Innovations in Educational Psychology
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Innovations in Educational Psychology

Perspectives on Learning, Teaching, and Human Development

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SPRINGER PUBLISHING COMPANY
New York
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More than a decade ago, one of the editors of this book suggested that the field of educational psychology was going through challenging times. He noted that fewer certification programs required courses in educational psychology, relatively few psychologists were involved in initiatives of educational reform, and educational psychology tended to be a marginalized field both in education schools and psychology departments (Sternberg, 1996). Nobody would have expected then that just a decade or so later, issues dealing with education would become so central to several subfields of psychology and related disciplines.

Indeed, over the last decade a number of changes have put educational issues back on the track of basic research. And although the institutional arrangements within many universities may not have necessarily favored this new development, a substantial part of recent educational research has been dealing with what we may consider fundamental scientific questions, such as the nature–nurture debate, the nature of human rationality and intelligence, and the role of culture in human development, among many others. The self-propelled movement of research has triggered some of these changes; others have been triggered by transformations originating outside science.

Thus, new discoveries in genetics and the biological sciences are increasing our understanding of the relation between our innate dispositions and the educational process. Contrary to what we may have expected, these new findings are challenging our understanding of the innate determinants of learning as something static and fixed. On the other hand, many advances in developmental psychology are enriching our understanding of the psychological consequences of schooling; they are also transforming our conception of the learning process and particularly of what we understand by expertise in teaching and learning. In fact, as Sternberg (1996) projected, in recent years the field has experienced an unprecedented growth of studies focused on expert teaching and expert learning (Bransford, Brown, & Cocking, 1999; Torff, 2003;
Not surprisingly, some of these initiatives have rapidly translated into classroom recommendations (Sternberg, 2002; Sternberg & Grigorenko, 2003a). Closely connected to these advances are new developments in both individual-differences and cognitive research, which have made important contributions to our understanding of the context-dependent, dynamic, and multifaceted nature of human abilities (Sternberg & Grigorenko, 2003b).

At the same time, findings from educational research have increasingly become a public issue. A central role has been played by the diverse initiatives of educational accountability, which today, for better or for worse, are blossoming around the world. Whereas the No Child Left Behind Act in the United States has sparked most of the recent accountability debate, in other areas of the world, that debate has been encouraged by the results of comparative studies such as the Trends in International Mathematics and Science Study (TIMSS) or the Program for International Student Assessment (PISA), which are informative of the level of achievement reached by different nations in a number of key educational variables (for some illustrations, see Stigler & Hiebert, 1999; Takayama, 2008). Since many of these initiatives comprehensively engage in implicit or explicit forms of teaching assessment, understanding the nature of teaching has become a hot topic in many latitudes and a challenge of utmost importance not only for researchers but also for makers of public policy.

The impact of globalization is making more common the adoption of a comparative stance in educational research (Grigorenko, Jarvin, Niu, & Preiss, 2007). Correspondingly, the last decade has seen renewed interest in the nature of teaching and how it differs across nations and cultures (Alexander, 2000, 2001; Givvin, Hiebert, Jacobs, Hollingsworth, & Gallimore, 2005; Loera, 2006; Preiss, 2009). Part of this interest has been prompted by the development of highly sophisticated technologies that rest on the use of videos for classroom observation, such as those proposed by advocates for TIMSS during the 1990s (Stigler, Gallimore, & Hiebert, 2000) and adopted by many scholars in other parts of the world (e.g., Loera, 2006).

Last but not least, the last decade has seen the proliferation of new technologies whose potential for teaching and instruction are just starting to be fully explored (Mayer, 2003; Preiss & Sternberg, 2005, 2006). More than a decade ago, data provided by the TIMSS reported a substantially low use of computers in an international sample of eighth-grade lessons: Instead of computers, the instructional materials used often in each country were quite “low-tech” and the chalkboard was still preva-
lent (Stigler, Gonzales, Kawanaka, Knoll, & Serrano, 1999). One decade later, the computerization of schools and use of the Internet has advanced significantly; but still, teacher adoption of the new technologies is a cause of concern for many. What is clear is that, far from the Skinnerian idea that teaching can be entirely replaced by universal machines, the new discoveries advanced during the current decade reveal that teachers play an essential role in mediating and making real the intellectual potential of the new technologies (e.g., see Lin, 2001). Still, our understanding of how the traditional and steady routines of teaching and learning can be transformed by using ever-changing technologies is limited.

Given the situation as we have described it, we believed the time was ripe to produce a collection of some of the new findings that are helping to rekindle interest in educational issues among basic researchers and that also are instrumental to communicating these findings among the general public. Particularly, the purpose of this book is to assemble a collection that reviews the current state of the art in several areas of educational research with a view toward contributions that link teaching, learning, and human development and that are, consequently, naturally interdisciplinary. Thus, we expect that this book will help to publicize a number of findings that have high scientific value but do not necessarily receive the attention they deserve. We further hope it will help to advance research in education by providing a single-volume review of important recent discoveries. Finally, we hope that this book will help make education a more attractive endeavor for future scholars by showing how exciting research in this field can be.

Each chapter includes a review of contemporary discoveries the authors deem to be novel and forward-thinking and that are having a major impact on the field. Each author (or group of collaborators) devotes a substantial part of the review to his or her own work. The review includes the nature of the questions that have been addressed with regard to his or her topic, how these questions originated, how they have been commonly answered, how the author and others have addressed these questions, and how the proposed approach compares to and contrasts with others. Authors have been encouraged to place their reflections in an interdisciplinary context and to relate teaching, learning, and human development. The chapters have been written in a way that is understandable to first-year graduate students in psychology or education and related disciplines. Yet we are sure that the book will appeal to a diverse audience.

