

*The International Journal for Transformations of Consciousness* (2014, In Press).

For Subscriptions: [chandrankunnel@gmail.com](mailto:chandrankunnel@gmail.com)

## **An Evolutionary RNA/DNA Psychogenomic Theory of the Transformations of Consciousness:**

### **The Quest for Therapeutic Mind/Gene Search Algorithms**

Ernest Rossi and Kathryn Rossi

#### **Abstract**

This review integrates evolutionary, epigenomic, mathematical and informational data for an evidence-based RNA/DNA psychogenomic theory of the transformations of consciousness that is suitable for therapeutic applications in translational medicine, psychiatry and psychology. Many states of psychobiological arousal such as pain, stress, novelty, REM sleep, the basic rest-activity cycle and creative moments in everyday life, the arts, humanities and the sciences are conceptualized here as phenotypes of mind/gene algorithms that are in part subject to voluntary memory, learning and training. The quest for such voluntary mind/gene search algorithms that could facilitate the behavioral epigenomics of meditation, psychotherapy, therapeutic hypnosis, placebos and the healing arts are proposed as scientific updates of many pre-scientific approaches that were originally given many different names by different cultures and spiritual traditions such as yoga, Wu wei, grace, prayer, Buddha consciousness, satori, Zen and so forth. RNA/DNA microarray technology, epigenetic software and genomic insights are recommended to bridge the artificial Cartesian philosophical divide between mind, body and matter.

#### **Introduction: The Evolutionary RNA/DNA Psychogenomic Theory of Adaptive Consciousness**

The perennial philosophy about the evolution of the transformations of human consciousness is summarized in the mathematical illustration of figure 1.<sup>1,2,3,4</sup> From an idealized perspective it was originally believed that the highest state of consciousness could be achieved *via negativa*: an experiencing of *God* that supposedly went beyond mere human cognition. This was also described as “*the cloud of unknowing*” by mystics of the Middle Ages.<sup>4,5</sup> It was called “*Point Omega*” by the geologist and theologian Teilhard de Chardin<sup>6</sup> who believed that it was the maximum level of complexity and cosmic consciousness<sup>7</sup> towards which the universe was evolving. The yoga traditions of India described such positive evolutionary transcendental states of consciousness as *Nirvana or Samadhi* achieved with seeming paradox by stilling the mind.<sup>8a,b,c</sup> Carl Jung described these experiences as self-realization<sup>9</sup> achieved through a life-time of observing and facilitating the so-called archetypal evolution of the unconscious.

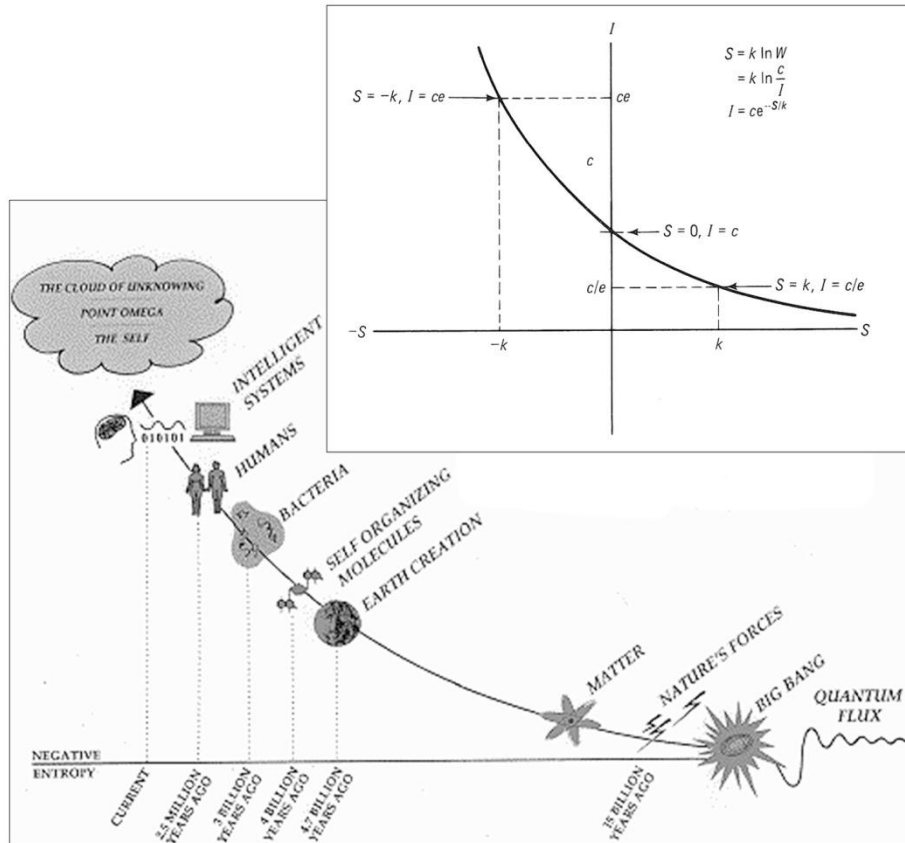


Figure 1. The Evolutionary RNA/DNA Psychogenomic Theory of the Transformations of Human Consciousness is illustrated as the co-evolution of information and entropy. The big bang ~15 billion ago, formation of earth ~ 4.7 billion years ago, the appearance of self-organizing molecules ~4 billion years ago, the emergence of bacteria ~ 3 billion years ago and humans ~ 2.5 billion years ago.<sup>2,4,5</sup>

Current research documents the use of DNA microarrays for assessing a variety of these top-down psychobiological experiences of the transformations of human consciousness that were originally given many different pre-scientific names by many diverse cultural, historical and spiritual traditions of mind-body healing. This review proposes that the perception, understanding and utility of such experiential states could be optimized by reframing them within a new epigenomic research paradigm as mind/gene search algorithms in pursuit of stress reduction as well as healing, meaning and satisfaction in life. The Darwinian natural variations and selection in this apparently adaptive quest for mind/gene search algorithms could be the scientific rational for the evolution of self-reflective consciousness.<sup>3,5,10-14</sup>

The mathematical model for the evolution of consciousness as information and entropy presented in figure 1 comes from a blend of theory, research and speculation about the origin of the cosmos in a quantum big bang about 13.7 billion years ago.<sup>2,4,5,15</sup> Noteworthy in figure 1 are a few fundamental stages in the epigenomic RNA-DNA evolution of life as we currently know it.<sup>16</sup> Epigenomic insights begin with “An RNA World model for the successive appearance of RNA, DNA and proteins and during the evolution of life beginning on earth” about 4 billion years ago.<sup>17</sup> The original *RNA World Hypothesis* proposed that RNA assembled itself as the first indispensable self-replicating molecule of life.<sup>18,19</sup> DNA came later, presumably as a mutation of RNA.<sup>20</sup> The evolution of life and consciousness apparently began with *RNA specializing as a signaling molecule* between the environment and *DNA, which*

functioned as the specialized memory molecule of life.<sup>21</sup> This co-evolutionary model integrating the functions of RNA and DNA facilitated the next stage of life's evolution when the cellular level morphed to the organismic level by random variation and natural selection ~3 billion years ago.

Four concentric cycles illustrate the RNA-DNA psychogenomic theory at the neuroscience level of human consciousness, sleep, dreams, brain plasticity, memory and learning (outer cycle) in figure 2. Before the advent of neuroscience these natural psychogenomic processes were understood only in their phenotypic cognitive-behavioral mythological garb as teaching tales for facilitating adaptation (next inner cycle<sup>22</sup>). This review proposes that such teaching tales are mythological and allegorical personifications of natural evolutionary RNA-DNA relationships; such teaching tales are pre-scientific metaphors for *mind/gene search algorithms for optimal adaptation*.<sup>14,23,24</sup> The two innermost circles of figure 2 represent the corresponding 4-stage creative cycle of human cognition, consciousness, experience and invention in everything from mathematics<sup>25</sup> music, and dance<sup>26</sup> to psychotherapy.<sup>3,4,5,13,27,28</sup>

