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Biosocial Influences on the Family: A Decade Review

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Abstract

The past decade brought a remarkable increase in the number and quality of biosocial studies of family processes. The current review summarizes recent advances in biosocial family research by providing key exemplars of emerging research paradigms. Research in the past decade has substantiated the claim in the previous Decade Review (Booth, Carver, & Granger, 2000) that bidirectional influences between all levels of analysis are paramount. There is an emerging consensus that integrating factors at multiple biological and social levels is highly informative. Because ignoring biological factors often will underestimate mediating or moderating mechanisms, the review provides recommendations for biosocial family research. We also highlight the need for researchers who understand complex family environments to lend their expertise to biosocial studies.

Keywords

Family Process; Family Structure; Marriage and Close Relationships; Selection Effects; Social Context; Within-Family Design

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The historical reticence of many family researchers to consider biological factors (Freese, Allen Li, & Wade, 2003) is due to various philosophical and epistemological factors. For some researchers in fields that are focused primarily on institutions or larger social constructs, reservations about considering biological factors may reflect concerns about all individual level explanatory variables, whether biological or not (Freese, 2008). Many family researchers also fear that incorporating or focusing on biological explanations for behavior promote extreme views on biological reductionism, wherein social factors are ignored at the expense of biological explanations (Duster, 2006). Concerns about extreme biological reductionism are not unfounded, as some writers advancing genetic explanations have made extreme claims concerning the perceived limited importance of social processes in families. Likewise, claims dismissing outright the role of biological factors in families have also been made. Many of the arguments concerning the sole explanatory role of biological factors, however, have been based on unjustifiable and polarizing extrapolations of research findings (Rutter, 2002).

Recently, there has been a growing acceptance of the importance of biological factors in the study of family and social influences, as many researchers are now studying how biological *and* social factors act and interact. This greater acceptance of a biosocial perspective on family functioning is illustrated by the enormous number of biologically informed studies of social factors in the past decade. For example, numerous special issues on genetic factors have recently been published in Sociology journals (Bearman, 2008; Guo, 2006, 2008) and recent reviews in psychology (e.g., Adele, 2009; Cacioppo, Berntson, Sheridan, &

McClintock, 2000; Cicchetti, 2006; Granger & Kivlighan, 2003), psychiatry (Kendler, 2005b), and sociology (Freese et al., 2003) have explicitly called for an integration of biological and social factors. Family researchers, in particular, have discussed the importance of taking an integrated biosocial perspective (Booth et al., 2000). This growing acceptance is also reflected by publications from prominent workgroups commissioned to study the importance of considering biological, behavioral, and social factors (Hernandez & Blazer, 2006) and how social science research can incorporate biological measures into their studies (Finch, Vaupel, & Kinsella, 2001).

The astounding increase in our knowledge of the interplay of biological and social factors in the past decade is due, in part, to technological advances. For example, it is now commonplace to collect biomarkers using noninvasive procedures (e.g., collecting DNA and hormone levels from saliva) and analyze these measures inexpensively. These advances have made it possible to collect biological markers in large studies, including assessments of children, resulting in biologically informed studies using nationally representative or national samples. Research in basic neuroscience has also identified mechanisms through which biological and environmental factors act and interact in controlled settings. Advances in technologies that assess brain activity, which allows researchers to explore mental processes related to social constructs, have also led to an explosion of studies exploring family processes. Finally, advances in computational power and in quantitative software to statistically model factors at multiple levels and over time have enabled researchers to statistically test complex theoretical models.

The current review was commissioned by the Editorial Board of *JMF* to provide an update of the 2000 review (Booth et al., 2000) by discussing advances in our understanding of family process through various approaches, including genetic, physiological, biomarker, and imaging research. Because an in-depth analysis of how all these approaches have informed every aspect of marital and family functioning is beyond of the scope of one article, the current manuscript provides exemplars of research that considers both biological and social factors, highlighting the importance of numerous paradigms and research that integrate micro *and* molar levels of analysis. We scanned articles in multiple fields, including psychology, sociology, family studies, psychiatry, and medicine, as well as consulted with experts in numerous fields to select the exemplars.

The current review is separated into three major sections. The first section describes progress in the past decade in understanding the interplay of genetic and environmental influences related to family processes. This section initially provides a brief overview of research highlighting the importance of genetic factors and presents the basics of molecular genetics. The review subsequently covers research on how genetic factors influence environmental risks and how environmental factors interact with underlying genetic predispositions. The second major section of the review provides an introduction to the burgeoning transdisciplinary field of social neuroscience. The field, broadly construed, utilizes numerous designs to jointly explore biological processes in the context of social processes and vice-versa. These include animal models, psychophysiological assessments, assessments of physical health, and localized measures of brain functioning. We use examples of each to illustrate how these approaches shed light on the complexity of family functioning. In the third section we provide a critique of the research in the past decade and present recommendations for future biosocial research related to family and social processes. In sum, we hope to illustrate how a biosocial perspective enriches our understanding of *both* social and biological processes because ignoring factors at either level of analysis can have serious, negative implications for research on family functioning.

Genetic and Environmental Influences on Family Functioning

Whether genetic factors influence complex human behaviors and family functioning has frequently been construed as a contest (the Nature *versus* Nurture debate), which pits one against the other. Historically, researchers have used quantitative behavior genetic (BG) designs, research that relies on natural experiments, to explore the importance of genetic and environmental factors (Plomin, DeFries, McClearn, & McGuffin, 2008). These include the comparison of identical (or monozygotic, MZ) twins, fraternal (or dizygotic, DZ) twins, and adopted individuals. Initially, quantitative BG research sought to estimate the extent to which genetic and environmental factors accounted for variability in some outcome, typically contrasting the importance of genetic factors (referred to as heritability) to the amount of variability accounted for by environmental factors. Numerous psychological and sociological researchers have criticized this approach, saying that such BG research did not test underlying causal mechanisms, was based on potentially invalid assumptions, did not take developmental issues into consideration, did not study specific environmental risks, and was based on samples with limited generalizability.

Although there are threats to the validity of each BG design, the overall body of traditional BG research, which relies on numerous studies using many different approaches (each with *different* and offsetting threats to their validity), clearly demonstrates that all behaviors of interest to family researchers are partially influenced by genetic factors (Turkheimer, 2000). The same conclusion has been reached by many psychologists and psychiatrists (Kendler, 2005b; Rutter, Moffitt, & Caspi, 2006), as well as sociologists (Freese, 2008). There is, thus, a growing consensus that genetic factors must be considered when studying families.