The book is organized into five sections. We briefly describe each in turn.
Section I is devoted to new research on individual differences in human development. The first chapter, by Elena L. Grigorenko, Samuel D. Mandelman, Adam J. Naples, and Natalia Rakhlin, discusses what the authors define as “the seemingly eternal but incorrectly posed dichotomous question of genes versus environment” from the point of view of its educational implications. As this chapter illustrates, we may need to go beyond the mere decomposition of variance if we are to understand the dynamic nature of the interactions between genes and environment and what education has to do with it. The second chapter in this section, by Richard K. Wagner and Patricia T. Kantor, is devoted to reviewing recent findings regarding the causes of dyslexia, its identification, and ways to help those individuals affected by it. For many years, dyslexia has drawn attention of researchers for both basic and practical reasons. On the one hand, problems in reading are informative of many basic cognitive processes. On the other hand, as Wagner and Kantor note, the vast majority of students who receive assistance for specific learning disabilities have problems in reading, and problems in reading have long-term effects in human development. So a chapter on dyslexia could not be omitted in a book devoted to the dissemination of new research findings in education.

The second section is devoted to chapters that deal with the complex relation between schooling as a process of deliberate instruction and human development as a process of mental growth, broadly understood.

The first chapter in this section, by Terezinha Núñes and Peter Bry- ant, discusses several insights from everyday knowledge for mathematics education. The authors note that people with little school instruction typically solve proportion problems in everyday life by setting values in one-to-many correspondence across variables. The authors investigated the origin and uses of this schema of reasoning by schoolchildren. This schema often goes unnoticed in school, where multiplication is taught as repeated addition. The chapter therefore discusses the difference between these two conceptions of multiplication. Research shows why one-to-many correspondence reasoning offers a good foundation for teaching children about proportions in school.

The second chapter of this section, by Xiaodong Lin, Robert S. Siegler, and Florence R. Sullivan, describes several studies showing that not all students view learning as their primary goal in school and that students’ goals vary between and within cultures. The authors show that optimizing students’ learning requires attention to learner’s goals and values and that instruction leading students to adopt the goal of deeply
understanding the material that is being taught can produce superior learning.

The third chapter of this section, by K. Ann Renninger, focuses on the critical role of interest in learning and development. Renninger shows that interest will develop when the learning environment seeks to cultivate learner interest in relation to phase of interest, motivational profile, and principled knowledge of content. Learners need to feel that their efforts are respected and to receive ongoing support to recognize, take advantage of, and seek opportunities to think and reengage.

The third section is devoted to studies on what we call the refinement of mind. In the first chapter of this section, James C. Kaufman, Ronald A. Beghetto, and John Baer present a new model of creativity and discuss the phenomenon of creative polymathy. They consider multicroative potential in light of their “Four C” model and offer an alternate possibility to general and domain specific models of creativity by drawing on the Amusement Park Theoretical (APT) model.

The second chapter of this section, written by Lauren Resnick, Sarah Michaels, and Cathy O’Connor, discusses the process of reasoning within classrooms and how children can be taught to give reasons for their answers. The authors introduce methods of creating these competencies of what they call “accountable talk,” which have been tested by the authors within face-to-face, teacher-led learning environments. The authors present results showing that students who learn in classrooms guided by accountable talk standards are socialized into communities of practice in which respectful and grounded discussion prevails.

The third chapter of this section, by Keith E. Stanovich and Paula J. Stanovich, presents a tripartite model of mind that explains why rationality is a more encompassing construct than intelligence. Similarly, the authors subsume the construct of critical thinking under the construct of rationality as well. According to the authors, creating a generic model of the mind that has rationality as an overarching construct, which integrates critical thinking and intelligence, has the considerable benefit of placing the construct of critical thinking within contemporary cognitive science.

The fourth section of the book is devoted to the experiences of teaching and learning and their cultural grounds. The opening chapter of the section, by Alan H. Schoenfeld, describes a model of teaching-in-context, which explains, on a line-by-line basis, decision making by teachers during hour-long classroom lessons. The existence of such models provides tools for examining and improving teaching as well as
the possibility that decision making in other professions can be compara-
ably modeled.

The second chapter of the section, by Carrie Rothstein-Fisch, Pa-
tricia M. Greenfield, Elise Trumbull, Heidi Keller, and Blanca Quiroz,
describes the relevance of the value systems of individualism and collec-
tivism for learning, development, and education. The authors focus their
attention on situations where the home culture of collectivistic children
opposes the individualistic culture of schools, which creates a need for
educational intervention. One such situation is that of Latino children in
the United States. An educational intervention addressing their needs,
the Bridging Cultures Project, is presented.

The third chapter of the section, by Miguel Nussbaum, Florencia
Gomez, Javiera Mena, Patricia Imbarack, Alex Torres, Marcos Singer,
and María Elena Mora, discusses ways of transforming the learning
process into an interactive and collaborative process by using handheld
devices with wireless networks. The authors discuss a methodology for
technology-supported small-group collaborative learning that uses as-
essment to adapt teaching to meet learning needs. They report the re-
results of a detailed qualitative and quantitative study of the methodology,
which demonstrates that communication and social abilities are attained
with an improvement in learning.

The last chapter of the section, by David Preiss, presents a tentative
operationalization of the construct of folk pedagogy, discusses its appli-
cation to a context other than the one where this construct originated,
and presents three empirical illustrations based on studies done in Chile
and inspired by this theoretical framework. Preiss’s results provide clear
support for the hypothesis that there are country-specific patterns of
teaching. Preiss concludes that future public policy initiatives for edu-
cational reform should take into consideration the cultural basis of the
teaching patterns they want to transform and how permeable these pat-
terns are to initiatives originating outside of classrooms.

The last section addresses the old theme of school reform by intro-
ducing three new initiatives in this area. The first chapter of the section,
by Edward Zigler and Matia Finn-Stevenson, describes the School of
the 21st Century (21C), a preschool program that provides not only care
and education for preschoolers but also other family support programs
beginning at the conception of the child and throughout the school
years. This program has been implemented in more than 1,300 schools,
enabling educators to address the needs of children and families. In this
chapter, the authors describe 21C and review its research base, imple-
mentation, and impact, showing how the program is transforming education in the United States.

The second chapter of the section, by Alex Kozulin, focuses on four areas of research with a great potential of use for initiatives of school reform. These are the general conceptualization of the goals and framework of the educational process, the multicultural classroom, the evaluation of students’ learning potential, and emerging research on differences between such fundamental processes as thinking and learning.