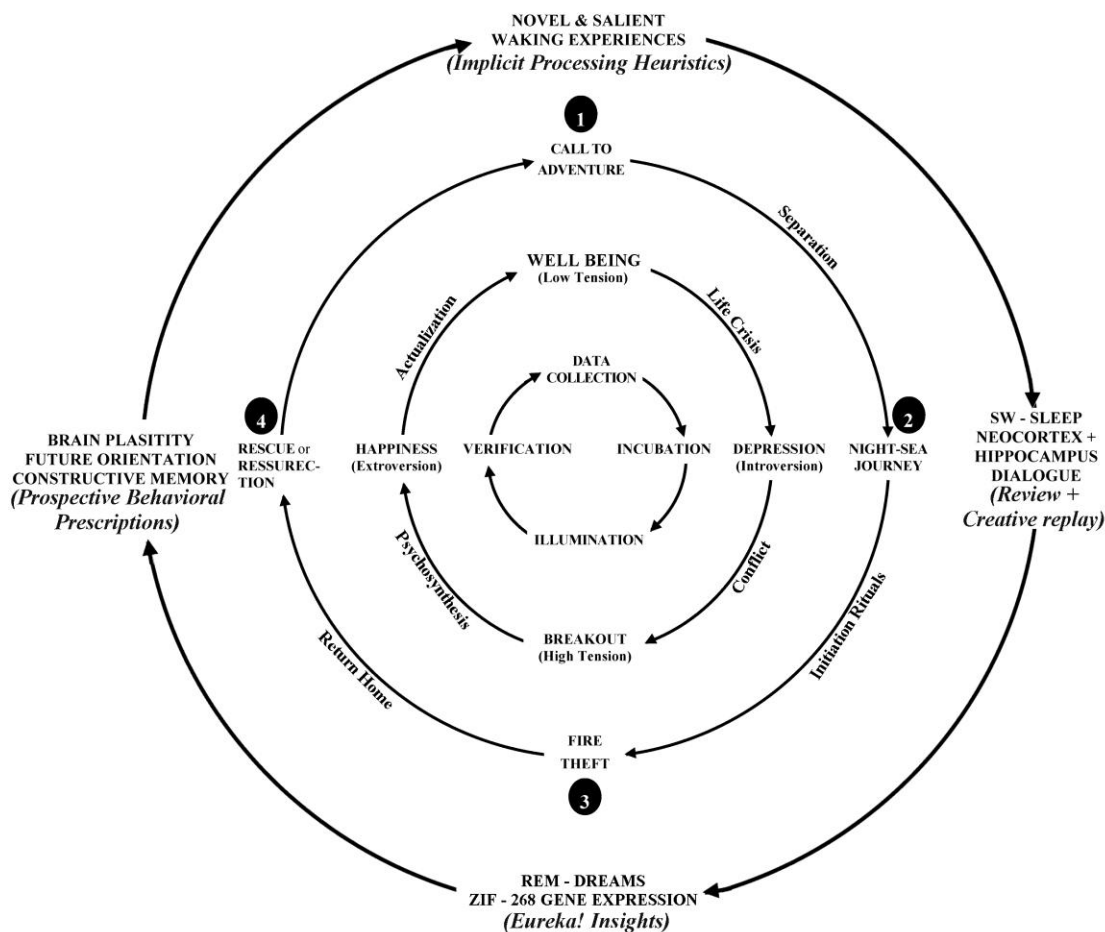


Figure 2. Four Levels of an Evolutionary RNA/DNA Psychogenomic Theory of the Transformations of Human Consciousness.

We now expand the outer neuroscience cycle of these natural psychogenomic processes of figure 2 with a detailed outline of the core evolutionary RNA/DNA psychogenomic theory of <sup>f 8a,b,c</sup>.

**The Core Evolutionary RNA/DNA Psychogenomic Theory of the Transformations of Consciousness.**

The central dogma of molecular biology<sup>29</sup> is updated to include current neuroscience research mind/brain/genomic model in four steps that underpin our proposed evolutionary RNA/DNA theory of the transformations of human consciousness outlined in figure 3. The psychogenomic perspective of Figure 3 presents an overview of how mind, particularly during the *salient crises and opportunities* of everyday life, activate mirror neuron eRNAs that promote the epigenomic human accelerated regions (HARs), brain plasticity and their consequent phenotypic transformations of adaptive human consciousness.<sup>30</sup>

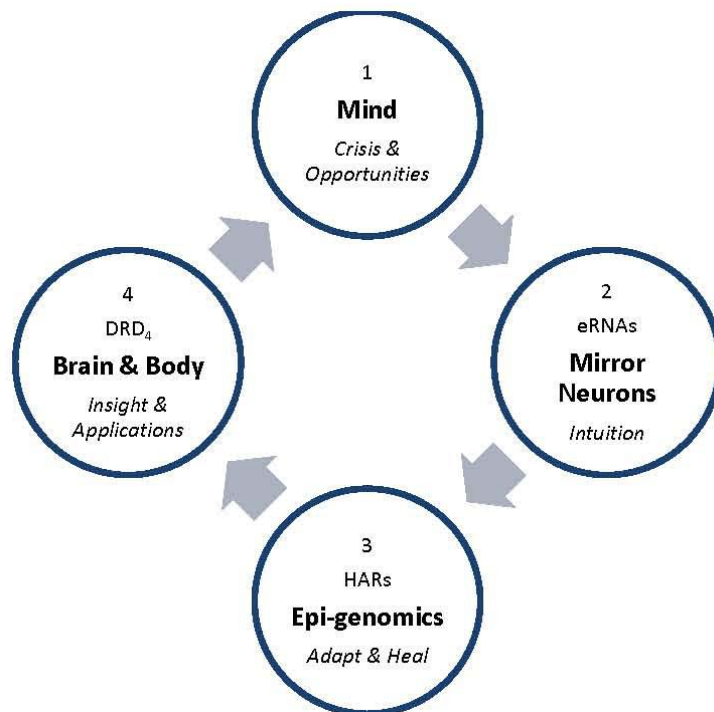


Figure 3. The Core Evolutionary RNA/DNA Mind/Gene Search Algorithm for Facilitating Transformations of Human Consciousness and Mind-Body Healing.<sup>4, 14, 71, 79</sup>

1. *Mind Responding to the Natural Crises and Opportunities of Life* is an epigenomic mind/gene signaling system that facilitates adaptation by activating mirror neurons in figure 3. The evidence for these psychogenomic mind/gene interactions comes from microarray data briefly reviewed here. In the past decade DNA microarray technology has made it possible to measure the expression levels of many thousands of genes simultaneously. This evidence-based research in molecular biology has become a new standard in personalized medicine.<sup>31</sup> Today these include RNA/DNA research on social variables<sup>32-36</sup>; the relaxation response,<sup>37</sup> therapeutic hypnosis,<sup>4,14,38-41</sup> meditation,<sup>42</sup> the therapeutic placebo<sup>43</sup> and yoga.<sup>44</sup> Such research is the first step in the documenting our evidence-based quest for mind/gene search algorithms to facilitate adaptive

states of human consciousness as well as the healing of stress related dysfunctions.<sup>45</sup> Further research is now required to standardize the efficacy of these mind/gene search algorithms in translational medicine recommended as a standard of clinical excellence by Insel,<sup>46-48</sup> director of National Institute of Mental Health.

2. *Mirror Neuron Research* explores how observing consciousness can function as a meta-level or secondary level of awareness wherein people engage in self-reflective cognitions, feelings and experiences about their own cognitions, feelings and experiences. Many types of multilevel self-reflection are generally taught, for example, as mind-body techniques for facilitating adaptation<sup>49-51</sup>). From this perspective mirror neurons can be conceptualized as *psychogenomic bridges* or *epigenomic* conversations between mind, nature and nurture.

How do these complex epigenomic adaptive systems<sup>52</sup> of self-reflective consciousness, culture and brain plasticity co-evolve? Kim et al.<sup>53</sup> recently described the identification of a new class of 12,000 enhancer Ribonucleic Acid molecules (eRNAs) that are involved in regulating gene expression during neuronal activity in mouse cortical brain tissue.<sup>54</sup> The significance of this research for bridging the Cartesian explanatory gap between the novel qualia of consciousness and their molecular-genomic infrastructure became apparent in related research on the genome of the zebra finch described as follows by Warren, Clayton *et al.*<sup>55</sup>

“The zebra finch is an important model organism in several fields with unique relevance to human neuroscience. Like other songbirds, the zebra finch communicates through learned vocalizations, an ability otherwise documented only in humans and a few other animals ... We show that song behavior engages gene regulatory networks in the zebra finch brain, altering the expression of long non-coding RNAs, microRNAs, transcription factors and their targets. *We also show evidence for rapid molecular evolution in the songbird lineage of genes that are regulated during song experience. These results indicate an active involvement of the genome in neural processes underlying vocal communication and identify potential genetic substrates for the evolution and regulation of this behavior.*” (Italics added, p. 758)

Clayton, one of the co-authors made the salient comment, “*this is the first time a microRNA has been shown to respond to a particular thought process*”.<sup>56</sup> We now propose eRNAs mediate between the novel qualia of activity or experience-dependent epigenomic expression that underpins adaptive brain plasticity and our quest for mind/gene search algorithms of therapeutic human consciousness. *From this psychogenomic perspective consciousness itself is a novelty-seeking mind/gene search algorithm that evolved as a sensitive detector qualia of human experience to facilitate rapid and creative adaptation to environments manifesting constant change with natural variation and selection* (p.135<sup>3</sup>).