Background on Molecular Genetics

How can genetics influence something as complex as human behavior in family context? Hereditary influences on behavior are conveyed primarily by DNA (although see below). Chromosomes within the nuclei of cells and within mitochondria are composed of long, complexly structured strands of DNA. DNA is composed of long chains of four organic compounds called nucleotides in varying sequences. The nucleotides are joined together in complementary pairs on a sugar-phosphate backbone in the shape of a double helix. The genetic code of DNA is carried in the specific sequence of the nucleotides. Although it is an oversimplification (Seringhaus & Gerstein, 2008), a gene is classically defined as a segment of DNA that is capable of directly or indirectly influencing the synthesis of proteins that compose structures in the body, such as functional parts of neurons, glands, and other systems involved in behavior. The vast majority of the DNA sequence is identical in all humans (which is why the same principles of biological and behavioral sciences apply to all of us), but some genes take several forms (i.e., are polymorphic). Under some circumstances, some of these variations in DNA can contribute to differences in protein based structures that, through transactions with the environment, influence behavior.

DNA is expressed, so that it influences the synthesis of proteins, in the two steps of transcription and translation. In transcription, some DNA segments of a gene drop out (introns) and others are recombined (exons) to create a single strand copy of the nucleotide sequence of the exons, called messenger RNA (mRNA). In the process of translation, mRNA leaves the nucleus and influences the synthesis of amino acids, which are the basis of proteins formed in ribosomes. In this way, a polymorphic gene can lead to the synthesis of different proteins in different individuals. If that protein is part of, for example, a receptor of a neurotransmitter in the brain (the chemical that helps the neurons in our brains communicate), then the gene could have downstream effects on behavior. For example, if a gene is associated with neuron that use the neurotransmitter dopamine, the resulting

differences in neural transmission could provide a partial basis for differences in aspects of behavior related to mood, reward, and related aspects of behavior.

Are there polymorphic genes that play a role in influencing complex behaviors and family functioning? The prevailing view is that most human behaviors are *genetically complex*—many genes influence each phenotype, and each gene accounts for little variance in the phenotype. In fact, recent research shows that complex psychological traits, such as schizophrenia, are influenced by many, many genes, each of which have small effects (The International Schizophrenia Consortium, 2009). Thus, it is inaccurate to describe the results of molecular genetic research as finding a gene "for" a particular complex trait (Kendler, 2005a), let alone complex interpersonal constructs.

To identify genetic polymorphism that influence behavior and other traits, two general strategies have emerged, candidate gene studies and genome wide association studies (GWAS). Candidate genes studies test theory-based hypotheses regarding the association between a limited number of specific genetic polymorphisms and measured behavior. In order to justify studies that focus on specific candidate polymorphisms, the hypotheses must be based on strong biological models of the gene's involvement in the phenotype (Moffitt, Caspi, & Rutter, 2005). This is facilitated when the candidate polymorphism is known to influence protein synthesis or has been associated with related constructs. For example, Dick et al. (2006) found that a gene that had previously been linked with alcohol dependence, GABRA2, was associated with a decreased probability of marrying and an increased risk of divorce, although the magnitude of the associations were small. Follow-up analyses revealed that personality characteristics, such as reward dependence, may partially explain how the gene is associated with both alcohol dependence and marital status. The specific processes involved are not yet clear, but reward dependence might promote alcohol dependence in certain environmental circumstances, which reduces chances of successful marriage. Other processes are quite plausible, too, however.

GWAS simultaneously tests for associations between a phenotype and hundreds of thousands of polymorphisms across the genome, often in large samples of unrelated individuals (Risch & Merikangas, 1996). Because GWAS casts a wide net that is not based on theory, they are useful in principle (1) when theory-based hypotheses are not available, and (2) for detecting previously unsuspected risk genes. One major disadvantage is that GWAS requires large sample sizes because the large number of polymorphisms requires steep corrections of the statistical significance level. As a result, most GWAS have the statistical power to identify only strong genetic effects. Furthermore, because tests of interactions between genetic polymorphisms and environments that may moderate genetic associations (gene-environment interactions, see below) requires far larger samples, few such tests can be conducted with adequate statistical power in affordable studies. At this point in time, therefore, it is not yet clear that the GWAS strategy will prove to be helpful in identifying genes associated with complex traits (Goldstein, 2009).

Studying the Interplay of Genetic and Environmental Factors

Recent research has shown that the dichotomous, either/or approach to studying genetic and environmental influences, which were evident in early quantitative BG and gene-finding approaches, is greatly misleading. As such, few current BG studies merely assess whether genetic factors influence some behavior. Rather, BG research now is using genetically informed designs (review in Plomin et al., 2008) to explore how both genetic and environmental factors act and interact—the *interplay* of genetic and environmental factors. By doing so, recent BG research is specifically addressing many of the criticisms researchers leveled against traditional BG research (review in Rutter et al., 2006). It is in the study of how genetic and environmental factors act and interact that family researchers who

understand the complex social environments in which our genes are expressed are most needed. The following sections describe general principles of how genetic and environmental factors, including family processes, work together.

Gene-Environment Correlation—Research in the past decade has continued to document that genetic factors influence the environments in which we live, referred to as gene-environmental correlation. For example, it is clear that genetic characteristics of individuals influence their exposure to parenting practices, stressful life events, social support, marital status, and marital quality (Kendler & Baker, 2007). Genetic factors influence exposure to environments through several general, complex processes (Scarr & McCartney, 1983). Passive gene-environmental correlation occurs when genes that influence parenting behavior (an environmental factor affecting the children's behavior) are passed down from the parent to their child. If these genes also influence the offspring's behavior, a correlation between the genes of the child and the parenting environment of the child is created. It is a passive correlation in the sense that the child's behavior does not create it. Active gene-environmental correlation occurs when genetic factors influence the types of environments an individual selects in the broad sense of that term (i.e., niche picking). For example, genes of the child may increase the likelihood of behaviors that result in friendships with deviant peers, who influence the child's risk for antisocial behavior. Evocative gene-environmental correlation arises when a genetically influenced trait of the child elicits particular reactions from others (e.g., parents responding to oppositional behavior with corporal punishment; Jaffee et al., 2004).

The phenomenon of gene-environmental correlation is an important aspect of the well-known problem in family studies of nonrandom selection into risky/protective environments. It is important to note that gene-environmental correlation poses serious concerns for traditional family and epidemiological studies, because gene-environmental correlation raises the possibility that genetic factors could account for outcomes incorrectly attributed to environmental risks. Indeed, many fields have ignored gene-environment correlation to their detriment:

> Currently, many quarters of social science still practice a kind of epistemological tacit collusion, in which genetic confounding potentially poses significant problems for inference but investigators do not address it in their own work or raise it in evaluating the work of others…Nothing makes the work of imperializing academics (whether from behavioral genetics or, e.g., economics) easier than an incisive, significant, and easily explained flaw shared by an entire literature." (Freese, 2008, p. S19)

Behavior Genetic Methods as Quasi Experimental Approaches—What may come as a surprise to many family researches is that BG methods actually provide a very powerful way of ruling out possible genetic confounding when testing causal hypotheses about particular environmental risks. Quantitative BG methods can be used as quasi experimental approaches, which help differentiate between alternative explanations for the association between putative risk factors and outcomes (Moffitt, 2005; Rutter, Pickles, Murray, & Eaves, 2001). We mention several such approaches, with examples of how these methods provide greater understanding about family factors by minimizing (or ruling out) genetic confounds.

