTC toxic dust, Cahill also found transition metals, acids, organic carcinogens and glass; the rounded glass shards had a mass peak in the 2.5 to 5 μm diameter range.57

The atoms found there correlated mathematically in a non-random way, in a fairly distinct and narrowly homogeneous dispersal, evidence that highly complex and energetic explosions took place, giving origin to “a complete smorgasbord of the Periodic Table”,67 including “an alphabet soup of heavy metals”.68

The presence of rare trace elements such as Ce, La and Y is enough to raise eyebrows, let alone in quantities of 50 ppm to well over 100 ppm, quantities that varied widely by location correlating with each other according to the relationships expected from a **nuclear fission** for the atoms analyzed.67

It seems that fission did not stop producing only two fission fragments or elements, many of these fragments experienced further fission into smaller atoms (Figure 4) by the intense concentrated neutron radiation in and underneath the building (Figure 4); such seems to be the signature of advanced underground nuclear devices perhaps coupled to a reactor to weaken the under infrastructure of the towers, plus additional destructive sources at the surface (*v.gr.*, “active thermitic material”54 seen as “flashes”, at the moment of the fall, as witnessed by firefighters etc.) (See references l and o).

Pu[m] is the element that seems to be the one that was split and started the reactions, with its products following **a synchronous race**: ***Pu*** = Sr + [Ba = K + (Rb = Mn + Mg)].

A similar exercise can be done for Sr in the 9/11 WTC dust chemistry done by X-ray fluorescence: [(Mg + Al = Mn) + Al = Sr] + Ba = ***Pu***.

Lung transplant 69 or synthetic lung replacement,70 bone marrow,71 hematopoietic stem cells,72 lymphocytes,73 and other blood cells 74 are possible options for the affected, both responders and residents.

If genetic damage reached the gametes, it would be best if the persons exposed to the 9/11 WTC dust and vapors did not intermarry, given the risk of expressing genetic problems similar to what happens in consanguineous heredity.

“The fetus may be 10-fold more susceptible to DNA damage than the mother” and “*in utero* exposure to polycyclic aromatic hydrocarbons (PAH) may disproportionately increase

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[k] The 15th Chairman of the Joint Chiefs of Staff, Vice-Chairman who acted as Chairman on 9/11 in the absence of the 14th Chairman, wrote that the way the twin towers fell “…*evoked a* ***nuclear*** *explosion*” [Myers, R. B., McConnell, M. 2009. Eyes on the horizon. Ch. 8. P. 154. *Simon and Schuster*. New York. 339 p. preserved at: http://www.webcitation.org/5wZiVnNpX] Beta radiation activity was twice the background level in the three samples of the 9/11 WTC dust analyzed by Lioy et al (2002),88 which may help explain the high correlation between Ba (56), La (57) and Ce (58). Atomic numbers in parentheses ( )

[m] Apparently nobody quantified Plutonium (***Pu***) at the 9/11 WTC. It seems that ***Pu*** did split, starting the fission reactions.

carcinogenic risk”,75‚76 this plus additional damages to the 9/11 WTC related offspring. 50‚77‚78

Impotence has also been demonstrated as another symptom of exposure to the WTC 9/11 contaminated dust 79 as well as chemosensory loss,80 *v.gr.*, the odor identification ability. 81

The entrance of atoms from the 9/11 WTC toxic dust to the **indoors** of the Manhattan residences can be seen as being very high, showing in the indoors similar or even higher levels than in the outdoors (in parentheses the percent outdoors *vs* the percent indoors which appears in bold): Ti-rich (0–0.1 *vs* **0–0.6**), Zn-rich (0.2–0.4 *vs* **0.1–0.6**), Pb-rich (not determined *vs* **0–0.03**), Fe-rich (0.2–1.3 *vs* **0.1–1.1**82). Also particles rich in **strontium** and in other elements were found, with no report of their levels indoors and outdoors.82‚53 For two samples revealing similar or higher indoors presence of atoms following a parallel coordinated pattern, go to Figure 2 (Samples 20 and 36).10