The next chapter of the section, by Robert J. Sternberg, advances the WICS model as a possible common basis for the development of skills and attitudes in college. WICS is an acronym standing for wisdom, intelligence, and creativity, synthesized. Wisdom, intelligence, and creativity are sine qua nons for the citizens and professionals of the future and really for anyone who wishes to achieve meaningful success in his or her life. Sternberg discusses each of these attributes and describes methods for developing and measuring the attributes.

In the closing chapter, on the subject of adopting a perspective based on the development of education as a discipline, David R. Olson integrates all the findings presented in this book. He examines the possible ramifications of this work for educational reform, educational practice, and educational research.

David Preiss’s work on the preparation of this book was supported by the Center for Research on Educational Policy and Practice, Grant CIÉ01-CONICYT and Grant Number 11060389 from FONDECYT (Fondo Nacional de Desarrollo Científico & Tecnológico). He dedicates this book to his daughters Ilana and Meital, whom he expects may benefit at their schools, present and future, from practices inspired by good educational research. Bob Sternberg dedicates the book to his graduate advisor, Gordon Bower, who has inspired him throughout his career to apply his ideas from psychology to education.

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Robert J. Sternberg

REFERENCES


Individual Differences in Human Development
In science, ideas come and go. Some ideas are driven out by an accumulation of opposing scientific evidence; others seem to take forever to get rid of, no matter what the evidence suggests. The nature–nurture controversy—the long-standing debate over whether heredity (i.e., influences from within, inherited from or transmitted by previous generations) or environment (i.e., influences from the outside, encountered throughout the life span) is more important in human development—is just one of these hangers-on. In the field of scientific inquiry, no matter how much evidence accumulates on the etiology of human behavior, this controversy continues to be invalid as a logical premise. In other words, the nature–nurture debate continues to exist, despite the false dichotomy it poses.

A clearer understanding of the relationships between heritable and nonheritable factors and behavior is something that psychologists and educators have been interested in for a long time. Since the early work of Sir Francis Galton (Galton, 1869), the question of what is hereditary and what is not has been asked about many human traits in many contexts. Approximately a century and a half later, it appears that, with the exception of inconsequential or poorly measured human traits, pretty much all traits demonstrate some degree of heritability. The interpretation of heritability as a statistic is typically focused on two of its aspects:
(a) whether it is statistically different from zero and (b) what its magnitude is when its confidence interval is taken into account. When the heritability is statistically different from zero, the statistic indicates that the population/sample–phenotypic variability is attributable in part to genetic population/sample variability. The magnitude of the heritability estimate itself indicates the magnitude of such attribution.

A few decades of research in behavior genetics, an interdisciplinary field that attracts both psychologists and geneticists, indicate that the majority of complex human traits, especially those associated with cognitive functioning and educational achievement, areheritable (meaning that at least a portion of the phenotypic variance in the trait is associated with genetic variance and that that portion is statistically different from zero). However, similarly, the majority of such traits are also susceptible to environmental impacts (i.e., the phenotypic variance is also, at least in part, attributable to environmental variance). In fact, it is difficult to find a trait—at least one that has been approached with well-designed studies and reasonably large samples—for which the variance underlying the observed individual differences is primarily either genetic or environmental. Typically, there is a mixture of influences, and estimates of the ratio for this mixture can fluctuate developmentally, but rarely if ever is it either/or. Thus a substantial investment of time and money spent in attempting to resolve the controversy has resulted in the realization that it cannot be resolved. So, why does the nature–nurture issue keep popping up?

It has been suggested that the long life of this controversy is attributable to the truly complex reality of the relationships among the genome, the brain, and behavior; this reality has been described as unfolding on a number of time scales, ranging from a million years of human evolution to split-second decision making in extreme situations (Robinson, 2004). The multidimensional connection between the genome and behavior is indirect and mediated by the brain, which, in turn, is built by proteins encoded by the genes, the essential building blocks of the genome. However, the brain’s “construction zone” is not situated in a galactic vacuum but rather localized within the context of a particular environment that, in turn, impacts the machinery of the genome and the brain’s edifice and function (Robinson, Fernald, & Clayton, 2008). This environment changes over time, calling for matching changes in the genome by both impacting it directly and signaling it through the brain. Thus what should replace the concept of the nature–nurture controversy is the concept referred to by Robinson as “the dynamic genome” (Robin-
son, 2004, p. 399)—an open structure whose function is shaped by both heritable (i.e., “old,” preexisting in some form, transmitted across generations) and nonheritable (i.e., imposed anew, emerging in a particular individual) forces.

What does this new perspective mean for the field? What will happen to the seemingly eternal but incorrectly posed dichotomous question of genes versus environment? Here, it is argued that this question can never be answered and thus should nevermore be asked. When it was asked by Galton in the middle of the 19th century, the value of this question was very different from its value today, here at the beginning of the 21st century. Asked then, it seemed priceless, opening a new direction of scientific inquiry; asked now, it is meaningless.

Galileo Galilei’s action in dropping balls from the Tower of Pisa and Isaac Newton’s observation of falling apples at Trinity College, Oxford, stimulated the formulation of the laws of gravity. Now, if a child asks why apples fall down instead of up or float in the air, a clear answer can be provided based on the modern understanding of the laws of gravity. There is no need for humanity to deal with balls and apples for the sake of understanding gravity: we have captured its meaning! Similarly, we now also know the answer to the genes-versus-environment question and thus should put the nature–nurture controversy to rest. Yet “should” is not always easily converted into “is.”

The statement that cutting-edge science has moved far beyond the nature–nurture controversy, of course, does not mean that there are no other interesting questions to ask in our quest to understand how the dynamic genome realizes itself in human behavior. Similarly, although the laws of gravity have been formulated in principle, there are endless subsequent important qualifiers and addenda to these laws. Searching for answers to the how question is, arguably, the most productive way of generating new data on the connection between the genome and behavior. This broad question can be reformulated in many different ways. Among these rephrased questions are these: How did evolution make our genomes the way they are? How does an individual genome form from the genomes of its progenitors? How does it change through stages of life, distancing itself from its original genome? And there are many others. This broad question of how (or one of its variants) is central to the discussion in this chapter, the main purpose of which is to draw four observations from the data that are accumulating in response to the how query. These observations are made with references to both human and animal data, and follow the footsteps of the field in an attempt to
understand the connection between the dynamic genome and human development in general and cognitive development in particular. Of particular interest here is the formulation of hypotheses with regard to the contribution of education to this connection.

