Expectations of Hypnosis Future: A New Neuroscience School of Therapeutic Hypnosis, Psychotherapy, and Rehabilitation

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Abstract:
We outline our expectations for a new bioinformatic and neuroscience of therapeutic hypnosis, psychotherapy, and rehabilitation based on the Human Genome Project. Just as The Human Genome Project identified the psychobiological foundations of modern medicine with the new technology of sequencing DNA during the past decade, we propose extending this bioinformatic knowledge base with the technologies of DNA/proteomic microarray research and brain imaging. We would implement this research program with an International PsychoSocial and Cultural Bioinformatics Project to explore the clinical foundations of therapeutic hypnosis, psychotherapy, and rehabilitation on all levels from the molecular-genomic to the psychological, cultural, social, and spiritual.

Key Words:
Bioinformatics, brain plasticity, psychosocial genomics, psychotherapy, rehabilitation, therapeutic hypnosis.

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Those who cannot outgrow

Limitations of Paradigms Past

Forever are constrained by them.

Introduction

An excellent review on "Remembrance of Hypnosis Past" by Kirsch & Mazzoni (2006) inspires us to write this complementary paper on our "Expectations of Hypnosis Future." We accept as axiomatic the prescient statement by Kirsch & Mazzoni, "Perhaps, someday, neurophysiological markers of a hypnotic state will be found, and perhaps they will be found to be a necessary precursor for the experience of a least some suggestive phenomena (Kallio & Revonsuo, 2003)." We believe that the "neurophysiological markers of a hypnotic state," and indeed, all salient psychosocial states of consciousness which Kirsch & Mazzoni describe, are currently being mapped by the emerging sciences of bioinformatics and neuroscience. This motivates us to outline a few principles of research that we are exploring in our new neuroscience school of therapeutic hypnosis, psychotherapy, and rehabilitation in the healing arts.

Discussion

1. Bioinformatics and neuroscience are developing empirical databases for bridging the Cartesian dichotomy between mind and body for the next generation of innovation in therapeutic hypnosis, psychotherapy, and rehabilitation.

The psychosocial bioinformatics cycle of figure one (below) provides an overall impression of the major circular pathways of information transduction between novel and enrichening experiences of (1) Observing Consciousness, (2) Mirror Neurons, (3) the Gene Expression/Protein Synthesis Cycle and (4) Brain Plasticity (Rossi, 2002, 2004a,b,c; Rossi & Rossi, 2006).

We believe the mind-body map of psychosocial bioinformatics broadly painted in figure one is consistent with Kirsch & Mazzoni statement of the basic axiom of research in hypnosis.

> "Hypnotic suggestion produces some pretty remarkable effects, including involuntary movements, partial paralyses, memory distortions, hallucinations, and profound analgesia. Initially, this was thought to be the result of magnetism. Later, it was at-