Those atoms continued penetrating the indoors of the WTC Manhattan neighborhood during the six months that the WTC underground had very high temperatures;83 “indoor dusts generated higher pH levels (11.8–**12.4**) than outdoor dusts (8.2–10.4), indicating that outdoor dust samples had reacted with rainfall or other waters prior to collection”;84 “the coarse particulate mass, finer than typical soils, appeared to be derived from hot portions of the collapse pile itself as it persisted even after periods of rain and despite increasingly effective efforts to wet and cool the pile”.57

Cahill measured in October 2001 the WTC ‘aerosols’ in the dust and found (in ppm): Si: *abundant*; V: 30; Pb: 200; Ni: 30; Cr: 120; **Ba**: 290; he included the boiling point for each element, *v.gr.*, for V is 3,480 °C and for Ni is 2,834 °C,85 an allusion to the smoldering pit.

In Chernobyl, at least 600,000 persons n were closely exposed to radiation for a prolonged time after the rupture of a reactor and a series of explosions; their germ-line mutation rate was found to be **twice as high** as that in a control group of families in Britain; families in which the parents had resided in more contaminated districts (*v.gr.*, Belarus) had higher mutation rates than those from less-contaminated districts.86

A comprehensive article revealing significant abnormalities associated with irradiation, unrelated to age or sex (*v.gr.*, stable chromosomal aberrations), as well as other genetic and non-genetic pathologies were compiled by Nesterenko et al (2009),87 where we read that the genetic damage among descendants of irradiated parents will propagate to the population and will be carried through generations.

To melt the WTC iron and concrete, temperatures of 2,800 degrees Fahrenheit or more were needed, time during which multiple highly toxic elements were expelled. o

The news near the final submission of this manuscript are that “thousands of people believe they have illnesses caused by trade center dust”, “the lawsuits cited hundreds of different ailments, both serious and mundane, with the most common being a respiratory problem similar to asthma”.89

Tahil (2006) noticed 67 that the high presence of strontium was ignored in the 9/11 WTC dust site-location graphics done by Clark et al (2001).10‚ p Sr was drawn in their “Leach Figure 1” as leading the μg/L group of atoms. It should have been located above phosphorus and fluorine in the upper **mg/L** group. In their ‘Leach Figure 5’ and ‘Leach Figure 6’, they

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[n] http://www.iaea.org/NewsCenter/Features/Chernobyl-15/cherno-faq.shtml, http://www.webcitation.org/5wYAlIlGJ

omit Sr while including nine atoms that had lower concentrations: Al, Cr, Mo, Sb and Zn, Ba, Ni, Co, Mn, respectively. In their X-ray Chemistry we also found the omission of Sr in their dust site-location graphics,[q] even when their “Chemistry Figure 1” included it as atom 13 between the more abundant barium and the less abundant zinc. However, while presenting Zn in their “Chemistry Figure 4”, strontium was omitted once more in an apparent “negative information action”[90] not by the researchers themselves (see references 68 and 84 and footnote l).

Even if we never fully understand the precise twin towers and nearby buildings[r,s] demolition details, the generation of nano-particles (**carbon nanotubes**, etc.) and bioavailable atoms (**strontium**, etc.), and their distinctive and damaging presence inside the bodies of possibly 300,000 humans or more, speaks for itself.

Conclusions

In this article, a second set of rules of variation, the genomic rules, is proposed to compare biological sequences and to find compatible genomes; these rules are: 1) the comparison of genomes to determine their compatibility between organisms, 2) the production of a healthy and fertile offspring, and 3) the study of their homologous recombination, rules that build up over the normal working of the code rules of variation.[4] By observing these three new aspects we may be capable of advancing the current status of knowledge and to preserve endangered organisms by performing backcrosses with non-endangered members of the same “theme” or “genomic species”; we may also be able to develop new varieties or subspecies based on the novel understanding of the natural order as presented here.

Comparative genomics used in compatible genomics is presented as a tool for studies of species and populations, including studies in the recent fields of population and ecosystem biosemiotics, to further the knowledge of the consequences of biological information, and of its signs and signaling.