A particularly powerful approach for exploring individual level environmental risks, when those risks are not shared by siblings in a family, is the co-twin control design. Hypotheses regarding the underlying causal mechanisms responsible for the association between a particular risk factor and some outcome are tested by comparing MZ twins reared together

but who are differentially exposed to the putative environmental risk. The design rules out all confounds related to DNA sequences because the twins are genetically identical in this sense; the design also rules out environmental factors that influence all siblings in the family similarly (for rationale see Caspi et al., 2004). In one such study, Caspi and colleagues (2004) compared identical twins differentially exposed to levels of maternal negativity using a longitudinal design. The study found that the MZ co-twin that was exposed to more negativity had more antisocial problems while controlling for previous levels of antisocial problems, supporting the inference that maternal negativity causes increased behavior problems over time. Lichtenstein and colleagues (1998) used a similar approach to support a causal inference between spousal bereavement and mortality.

Researchers are also using multivariate twin studies to explore putative environmental risks. Multivariate twin studies examine more than one behavior at a time to explore the underlying mechanisms for the covariation between them (i.e., do genetic or environmental factors explain why two measures co-occur?; Plomin et al., 2008). Many multivariate studies include "environmental" measures to explore the underlying mechanisms through which the environmental factor is associated with some "outcome." For example, Ganiban and colleagues (in press) used a multivariate twin approach to explore how the genetic and environmental influences on personality help account for the associations between marital quality and parenting.

Researchers have also used the sibling comparison method, an approach which helps to rule out genetic and environmental confounds, to study early environmental risks for which siblings can differ (Lahey, D'Onofrio, & Waldman, 2009). Under certain conditions, the design rules out all genetic confounds when studying early risk factors because the process of meioses randomly distributes parental genes equally across siblings (ruling out confounds due to passive gene-environment correlation) when comparing full siblings. The design also rules out active/evocative gene-environmental correlation when studying early risk factors (e.g., pregnancy related risks) where there is no possibility of child effects. Sibling comparisons also control for environmental risks that equally affect members of the same family. D'Onofrio et al. (2009) explored the association between maternal age at childbearing and offspring disruptive behaviors using the approach. Although previous studies had suggested that background familial factors account for the increased risk of behavior problems in offspring of young mothers, offspring born when the mothers were younger had more problems than their siblings who were born when the mothers were older, an effect moderated by birth order. These results help support the inference that something about the environments provided by younger mothers exerts a causal influence on their children's disruptive behavior.

In the past decade, researchers also increasingly utilized the Children of Twins (CoT) approach to study environmental factors that influence all siblings in a nuclear family (D'Onofrio et al., 2003; Silberg & Eaves, 2004). In its most basic form, the approach compares offspring of adult twins who are discordant for a particular characteristic (e.g., one co-twin is divorced but his/her co-twin is not). The design is an extension of the cousin comparison approach, which has been extensively used in sociological and economic studies, and, therefore, controls for unmeasured environmental factors that influence all members of an extended family similarly. The CoT approach can also help rule out genetic factors passed down from twin parents to their offspring. The offspring of MZ twins are genetically related as half siblings (sharing 25% of their genes), although socially they are cousins. Offspring of DZ twins share only 12.5% of their genes. The comparison of offspring of MZ twins accounts for more genetic factors than the comparison of DZ twins, allowing researchers to estimate the extent to which shared genetic liability or environmental confounds account for intergenerational associations. Research on the

intergenerational transmission of conduct problems using the CoT approach suggests that the mechanisms responsible for the increased risk of child conduct problems when parents have a history of conduct problems depends on the gender of the offspring (D'Onofrio et al., 2007). For women, the familial risk was due to shared genetic liability in both the parents and the offspring; whereas environmental factors specifically associated with parental conduct problems increase the risk for men, consistent with causal inference.

The past decade has also seen the continued use of adoption studies to explore environmental risks, although it is becoming more difficult to conduct such research relative to conducting twin studies. The adoption design represents the cleanest break between environmental and genetic risk because adopted away children are not raised by their biological parents (Plomin et al., 2008). Researchers have used the approach to study the effects of parental divorce, finding that adopted children have more behavior problems when their adoptive parents divorce than adopted children from continuously married parents, minimizing the possibility of genetic confounding (Burt, Barnes, McGue, & Iacono, 2008).

What has been particularly striking about the advances in quantitative BG research related to social risks is the use of multiple designs to test the environmental and genetic processes responsible for hypothesized environmental effects. Certainly, the field as a whole is providing converging evidence concerning particular environmental risks. For example, adoption studies (Burt et al., 2008) exploring the effects of parental divorce provide similar answers to CoT studies (e.g., D'Onofrio et al., 2005). Researchers are going further, though, to simultaneously include numerous quantitative BG approaches in the same analyses. For example, researchers have combined the CoT approach with multivariate twin studies of twin children and their parents to help differentiate passive gene-environmental correlation from active/evocative gene-environmental correlation and causal environmental processes. Use of both designs in the same study suggest that the association between parental over involvement and adolescent depressive problems is primarily due to evocative gene-environment correlation, highlighting the importance of considering child effects (Narusyte et al., 2008). In fact, some researchers have utilized large scale studies that include over 80 different family relationships to study the processes underlying the familial resemblance for traits (Eaves et al., 1999). These are only a few examples of how researchers are using novel approaches to studying putative environmental risk factors, taking great care to test the underlying assumptions and limitations inherent in each method. Again, each quasi experiment has its own strengths and weaknesses, primarily in the generalizability of the findings, but BG designs provide some of the most powerful quasi experimental methods for testing causal hypotheses (Moffitt, 2005; Rutter et al., 2001).

Gene-Environment Interaction—Social science research has shown that there is enormous variability in responses to family and social influences. In recent years, it has become clear that genes and environments influence our behavior in a complex interplay that often involves the genetic moderation of environmental influence, a phenomenon referred to as gene-environment interaction. Indeed, it now seems quite possible that genetic disposition is necessary but not sufficient for the expression of most, if not all, complex behaviors. For example, it now seems likely that inadequate parenting and other social factors often influence whether genetic vulnerabilities lead to mental disorders (Rutter, 2008).

Traditionally, twin studies were based on the simplifying assumption that genetic and environmental factors act in isolation, so that their independent effects add up in linear fashion to account for variability in a particular outcome. Newer computational and analytical strategies (Purcell, 2002; Rathouz, Van Hulle, Rodgers, Waldman, & Lahey, 2008) however, allow BG researchers to demonstrate that the degree to which genes

influence behavior often depends on the environment and vice versa. For example, Jaffee et al. (2005) used a twin study to explore whether physical maltreatment interacted with genetic risk to influence children's disruptive behavior. The authors used the zygosity of the twin pairs (either MZ or DZ) and the co-twin's behavior to create groups of individuals indexing increasing inferred genetic vulnerability to conduct problems (e.g., an individual with a MZ co-twin with a history of conduct problems was at greater genetic risk than an individual with an MZ co-twin without a history of problems). The study found that experiencing physical maltreatment was a stronger predictor of conduct problems in the child when the child was at greater genetic risk.