A pronounced limitation of this overview is its inability to cite literature that is directly related to education; there is virtually no such literature. Yet there are massive amounts of related literatures on humans and animals that form the foundation for formulating hypotheses with regard to the connections between these literatures and education. Thus, this chapter is structured around the discussion of four observations and concludes by linking these observations to issues of education. These observations are on (a) the role of the dynamic genome in the evolution of uniquely human traits; (b) associations between the genome, the brain, and subsequently cognition; (c) attempts to localize cognition in the genome; and (d) the correspondences between the degree of complexity of particular behaviors and the genetic mechanisms governing them.

Of note is that, in the 20th century, psychology and education, as scientific disciplines, have been predominantly driven by research paradigms that rest on the assumed necessity of formulating a priori hypotheses before collecting data and capitalizing on inferential–statistical frameworks of data analyses. Quite to the contrary, the genomic sciences, especially within the last decade, prior to and since the sequencing of the human genome, have been predominantly inspired by exploratory paradigms and are open to data mining and the engagement of posterior probabilities approaches. The illustrations of the connections between the dynamic genome and complex behaviors, presented below, highlight the impact of explorations characteristic of modern genomic sciences. They do not necessarily fit or verify higher-order theories; they try to capture and describe characteristics of the dynamic genome with regard to its relationship to complex human behaviors.

**OBSERVATION 1: EVOLUTION AND UNIQUELY HUMAN COMPLEX TRAITS**

For many subfields of psychology (e.g., clinical and social in particular), it is important to know how certain human behaviors evolve and what the “wild” (i.e., the initial or ancestral) versus acquired (i.e., modified by human civilization and culture) behaviors are. This evolutionary metric can aid both in understanding typical and atypical behaviors and in
defining the parameters of the modifiability of human behavior in response to social pressures. At what behavioral junctions did humans acquire the needed degrees of freedom to deviate from the repertoire of animal behavior? Which genes provided us with the opportunity to gain distance from our "wild" animal genome and attain such traits as free will and creativity, which are as nonanimal as any human traits that we know of? And how did they gain this distance?

A tremendous degree of overlap between the structures of the genome of high apes and modern Homo sapiens suggests that evolution is rather unlikely to operate in straightforward and direct ways, building new genetic structures to support new human-specific functions. Given the compact size of the human genome, one hypothesis is that a gain of function is related not to an increase in the size of the genome itself through the addition of new genetic material but rather to reusing existing genetic material in novel ways. This hypothesis assumes that there are some regulatory elements in the genome that guide the usage of the genetic materials, allowing for its differential transcription (i.e., differential gene expression).

To illustrate, a recent investigation (Prabhakar et al., 2008) focused on a particular type of such DNA regulatory material, the so-called cis-regulatory elements, a DNA region that regulates the transcription of genes located on the same DNA strand. More specifically, using bioinformatic approaches, these researchers identified a particular cis-element they described as “the most rapidly evolving human noncoding element yet identified” (p. 1346). Specifically, they identified a 546-base-pair piece of DNA termed human-accelerated conserved noncoding sequence 1 (HACNS1). This sequence is conserved and nonvariable in all sequenced vertebrate genomes; however, during the period of approximately 6 million years since the evolutionary differentiation between the human and the chimpanzee, it has accumulated 16 human-specific changes in the DNA structure. A rapid divergence such as that exhibited by HACNS1 is highly unlikely unless a positive selection pressure that might have altered the function of HACNS1 is assumed. Researchers (Prabhakar et al., 2008) have presented evidence that HACNS1 appears to be acting as an enhancer of gene expression that is localized to limbs. Their argument is especially appealing because of their molecular comparative analyses, according to which chimpanzee and rhesus macaque copies of this element do not result in such a comparative enhancement. In order words, the pattern of gene expression enhanced by this element might be directly related to the limb/thumb patterning that differentiates humans from their closest evolutionary relatives.
Based on this observation, it is possible to assume that similar mechanisms might have been involved in the evolution of language. Although currently there are no clear molecular “candidates” for the emergence of human language or its precursors, there are threads of indirect evidence supporting the general idea of the involvement of the genome in such differentiation. Two relevant ideas are discussed here.

First, it has been hypothesized that the differentiation of human languages corresponds to the differentiation of genetic variation between different human populations (Cavalli-Sforza, Piazza, Menozzi, & Mountain, 1988). Researchers have attempted to verify this initial hypothesis, but with mixed success (e.g., Barbujani & Pilastro, 1993; Barbujani & Sokal, 1990; Dupanloup de Ceuninck, Schneider, Langaney, & Excoffier, 2000; Excoffier, Smouse, & Quattro, 1992; Poloni et al., 1997; Rosser et al., 2000). The range of opinions and data collected in an attempt to verify this hypothesis has been broad, extending from the view that “genetic and linguistic features are tightly correlated” (Cavalli-Sforza et al., 1988) through the idea that “these features are correlated, but only in certain regions of the Old World” (Nettle & Harriss, 2003), to “these features are not correlated” (McMahon, 2004). According to these hypotheses, genetic and linguistic variations in different populations are correlated but might not necessarily be causally related.