Now, by taking the naturally compatible interbreeding to the molecular level and by the use of the rotating circular genetic code or other related software, we may be able to detect fully compatible genomes that have the same number of significant nucleotides. Also, with compatible genomics in mind, we can redefine the concept of ‘species’ at the molecular level as “the ability to interbreed and to produce a healthy fertile offspring by the compatible genomes present in two organisms: male and female”.

When the rules of variation[4] are broken, the molecular quality control mechanisms are unable to repair the excessive amount of damage, such as the damage imposed by radioactive and/or toxic contaminants, resulting in possible mutations to the DNA, damaging the newborns’ genes.[75,76,77,78]

The dust contaminated on 9/11, as it happens in consanguinity, may increase the probability to manifest hereditary diseases. Very sadly, the same can be said in relation to Japan and the

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[p] http://pubs.usgs.gov/of/2001/ofr-01-0429/leach1/index.html (leach figures 2 to 6, http://www.webcitation.org/5wYBFTMEN). Preserved at: http://www.webcitation.org/5wYBljfuw, http://www.webcitation.org/5wYCBbX2d, http://www.webcitation.org/5wZQ0qbDY.

[q] http://pubs.usgs.gov/of/2001/ofr-01-0429/chem1/index.html (chemistry figures 2 to 4, http://www.webcitation.org/5wYBOVn5q) Preserved at: http://www.webcitation.org/5wYCMQmL3, http://www.webcitation.org/5wYCTz9wm.

[r] http://www.youtube.com/watch?v=iOLIlKHDd78, WTC7 demolition to the ground of east penthouse ~7 seconds before the whole building.

[s] http://www.youtube.com/watch?v=7RhdBxEe_6M, WTC6 molten concrete (~2150°C) engulfing metals and perhaps carbonizing paper.

recent meltdown of its reactors. The novel field of compatible genomics should restrain consanguinity.

Abundant fumes, gases, vapors and volatile elements were produced during months by the smoldering WTC underground and were even more dangerous than the atoms generated at the fall of the 9/11 WTC (Cahill to Jenkins, 2007).59

In consanguinity, equally mutated regions of the genome increase the probability of expressing hereditary diseases in the offspring. Man-made disasters such as 9/11 may produce similar genetic effects.

If we advance a model for population biosemiotics as the reproductive compatibility of variations of a common theme, a compatible genomic population may be considered as a group with internal variations such as the synonyms of a ‘word’ or the different versions of a ‘book’.

As with variation, we consider a different version of pencil or of pen, just like a different but equally efficient variety, being the rules of variation fuelled by reversible changes highly dependent on the ecosystem and its environment. The adaptation of living organisms is engrained in the perfection of their intelligent design. Under the current normal and natural conditions, **selfless changes in the nucleotides of their ancestors** are helping their descendants, not themselves, to be a better fit **for a changing environment**.

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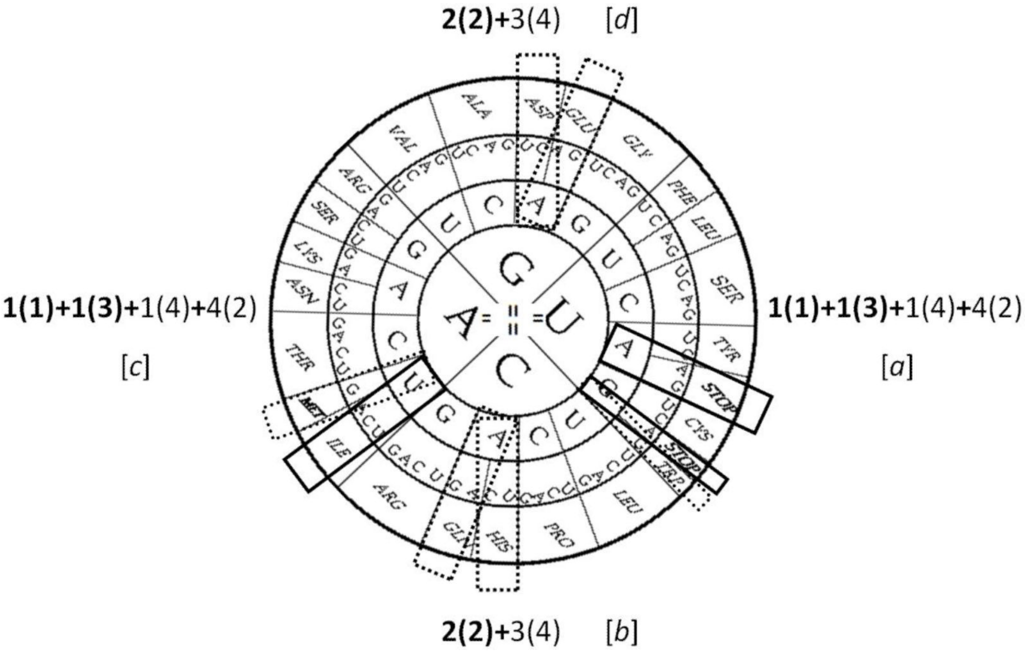