MicroRNAs apparently respond to thought by modulating activity-dependent transcription/translation via qualia-dependent search algorithms of epigenomics. Culler et al.<sup>57</sup> reported a proof-of-principle experiment wherein they showed how RNAs function as “sensing-

actuation devices” transmitting the qualia of information from the environment to modulate the gene expression of DNA within cells as follows.

“Cellular decisions, such as differentiation, response to stress, disease progression, and apoptosis, depend upon regulatory networks that control enzymatic activities, protein translocation, and genetic responses. Central to the genetic programming of biological systems is the ability to process information within cellular networks and link this information to new cellular behaviors, in essence rewiring network topologies ... *RNA is a promising substrate for platforms to interface with cellular networks because of the versatile sensing and actuation functions that RNA can exhibit and the ease with which RNA structures can be designed. RNA-based sensing-actuation devices have been engineered that respond predominantly to externally [environmental] applied small-molecule and nucleic acid inputs and control gene expression through diverse mechanisms.*” (p. 1251, italics added here).

From an evolutionary perspective it appears that sensitive and fragile “RNA-based sensing-actuation devices” were the primordial molecular signaling epigenetic information from the environment of early earth to the more stable DNA memory molecule. One possibility is that DNA may have been a mutation in RNA world that began to function as memory molecule which eventually made natural evolution possible from one generation to the next. *We propose that this adaptive coordination between the sensing (qualia), signaling, and catalytic self-replicating properties of RNA (with A-U, G-C base pairings) interacting with the more stable memory properties of DNA (due to A-T, G-C base pairing) was the original bridge over the Cartesian explanatory gap between the molecular-genomic qualia and functions of life and consciousness.* Wang et al.<sup>58</sup> expressed it in this way:

“A major surprise arising from genome-wide analyses has been the observation that the majority of the genome is transcribed, generating noncoding RNAs (ncRNAs). It is still an open question whether some or all of these ncRNAs constitute functional networks regulating gene transcription programs. However, in the light of recent discoveries and given the diversity and flexibility of long ncRNAs ... *it becomes likely that many or most ncRNAs act as sensors and integrators of a wide variety of regulated transcriptional responses and probably epigenetic events ... Together, the ncRNA sensor code appears to be a robust and critical strategy underlying a wide variety of gene regulatory programs.*” (Italics added here pp. 279 & 289)

If we are willing to take a philosophical, linguistic and quantum leap from “ncRNA sensor code” to “ncRNA qualia code” such research could be another ingredient in our evolving theory of the origin of life and the qualia of consciousness via the psychogenomic dynamics of RNA/DNA coordination during transcription and translation. *Current research implies that the more fragile but versatile molecular RNA signaling software of RNA world became integrated with the more stable DNA memory hardware to initiate the evolution of life as we know it.* It is interesting coincidence to note that when Gilbert<sup>18</sup> first introduced the concept of “RNA world” in a bottoms-up approach to the evolution of life and mind. At the same time Rossi<sup>27</sup> independently

began exploring such research from a top-down approach. A comprehensive theory of adaptive consciousness, of course, requires an integration of both approaches to fill in the Cartesian psychogenomic gaps that remain between them. In the following sections we review the incredibly wide range of *qualia-dependent molecular-genomic processes* that underpin the deep psychogenomic rhythms of human consciousness and experience.<sup>59, 60</sup>

3. *Uniquely Human Epigenomics* is described by Pollard *et al.*,<sup>61</sup> as follows.

“The developmental and evolutionary mechanisms behind the emergence of human-specific brain features remain largely unknown. However, the recent ability to compare our genome to that of our closest relative, the chimpanzee, provides new avenues to link genetic and phenotypic changes in the evolution of the human brain. *We devised a ranking of regions in the human genome that show significant evolutionary acceleration. Here we report that the most dramatic of these ‘human accelerated regions’, HARI, is part of a novel RNA gene (HARIF) that is expressed specifically in Cajal–Retzius neurons in the developing human neocortex from 7 to 19 gestational weeks, a crucial period for cortical neuron specification and migration. HARIF is co-expressed with reelin, a product of Cajal–Retzius neurons that is of fundamental importance in specifying the six-layer structure of the human cortex. HARI and the other human accelerated regions provide new candidates in the search for uniquely human biology.*” (Italics added here, p. 167)

Pollard provides more detail about the uniquely human accelerator regions as follows.<sup>62</sup>

“Studies in a variety of different organisms support the importance of regulatory mutations in the evolution of closely related species. Similarly, many of the fastest evolving sequences in the human genome are outside of genes in regulatory DNA. *These uniquely human regulatory sequences, called Human Accelerated Regions (HARs), are located near and likely control a very important collection of genes, many of which are involved in development and human disease. Because many of the genes with HARs are transcription factors that control the expression of other genes, it is easy to see how a relatively small number of mutations in regulatory sequences could alter the function of an entire network of genes and thereby influence a trait, such as pelvic morphology or brain size.*

But individual mutated bases of DNA are not the whole story. During evolution, stretches of DNA can be copied, deleted, or rearranged in a species’ genome. These structural variations can lead to destruction or change in the functions of the genes and regulatory sequences they contain. The consequences are often detrimental, but occasionally beneficial ... *These dynamic regions likely harbor much of what makes us genetically human. As novel technologies enable us to study a wider range of molecular data, geneticists will be digging even deeper for what makes us human. Sequencing hundreds of living and extinct human genomes will help to pinpoint the genetic changes that make us modern humans, in contrast to those that distinguish hominins as a group from chimps and other primates.*” (Italics added here, p. 184).

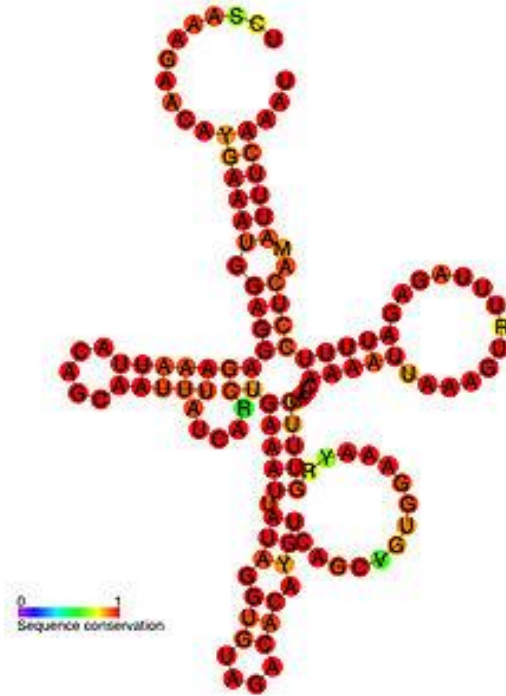


Figure 4. An illustration of the human accelerator region (HAR) adopted from Wikipedia creative commons.

4. *Brain and body adaptation and plasticity are epigenomic expressions of the dynamic interaction between mind, nature and nurture that generate the phenotypic transformations of consciousness that we experience as the natural reframing and transformations of our phenotypic attitudes, behavior, emotions, memory, learning, etc. A recent example of the far reaching implications for the psychosocial genomics of the novelty-seeking dopamine D4 receptor (DRD4) gene and human migration behavior, for example, has been summarized by Matthews and Butler as follows.*<sup>63</sup>

*“Numerous lines of evidence suggest that Homo sapiens evolved as a distinct species in Africa by 150,000 years before the present (BP) and began major migrations out-of-Africa ~50,000 BP. By 20,000 BP, our species had effectively colonized the entire Old World, and by 12,000 BP Homo sapiens had a global distribution. We propose that this rapid migration into new habitats selected for individuals with low reactivity to novel stressors. Certain dopamine receptor D4 (DRD4) polymorphisms are associated with low neuronal reactivity and increased exploratory behavior, novelty seeking, and risk taking, collectively considered a novelty-seeking trait (NS) ... Furthermore, additional loci surrounding DRD4 are now recognized to influence novelty-seeking.”* (Italics added here, p. 382).