Second, it has been hypothesized that there might be causal relationships connecting the genetic variation in a given population and certain linguistic feature(s) that characterize the language used by this population. For example, it has been proposed that the emerging variation in certain genes—such as genes involved in such functions as corticogenesis (e.g., *H. sapiens* abnormal spindles mRNA, *ASPM* or *MCPH5*, located at 1q31, and *Microcephalin, MCPH1*, located at 8p23, genes)—might be causally related to linguistic variation, but in an indirect fashion. Specifically, it is possible that the variation in these genes is related to differences in the size and organization of the cerebral cortex, which, in turn, might be related to a subtle cognitive bias in the processing and acquisition of linguistic tone and, correspondingly, to the presence or absence of tone in world languages (Dediu & Ladd, 2007). This hypothesis appears also to be supported by evidence pointing to the young age and relatively quick propagation of the derived variants of both *ASPM* and *Microcephalin* (5,800 and 37,000 years respectively) and suggests, as in the example of *HACNS1* above, the presence of a positive selection force that capitalized on a particular genetic feature magnifying the possibility of certain human traits to arise (Evans et al., 2005; Mekel-Bobrov et al., 2005).
Although the lines of investigation described above are of great interest, they face the major challenge of being translated from generic mechanisms to illustrations pertaining to specific human traits. And this translation is at its very beginning and not without controversies. For example, researchers (Mekel-Bobrov et al., 2007) have performed a large-scale genetic association study attempting to investigate the connection between the adaptive alleles of the *MCPH1* and *MCPH5* genes and normal variation in several measures of IQ in a sample of approximately 3,000 participants. They did not reveal an association that could have supported the connection between the recent adaptive evolution of either the genes or changes in IQ. Yet another study attests to the presence of genetic associations connecting variation in the *MCPH1* gene with both linguistic and nonverbal intelligence (Christiansen, Kelsey, & Tomblin, 2008).

Thus the findings are perhaps contradictory. Yet they are very exciting in terms of their potential to help identify both coding and noncoding regions in the human genome, whose evolution might underlie the emergence of uniquely human traits (e.g., language, as discussed above). In short, the findings presented here permit the observation that the emergence of human features (e.g., the differentiation of the prehensile thumb and the emergence of human language) are related to specific changes in the genome. It appears that different regions of the human genome differentiate at different rates, both presenting the link between *H. sapiens* and the evolutionary tree and allowing the species to distance itself from this tree by acquiring uniquely human features. It is possible that it is those regions in the human genome that accumulate rapid structural changes that are particularly pertinent to understanding the connection between the genome and education. Having identified such rapidly evolving regions, the field might be able to focus on them in a more systematic way in its attempt to understand the genetic bases for individual differences in such traits as the acquisition of literacy and numeracy.

**OBSERVATION 2: BRAIN STRUCTURE, GENES, AND COGNITION**

One of the axioms of modern cognitive science is that variation in cognitive performance is related to variation in the brain. Generally speaking, the variation in the brain is attributable to differences in (a) brain size, (b) brain structure, and (c) brain activation patterns. Correspondingly,
researchers attempt to correlate individual differences in cognition and cognitive tasks with all these sources of variation (for a more detailed discussion of this issue, see Mandelman & Grigorenko, in press).

There is a substantial literature that connects cognition with brain size and structure. For example, the average correlation between brain size and intelligence has been reported to be approximately .33 (McDaniel, 2005). It also has been argued that this correlation is attributable to genetic factors (Posthuma et al., 2002; Posthuma, de Geus, & Boomsma, 2003; Toga & Thompson, 2005; Winterer & Goldman, 2003). This hypothesis was suggested in particular based on the observation that the correlation between the brain properties of monozygotic twins and their intelligence is higher than in dizygotic twins (Posthuma et al., 2002). Summative interpretations of the literatures on intelligence and the brain (e.g., Hulshoff Pol et al., 2004) point to the connection between IQ and the volume and density of gray and white matter in the brain network that engages the regions of the right medial frontal, occipital, and right parahippocampal (gray matter) regions of the brain and the regions of the superior occipitofrontal fascicle and corpus callosum (white matter connecting the corresponding gray matter regions) of the brain.

Developmentally, increases in gray and white matter volume and density (i.e., increases in cortical thickness) are associated with brain (and correspondingly cognitive) maturation. This maturation is the result of numerous morphological changes, including the formation of new neuronal connections by dendritic spine growth as well as changes in the strength of existing connections (Chklovskii, Mel, & Svoboda, 2004), and axonal remodeling and increased soma and nuclei of neurons (Kleim, Lussnig, Schwarz, Comery, & Greenough, 1996). These changes have been attributed to both genetic and environmental effects that unfold in a complex systematic fashion (Shaw, 2007). Although the causal hypothesis connecting brain maturation to the development of intelligence has been rooted in animal literature and supported primarily by it, there are many correlational studies in humans that indirectly buttress this hypothesis.

Specifically, postmortem studies indicate that the brains of individuals with higher IQ and higher levels of education are characterized by a greater number of dendrites and more dendritic branching (Jacobs, Schall, & Scheibel, 1993; Jacobs & Scheibel, 1993) compared with individuals with very low IQs (Huttenlocher, 1991). Yet recent evolutionary analyses of the covariation between brain size and intelligence indicate
that there is an evolutionary preference for strong stabilizing (average is better) selection (Miller & Penke, 2007). Thus, although within a given population there is a tendency for intelligence and brain size to correlate, there is no evidence that evolution systematically “promotes” big brains and/or high levels of intelligence. One possible hypothesis here might be that this tendency toward being average in terms of having more stable, biologically controlled traits (e.g., brain size and structure) might explain the greater flexibility and diversity in more dynamic traits such as styles of information processing.

Similarly, there is ongoing interest in behavior–genetic studies of brain anatomy. Although this is a relatively new line of research, the data accumulated so far have indicated that heritability estimates vary for different regions and different ages (Lenroot et al., 2009). They also appear to vary depending on how fine-grained the investigated regions are, with heritabilities being smaller (.00–.50) for smaller regions, such as the thalamus and hippocampus (Wright, Sham, Murray, Weinberger, & Bullmore, 2002), and higher for large brain subdivisions (.60–.80) such as the frontal, parietal, and temporal lobes (Baare et al., 2001; Geschwind, Miller, DeCarli, & Carmelli, 2002; Wallace et al., 2006; Wright et al., 2002). There have also been attempts to investigate the structure of genetic variance by means of factorial techniques, but the results have been inconsistent, with some suggesting (Lenroot et al., 2009) and others negating (Wright et al., 2002) the presence of a major single factor accounting for the majority of genetic variability in the brain anatomy.