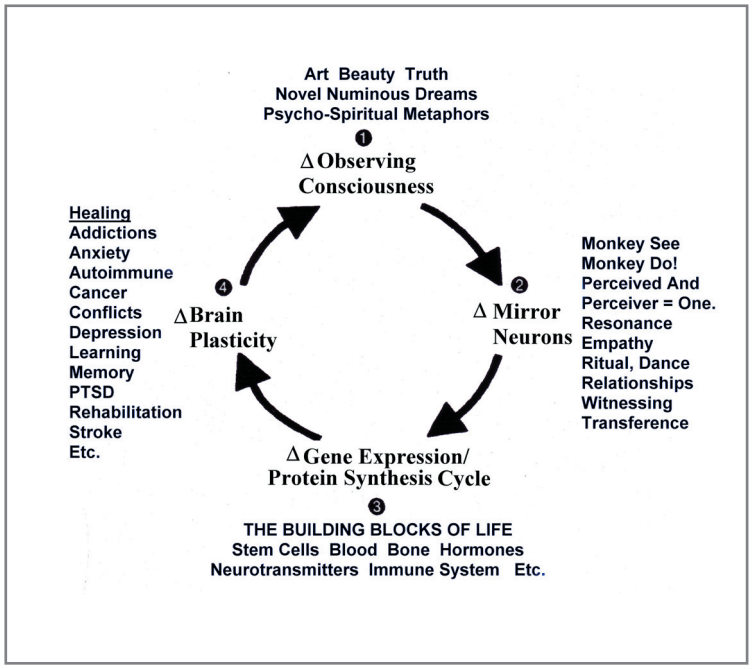

Fig. 1. The Psychosocial Bioinformatic Cycle of Information Transduction Between Observing Consciousness, Mirror Neurons, the Gene/Expression Protein Synthesis Cycle, and Brain Plasticity (Rossi, 2007 In Press).

> tributed to the induction of a trance state. Later still, first clinicians, and then researchers, reported that the same responses could be obtained without the induction of hypnosis. This discovery generated a basic axiom of research in hypnosis: *'No behavior following hypnotic induction can be attributed to hypnosis unless the investigator first knows that the response in question is not likely to occur outside of hypnosis in the normal waking state.'* (Sheehan & Perry, 1976, p. 55)

Current research in bioinformatics and neuroscience documents how heightened experiences of art, beauty, and truth can stimulate (1) Observing Consciousness, which activates (2) Mirror Neurons and associated experiences of empathy, transference, and rapport to turn on their (3) Gene Expression/Protein Synthesis Cycle to create the Building Blocks of Life, which generate (4) Brain Plasticity and the possibility of healing many body dysfunctions on the molecular-genomic level Rossi, 2004a,b,c). Note the self-perpetuating nature of the basically positive biofeedback cycle in figure one: every cycle leads to the possibility of another round of observing consciousness, which in turn activates another iteration of activity-dependent gene expression, brain plasticity, and the possibility of mind-healing (Rossi, 2007 in press).

This entirely normal mind-body loop of communication, self-creation, and healing of figure one that cycles every ~90 – 120 minutes throughout the ~ 24 hour circadian day in humans, is a symphony of integrated life processes, which future research may recruit as the natural neurophysiological markers of a hypnotic state (Rossi, 2002, 2004a,b,c, 2005a,b,c). Stress, trauma, malfunctions, and diseases of all sorts can disrupt the natual bioinformatic periodicity of figure one leading to illness (Lloyd & Rossi, 1992/2008; Rossi & Nimmons, 1991). New research models are required to demonstrate how each of the four stages of the psychosocial bioinformatics cycle of figure one may be a widow of opportunity for therapeutic suggestion to access and facilitate our inner resources for mind-body healing. We will briefly summarize the types of current bioinformatic and neuroscience data that are consistent with this prospect of a program of research that could implement our expectations for a more efficacious therapeutic hypnosis in the future.

2. What Makes Us Human? Heightened levels of psychosocial behavior activate elevated levels of neuronal activity, gene expression, and brain plasticity that distinguish human brains from other primates.

There is an explosion of bioinformatic research that is clarifying the differences between humans and other primates that profoundly expands our understanding of how we may access and utilize the potentials implied in the psychosocial bioinformatics cycle figure one. Ponting and Lunter (2006), for example, describe the current research frontier exploring how the human brain is different from other primates as follows.

> "So which parts of our genome have seen the most change, and are these genomic innovations linked directly to our unique brain structure and function? . . . Pollard et al (2006) describe how they have clocked the speed at which various human genome regions have changed in recent times. The clear winner of this race is human accelerated region 1 (HAR1), part of an RNA gene whose pattern of expression is suitably poised to influence the migration of neurons in the developing cortex. The authors' second and equally important finding is that all but two of the most-accelerated regions lie outside protein-coding sequences — in the enigmatic 'dark matter' of the human genome. . . Their study reveals a set of 49 regions (HAR1–HAR49), each with a sequence that is highly evolutionarily conserved among many mammals, but that has diverged rapidly in humans since our last common ancestor with chimpanzees. How might these extraordinary changes be linked to the human brain's increased cognitive capabilities? The first clue came from the finding that HAR1F, one of two RNA genes containing HAR1, is expressed in the developing neocortex in the brains of humans and in those of another primate,

the crab-eating macaque. This is intriguing, as the neocortex is most often associated with higher cognitive functions.