Using an approach that assesses continuous genetic and environmental liabilities, Turkheimer et al (2003) explored whether family socioeconomic status moderated genetic influences on child intellectual abilities. The results indicated that genes had little influence on childhood IQ in very poor families. In high socioeconomic families, in contrast, genetic factors accounted for most of the variability in childhood IQ, with the remainder of the variability being due to environmental factors specific to each child. This and other studies (Rutter et al., 2006) strongly suggest that importance of genetic factors depends on environmental risk (and vice-versa).

A number of studies exploring the interaction between specific measured genes and environments have also provided early clues for how we should conceptualize the joint action of genes and environments. For example, there is now replicated evidence that early exposure to physical maltreatment interacts with variants of the offspring's monoamine oxidase-A gene to influence the offspring's risk for violent behavior (Kim-Cohen et al., 2006). In addition, some research suggests that social stressors may interact with a polymorphism of the serotonin transporter gene to influence risk for major depression and suicidal behavior (e.g., Caspi et al., 2003). Not all researchers agree that this is the case, however (Risch et al., 2009).

It is important to note that there is currently great disagreement regarding molecular genetic research. Gene-finding studies suggest that studies need enormous sample sizes (tens of thousands) to detect genes of small effects, but many small studies (sometimes with hundreds of subjects or less) are reporting gene-environment interactions. Could gene-environment interactions be hindering gene-finding studies? Are researchers reporting gene-environment interactions relying on spurious findings? The study of measured gene-environment interactions is still in its infancy, and many analytical, assessment, and technical issues remain. In spite of these problems we expect the conceptual framework of the approach (individuals vary in their genetic vulnerability to family influences) will be central to family studies in the future.

Mechanisms of Gene-Environment Interactions—How can the external social environment alter the ways in which genes, which are located deep within our cells, influence behavior? There are several ways in which this can happen.

1. Gene-environmental interaction *based on the social context of behavior*. It is likely that gene-environmental interaction often reflects environmental influences and limits on behavior (see Shanahan & Hofer, 2005 for a review of different models). For example, youth who are genetically predisposed to be aggressive who live in sparse rural environments may be less likely to engage in violence than youth living in urban environments because of the greater density of gangs in densely populated environments.
2. Gene-environmental interaction *based on epigenetic factors*. Research during the last decade has dramatically changed our understanding of how DNA operates and

has revealed that gene-environmental interaction often reflects indirect environmental influences on gene expression at the molecular level. Exciting new research, mostly using animal models to date, illustrates how social environments can alter the expression of genes. Environmental factors do not alter the sequence of DNA, but they influence whether genes are "turned on" or "turned off" (Rutter et al., 2006). DNA is typically in a quiescent state. It is not expressed as messenger RNA until specialized substances, such as transcription factors (proteins that bind with the promoter regions of genes), effectively turn on genes. Simply put, because levels of some transcription factors are strongly influenced by the social environment, the social environment can regulate gene expression by influencing levels of transcription factors. For example, cortisol (a stress hormone) can serve as a transcription factor (Cole et al., 2007) and the experience of harsh parenting is associated with elevated levels of cortisol in children (Gunnar & Quevedo, 2007). Thus, it is plausible that harsh maternal parenting could influence gene expression by influencing levels of cortisol (and perhaps other transcription factors that regulate gene expression) in offspring.

The social environment also can initiate a chain of much longer lasting biological events that alter the availability of DNA to transcription through the process of *epigenetic programming* (Szyf, McGowan, & Meaney, 2008). DNA consists of meter long strands that are condensed within the nuclei of cells by being wound tightly around histone blocks to form structures called chromatin. Aspects of the social environment, such as variation in maternal care, have been shown to alter the structure of chromatin. Specialized molecules, particularly methyl and acetyl groups, can bind to DNA in ways that makes DNA more or less available to transcription factors, which influence whether particular genes are actually expressed (Meaney, Szyf, & Seckl, 2007). Indeed, controlled studies of nonhuman animals suggest that this is a key mechanism through which maladaptive early parenting influences the health of offspring (Meaney, 2006). In some cases, altered chromatin is passed through germ cells (eggs and sperm) to offspring, providing an "epigenetic memory" for social experiences that is passed on to the next generation independent of DNA sequences (Meaney, 2006). Although such research is in its infancy, the existing studies suggest that parents pass down the sequence of their DNA *and* modified chromatin to their children.

Whereas most research on epigenetic factors has been conducted with nonhuman animals, recent work has provided evidence of the importance of epigenetic mechanisms related to social factors in humans. For instance, researchers have found associations between social isolation and gene expression (Cole et al., 2007). Although it is impossible to determine the direction of causality in such studies, the findings suggest possible mechanisms through which social isolation might operate—altering which genes are expressed and silenced. Interestingly, researchers are now beginning to study epigenetic mechanisms in humans using randomized control studies. For example, Irwin et al. (2006) found that experimentally inducing sleep deprivation caused differences in the expression of genes relevant to the immune system. When we learn which aspects of the family environment shape gene expression and how this happens we will have enormously powerful new tools for preventing mental, physical, and social problems (Meaney et al., 2007). Indeed, this is a fundamentally important topic for future research on all aspects of family life (Feinberg, 2008).

Joint Estimation of Gene-Environment Correlation and Interaction—In order to fully understand the interplay of genes and environments, researchers must consider both gene-environmental correlation and gene-environment interaction because the correlation between genes and environmental factors may confound the interactions between them (Jaffee & Price, 2007). Eaves and colleagues (2003) explored numerous environmental and

genetic processes influencing the etiology of anxiety and depression over time. The results suggested that the same genetic factors that influence anxiety problems before puberty influence depression after puberty. The same genetic factors also influenced exposure to stressful life events (gene-environmental correlation) *and* made individuals more susceptible to the depressogenic effects of those life events (gene-environment interaction). Stressful life events also influenced later depression to some extent independently of each youth's genetic vulnerability. Although it awaits replication, this study provides a powerful example of the complexity of gene-environment interplay over the course of development. The study shows how solely focusing on genetic factors misses the importance of environmental stressors. Ignoring genetic factors misses the nonrandom selection into stressful life events and the fact some individuals are more vulnerable to such events. Summary of Genetic and Environmental Research on Families Quantitative BG methods provide a number of rich and powerful designs that are shedding light on the complex interplay of environmental and genetic influences on family and other social processes. Quantitative BG research provides powerful methods for studying family influences while controlling for genetic factors (gene-environment correlation) and is asking for whom, under what conditions, and in what manner do genetic *and* environmental factors influence behavior (gene-environment interaction). Modern BG approaches are also providing important clues for research focused on molecular genetic processes. Molecular genetic studies illustrate that there are no "genes for" complex traits that are of interest to family researchers. Rather, the research demonstrates that many genes have small effects and interact with environmental factors, particularly familial characteristics, to confer risk or resilience for complex traits. The rapidly growing research literature on measured gene-environment interaction and epigenetic factors strongly suggest that considering the role of environmental factors on genetic expression is crucial for understanding how heredity influences behavior. The pathways between genes, environments, and behaviors are not unidirectional (e.g., gene to protein to brain to behavior), but, rather, complexly bidirectional (Gottlieb, 2003). As such, behavior genetic research over the past decade has highlighted the necessity of simultaneously examining the interplay of biological and social factors.