The profound implications of novelty-seeking as part of a general mind/gene search algorithm for human cognition and the qualia of positive human consciousness (happiness, empathy) as well as human migration patterns is described by Kluger *et al.* as follows.<sup>64</sup>



“The familiar notion that the descendents of immigrants, whether they arrived from old Europe 300 years ago or Asia last year, are heirs to a genetically optimistic temperament makes intuitive sense. ... If genes play a role in shaping immigrant temperament, they do it in a subtle way. Serotonin and dopamine are often, simplistically, thought of as feel-good neurotransmitters. The more you have of them, the happier you are. But in the case of immigrants at least, the power of the chemicals is that they regulate what researchers straightforwardly call search activity—forward-looking behavior that often occurs in pursuit of a specific goal. *Search activity simply feels good*—a fact that helps explain why shopping for something is often more fun than buying it, hunting can be more enjoyable than actually bagging your prey, and so many politicians appear to have a better time running for office than holding it.

What is more, explains Dr. Vadim Rotenberg, a psychiatrist and psychophysicologist at Tel Aviv University, *the feel-good search experience can stimulate people to continue perusing a goal even when they are having trouble achieving it*. That’s as good an explanation for immigrant persistence as there ever was. So how does the brain bred for the joy of pursuit react to stress and a climate of near constant distractions—both grindingly consistent features of the post-industrial world?

At the neurological level, happiness is a very complex thing, and lots can go wrong. Studies of the brain conducted with functional magnetic resonance imaging (fMRI) show varying levels of happiness-related activities in the left prefrontal cortex and the more primitive basal ganglia, which form part of the reward loop; the amygdala, which processes a range of basic emotions; the septal area, which is involved in the experience of empathy; and the anterior insula, which helps focus our attention on the things that are making us happy in the first place.” (Italics added here, p. 27-28)

This brief overview of the evolutionary core of Mind/Gene Search Algorithms leads us to propose how they could function as the self-rewarding psychogenomic underpinning of the 4-stage creative cycle. It feels good to experience these ubiquitous and universal motivational positive qualia of human search behavior. In this sense they function as the epigenomic integration between mind, nature and nurture. It is now important to determine to what degree they are also phenotypes of the genotypes of the human accelerator regions (HARs).

In the following sections we will review some salient implications and therapeutic applications of qualia-dependent mind/gene search algorithms that require further empirical documentation via research in behavioral epigenomics [<http://epigenie.com/nih-roadmap-epigenomics-program-data-resource>].

### **Qualia of Consciousness during the Basic Rest-Activity Cycle (BRAC)**

Table 1 presents the contrast between the qualia of the Basic Rest-Activity Cycle (BRAC) as typically experienced during the *Ultradian Healing Response*, when people take appropriate rest-breaks every 90-120 minutes or so throughout the day, with the *Ultradian Stress Response* when people chronically attempt to forego taking appropriate rest periods.<sup>28,65</sup>

THE ULTRADIAN HEALING RESPONSE	THE ULTRADIAN STRESS SYNDROME
1. <i>Recognition Signals:</i> An acceptance of nature’s call for your need to rest and recover your strength and well-being leads you into an experience of comfort and thankfulness.	1. <i>Take-a-Break Signals:</i> A rejection of nature’s call for your need to rest and recover your strength and well-being leads you into an experience of stress and fatigue.
2. <i>Accessing the Deeper Breath:</i> A Spontaneous deeper breath comes all by itself after a few moments of rest as a signal that you are slipping into a deeper state of relaxation and healing. Explore the deepening feeling of comfort that comes spontaneously. Wonder about the possibilities of mind/gene communication and healing with an attitude of “dispassionate compassion.”	2. <i>High on your Hormones:</i> Continuing effort in the face of fatigue leads to the release of stress hormones that short-circuits the need for ultradian rest. Performance goes up briefly at the expense of hidden wear and tear so that you fall into further stress and a need for artificial stimulants (caffeine, nicotine, alcohol, cocaine, etc.).
3. <i>Mind-Body Healing:</i> Spontaneous fantasy, memory, feeling-toned complexes, active imagination, and numinous states of being are orchestrated for healing and life reframing.	3. <i>Malfunction Junction:</i> Many mistakes creep into your performance, memory, and learning; emotional problems become manifest. You may become depressed or irritable and abusive to yourself and others
4. <i>Rejuvenation and Awakening:</i> A natural awakening with feelings of serenity, clarity, and healing together with a sense of how you will enhance your performance and well-being in the world	4. <i>The Rebellious Body:</i> Classical psychosomatic symptoms now intrude so that you finally have to stop and rest. You are left with a nagging sense of failure, depression and illness

Table 1. The contrast between the qualia experienced during the Ultradian Healing Response, when people take appropriate breaks throughout the day, versus the Ultradian Stress Response leading to behavioral, cognitive and emotional problems or psychosomatic symptoms when they do not take appropriate healing breaks throughout the day to optimize gene expression and healing.<sup>4, 14</sup>

Figure 5. The Qualia of Darwin’s daily and hourly work experienced as the 4-Stage Creative Cycle in one 90-120 minute basic rest-activity cycle of human consciousness.