Figure 1.

Balance of codons in the classic circular genetic code. Rectangles are surrounding the odd-numbered codons present in quadrants one and three and the paired groups of codons that are present in quadrants two and four ([a]-[d], quadrants 1-4, respectively). Only quadrants two and four are fully symmetrical, both by number and by position. Here, the rectangles specifically represent the quasi-symmetrical position of the odd-numbered groups of codons for quadrants one and three, and of paired groups of codons for quadrants two and four, having equilibrium in the net sum for these codons per quadrant (numbers in bold). A similar numerical balance is seen in the essential hydrophobic amino acids with U at the center of their codons (ref. 4).

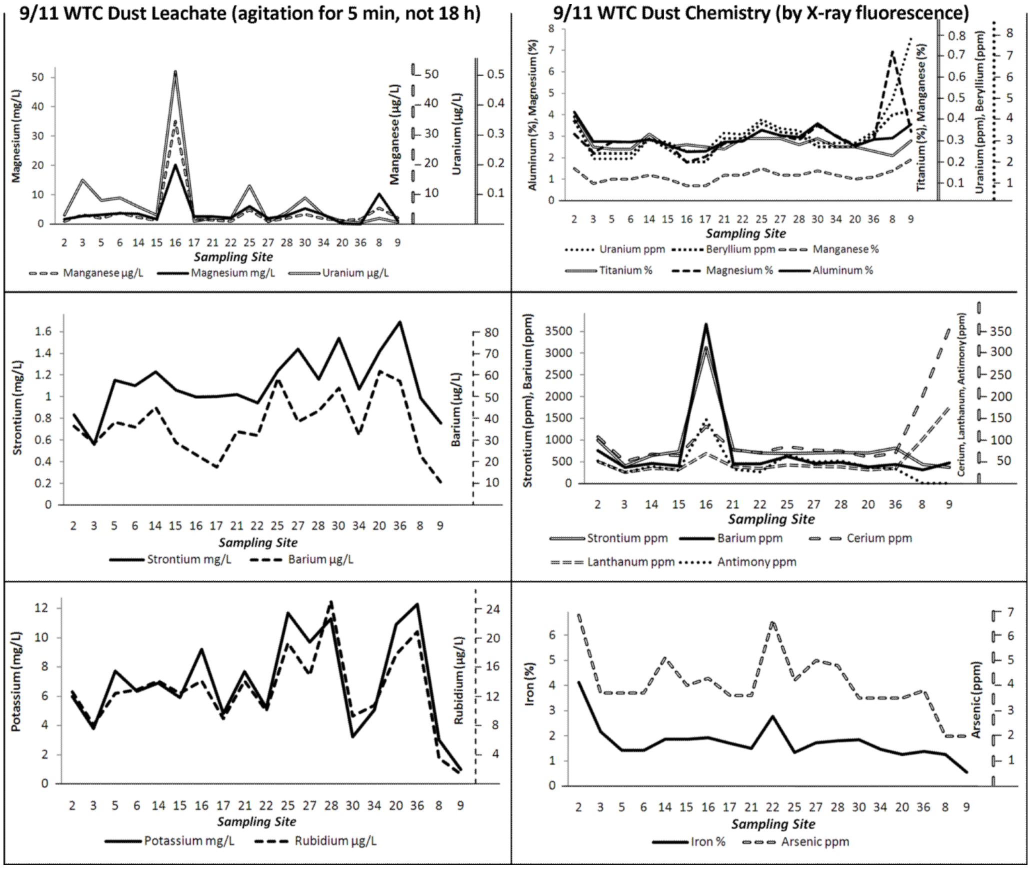

Figure 2.