Social Neuroscience

Social neuroscience, a field that emerged in the 1990's, has greatly advanced the understanding of biosocial processes during the past decade. This field, which includes many disparate research strategies and content areas, stresses the necessity of taking a transdisciplinary approach to social phenomena. In particular, the field is, "devoted to understanding how biological systems implement social processes and behavior, capitalizing on biological concepts and methods to inform and refine theories of social processes and behavior, and using social and behavioral concepts and data to inform and refine theories of neural organization and function" (Cacioppo, Amaral et al., 2007, p. 100). Social neuroscience research posits that all social behavior is "implemented biologically", but explicitly rejects the notion that micro levels of analysis provide the most salient explanations for social phenomenon. Rather, the field relies on a consideration of interplay between levels of analysis to more fully understand complex behaviors and social phenomena (Cacioppo et al., 2000; Harmon-Jones & Winkielman, 2007). This section includes a number of examples, including animal studies of parenting behavior; studies of social neurology, immunology, endocrinology; and the use of brain imaging techniques. These approaches illustrate how social neuroscience research is expanding our knowledge of biosocial influences on the family.

Animal Studies of Parenting Behavior

Parent child interaction is the earliest and certainly one of the most important forms of social behavior for mammals (Suomi, 2006). Not only is parental care necessary for survival,

variations in the quality of mother-child interactions are associated with long term health consequences in humans. Maternal behavior in nonhuman mammals has been the subject of intensive biological study for over 50 years, with extensive gains in knowledge (Numan, 2007). We present a greatly simplified overview of a few key findings and models to stimulate biosocial studies of maternal (and paternal) behavior in humans.

First, research on rodents has found that key brain structures form a system that mediates maternal behavior in animals (the MPOA/BNST system). Surgically removing the system disrupts a broad range of maternal behaviors, without disrupting nonmaternal behavior (Gammie, 2005). This brain system releases a neurotransmitter that inhibits the brain circuits involved in maternal aversion to baby pubs and activates the brain's reward system. These processes result in the mothers finding contact with infants more rewarding (Brunton & Russell, 2008).

Second, neuroscience research has identified a neurohomone, oxytocin, which plays a key role in maternal behavior, including both recognition memory for offspring and social bonding in animals (Brunton & Russell, 2008). Oxytocin functioning is increased during the postpartum period, partly because it is modulated by the hormone estrogen. Following estrogen priming, injections of oxytocin induce maternal behaviors, even in rats who have never given birth (Campbell, 2008). In primates, estrogen increases the rewarding properties of contact with infants by influencing oxytocin and the reward system (Pryce, Dobeli, & Martin, 1993). In addition to playing a key role in maternal nurturing behavior, oxytocin also is involved in the modulation of stress responsiveness, anxiety, and aggression (Neumann, 2008), all of which are related to maladaptive parenting behaviors.

Third, in some species the release of opium-like substances manufactured in the brain (endogenous opioids) during and after birth also plays a role in the positive affect associated with maternal parenting and bonding. The MPOA/BNST brain system that influences maternal behavior and the brain's reward system contain receptors for these chemicals, which allow opioids to influence their functioning (Gulledge, Mann, Bridges, Bialos, & Hammer, 2000). When the action of endogenous opioids is chemically blocked, suckling, maternal caregiving and protective behaviors are reduced in mammals (Broad, Curley, & Keverne, 2006).

Although the neurobiological systems involved in maternal behavior are highly conserved across mammalian species, there are obviously important differences between humans and other mammals (Broad et al., 2006). The more developed frontal cortex, for example, plays a greater role in maternal behavior in humans and other primates than in other mammals. And, maternal behavior is not restricted to individuals who have been exposed to hormones when pregnant and giving birth in humans, as adoptive human parents can form strong parent-child bonds quite successfully.

Such social neuroscience research using nonhuman animals, however, provides strong theory and evidence-based models for exploring the causes of adequate and inadequate parenting in humans, especially during infancy. Potentially, dysfunctions of particular brain regions (the MPOA/BNST system), oxytocin, and endogenous opiod systems in humans could increase the risk of harsh parenting, including abuse. A number of recent human studies are consistent with this hypothesis. A study of humans found significant correlations between levels of oxytocin in plasma measured during pregnancy and in the first month after birth and several aspects of maternal behavior (Feldman, Weller, Zagoory-Sharon, & Levine, 2007). It is important to note, however, that the human literature on oxytocin is currently mixed (Campbell, 2008). Brain imaging studies have also added important information on the neurobiology of maternal parenting in humans. A review of the first five

functional magnetic imaging (fMRI) studies of mothers' neural responses to infant cries versus control stimuli found consistent activation in areas of the brain implicated in the current animal model of maternal behavior (Swain, Lorberbaum, Kose, & Strathearn, 2007). Future animal and human research will no doubt, provide us with a greater understanding of the role of brain structures that influence parenting behavior, as well as the biological and environmental factors that influence such processes.

Social Neurobiology, Immunology, and Endocrinology

Researchers have made great strides in incorporating new or greatly improved methods of assessing psychophysiology in studies of social processes (Cacioppo, Tassinary, & Berntson, 2007). We briefly review studies related to the neurobiology of stress reactivity, psychoneuroimmunology, and social endocrinology to illustrate how studies that include assessments of biological processes are revealing new information about important family processes.

Family Processes and the Neurobiology of Stress Reactivity—The past decade has seen a great increase in our knowledge concerning the biological mechanisms involved in responses to stress (review in Gunnar & Quevedo, 2007). The human stress response is primarily driven by two separate but related systems, the sympathetic-adrenomedullary (SAM) and hypothalamic-pituitary-adrenocortical (HPA) systems. The SAM system is responsible for preparing humans for quick action in response to stresses. The SAM system helps quickly increase arousal and vigilance, the amount of available glucose for energy, and blood flow to the brain and muscles. While these reactions are helpful in the short term, the response comes at the expense of other necessary physiological processes. Thus, prolonged activation of the SAM system has adverse health consequences (Gunnar & Quevedo, 2007).