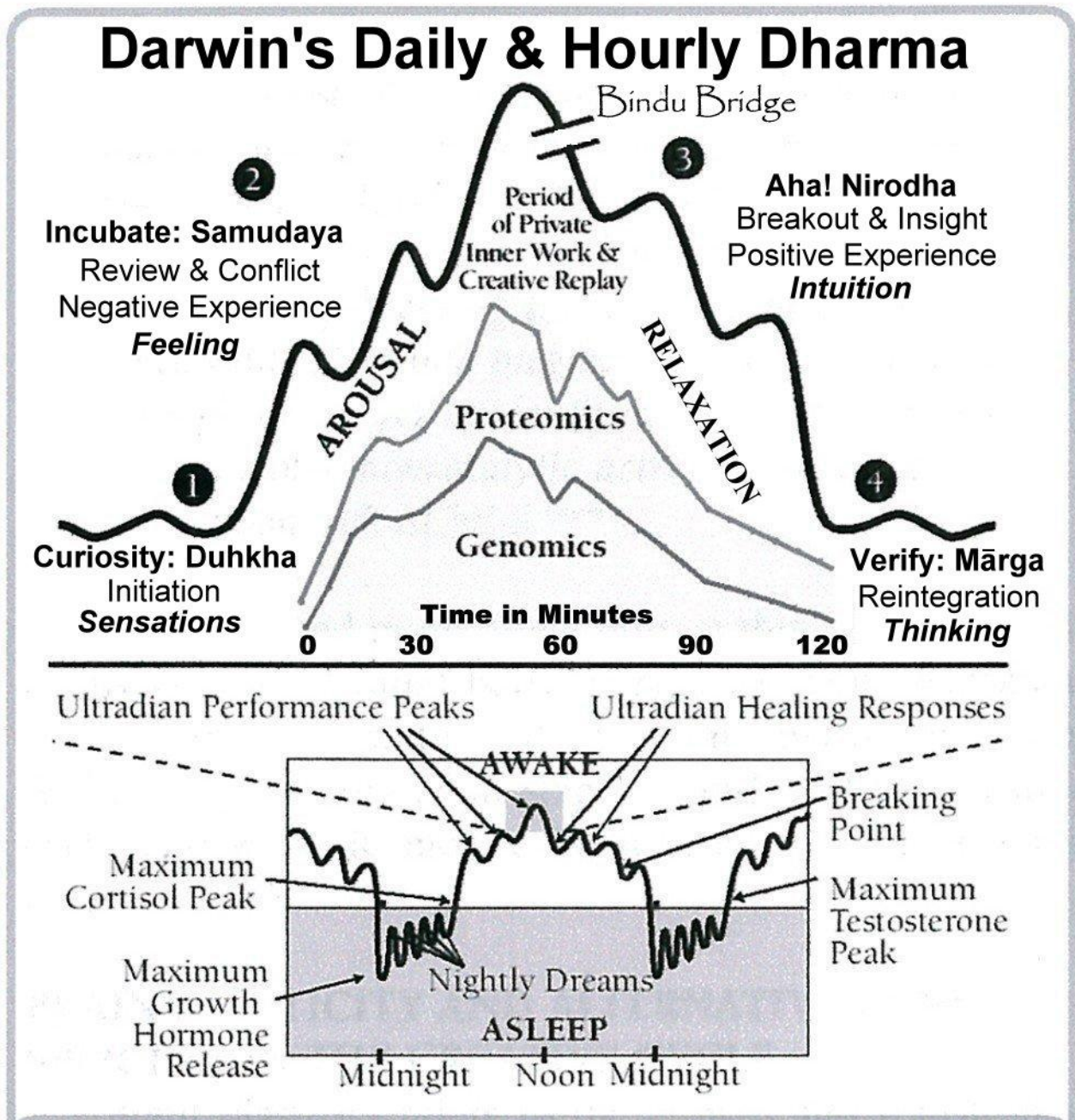


Figure 5. *Qualia* of Darwin's daily and hourly dharma experienced as the 4-Stage Creative Cycle in one 90-120 minute basic rest-activity cycle (top) of the ~24 hour circadian cycle (bottom). The Sanskrit terms that accompany each stage represent the *qualia* of the pathways of Buddha's Four Noble Truths, which we hypothesize are experientially identical with the cyclic 4-stage creative process. The proteomics (protein) profile in middle curve depicts the energy landscape for protein folding within neurons of the brain into the correct structures needed for brain plasticity.<sup>66</sup> This proteomic profile arises from the functional concordance of co-expressed genes illustrated by the genomics profile below it (Adapted from Levsky et al.,<sup>67</sup>). This genomics curve represents the actual gene expression profiles of the immediate-early gene *c-fos* and 10 other genes (alleles) over the typical Basic Rest-Activity (BRAC) period. The lower diagram illustrates how these ultradian dynamics of the *qualia* of consciousness

are typically experienced as Kleitman's 90–120 minute Basic Rest-Activity Cycle within the normal circadian cycle of waking and sleeping.<sup>3</sup>

Table 2 outlines the qualia of mind/gene search algorithms during psychotherapy that turn on experience-dependent gene expression and brain plasticity, which we call, “the Novelty-Numinosum-Neurogenesis Effect,” from two complementary perspectives: the bottoms-up approach of neuroscience<sup>3</sup> and the top-down approach of heightened states of purported spiritual experience that are called, “the numinosum”.<sup>9,68</sup>

**Qualia of Human Experience Associated with  
the Novelty-Numinosum-Neurogenesis-Effect (NNNE) in  
Neuroscience and the Numinosum in Spiritual Practice.  
(Rossi, 2002-2013)**

<b>Neuroscience</b>	<b>Numinosum</b>
<ul style="list-style-type: none"> <li>▪ <b>Activity</b></li> <li>▪ <b>Novelty</b></li> <li>▪ <b>Enrichment</b></li> </ul>	<ul style="list-style-type: none"> <li>▪ <b>Fascination</b></li> <li>▪ <b>Mysterious</b></li> <li>▪ <b>Tremendous</b></li> </ul>
<p><b>Kempermann, 2006</b> <b>Ribeiro et al., 2008</b> <b>Dalai Lama, 2005</b></p>	<p><b>Otto, 1923</b> <b>Jung, 1958</b> <b>Lahiri, 2000, 2009</b></p>

*Table 2. The three qualia associated with experience-dependent gene expression and brain plasticity by neuroscience and the corresponding three qualia experienced during the heightened states of consciousness associated with spiritual experience.*<sup>4, 5, 8a,b, c, 13, 14</sup>

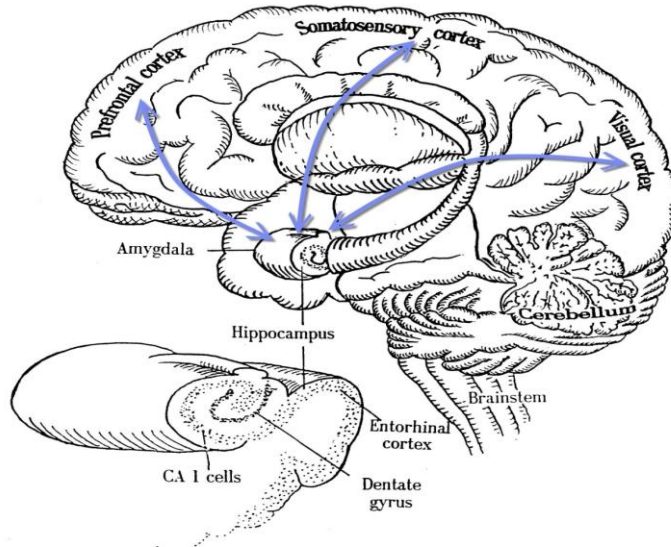
**Qualia of the Molecular Biology of Memory & Learning during Sleep and Dreaming**

Figure 6 illustrates our psychosocial genomic model of psychotherapy that emulates the natural process whereby novel qualia experienced in our waking hours induce mind-brain-gene dialogues during slow wave sleep and re-plays during REM state dreaming.

There is striking experimental evidence for the role of novel, surprising and unusual qualia in turning on experience-dependent gene expression and brain plasticity during REM dreaming. When experimental animals experience a day lacking new activity, novel stimuli or challenges the arc and zif-268 genes that generate brain plasticity do not turn on.<sup>69-72</sup> More recently Ribeiro has updated the entire field of sleep-dependent brain plasticity and the cortical-hippocampal circuits with these questions.<sup>70</sup>

Many intriguing questions about the mechanisms of sleep-dependent plasticity remain completely or partially unanswered. What is the exact role played by dopamine? Is acetylcholine, highly abundant during REM, also involved? What is the role of cortisol? What kind of neuronal and local field potential activity is necessary to trigger or deactivate the cAMP/PKA pathway during sleep? How are synapses tagged by waking experience for subsequent sleep plasticity? What is the contribution of these mechanisms for the displacement of memory traces across hippocampo-cortical circuits? (p. 120)

**A PSYCHOSOCIAL GENOMIC MODEL of PSYCHOTHERAPY**  
**Novel Qualia Induced Mind-Brain-Gene Dialogues of Sleep & Dreams**  
**Selectively Activate the Arc & Zif-268 Genes for Brain Plasticity.**

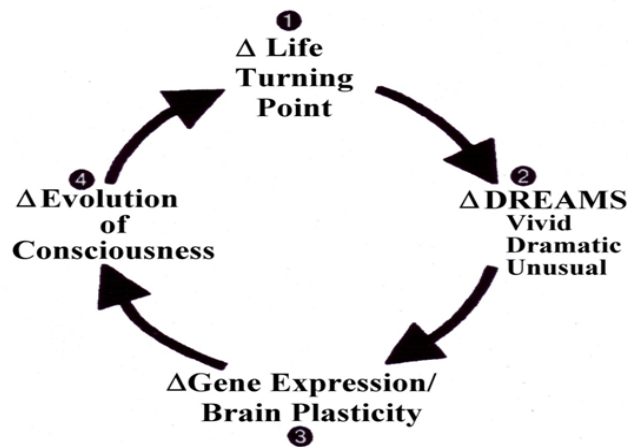


7

Figure 6. The brain pathways that are engaged during REM dreaming. The arrows signify the natural mind/gene search algorithms operative during molecular-genomic dialogues initiated by the various areas of the cortex with the hippocampus. The psychosocial genomic approach to psychotherapy is modeled on these natural RNA/DNA dynamics of experience-dependent gene expression in REM Dreaming in response to novel qualia during the previous waking period.<sup>69,70</sup>

Figure 7 illustrates how the intense qualia of important life turning points in real life (adolescence, marriage, divorce, trauma, war, etc.) are associated with vivid dreams, which turn on experience-dependent gene expression, brain plasticity and the adaptive reframing of personal consciousness.

**The Qualia of Life Turning Points & Vivid Dreams Turn On Activity & Experience Dependent Gene Expression that facilitates the Evolution of New Consciousness.**



8

Figure 7. The cyclic dynamics of the qualia of significant life turning points that tend to activate vivid, dramatic and unusual dreams associated with experience-dependent gene expression and brain plasticity that generates adaptive transformations of human consciousness and cognition.<sup>4,5,14</sup>

Figure 8 illustrates the axioms of Galois group theory as an adaptive algorithm that underpins the activity-dependent genomics of cognition in the interplay between mathematics and the narratives we tell ourselves at important life turning points.<sup>73</sup>

### Axioms of Galois Group Theory Re-Visioned as an Adaptive Algorithm for Facilitating Transformations of Human Consciousness.