Examples of coordinated changes in elements from the 9/11 WTC dust and its leachate tested at different sites. **Left Column**: 'Codissolved' in the leachate with a similar pattern per collecting site we have: uranium, manganese and magnesium; barium and strontium; rubidium and potassium. **Right Column**: A similar dust pattern was observed by uranium, beryllium, manganese, titanium, magnesium and aluminium; by strontium, barium, lanthanum, cerium and antimony; by iron and arsenic (flat regions, sites that were not measured). Two values at the right of each graphic (08 and 09) correspond to the girder coatings while samples 20 and 36 at their left side correspond to the indoors. Symbols: mg/L—milligrams per liter; µg/L—micrograms per liter; ppm—parts per million.

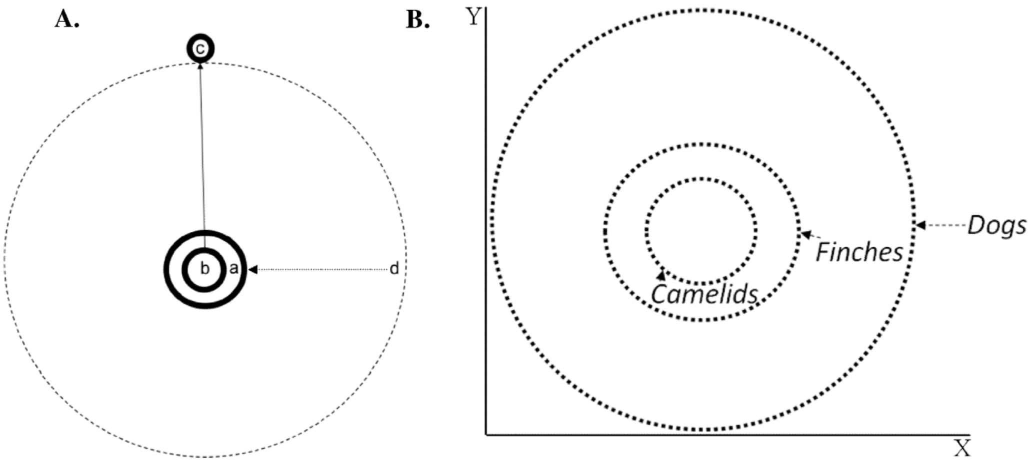

Figure 3.

a) Prospects for the genomic rules of variation: The generation of biodiversity, represented by circle **c** (cluster **c** contains new hypothetical varieties to be developed by humans), the preservation of endangered biodiversity is represented by circle **b**, while all organisms with compatible genomes are represented by circle **a**, which currently includes endangered organisms; circle **d** represents the currently over-inflated number of species, including ‘phenotypic species’ and ‘behavioral species’. Notice that once the factor of compatible genomics is added, the currently over expanded number of ‘species’ will dramatically shrink, moving down from **d** towards **a** (horizontal arrow). b) Each orbit of organisms with compatible genomes is one and the same theme, the same genomic species or genomic population. Each dot on each expanding circle represents a different variety for the compatible species that are represented by the complete orbit. The molecular genetic language spoken by all the dots within each orbit is the same, spoken through different local accents: their phenotypes and behaviours.