HARs seem to be particularly rare in protein-coding sequences. Instead, they often lie near protein-coding genes that have neuro-developmental functions, perhaps within regions that are involved in regulating when and where these genes are turned on. Rapid human-specific evolution, and particularly the evolution of brain morphology and of behavioural traits, may thus be associated more with fine-tuning the spatial and temporal expression of protein-coding genes than with altering the molecular functions of their encoded proteins." (p. 149-150).

Cáceres et al. (2003) summarize their research in this area in an even more intriguing manner as follows.

"To investigate the genetic basis of human specializations in brain organization and cognition, we compared gene expression profiles for the cerebral cortex of humans, chimpanzees, and rhesus macaques by using several independent techniques. We identified 169 genes that exhibited expression differences between human and chimpanzee cortex, and 91 were ascribed to the human lineage by using macaques as an outgroup. Surprisingly, most differences between the brains of humans and nonhuman primates involved up-regulation, with ~90% of the genes being more highly expressed in humans . . . *The increased expression of these genes could provide the basis for extensive modifications of cerebral physiology and function in humans and suggests that the human brain is characterized by elevated levels of neuronal activity.*" (p. 13030, italics added)

Such research implies that DNA microarrays may be more sensitive, comprehensive, and reliable measures of psychological experiences and states of consciousness, emotions, behavior, and brain plasticity in stress, injury, disease, and psychotherapy in general. It is currently believed that subjective states that have been difficult to measure objectively may all have their own distinct profiles of gene expression on highly quantifiable molecular levels. Cáceres et al. (2003), for example, go on to describe how elevated gene expression levels that differentiate human from non-human primate brain functioning actually generate heightened neuronal activity as the substrate of consciousness and cognition.

"The identification of the genes that exhibit regulatory changes in adult human cortex provides clues to the biochemical pathways and cell-biological processes that were modified during evolution. *The apparent up-regulation of so many different genes suggests, among other things, that the general level of neuronal activity and the metabolic processes that support it may be unusually high in human cortex.* . . .Recent studies with imaging techniques to measure cerebral glucose metabolism in the conscious state suggest that metabolic rates are as high or even higher in humans than in macaques. *Higher levels of neuronal activity are likely to have important consequences in cognitive and behavioral capacities, and of the genes up-regulated in humans*" (pp. 13034, italics added here)

At the present time here is a considerable gap between the research literature in current bioinformatics, neuroscience, and the clinical applications of therapeutic hypnosis, psychotherapy, and rehabilitation. How can we bridge this gap?

3. Expectations of New Research Paradigms for Hypnosis Future: A new generation of factor analytic studies integrating the psychosocial bioinformatics cycle with traditional scales of hypnotic susceptibility?

We believe a very important updating is now required in our standardized scales of hypnotic susceptibility and related subjective psychological states mentioned by Kirsch & Mazzoni, such as the Tellegen Absorption Scale (http://socrates.berkeley.edu/~kihlstrm/TAS.htm). We need to update our paradigms of "Remembrance of Hypnosis Past" with the emerging databases of bioinformatics and neuroscience of the present and future that associate heightened states of psychosocial behavior with heightened

states of gene expression, neuronal activity, brain plasticity, as well as new profiles of sleep, dreaming, and creative consciousness (Ribeiro, 2004; Ribeiro et al., 1999, 2002, 2004; Rossi, 1972/2000; Rossi, 2007, in press).

In brief, we need a new generation of factor analytic studies relating our psychosocial scales with (1) microarray technologies for measuring gene expression (genomics) and proteins (proteomics) and (2) brain imaging technologies (fMRI and PET) to evaluate the anatomical location and levels of neuronal activity of the brain to more adequately assess the efficacy profiles of all the therapeutic approaches to behavior, cognition, and healing.