The parallel HPA system produces glucocorticoids, which are steroid hormones, including cortisol. The effects of glucocorticoids are slower and longer lasting than the effects of SAM system because glucocorticoids primarily influence stress responses through changes in gene expression and neural functioning (Gunnar & Quevedo, 2007). Glucocorticoids influence both the basal rates of neural responsiveness and changes in neural reactivity in response to stress. Whereas these steroid hormones can have positive effects on neuronal functioning in the short term, prolonged exposure to high levels can hinder brain functioning, especially related to learning and memory, and cause death of neurons in the brain.

When stressors are prolonged, the detrimental effects of stress responses can outweigh the benefits. When describing the joint effects of both the SAM and HPA systems, researchers typically refer to the cost involved with chronic and intense stress as allostatic load. Recent research on stress reactivity has emphasized a number of key findings related to family processes (Gunnar & Quevedo, 2007). First, the effects of stress are most pronounced during times of rapid development (e.g., during pregnancy, early childhood, and puberty) because of the deleterious physiological consequences on changing brain structures. Second, social factors, primarily the parent-child relationship, shape a child's stress neurobiology, which has long-term mental and physical health consequences. Third, although stressors early in development have long lasting consequence, stress reactivity is also highly responsive to changes in the environment, indicating that social influences in later development could provide protective factors to enhance resiliency. Finally, individual differences (both environmentally and genetically influenced) may be critically important when considering the effects of stress. Indeed, when considering the impact of stress, researchers must consider key features in both (a) the types of stressors and (b) individual characteristics of the person (e.g., their vulnerability and actual stress responses) (Miller, Chen, & Zhou, 2007).

Recent research that measures these steroid hormones (e.g., cortisol) has highlighted the importance of taking a biosocial perspective when considering numerous familial stressors, including both normal and extreme measures of poor family relationships (Repetti, Taylor, & Seeman, 2002), parental conflict (Davies, Sturge-Apple, Cicchetti, & Cummings, 2008), and childhood poverty (Evans & Kim, 2007), to name a few examples. Great advances have been made in the use of cortisol as a measure of stress reactivity, but many questions remain given intra-individual variability (Hruschka, Kohrt, & Worthman, 2005) and the fact that cortisol only indirectly assesses stress reactivity (Hellhammer, Wüst, & Kudielka, 2009).

Physiological and Immunological Responses to Marital Conflict—Neuroscience research has also clearly demonstrated that physiological systems that were once thought to be separate are, in fact, quite interrelated. As a result, researchers are assessing multiple domains within each level of analysis (in addition to factors at multiple levels). For example, negative and hostile behaviors among couples are associated with cardiovascular and immune functioning problems, in addition to endocrine responses (review in Robles & Kiecolt-Glaser, 2003). Marital interaction studies assessing blood pressure and heart rate suggest that couples show increased cardiovascular reactivity to marital conflict, although men and women respond to qualitatively different demands. Similar studies have also demonstrated that marital conflict can have profound impacts on immune functioning, highlighting an important mechanism through which family processes can influence long term health and mortality (Kiecolt-Glaser, McGuire, Robles, & Glaser, 2002). The studies of marital conflict, part of the growing field of psychoneuroimmunology (Miller, Chen, & Cole, 2009), highlight how psychophysiological and biological measures allow researchers to test underlying mediating mechanisms and test processes that cannot be assessed using self report measures and other assessments.

Social Endocrinology Studies of Testosterone—Numerous family studies have also explored the role of sex hormones, such as testosterone. While higher levels of testosterone are correlated with aggression, the relation is quite complex (Booth, Granger, Mazur, & Kivlighan, 2006). Recent research on sex hormones highlights three important points. First, the association between levels of testosterone and health outcomes appears to be curvilinear —both low levels and high levels are associated with measures of antisocial behavior, employment, and marital functioning in men (Booth, Johnson, & Granger, 1999). Second, recent biosocial studies have highlighted the importance of social factors in understanding the relation between testosterone and negative (and positive) behaviors. For instance, research on peer influences illustrates that proximal social influences moderate the association between testosterone and behaviors. Men with high levels of testosterone showed greater leadership skills when surrounded by positive peers, whereas high levels of testosterone were associated with disruptive behaviors when surrounded by deviant peers (Rowe, Maughn, Worthman, Costello, & Angold, 2004).

Third, a recent review also highlights the reciprocal relation between testosterone (and other sex hormones) and environmental factors (van Anders & Watson, 2006). Most researchers have primarily focused on how hormones influence behaviors, such as competition, partnering, sex, and parenting. Many studies, however, highlight how these behaviors and environmental factors influence levels of testosterone. For example, informal contact for five minutes with a female confederate increased testosterone levels in men, especially those with aggressive personalities (van der Meij, Buunk, van de Sande, & Salvador, 2008). Definitive conclusions about the implications of these reciprocal relations over time are lacking, given the limited research in this area, but advances in collecting hormonal assays (e.g., through saliva samples), makes this understudied area of social endocrinology particularly important (van Anders & Watson, 2006), especially to family functioning.

Brain Imaging Studies of Social Processes

Advances in the techniques to assess brain functioning in living persons have also grown exponentially in the past decade. Whereas there are numerous methods for imaging brain functioning in humans (Cacioppo, Tassinary et al., 2007), we will briefly highlight how functional magnetic resonance imaging (fMRI) can be used to test hypotheses regarding family influences in a biosocial framework. fMRI studies use the magnetic differences between oxygenated and deoxygenated blood to localize differences in metabolism in the brain, which is assumed to reflect greater neuronal activity (Huettel, Song, & McCarthy, 2004). fMRI studies contrast brain activation under differing conditions (e.g. activation when presented with emotional stimuli versus a baseline condition, such as focusing on a neutral, fixed stimulus). The differences in blood oxygenation, therefore, provide an in vivo measure of brain activity throughout the brain. fMRI provides a much more precise spatial resolution of the loci of brain activation than other assessment of brain function (e.g., electroencephalography; EEG), although the approach is somewhat limited in its temporal resolution because of the lag between neuronal activation and the flow of oxygenated blood. Technological advances and developments in study design in the past decade have enabled more researchers to utilize fMRI techniques to study social phenomena. Whereas early fMRI research was criticized for searching for the brain structure "responsible for" or "necessary for" certain mental activities, fMRI studies are currently focused on testing different theories by exploring the neural systems activated during various activities (Harmon-Jones & Winkielman, 2007).

Longitudinal and cross sectional studies using structural MRI (and other brain imaging techniques) have identified key differences in the development of various brain structures, which are very important for understanding family dynamics. For instance, the prefrontal cortex (the frontal most portion of the brain), which is involved with executive functioning (e.g., planning, self regulation, monitoring, and evaluating situations), is still undergoing normative developmental changes during late adolescence and early adulthood (Casey, Tottenham, Liston, & Durston, 2005). This is in contrast to the brain systems that are responsible for the processing of emotional stimuli. Longitudinal brain imaging studies, therefore, provide for a context for understanding children's and adolescents' poorer ability to engage in so-called higher order processing. For example, one study found that the volumes of prefrontal areas and the amygdala, a brain structure involved in emotional processing, were correlated with adolescent affective behaviors (e.g., aggressive and dysphoric behaviors) during parent-child interactions (Whittle et al., 2008).