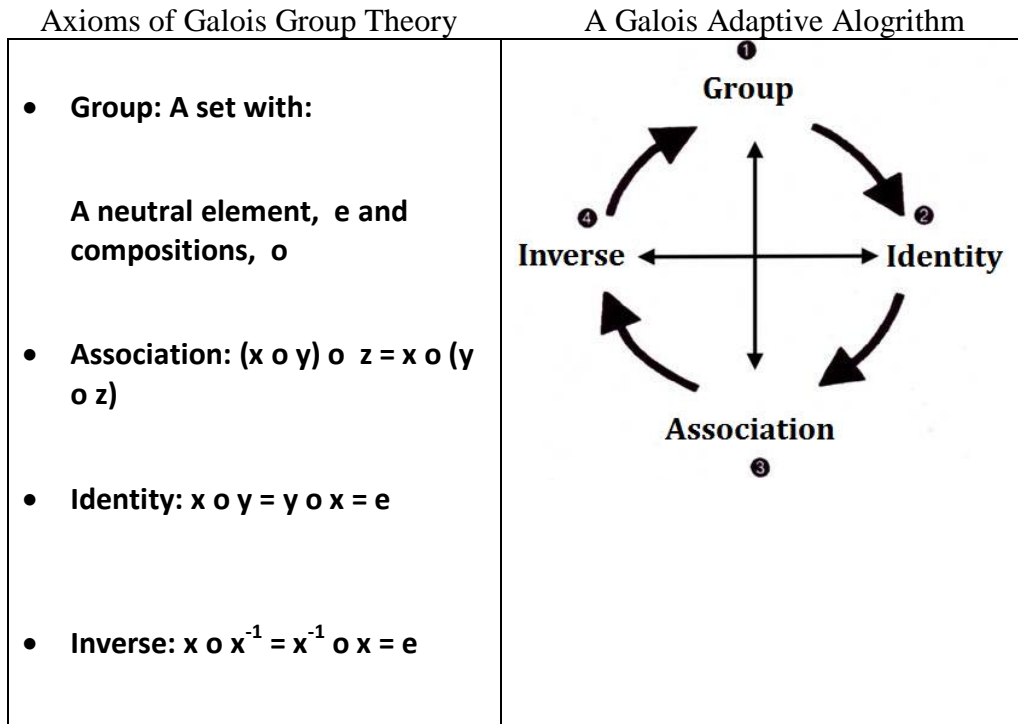


Figure. 8. Galois Group Theory Re-Visioned as Adaptive Transformations of Human Consciousness Via Mind/Gene Search Algorithms.<sup>4,13</sup>

The four basic axioms of Galois Group Theory are used in understanding the solutions of equations in higher mathematics in a manner somewhat analogous to Euclid’s axioms in proving the theorems of geometry. Modern Galois group theory has been called, “the supreme art of abstraction”<sup>74</sup> The linear list of Galois axioms in the left-hand column of figure 8 deals with sets of anything (numbers, psychological concepts, suggestions, etc.) with a very general notation for composing relations between elements of the sets. These axioms are re-visioned as a circular dynamic algorithm in the right-hand column. We can use such algorithms for integrating many of the *psycho-analytic* (Freudian) and *psycho-synthetic* (Jungian) dynamics to facilitate the “transcendent function” (bridging the conscious and unconscious) for resolving the “*problem of the opposites*” during stressful mental experience via qualia and experience-dependent gene expression and brain plasticity.<sup>3,4,13</sup>



**Qualia of the Creative Psychosocial Genomics Via Transformations of Human Consciousness During Mind-Body Healing.**

Figure 9 is an overview of the therapeutic applications of a new protocol, the “*Creative Psychosocial Genomics Healing Experience*,” for facilitating problem solving and mind/body healing in psychotherapy and translational medicine via the core RNA/DNA psychogenomic theory of adaptive consciousness.<sup>4</sup>

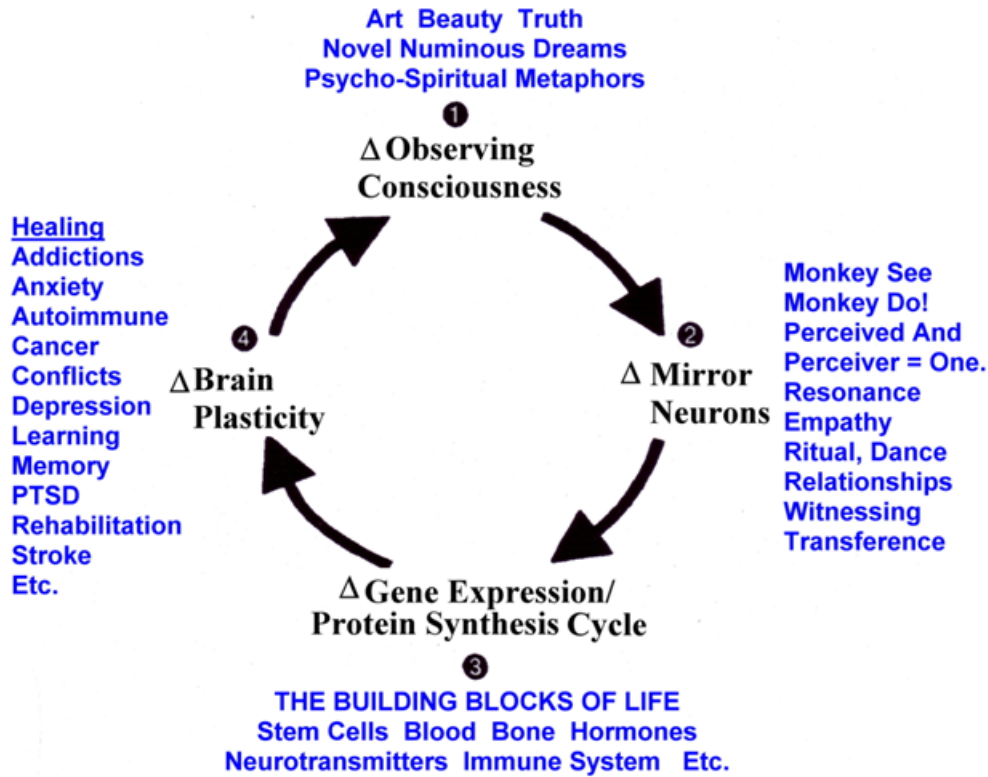


Figure 9. An Overview of the Transformations of Human Consciousness Via The Creative Psychosocial Genomic Healing Experience.<sup>4, 5, 14</sup>

Figure 10 is a simple model of the experimental/experiential quest for therapeutic mind/gene search algorithms in the Evolutionary RNA/DNA Psychogenomic Theory of Adaptive Consciousness that could guide students, researchers and therapists.

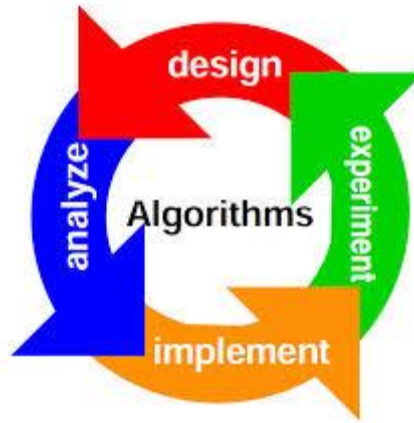


Figure 10. A Model for Mind/Gene Search Algorithms useful for facilitating the evolutionary RNA/DNA psychogenomic theory of the transformations of human consciousness, stress reduction and healing that corresponds well with the 4-stage creative cycle <https://www.google.com/search?q=search+algorithm>.

Models for Mind/Gene Search Algorithms suggested by Figure 10 are the self-rewarding psychogenomic essence of the 4-stage creative cycle. They are the motivational essence of the 4-stage creative process because it feels good to experience them. It is now a researchable project to determine if they are also, from a behavioral epigenetic perspective, a phenotype of the human accelerated region (HARs)<sup>75-84</sup>

### Summary and Conclusions

Life apparently began in *RNA World* about 4 billion years ago with *RNA specializing as a signaling molecule* between the environment and *DNA, which functioned as the specialized memory molecule* of life. This co-evolutionary epigenomic RNA/DNA development is the origin of the current psychogenomic RNA/DNA theory of the transformations of human consciousness and our quest for therapeutic mind/gene search algorithms. This brief review of the evolutionary source of mind/gene search algorithms documents how they can function as the self-rewarding underpinning of the natural 4-stage basic rest-activity cycle every 90-120 minutes throughout the 24 hour circadian day. It feels good to experience these ubiquitous and universal qualia of human search behavior. They are the motivational essence of the 4-stage creative process for problem solving and mind/body healing in counseling, neuroscience, psychotherapy, psychiatry and translational medicine.