Similarly, studies of patterns of brain activation in people who are engaged in cognitive tasks have also produced a pattern of results that is rather difficult to interpret. It has been reported that individual differences in patterns of brain activation in people engaged in working-memory (N-back) tasks are attributable, at least partially, to genetic variation (Blokland et al., 2008). Likewise, it appears that heritability estimates of lateralization for such functions as language (Sakai, Miura, Narafu, & Muraishi, 2004; Sommer, Ramsey, Mandl, & Kahn, 2002), although statistically significant, differ depending on a number of “other” variables, such as handedness (Sommer et al., 2002) and training relevant to developing the tested cognitive function (Sakai et al., 2004). Yet, the activation patterns of the ventral visual cortex in response to language stimuli (pseudowords) were reported as not heritable, whereas the neural activity outlines in the same area, but in response to face and place stimuli, showed genetic influences (Polk, Park, Smith, & Park, 2007). Researchers (Matthews et al., 2007) also reported the presence of
genetic influences on the patterns of activation of the anterior cingulate during interference processing.

Thus, in general, the findings in this domain of research are once again rather contradictory. A possible new avenue of inquiry has recently been introduced by an elegant study that blended an investigation of individual differences in activation patterns in response to a particular task, regardless of what that task was, with an objective of differentiating brain networks that are engaged in response to different tasks, in this case, frontoparietal spatial networks and language-related networks (Koten et al., 2009). Perhaps surprisingly, the highest genetic influences were seen not in conjunction with the details (i.e., intensity or temporal resolutions) of patterns of activation but in the general selected cognitive strategy. Interpreting their data, researchers suggested that genetic effects are more related to qualitative, strategy, and style-based differences than to quantitative differences in patterns of activation.

This finding rings true for educators. The educational literature is replete with observations about individual styles of learning that students demonstrate in the classroom. It is these holistic stylistic preferences that differentiate students, not specific peculiarities like the details relating to how they acquire the alphabet or hand-write the letter “o.” Learning about how the genome contributes to the formation of such stylistic preferences might enhance the field’s understanding of how to address these styles in a classroom. It might also aid in focusing pedagogical efforts on those traits that are more modifiable and more open to intervention than others.

**OBSERVATION 3: LOCATIONS IN THE GENOME FROM WHICH COGNITION ORIGINATES**

For the last two decades or so, researchers have been engaged in a search for the specific genes involved in the etiology of intelligence and intellectual abilities and disabilities. Such searches usually unfold in one of two ways: as exploratory whole-genome investigations/screens (often also referred to as “scans”) or as hypothesis-driven studies of candidate regions in the genome or candidate genes (for a more detailed discussion of this issue, see Mandelman & Grigorenko, in press).

Up to now there have been six genomewide scans for genes contributing to intelligence and cognition (Butcher, Davis, Craig, & Plomin, 2008; Buyske et al., 2006; Dick et al., 2006; Luciano et al., 2006; Post-
The results of these scans are quite variable but there are interesting partial overlaps. Specifically, the findings coincide in regions on chromosomes 2q (for 4 out of 6 studies), 6p (for 5 out of 6 studies), and 14q (for 3 out of 6 studies). These overlapping regions have been putatively interpreted as indicative of the presence of genes that could explain some of the variance in IQ.

A number of observations can be derived from these results. The first pertains to the variety of the measures used in these studies. In fact, only one study (Butcher et al., 2008) utilizes an indicator that was referred to as measuring the general factor of intelligence, the $g$-factor. The remaining studies used a range of indicators of both achievement and abilities and generated a wide spectrum of findings, allegedly implicating 13 (out of 22) autosomal chromosomes, 5 of which reportedly demonstrated the signals on both arms, $p$ and $q$. Thus, between all of these phenotypes and all of these regions, the resulting picture is rather difficult to interpret. Second, of note is the observation that the magnitudes of the presented statistics and $p$ values are rather modest. When such effect sizes are estimated (e.g., as in Butcher et al., 2008), they are reported to be very low (topping out at 0.4%). Third, it is important to note that these studies are not independent of each other. They are collectively presented by four groups (two of which, the Dutch and the Australian group, have also published on samples together [Posthuma et al., 2005]), and it appears that there is a substantial overlap in the samples of participants (e.g., Buyske et al., 2006; Dick et al., 2006; Luciano et al., 2006; Posthuma et al., 2005; Wainwright et al., 2006). Given that the presentations are split based on the availability of a complete (or, in some cases, semicomplete) IQ battery versus the availability of specific subtests from IQ tests and/or other cognitive tests and different inclusion/exclusion criteria (e.g., as in Buyske et al., 2006; Dick et al., 2006, Luciano et al., 2006; Wainwright et al., 2006), one may ask whether any of the reported signals would survive if a conservative but traditional approach to correcting for multiple comparisons were applied. Fourth, it is important to note that these studies used a variety of designs and methodologies, analyzing both pooled DNAs for groups of individuals (i.e., mixing DNA from different individuals in one tube) and individual DNAs (i.e., keeping DNA from different individuals in different tubes), recruiting family members and singletons, and covering the genome with genetic markers at highly variable densities. All of these “differences and similarities” must be carefully taken into account in considering the patterns of consistencies and inconsistencies in these findings. Fifth, none
of these studies were specifically created to investigate the genetic bases of intelligence, however defined. In fact, the same genetic data were used to investigate linkage/association with multiple other phenotypes in different subsamples of the same samples. At this point, the impact of such reutilization of data on inferential statistics has not been carefully appraised, but there have been concerns in the literature regarding the effect of such reutilization on \( p \) values, the definition of replicability, and the generalizability of the results (e.g., McCarthy et al., 2008).

In summary, although these scans present interesting data, the reported findings must be interpreted with caution. Yet these studies are considered interesting enough to suggest that further investigations of the genetic bases of intelligence (broadly defined) are warranted.