A hint of what we are looking for is illustrated in figure two, which is our greatly simplified graph of a linear relationship between gene expression, brain plasticity, and an easily accessible and quantifiable behavioral index of sleep time that was recently described by Ganguly-Fitzgerald, Donlea, and Shaw (2006).

> "Sleep is critical for survival, as observed in the human, mouse, and fruit fly, and yet, its function remains unclear. Although studies suggest that sleep may play a role in the processing of information acquired while awake, a direct molecular link between waking experience, plasticity, and sleep has not been demonstrated. We have taken advantage of Drosophila genetics and the behavioral and physiological similarities between fruit fly and mammalian sleep to investigate the molecular connection between experience, sleep, and memory.
>
> Sleep is a vital, evolutionarily conserved phenomenon, whose function is unclear. Although mounting evidence supports a role for sleep in the consolidation of memories, until now, a molecular connection between sleep, plasticity, and memory formation has been difficult to demonstrate. We establish Drosophila as a model to investigate this relation and demonstrate that the intensity and/or complexity of prior social experience stably modifies sleep need and architecture. Furthermore, this experience-dependent plasticity in sleep need is subserved by the dopaminergic and adenosine 3',5'-monophosphate signaling pathways and a particular subset of 17 long-term memory genes." (p. 1775)

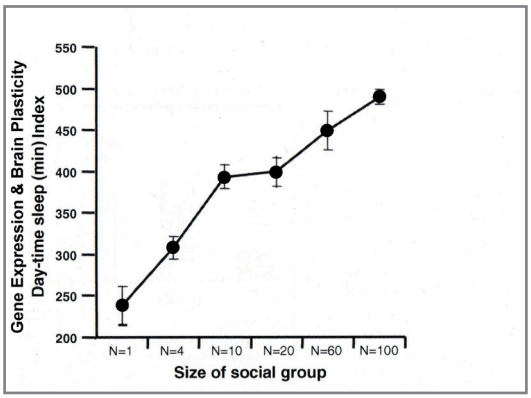

Fig. 2. The Relationship Between Social Group Size, Gene Expression, Brain Plasticity, and an Easily Quantified Behavioral Index of Sleep Need in Drosophila (Modified from Ganguly-Fitzgerald, Donlea, &. Shaw, 2006).

The intensity and/or complexity of prior social experience, which modifies sleep need in Drosophila, is related to the size of the social group as the independent variable on the horizontal axis in figure two. That is, the size of the social group turns on gene expression, brain plasticity, and increased need for daytime sleep in Drosophila. This is a general finding in genomic research: from bacteria to fruit flies and mammals nothing seems to turn on gene expression as much as the presence of another organism of the same species. From an evolutionary perspective we can understand how this association could have selective value for survival. From a historical perspective we recall that impressive demonstrations of hypnosis were frequently staged in front of large groups. It really seems like a bit of a stretch to generalize from sleep need in fruit flies to hypnosis in humans. This hypothesis, however, is entirely consistent with what we might expect from the psychosocial bioinformatics cycle of figure one where a heightened focus of attention and observing consciousness in large social groups leads to a heightening of mirror neuron activity, which in turn generates gene expression and brain plasticity. It is also consistent with the late Carl Rogers' belief that "the size of the professional crowd"

observing his demonstrations of client-centered psychotherapy was an important factor in their success (personal communication with the senior author). Such anecdotal observations, of course, cannot resolve this issue. Updated hypnotic susceptibility scales possibly could

The acute contemporary research issue raised by figure two is how to document similar relationships between gene expression and brain plasticity with a practical index of easily measured behavior in humans such as their responses on paper and pencil tests or the new game-like devices and software that are purported to facilitate brain activity and changes in social attitudes (http://www.nickyee.com). Ganguly-Fitzgerald, Donlea, and Shaw were able to grind up the heads of fruit flies to assess their profiles of gene expression with DNA microarrays, but it might be difficult to find human volunteers for such an experimental approach. Our expectations for hypnosis future is that a new generation of factor analytic studies relating hypnotic susceptibility and psychological scales with DNA microarray and brain-imaging technologies will more adequately assess the efficacy profiles of our clinical approaches to therapeutic hypnosis, psychotherapy, and rehabilitation.