In this sense they are the psychosocial genomic integrations between mind, nature and nurture that resolve the Cartesian philosophical problems of artificially separating mind, body and matter. It is now important to determine if mind/gene search algorithms are also the phenotypes of the human accelerator regions (HARs) that underpin many of the advanced qualia of consciousness as well as psychological attitudes, behaviors, emotions, traits and subjective experiences.

Current research documents the use of DNA microarrays for assessing a variety of top-down mind/gene search algorithms of consciousness that were originally given many different pre-scientific names by many diverse cultural, historical and spiritual traditions of mind-body healing. We now need more inclusive cognitive-behavioral data bases and psychosocial genomic software, which could integrate psychological and biological search terms for guiding future theory, research and therapeutic practice of facilitating transformations of human consciousness in psychology, psychotherapy, psychiatry and translational medicine.



## References

1. Huxley, A. (1946). *The Perennial Philosophy* (1st. ed.). London: Chatto & Windus.
2. Stonier, T. (1990). *Information and the internal structure of the universe: An exploration into informational physics*. NY: Springer-Verlag.
3. Rossi, E. (2002). *The Psychobiology of Gene Expression: Neuroscience and Neurogenesis in Hypnosis and the Healing arts*. NY: W.W. Norton.
4. Rossi, E. (2012). *Creating Consciousness: How Therapists Can Facilitate Wonder, Wisdom, Truth and Beauty: The Selected Papers of Ernest Lawrence Rossi, Vol. 2*. Phoenix: AZ., The Milton H. Erickson Foundation Press.
5. Rossi, E. (2007). *The Breakout Heuristic: The New Neuroscience of Mirror Neurons, Consciousness and Creativity in Human Relationships: Vol. 1, Selected Papers of Ernest Lawrence Rossi*. Phoenix, AZ: The Milton H. Erickson Foundation Press.
6. Teilhard de Chardin, P. (1955/1959). *The Phenomenon of Man*. NY: Harper & Row.
7. Bucke, M. (1901). *Cosmic Consciousness: A Study in the Evolution of the Human Mind*. NY: Innes & Sons, Penguin Books.
- 8a. Lahiri, S. (2000) in Chatterjee, A.K. (2000). *Purana Purusha: Yogiraj Sri Shama Churn Lahiree (A Complete Biography)*. Kolkata, India: Yogiraj Publication.
- 8b. Lahiri, S. (1991) in Giri, S. (1991). *The Bhagavad Gita Interpretations of Lahiri Mahasay. Complete Works of Lahiri Mahasay, Vol. 2*. ISBN 1-877854-16-6, The Sanskrit Classics, P.O. Box 5368, San Diego, CA, 92165.
- 8c. Lahiri, S. (2009) in Wyder, H. (2003/2009). *Footsteps to Freedom: Four Spiritual Masters of Kriya Yoga and a Beginner*. UK: Kriya Source Publishing, printed by Lulu.com.
9. Jung, C. (1958). *Psychology and Religion. Bollingen Series XX, Vol 11*. NY: Bolingen Foundation.
10. Hofstadter, D. (1979). *Gödel, Escher, Bach: An Eternal Golden Braid*. NY: Basic Books.
11. Hofstadter, D. (1985). *Metamagical Themes: Questing for the Essence of Mind and Pattern*. NY: Bantam Books.
12. Poundstone, W. (1985). *The Recursive Universe: Cosmic Complexity and the Limits of Scientific Knowledge*. Chicago: Contemporary Books.
13. Rossi, E. (2004). *A Discourse with Our Genes: The psychosocial and cultural genomics of therapeutic hypnosis and psychotherapy*. Available in English and Italian. (ISBN –89396-01-6) San Lorenzo Maggiore, Italy: Editris s.a.s. Phoenix, Arizona: Zeig, Tucker and Theisen.
14. Rossi, E. and Rossi, K. (2013). *Creating New Consciousness in Everyday Life: The Psychosocial Genomics of Self-Creation. A Video eBook available @ Amazon.com*. Los Osos, CA: The Psychosocial Genomic Institute of the Central California Central Coast.
15. Vedral, V. (2010). *Decoding Reality: The Universe as Quantum Information*. NY: Oxford University Press.
16. Atkins, J., Gesteland, R., & Cech. (2011). *RNA Worlds: From Life's Origins to Diversity in Gene Regulation*. NY: Cold Spring Harbor Laboratory Press.
17. Cech, T. (2011). The RNA worlds in context. In Atkins, J., Gesteland, R., & Cech. (2011). *RNA Worlds: From Life's Origins to Diversity in Gene Regulation*. NY: Cold Spring Harbor Laboratory Press.
18. Gilbert, W. (1986). Origin of Life: The RNA World. *Nature*, 319. 618.
19. Darnell, J. (2011). *RNA: Life's Indispensable Molecule*. NY: CSH Press.
20. Yarus, M. (2010). *Life from an RNA World: The Ancestor Within*. Cambridge, MA: Harvard University Press.
21. Breaker, R. (2011). Riboswitches and the RNA World. In Atkins, J., Gesteland, R., & Cech (Eds.). *RNA Worlds: From Life's Origins to Diversity in Gene Regulation*. NY: CSH Press pp. 63-77.
22. Campbell, J. (1949). *Hero with a Thousand Faces*. NY: Pantheon.

23. Berlinski, D. (2000). *The Advent of the Algorithm: The 300-Year Journey from an Idea to the Computer*. Orlando, FL: Harcourt.
24. Sedgewick, R. and Wayne, K. (2011, 4<sup>th</sup> Edition). *Algorithms: What Every Serious Programmer Needs to Know*. NY: Addison-Wesley.
25. Hadamard, J. (1945). *An essay on the psychology of invention in the mathematical field*. NY: Princeton University Press.
26. Meekum, B. (2002). *Dance Movement Therapy: Creative Therapies in Practice*. London: Sage. *Nature* 443, 167-172 (14 September 2006)
27. Rossi, E. (1986). *The Psychobiology of Mind-Body Healing: New Concepts of Therapeutic Hypnosis* NY: W.W. Norton.
28. Rossi, E. (1996). *The Symptom Path to Enlightenment*. Los Osos, California: Palisades Gateway Publishing. Kathryn@ErnestRossi.com.
29. Crick, F. (1970). Central dogma of molecular biology. *Nature*, 227, 561-563.
30. Rossi, E. and Rossi, K. (2014). Opening the Heart and Mind with Single Session Psychotherapy and Therapeutic Hypnosis: A Final Meeting with Milton H. Erickson, M.D. in *Capturing the Moment: Single-Session Therapy and Walk-In Services*. VT: Crown House Publishers.
31. Eisen, M., Spellman, P., Brown, P. and Botstein, D. (1998). Cluster analysis and display of genome-wide expression patterns. *PNAS*. 95, (25), 14863-14868.
32. Cole, S. (2009). Social regulation of human gene expression. *Current Directions in Psychological Science*, 18, 132-137.
33. Cole, S., Yan, W., Galic, Z., Arevalo, J., Zack, J. (2005). Expression-based monitoring of transcription factor activity: the TELiS database. *Bioinformatics*, 21, 803–810.
34. Cole, S., Hawkey, L., Arevalo, J., Sung, C., Rose, R., Cacioppo, J. (2007). Social regulation of gene expression in human leukocytes. *Genome Biology*, 8, R189–R189.13.
35. Cole, S., Arevalo, J., Takahashi, R., et al. (2010). Computational identification of gene–social environment interaction at the human IL6 locus. *Proc. Natl. Acad. Sci.* 107, 5681–5686.
36. Cole, S., Hawkey, L., Arevalo, J., Cacioppo, J. (2011). Transcript origin analysis identifies antigen-presenting cells as primary targets of socially regulated gene expression in leukocytes. *Proc. Natl. Acad. Sci.* 108, 3080–3085.
37. Dusek, J., Otu, H., Wohlhueter A., et al (2008). Genomic Counter-Stress Changes Induced by the Relaxation Response. *PLoS ONE* 3(7): e2576. doi:10.1371/journal.pone.0002576.
38. Atkinson, D., Iannotti, S., Cozzolino, M., Castiglione, S., Ciatelli, A., Vyas, B., et al. (2010). A new bioinformatics paradigm for the theory, research, and practice of therapeutic hypnosis. *American Journal of Clinical Hypnosis*, 53 (1), 27-46.
39. Cozzolino, M., Tagliaferri, R., Castiglione, S., et al. (In Press, February 2014). The New Mind-Body Healing Experience (MHE). In Rossi, E., Erickson-Klein, R. & Rossi, K. (Editors), *The Collected Works of Milton H. Erickson*, Phoenix, Arizona: The Milton H. Erickson Foundation Press.
40. Lichtenberg, P., Bachner-Melman, R., Gritsenko, I., and Ebstein, R. (2000). Exploratory Association Study between catechol-O-methyltransferase (COMT) high/low enzyme activity polymorphism and Hypnotizability. *American J. Medical Genetics*, 96, 771-774.
41. Lichtenberg, P., Bachner-Melman, R., Ebstein, R., Crawford, H. (2004). Hypnotic Susceptibility: Multidimensional Relationships with Cloninger's Tridimensional Personality Questionnaire, COMT polymorphisms, absorption, and attentional characteristics. *International Journal Clinical of Experimental Hypnosis*, 52, 47-72.
42. Creswell, J., Irwin, M., Burklund, L., Lieberman, et al. (2012). Mindfulness-Based Stress Reduction training reduces loneliness and pro-inflammatory gene expression in older adults: A small randomized controlled trial. *Brain, Behavior, and Immunity*, DOI: 10.1016/j.bbi.2012.07.006.
43. Sliwinski, J. and Elkins, G. (2013). Enhancing placebo effects: insights from social psychology. *American Journal of Clinical Hypnosis*. 55: 236-248.