Although such genomewide scans have not generated specific candidate genes for intelligence, other types of studies have implicated specific genetic regions or specific genes. A comprehensive review of so-called candidate genes for cognition, of which there are many, is beyond the scope of this chapter (for a more detailed discussion, see Mandelman and Grigorenko, in press); thus, only main conclusions relevant to the main argument of this chapter are outlined. First, of note is the fact that these candidate genes are numerous, with sparks of evidence both supporting and disputing the involvement of pretty much each of these genes with the etiology of cognition. Second, these genes are of rather diverse functions (i.e., belonging to families of genes connected to different groups of proteins with known functions in the brain), indicating, presumably, that the genetic pathways to cognition are complex or multilayered. Third, in many of these studies of genes and cognition, the behavioral variables of interest are defined beyond IQ. In fact, they encompass a whole gamut of characteristics of intelligence (verbal and nonverbal, at the minimum) and cognition (e.g., executive functioning, creativity, working memory, and IQ itself). Finally, the participants in whose samples these candidate genes have been investigated differ in age, suggesting that these diverse findings might reflect some developmental variability that is yet to be understood.

Nevertheless, although there have been no or only failed attempts to replicate the findings from some of these candidate-gene studies, there is a degree of consistency in correlating variation in selected genes with variation in cognition. The establishment of these specific associations between genes and cognition is a fundamental breakthrough, a switch from the hypothetical decomposition of variance that was characteristic of earlier heritability studies to a firm “grounding” of these heritabilities
in the genome. The hope is that, by understanding the functions of these genes and their interactive proteins networks, the field will gain some additional understanding of how the general biological (and the specific genetic) machinery of intelligence, cognition, learning, and academic skills works. Such discoveries might lead to discussions of the degree to which human potential can be maximized, but with pedagogical and perhaps pharmacological efforts.

**OBSERVATION 4: THE COMPLEXITY OF THE STRUCTURE OF COGNITIVE PROCESSES DOES NOT NECESSARILY CORRELATE WITH THE COMPLEXITY OF THE CORRESPONDING GENETIC MECHANISMS**

Quite often, in formulating initial hypotheses, researchers start by generating default assumptions that are maximally parsimonious. For example, one such assumption is that a simple behavior or a cognitive process is more likely to be guided by a simple genetic mechanism and a more complex behavior or process is more likely to be controlled by a more complex genetic mechanism. Yet although it is logical, this assumption does not seem to be consistently supported by the literature on how the dynamic genome behaves.

On the contrary, the literature today (for a review, see Robinson, 2004) contains rather surprising examples of complex sustainable behaviors in animals (e.g., pair bonding, foraging, and care of offspring), which are apparently controlled by relatively simple genetic mechanisms. Of interest is the fact that some of these behaviors involve molecules known to be present in humans and therefore likely to be involved in similar types of human behaviors. This literature delivers many interesting observations, two of which appear to be particularly remarkable. The first is that really complex behaviors can be controlled by a single polymorphism in a single gene. The second is that relatively simple (or low-level, componential) behavior can require the coordinated action of many genes.

Consider relevant illustrations. Researchers have explored the molecular bases of mating preferences in two species of voles, the monogamous prairie vole and the polygamous meadow and mountain vole (for a review, see Donaldson & Young, 2008). It has been reported that monogamous versus polygamous behaviors can putatively be associated with a highly polymorphic, complex, repeat-containing DNA element (referred to as a microsatellite) located in the so-called 51-region of the
vasopressin receptor, or AVPR1A, gene (Donaldson & Young, 2008). Moreover, there is growing evidence in the literature that genetic variation in the human variant of this gene, the AVPR1A gene, is important for human behaviors as well. Specifically, there are reports on associations between different variants of the AVPR1A gene and such human traits/behaviors as fat intake (Enhorning et al., 2009), personality traits such as altruism (Israel et al., 2008; Prichard, Mackinnon, Jorm, & Easteal, 2007) and aggression (Caldwell, Wersinger, & Young, 2008), and pair bonding (Walum et al., 2008).

To illustrate this last observation, the researchers asked members of 552 Swedish twin pairs, all of whom were living at a given time with a partner, to answer a brief self-report questionnaire with items targeting partner bonding, marital status, and marital problems. All participating twins were genotyped for the 51-microsatellite of the AVPR1A gene. It was reported that a particular allele of this polymorphism (the allele RS3 334) was associated with significantly lower scores on the partner-bonding items. This association was true for males only, so that males who were homozygous for this allele were twice as likely to have experienced marital problems or threat of divorce and half as likely to be married if involved in a committed relationship. Moreover, the presence of this allele in the male partner was reported to be correlated with reports of the quality of the relationship’s quality as reported by the female partner (Walum et al., 2008).

The second illustration is related to the concept of endophenotypes, which is widely used in the work by Gottesman and colleagues (Gottesman & Gould, 2003) and their many followers. The concept was initially proposed about 35 years ago by Gottesman and Shields (Gottesman & Shields, 1972) and was defined later as a measurable component “unseen by the unaided eye along the pathway between disease and distal genotype” (Gottesman & Gould, 2003, p. 636). When this concept was introduced, the intention, according to the authors, was to fill the gap between the holistic manifestation of the disorders and the gene or genes that govern them. According to the argument for this concept, there is a strong association between the number of genes affecting specific disorders and the number of relevant endophenotypes. In other words, the fewer the genes involved in the manifestation of a particular disorder, the fewer the componential dimensions (i.e., endophenotypes) required to describe and characterize the phenotype; the more genes involved and the more complex the genetic mechanism, the more complex the phenotypic manifestations of the phenotype. From this point
of view, the impact of a single gene might be adequately captured by a single dimension of the holistic phenotype, but more dimensions would be required to reflect differentially the impact of multiple genes. Logically, then, it is often assumed that the genetic mechanisms controlling an endophenotype might be simpler for such an endophenotype than for the disorder (or a more complex holistic trait) with which this endophenotype is associated. However, at this point, there is growing evidence that these assumptions might not be quite true.