Social neuroscience studies using fMRI have made big strides in our understanding of social processes that occur outside of conscious awareness, such as some aspects of sexual decision making. For example, women prefer more masculinized faces closer to ovulation, but the underlying mechanisms are poorly understood. An fMRI study of women's preferences for masculinized and feminized faces indicated that brain activation in areas associated with decision making and reward processing depend on hormonal and psychosexual factors (Rupp et al., 2008). Interestingly, some of the same brain structures were activated in another study that explicitly provided women information about sexual risks during a sexual decision making task, suggesting similar cognitive processes may be occurring (Rupp et al., 2009). Thus, fMRI results may provide insights into the cognitive processes involved in women's perception and evaluation of potential sexual partners, noting the critical role of both hormonal levels (based on their menstrual cycles) and psychological traits.

Importantly, fMRI studies have shown that patterns of brain activation may be greatly influenced by family environmental factors. For example, a study by Taylor and colleagues (2006) found that adults who had experienced risky family environments during childhood

had different patterns of brain activation in prefrontal areas and the amygdala (a brain structure highly associated with emotional reactivity) when shown emotional stimuli than individuals who did not. Furthermore, the study found that the functional connectivity between activation in the amygdala and prefrontal cortex, which may be involved in emotional regulation, was also quite different in subjects from low and high risk families. This study illustrates how fMRI studies can be used to look at functioning brain networks, rather than at separate brain structures.

Although the Taylor et al. (2006) study is important in suggesting that family environments are associated with brain activation patterns related to emotional processes, it is impossible to determine causality given the correlational nature of the data. Experimental studies, however, have demonstrated that social factors influence the neural activation related to potential threats. Coan and colleagues (2006) studied whether holding hands with a spouse or an anonymous male experimenter would influence emotional regulation during threat of electrical shock for women. Both spouse and stranger hand holding helped regulate brain activation to the threat cues in prefrontal cortex areas, but spousal hand holding was a stronger moderator of the brain activation. Furthermore, the regulatory influence of spousal hand holding varied according to level of marital satisfaction—women reporting the highest marital quality showed the least neuronal activation to the threat cues while holding their spouse's hand. The study provides a mechanism through which social influence can help regulate one's responses to threats.

fMRI research, especially related to social constructs, is not without controversy, however. The initial focus on whether particular brain regions are responsible for mental processes was overly simplistic. Recent advances now enable researchers to consider overlapping and interacting *networks* that are highly plastic. Recent work also illustrates how the study of mental processes must also consider hormonal, psychological, and social factors. Finally, the analysis and interpretation of fMRI data remains controversial (Vul, Harris, Winkielman, & Pashler, 2009).

Summary of Social Neuroscience Research on Families

Brain imaging techniques, along with animal studies and social psychophysiological approaches, provide researchers with a set of research tools to explore both biological and social influences. We have only listed a few examples of social neuroscience research, as the field has advanced rapidly over the past decade (reviews in Cacioppo, Amaral et al., 2007; Harmon-Jones & Winkielman, 2007), but social neuroscience, again broadly construed, is providing great insights into family influences. One particularly exciting aspect of the field is the fact that the numerous research methods provide the opportunity to provide converging evidence concerning etiological mechanisms (e.g., do animal *and* human studies yield consistent findings?). Yet, what may be of most interest to family researchers, especially those studying broader social influences, is the conceptual framework that underlies the field. Social neuroscience as a field specifically aims to improve our knowledge of *both* biological and social mechanisms. And, the field emphasizes that "molecular" or biological explanations may not be the best or most appropriate level of explanation for social behavior.

Current Status of Biosocial Studies of Family Processes

Certainly, there is a growing acceptance of genetic and biological influences on family functioning, but many researchers in the field remain hostile to the notion or ignore the possibility that biological factors may be important when studying family processes. Recent efforts have been made to publish special issues on biological factors in sociology and family studies journals (e.g., Bearman, 2008; Guo, 2006, 2008), but most relevant papers

that take a biosocial perspective on family processes are still not published in journals specifically related to those fields. For instance, only a handful of papers have been published in *JMF* in the past decade that included consideration of biological factors.

This is very problematic, as the lack of family researchers engaging in biosocial research has negative consequences for both biological research and for family studies. Family researchers have vital information that can help guide biological research (e.g., the understanding of multilevel systems, the importance of social context, the need for proper assessment of environments, and exploring how families change over time). Likewise, ignoring biological influences has hindered family studies, especially given the widespread acceptance of the importance of biological factors in many related fields (e.g., psychiatry and psychoneuroimmunology). Failing to take a biosocial perspective, in fact, has the potential to leave family studies isolated as a discipline (Freese, 2008).

From our perspective, the most glaring weakness of the biosocial influences on the family in the past decade as a whole is the lack of developmental considerations. Many (but certainly not all) studies relied on cross-sectional samples and/or static models of interactions between biological and environmental influences. Yet, biological processes, human behavior, and family processes are all dynamic systems over time (Cicchetti, 2006; Smith & Thelen, 1993). As such, researchers must be aware of different developmental trajectories, the potential presence of sensitive periods, and the importance of understanding cascading events over time. Thus, researchers must explore how biological influences, social factors, and one's own behavior act and interact over time, a need stressed by the last decade review (Booth et al., 2000). For instance, biosocial research suggests that hormone levels influence and are influenced by social environments (van Anders & Watson, 2006). Furthermore, when studying family processes researchers must also explore how multiple people of different ages are developing and changing time, how the family system is changing over time, and how their communities are changing over time. Although some advances are being made (e.g., Adele, 2009), biosocial research in the next decade must focus on understanding mechanisms of change. As such, family researchers can play a crucial role in the design, implementation, and interpretation of biosocial research by stressing the need to incorporate developmental considerations at multiple levels of analysis.

Great advances have been made in the past decade, but from a historical perspective research that integrates family and social influences with biological considerations is still in its infancy. Each quasi experimental design has its limitations (Rutter et al., 2001), the conduct and interpretation of gene-environment interaction studies is controversial (Risch et al., 2009), questions remain on whether the results from animal study apply to humans (Broad et al., 2006), the study of stress hormones only provides a proxy of stress reactivity (Hruschka et al., 2005), and the interpretation of fMRI data remains controversial (Vul et al., 2009), to name a few examples. The question for family researchers is whether to engage with researchers from these disparate (and historically, competing) fields or continue to conduct research on social factors without consideration from these other disciplines.