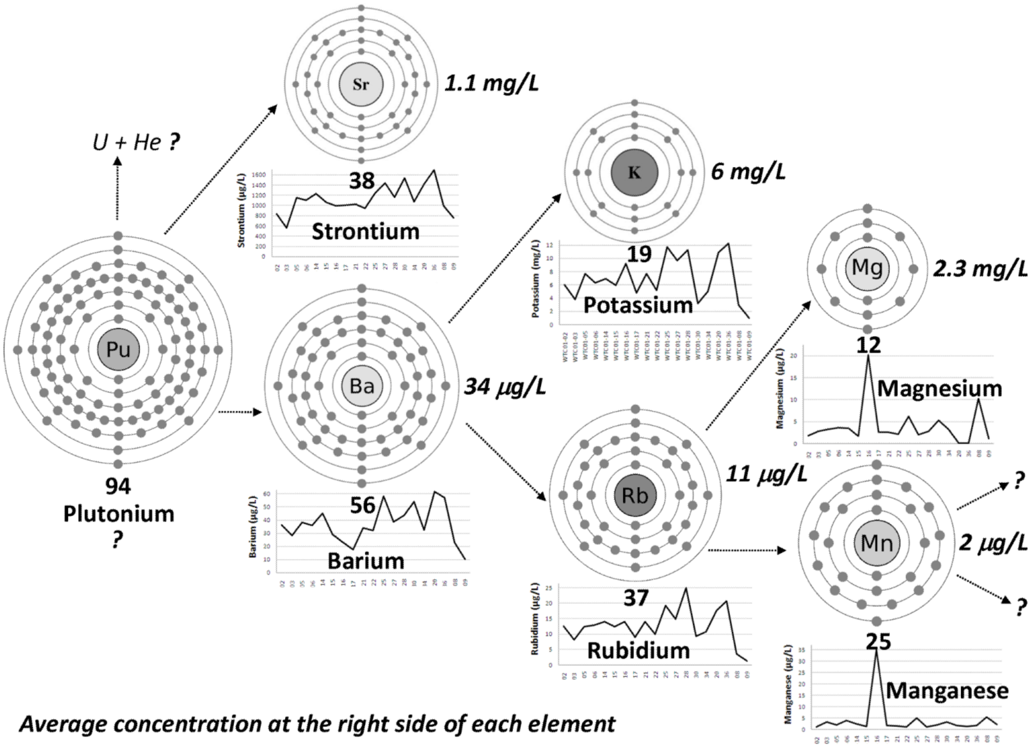

Figure 4.

Representation of atoms produced by **possible** nuclear fissions of plutonium (***Pu***), Barium (**Ba**), and Rubidium (**Rb**) as followed by the uniquely **coordinated patterns** of bio-available metals present on the soluble leachate of the 9/11 contaminated dust reported by the *USGS*.10 Atomic numbers are shown with the graphic of the dust (Fig. 2). “Cracks emerged” inside the preserved 9/11 WTC “compressions”, also called the 9/11 WTC “meteorites” (see http://www.webcitation.org/5y2mJY9Be and footnote o).

Table 1

Allele Frequencies in *HapMap* Populations; comparison of two polymorphisms predominant in humans with African origin for the gene LDLRAP1; in bold, similarity of percentages for the four upper and lower extremes, being the four in italics more compact [P = 0.0005] for both comparisons. Japanese matched closer to Indians, Toscans and Mexicans than to Chinese (*v.gr.*, P = 0.002 for rs3856239).

rsl 2096438 **Description [in brackets, panel in a 3 and 1 letter code]**	**Frequency of C (%)**	**Frequency of T (%)**
Luhya in Webuye, Kenya [LWK, L]	**68**	**32**
Yoruba in Ibadan, Nigeria [YRI, Y]	**68**	**32**
African ancestrv in Southwest USA [ASW, A]	**65**	**35**
Maasai in Kinyawa, Kenya [MKK, K]	**58**	**42**
Chinese in Metropolitan Denver, Colorado [CHD, D]	52	48
Utah residents with Northern and Western European ancestry, CEPH [CEU. C]	50	50
Han Chinese in Beijing, China [CHB, H]	49	51
Mexican ancestry in Los Angeles, California [MEX, M]	***44***	***56***
Gujarati Indians in Houston, Texas [GIH, G]	***42***	***58***
Japanese in Tokyo, Japan [JPT, J]	***41***	***59***
Toscans in Italy [TSI, T]	***40***	***60***

rs3856239 **Description [in brackets, panel in a 3 and 1 letter code]**	**Frequency of A (%)**	**Frequency of G (%)**
Yoruba in Ibadan, Nigeria [YRI, Y]	**68**	**32**
Luhya in Webuye, Kenya [LWK, L]	**64**	**36**
African ancestry in Southwest USA [ASW, A]	**62**	**38**
Maasai in Kinyawa, Kenya [MKK, K]	**56**	**44**
Chinese in Metropolitan Denver, Colorado [CHD. D]	52	48
Utah residents with Northern and Western European ancestry, CEPH [CEU, C]	49	51
Han Chinese in Beijing, China [CHB, H]	49	51
Gujarati Indians in Houston, Texas [GIH, G]	***43***	***57***
Japanese in Tokyo, Japan [JPT, J]	***41***	***59***
Mexican ancestry in Los Angeles, California [MEX, M]	***39***	***61***
Toscans in Italy [TSI, T]	***39***	***61***