For example, in the field of intelligence, it has been assumed that the holistic trait of intelligence can be captured by a variety of endophenotypes. Plausible endophenotypes are chronometric indicators such as reaction time, inspection time, and so forth, which are often assumed to be examples of the lower-level cognitive processes that contribute to the complex texture of the g-factor of intelligence. It has been argued that the “location” of these phenotypes, being “closer” to the genome than the trait of intelligence itself, should mean that they are governed by less complex genetic mechanisms than those controlling intelligence. Correspondingly, having understood the nature of these genetic mechanisms, the field would have been closer to understanding the genetic nature of intelligence itself. Yet various quantitative–genetic studies indicate that, if anything, there appear to be more genes involved in the control of the variability in chronometric indicators of cognitive processing than for more complex, higher-order cognitive traits. Thus, at least with regard to the number of genes involved in the manifestation of the so-called endophenotypes for intelligence as its chronometric indicators, the assumption that less complex traits are governed by less complex mechanisms might not be either true or helpful in understanding the ways the dynamic genome exerts its influences on cognition.

These observations might also be directly related to classroom practices by informing the differentiation (i.e., lower- vs. higher-level processes) of pedagogical intervention targets.

### PSYCHOLOGICAL, EDUCATIONAL, AND GENOMIC SCIENCES: AN EMERGING PLATFORM FOR INTERPRETING INDIVIDUAL DIFFERENCES

Four observations connecting the dynamic genome with complex human behaviors have been made. First, it appears that the different regions of the human genome appear to evolve at different rates; it is assumed
that rapidly evolving regions of the dynamic genome might be responsible for the acquisition of specific human traits. Second, although the assumption of the field that the genome controls the brain, which then controls human behavior, remains dominant in the field, the specifics of these connections are rather complex, nonlinear, and perhaps not sequential. These connections reflect an emergence of a true complex dynamic system, where it might be the case that, although the lower levels of the system might arise first developmentally, it is the higher levels of the system that are more constrained genetically. Third, the current evidence indicates that human cognitive functions are not rooted in a particular spot of the brain but rather are routed through its multiple regions. This routing underlies the formation of diverse information processing networks that are amenable to modification through teaching and learning. Fourth, we observed that the complexity of a cognitive process does not necessarily correlate with the complexity of the corresponding genetic mechanism; in fact, more complex cognitive functions can be governed by simpler genetic mechanisms, and simpler genetic mechanisms might be controlled by more complex genetic architecture. Thus, the connections between the dynamic genome and human behaviors are diverse: they range from those that form the foundations for uniquely human behaviors to those that underlie the architecture of cognitive traits.

In concluding this discussion, we point to some of the numerous junctions between the dynamic genome and behavior that are of interest to the fields of psychology and education.

First, development is characterized by a tremendous amount of interindividual variation, which forms the foundation for individual differences. Numerous studies of a variety of human traits, typical and atypical, that have been carried out with genetically informed designs (i.e., designs including pairs or larger groups of genetically related individuals) have indisputably demonstrated that the genome is a major source of these differences. Many researchers are currently working on translating the structural variation in the genome into potentials for individual differences in human behavior in general and cognition in particular. These translations are unfolding in multiple directions, including (a) identifying structural variation in the human genome in specific genes whose proteins can be targeted by pharmacological agents for the purposes of both enhancement and prevention of deterioration of cognitive functioning; (b) understanding the degree of malleability of particular complex behaviors whose manifestation is, at least partially, controlled
by genes, especially in response to pedagogical interventions; and (c) developing diagnostic procedures based on identifying genetic risk factors for developmental disorders that present particular challenges for regular classrooms and call for the development and implementation of special pedagogies.

Second, human behavior is governed by the brain in general and by its specific circuits in particular. Many of these specific circuits have now been delineated, at least in broad strokes, allowing researchers to start filling in the specifics of connections between the dynamic genome and these circuits. Yet the field is at its very beginning with regard to its attempts at translating these associations into targeted clinical and educational practices. Much more work is needed to identify the specifics of the dynamics of corticogenesis, the genes that are involved in this process, and the elements in the chain connecting the dynamic genome and the brain that are open to both evolution and targeted, human-orchestrated influences.

Third, the specificity of brain circuits is established anatomically by particular patterns of signal transduction and neuromodulation that develop functionally, in response to environmental stimulation. All these “contributors” to specificity and plasticity are, in turn, governed or assured by specific proteins synthesized by specific genes. Understanding what these genes are and how they function is of direct importance for understanding the regulation of human behavior by the brain. Moreover, such understanding will result in establishing both the sequence and the structure of higher-order functions and inform education with regard to the development of pedagogies best suited to these sequences.

Fourth, brain circuits are responsible for processing and merging information from stimuli that are internal and external to an individual. These stimuli form streams of information that are captured and transduced by various sensory pathways. Identification of the genes engaged in the formation of the biological foundation for these sensory pathways will be important for understanding the connection between the genome and information processing. Having this fundamental bit of understanding in place will inevitably help the field link the dynamic genome to the elusive texture of higher-order human functions such as thought and love. This, of course, will also have direct implications for education, indicating particularly effective strategies for teaching skills that are highly demanded by modern society, such as creativity and compassion.

Clearly this list is not exhaustive and can only grow as the field enhances its understanding of the structure and function of the dynamic
genome. Yet in going through this list and ticking off its items, the field formulates a new conceptual framework for further studies of the links between the genome and behavior. This framework brings us far beyond the nature–nurture controversy and opens new and exciting perspectives in understanding human complexity, from its evolutionary roots to its manifestations in the future. And among the many how questions there is one that is especially important—how to summarize this wealth of information, benefit from it, and bring it to school with the purpose of further understanding the nature and degree of malleability of individual differences in the classroom.

NOTE

1. A concept utilized to fill the gap between a clinical disorder phenotype and the genome. Other similar concepts are intermediate phenotype, subphenotype, biological marker, subclinical trait, vulnerability marker, and cognitive marker.

AUTHOR NOTE

Preparation of this chapter was supported in part by the following research grants from the National Institutes of Health: R01 DC007665 and P50 HD052120. Grantees undertaking such projects are encouraged to express their professional judgment freely. Therefore this chapter does not necessarily reflect the position or policies of the National Institutes of Health, and no official endorsement should be inferred. The authors are thankful to Ms. Mei Tan for her editorial assistance.

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