Given some reasonable degree of success in developing an updated psycho-bioinformatic scale of hypnotic susceptibility, we would be in a position to ask what our new theory of therapeutic suggestion would look like.

Figure three outlines one possibility of a psycho-bioinformatic theory of therapeutic hypnosis that would be consistent with the research review presented by Kirsch & Mazzoni (2006) in their Remembrance of Hypnosis Past as well as our Expectations of Hypnosis Future. Therapeutic suggestion and hypnosis as illustrated in figure three would be recognized as one example of the more general psychosocial bioinformatic cycle of information transduction between observing consciousness, mirror neurons, gene expression, and brain plasticity presented above in figure one. Notice how figure three identifies Weitzenhoffer's (2000) Ideodynamic Action Hypothesis of Hypnosis as a generator of the activity-dependent gene expression/protein synthesis cycle, which in turn leads to activity-dependent brain plasticity (synaptogenesis & neurogenesis) in the reconstruction

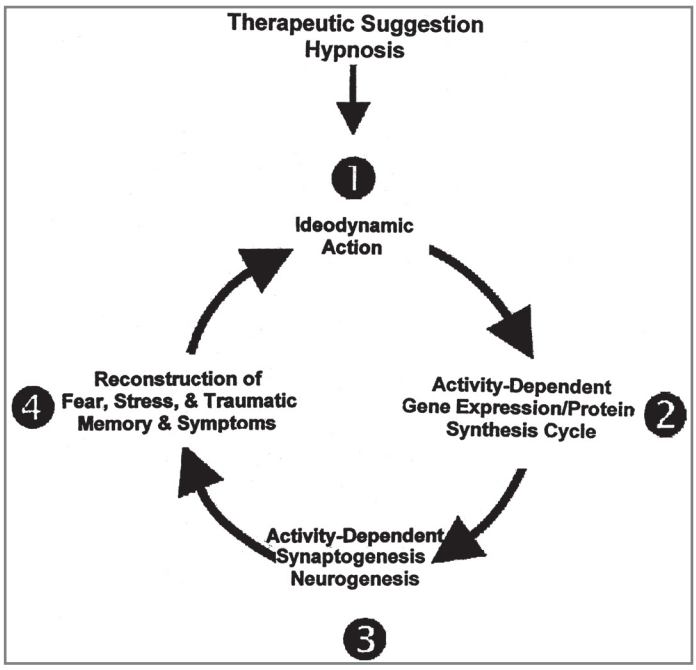

Fig. 3. An illustration of how Weitzenhoffer's Ideodynamic Action Hypothesis of Hypnosis could be upgraded to a Psycho-Bioinformatic Theory of Therapeutic Hypnosis (Rossi, Erickson-Klein, & Rossi, 2006)

of fear, stress, and traumatic memory and symptoms. A more complete discussion of figure three has been presented recently in an essay on How the Mind Heals the Brain (Rossi, Erickson-Klein, & Rossi, 2006).

Summary and Prospects

This paper proposes a bioinformatic and neuroscience approach to therapeutic hypnosis, psychotherapy, and rehabilitation based on the bioinformatics cycle of human experience on all levels from molecular-genomic to brain plasticity, and consciousness in sickness and health. Just as The Human Genome Project identified the molecular foundations of modern medicine with the new technology of sequencing DNA during the past decade, we propose that a new International PsychoSocial and Cultural Bioinformatics Project (IPCBP) could identify the profiles of gene expression and brain plasticity associated with stress, trauma, healing, and rehabilitation. We anticipate that the IPCBP would require a unique collaboration of academic institutions, researchers, and clinicians for a greatly enriched bioinformatics and neuroscience of mind-body healing, brain plasticity, memory, learning, and creative processing during optimal experiences of art, beauty, truth and health as well as therapeutic hypnosis and psychotherapy.

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