Table 2

Sequences with >22 bases of contaminating palindromic fragments of the *ZAP* adaptor in tandem. Examples taken from 1,803 results of the 'Nucleotide collection (nr/nt)' database [search done in Nov., 2010]. One example per contaminant variant per organism: **1**. *Vitis vinifera*, Adh7, **2**. *Triticum aestivum*, **3**. *Homo sapiens*, Hdac8, **4**. *Oryza sativa*, glycine-rich protein, **5**. *Gallus gallus*, major class I glycoprotein, **6**. *Plasmodium falciparum*, **7**. *Schistosoma japonicum*, triosephosphate isomerase, **8**. *Xenopus laevis*, Bmp1, **9**. *Mus musculus*, Le51, **10**. *Aspergillus oryzae*, **11**. *Salicornia herbacea*, tonoplast intrinsic protein gamma, **12**. *Rana japonica*, gonadotropin, **13**. *Micromonas sp*., Lhcp2.3, **14**. *Lupinus luteus*, ribosomal protein L30, **15**. *Cimex lectularius*, apyrase, **16**. *Danio rerio*, immunoglobin superfamily member 21, **17**. *Nicotiana tabacum*, carbamoyl phosphate synthase, **18**. *Ciona intestinalis*, IfB, **19**. *Felis domesticus*, Behab, **20**. *Hydra attenuata*, lamin, **21**. *Petroselinum crispum*, Mkk2. [**GC** in sequences 9–13 seems added by *host*].

#	GenBank ID	Position of the contaminating sequence, of the EcoRI recognition site, highlighted in bold
1	AF195867	701 CTCGTG**CCGAATTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 744
2	BT009354	5 GTG**CCGAATTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 45
3	AF230097	3 **AATTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 37
4	AF011331	5 **ATTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 38
5	Z54362	1140 CTCGTG**CCGAATTCGG**CACGAGCTCGTG**CC** 1169
6	AJ005572	37 **G**CACGAGCTCGTG**CCGAATTCGG**CACGAG 65
7	U50847	55 CTCGTG**CCGAATTCGG**CACGAGCTC 79
8	NM_001090275	40 GAGCTCGTG**CCGAATTCGG**CACGAG 64
9	AB094480	423 CTCGTG**CCGAATTCGG**CACGAGGCCTCGTG**CCGAATTCGG**CACGAG 468
10	AB226176	74 **CGAATT**CGGCACGAGGCCTCGTG**CCGAATTCGG**CACGAG 112
11	AY639596.2	13 **GAATT**CGGCACGAGGCCTCGTG**CCGAATTCGG**CACGAG 50
12	AB178055	1 **AATTCGG**CACGAGGCCTCGTG**CCGAATTCGG**CACGAG 37
13	BK006036	1 **ATTCGG**CACGAGGCCTCGTG**CCGAATTCGG**CACGAG 36
14	AJ223316	1 **GAATTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 36
15	AF085499	1 **TTCGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 33
16	CU458945	1 **CGG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 31
17	AJ319873	1 **GG**CACGAGCTCGTG**CCGAATTCGG**CACGAG 30
18	AJ298330	1 CACGAGCTCGTG**CCGAATTCGG**CACGAG 28
19	Z28367	1 **CGG**CACGAGCTCGTG**CCGAATTCGG**CAC 28
20	AJ005934	2161 CGAGCTCGTG**CCGAATTCGG**CACGAG 2186
21	AY533301	1 **GAATTCGG**CACGAGCTCGTG**CCG-ATTCGG**CACGAG 35