Recommendations for Future Biosocial Research on Families

The Institute of Medicine Committee on Facilitating Interdisciplinary Research published 14 broad recommendations for supporting research that incorporates numerous levels of analysis related to health outcomes. We highlight a number of these recommendations and elaborate key points to help facilitate more biosocial research on family issues (see NAS/NAE/IOM, 2004 for a full description).

First, the committee recommended that researchers conduct transdisciplinary, collaborative research, consistent with calls of researchers in numerous fields (e.g., Cacioppo et al., 2000;

Cicchetti, 2006; Freese, 2008; Granger & Kivlighan, 2003; Kendler, 2005b). This recommendation calls for consideration of causal processes at all levels of analysis, not just the biological level. Such research should be theory driven, based on evolutionary principles, animal studies, and human neuroscience research (e.g., Caspi & Moffitt, 2006). This research will require researchers to work in transdisciplinary teams, where knowledge flows back and forth among different disciplines, rather than merely working on interdisciplinary teams in which each group of researchers works on their own part of a larger project. Such collaboration can be difficult (e.g., Hernandez & Blazer, 2006), but it is impossible for a single researcher or team to have the expertise in all areas to conduct such research. We especially encourage the integration of quantitative BG designs (especially as quasi experimental approaches) and social neuroscience methods. Such collaboration would greatly help the field of social neuroscience draw stronger causal inferences about biological and social factors, and the collaboration would help behavior genetic studies further specify causal mechanisms (e.g., Shirtcliff, Coe, & Pollak, 2009).

Second, research must include key variables over the life course and consider social context. Researchers from relevant disciplines, such as sociology (Duster, 2006), can provide insights into key conceptual and measurement issues at social levels. For example, family researchers are particularly needed to help biologically informed studies conceptualize how social factors can moderate genetic risk for health related outcomes (Monroe & Reid, 2008; Shanahan & Hofer, 2005). This recommendation also stresses the importance of taking a developmental perspective, which we stressed above.

Third, researchers need to develop and implement analytical modeling strategies that build comprehensive statistical models of heterogeneous behaviors. Researchers, therefore, must recognize that the same risk/protective factors may lead to drastically different outcomes, depending on the person, and that the same objective behaviors may be the result of quite different causal mechanisms (Cicchetti, 2006). Although there is a gap between the complexity of our theoretical models of development and the ability to test such models, advances in analytical models (e.g., growth mixture modeling: Kreuter & Muthen, 2008), are providing researchers with the ability to test complex issues related to heterogeneity and development. The key conceptual issue underlying the recommendation is that individual level traits, as well as developmental issues, are crucial for understanding social influences, and, consequently, must be explored (Freese, 2008).

Fourth, the committee urged researchers to conduct studies in diverse groups and settings. This is a key recommendation for obtaining a full understanding of how biological and social factors influence and are influenced by family processes. Although there have been tremendous advances in our knowledge of biosocial processes, our understanding is quite limited by inadequate testing in diverse and representative groups. For example, most of the research on social endocrinology has been done on heterosexual men, which helped lead, in part, to an overly simplistic view of the role of hormones and behavior (van Anders & Watson, 2006). The enormous technological advances in collecting biomarkers now enable researchers to collect biological (and environmental) measures on diverse groups. Great strides in sampling were made in the past decade, but future biosocial studies of family influences over the next decade will need to explicitly study groups that heretofore have been ignored or rarely studied. In fact, creative research designs, such as studies with foster children, can provide great insight into the functioning of extremely at-risk families while also utilizing a quasi experimental approach (Jaffee, 2007).

Fifth, the committee encouraged researchers to enhance existing datasets and develop new, large scale datasets to more precisely assess biosocial effects. There are number of large scale studies that can be used to explore family processes from a biosocial perspective that

does not require additional data collection. For instance, Guo et al. (2006) used the twin sample and molecular genetic data from the National Longitudinal Survey of Adolescent Health (AddHealth) to explore the influences on age at first sexual intercourse. We encourage researchers to conduct more secondary data analyses using a biosocial perspective. Furthermore, we encourage ongoing studies to incorporate biomarkers to help facilitate such research (Finch et al., 2001); adding biomarkers to existing longitudinal studies is an efficient use of resources, which will highlight family processes.

Sixth, the committee called on researchers to expand the focus of their research. The move by the National Institutes of Health to focus on translational research (Zerhouni, 2005) highlights the need for basic research to inform intervention efforts and public policy initiatives and for the findings from interventions to inform basic research. Again, this will require collaboration across disciplines that have traditionally worked separately. One way of facilitating such research is to include relevant and informative biological measures in intervention studies (Beauchaine, Neuhaus, Brenner, & Gatzke-Kopp, 2008). Combining neuroscience measures with randomized controlled studies of couple and family therapy could shed great insight into family influences.

Finally, the growing appreciation for the biosocial perspective of family influences has enormous implications for the training we provide for undergraduate, graduate, and postdoctoral students. Graduate and postdoctoral training programs and classes, in particular, will need to incorporate multiple perspectives and facilitate students being able to work and collaborate across traditionally separate fields (e.g., McFall, 2006). Given the complexity of biosocial research training programs should focus on preparing students to be independent researchers capable of working on interdisciplinary teams. We have experience with developing and studying new curricula for transdisciplinary education. The training is greatly complicated by difficulties with basic terminology, differences in underlying assumptions, inherent biases based on past training, and differences in goals. Training students in a collaborative and transdisciplinary manner, however, is also incredibly exhilarating for both the students and the faculty. Such approaches will be essential for training the next wave of researchers, clinicians, and policy experts.

Summary

In the previous decade review on biosocial influences on the family, Booth and colleagues (2000) noted that the field was moving toward assessing and incorporating measures at multiple levels of analysis, while emphasizing the need to consider bidirectional influences across levels. Research during the past decade has further substantiated and strengthened their claims. The past decade has seen enormous growth in the number of family studies that incorporate both biological and social factors, due, in part, to technological advances that have made it easier and less expensive to collect biomarkers in studies of social influences. What has also developed over the past decade is a growing acceptance of a biosocial approach among researchers in disciplines interested in family influences. The growth in biosocial research has not diminished the importance of family and social factors; rather, it has highlighted and elaborated the importance of such influences. Biosocial research on the family is now using various paradigms, such as quantitative and molecular genetic approaches, as well as the various methods in the field of social neuroscience. These approaches have identified mechanisms through which biological and environmental factors act and interact with each other. It is time to break down the artificial and profoundly limiting barriers between fields of study. Biosocial research on family influences over the next decade will need to increasingly incorporate multiple levels of analysis, with a special emphasis on (a) studying how biological and environmental factors act and interact over time, and (b) sampling diverse groups of individuals and families to provide more

generalizable conclusions. Family researchers can play a critical role in biosocial research by informing biological research about these critical issues. Likewise, family research will only continue to benefit from a biosocial perspective. Indeed, ignoring the importance of either biological or environmental processes would greatly limit the validity and value of future research on families.

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