44. Lavretsky, H., Epel, E., Siddarth, P., et al (2013). A pilot study of yogic meditation for family dementia caregivers with depressive symptoms: effects on mental health, cognition, and telomerase activity. *Int. J. Geriatric Psychiatry*. 28(1):57-65.
45. Unternaehrer, E., Luers, P., Mill, J., Dempster, E., Meyer, A., Staehli, S., et al. (2012). Dynamic changes in DNA methylation of stress-associated genes (OXTR, BDNF) after acute psychosocial stress. *Translational Psychiatry*, 2, e150, doi:10.1038/tp.2012.77.
46. Insel, T. (2009). Disruptive insights in psychiatry: Transforming a clinical discipline. *Journal of Clinical Investigation*, 119 (4), 700-705.
47. Insel, T. (2010). Faulty circuits. *Scientific American*, 302 (4), 44-51.
48. Insel, T. (2012). Next-generation treatments for mental disorders. *Science Translational Medicine*, 4, Issue 155, p.155 ps19.
49. Iacoboni, M. (2008). *Mirroring People: The New Science of How We Connect with Others*. NY: Farrar, Straus and Giroux.
50. Rizzolatti, G. & Sinigaglia, C. (2008). *Mirrors in the Brain: How Our Minds Share Actions and Emotions*. NY: Oxford University Press.
51. Benedetti, F. (2009). *Placebo Effects: Understanding the Mechanisms in Health and Disease*. NY: Oxford University Press.
52. Mitchell, M. (2009). *Complexity: A Guided Tour*. NY: Oxford University Press.
53. Kim, T., Hemberg, M., et al. (2010). Widespread transcription at neuronal activity-regulated enhancers. *Nature*, 465, 182-187.
54. Ren, B. (2010). Transcription: Enhancers make non-coding RNA. *Nature*, 465, 173-174.
55. Warren, W., Clayton, D. et al. (2010). The genome of a songbird. *Nature*, 464, 757-762.
56. Saey, T. (2010). First songbird genome arrives. *Science News*, 177(9), 16.
57. Culler, S., Hoff, K., & Smolke, C. (2010). Reprogramming cellular behavior with RNA controllers responsive to endogenous proteins. *Science*, 330, 1251-1255.
58. Wang, X., Song, X., Glass, C., & Rosenfeld, M. (2011). The long arm of long noncoding RNAs: Roles as sensors regulating gene transcription programs. In Atkins, J., Gesteland, R., & Cech (Eds.). *RNA Worlds*. NY: Cold Spring Harbor Laboratory Press, pp. 279-292.
59. Lloyd, D. & Rossi, E. (Eds.) (1992). *Uladian Rhythms in Life Processes: An Inquiry into Fundamental Principles of Chronobiology and Psychobiology*. NY: Springer-Verlag.
60. Lloyd, D. & Rossi, E. (Eds.) (2008). *Uladian Rhythms From Molecules to Mind: A New Vision of Life*. NY: Springer.
61. Pollard K., Salama S., Lambert, N., et al. (2006). An RNA gene expressed during cortical development evolved rapidly in humans. *Nature*, 443 (7108): 167-172.
62. Pollard, K. (2012). The genetics of humanness. What makes us human? Answers from evolutionary anthropology. In Calcagno, J. and Fuentes, F. (Eds.) *Evolutionary Anthropology* 21: 184.
63. Matthews, L. and, Butler, P. (2011). Novelty-seeking DRD4 polymorphisms are associated with human migration distance out-of-Africa after controlling for neutral population gene structure. *Am. J. Phys. Anthropol.* 145(3):382-9.
64. Kluger, J. with Aciman, A. and Steinmetz, K. (2013). The Pursuit of Happiness. *Time*, (cover story), 24-32.
65. Rossi, E. and Nimmons, D. (1991). *The Twenty-Minute Break: The Uladian Healing Response*. NY: Zeig, Tucker, Theisen.
66. Cheung, M., Chavez, L., and Onuchic, J. (2004). The energy landscape for protein folding and possible connections to function. *Polymer*, 45, 547-555
67. Levisky, J., Shenoy, S., Pezo, C., and Singer, R. (2002). Single-cell gene expression profiling. *Science*, 297, 836-840.
68. Otto, R. (1923/1958). *The Idea of the Holy*. NY: Oxford University Press.

69. Riberio, S., Simões, C. & Nicolelis, M. (2008). Genes, Sleep and Dreams. *In Lloyd & Rossi (Eds.) Ultradian rhythms from molecule to mind*. NY: Springer. 413-430.
70. Ribeiro S. (2012). Sleep and plasticity. *Pflugers Arch*. 463(1):111-20.
71. Rossi, E. (1972/1986/2000). *Dreams, Consciousness & Spirit: The Quantum Experience of Self-Reflection and Co-Creation*. (3<sup>rd</sup> Edition of Dreams & the Growth of Personality). NY: Zeig, Tucker, Theisen.
72. Rossi, E., Erickson-Klein, R. & Rossi, K., (2008-2014). *The Collected Works of Milton H. Erickson, M.D. (16 Volumes)*. Phoenix: The Milton H. Erickson Foundation Press.
73. Doxiadis, A. and Mazur, B. (2012). *Circles Disturbed: The Interplay of Mathematics and Narrative*. Princeton, N.J.: Princeton University Press.
74. King, J. (1992). *The Art of Mathematics*. NY: Plenum Press.
75. O'Connor, T., and Mundy, T. (2013). Evolutionary Modeling of Genotype-Phenotype Associations, and Application to Primate Coding and Non-coding mtDNA Rate Variation. *Evolutionary Bioinformatics*, 9, 301-315.
76. Moriam, S. and Sobhani, M. (2013). Epigenetic Effect of Chronic Stress on Dopamine Signaling and Depression. *Genetics & Epigenetics*, 5, 11–16.
77. Trollope, A., Gutiérrez-Mecinas, M., Mifsud, K., Collins A, Saunderson, E. & Reul, J. (2012). Stress, epigenetic control of gene expression and memory formation. *Exp. Neurology*. 233(1):3-11.
78. Miller, G. (2010). The Seductive Allure of Behavioral Epigenetics. *Science*, 329 (5987), 24-27.
79. Maya-Vetencourt, J. (2013). Activity-Dependent *NPAS4* Expression and the Regulation of Gene Programs Underlying Plasticity in the Central Nervous System. *Neural Plasticity*, <http://dx.doi.org/10.1155/2013/683909>, 1-12.
80. Venter, B. & Pugh, F. (2013). Genomic Organization of Human Transcription Initiation Complexes. *Nature*, 502, 53-58.
81. Pyle, A. (2013). Non-coding RNA in Systems. *Journal of Molecular Biology*. Vol. 425, (19), 3577-3746. **This entire issue of JMB is devoted to Non-Coding RNA/DNA Dynamics.**
82. Doxiadis & Mazur. (2012). *Circles Disturbed: The Interplay of Math & Narrative*. Princeton Univ. Press.
83. Frenkel, E. (2013). *Love & Math: The Heart of Hidden Reality*. NY: Basic Books.
84. Cozzolino, M. *et al.* (2014, In Press). The Mind-Body Healing Experience (MHE) is associated with Gene Expression in Human Leukocytes. *International Journal of Physical and Social Sciences*.