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TRANSITION FROM TRADITIONAL MARKETING TO GENETIC MARKETING AND THE SPECIAL IMPACT OF MAOA

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ABSTRACT: After the last twenty years, when classical theories started to lag behind, the point reached has exceeded neoclassical approaches and it has been seen that genetic data has begun to be added to theories, especially in social sciences and behavioral sciences studies. Genetic data can enhance and validate existing theories of consumer behavior by illuminating the nature of relationships between traits and revealing the biological mechanisms underlying individual differences in behavior. Some of these applications are also used in the field of marketing, similar to the use of genetics in other fields of social sciences by their nature. This study aims to update consumer theory by revealing business strategies based primarily on genetic variables for segmentation and targeting, creative uses that enhance consumers' sense of community and personalization, the use of genetically informed study designs to test causal relationships, and the biological mechanisms underlying behavior. In addition, in the article aiming to add the term genomarketing to the Turkish literature, a special place is reserved for monoamine oxidase A. The MAOA gene, whose effect on other economic decisions, especially on purchasing, has been revealed by other studies, has been genetically identified and some studies that are important in the literature have been examined in terms of their results.

KEYWORDS: Genomarketing, MAOA, Behavioral Genetics

1. INTRODUCTION

The fact that people try to predict the next behavior of the person in front of them is as old as human history. That's what mediums or seers do. The question is "behavior". According to Turkheimer (2000), behavior emerges through complex, nonlinear developmental processes. Ethical considerations prevent us from controlling most human development processes through experimental controls. For this reason, it is difficult to understand the complex behavior patterns of human beings and it is a more complex process than the behavior itself.

According to scientists, if the effect of a certain gene or gene group on a behavior can be identified, it may be possible to test the probability of the behavior caused by variations in these genes in humans. Moreover, thanks to the development of tests that accurately predict human behavior, it may be possible to talk about the probability of a behavior occurring in a person.

When we evaluate the behavioral output as a phenotype, estimation of the heritability of this phenotype will again be possible with behavioral genetics. Because, this field, which has entered the literature as behavioral genetics, forms the basis of scientific researches in many different fields, from physical characteristics to physiological and psychological diseases, from personality to mood disorders, thanks to its unique working methods. The study methods of behavioral genetics are also used in research conducted in cooperation with the fields of genetics and social sciences. New generation marketing, which is referred to as genomarketing in the literature and has brought up one of the most discussed issues in recent years, is one of the partnerships of social sciences and genetics in its sub-discipline.

In this study, behavioral genetic study methods that can be used in the field of genomarketing will be mentioned and some studies that are expected to have a say in the marketing of beauty products will be mentioned.

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2. PHENOTYPE HERITABILITY AND BEHAVIORAL GENETICS

With the beginning of the investigation of the human genotype before the 1980s, laboratory research began to be carried out on many subjects, including protein or enzymes, which are gene products. A typical example of this is the presence of A, B, O and Rh blood groups for detecting the genotype from the reaction of gene products with certain chemicals. By the mid-1980s, it was seen that there was a great leap forward in studies with the possibility of DNA itself to determine the genotype. Now, genetic researchers have started to examine DNA directly, instead of trying to search for genotypes by examining gene products (enzymes and proteins), which is a laborious process (Güngör, 2020). With the "Human Genome Project", which started in 1990 and announced all the results in 2003, important information about the genetic structure of humans was presented to the scientific world. With the completion of this project, we finally have important information about the approximate number, location, structure and function of genes today. This information allowed us to determine the roles of genes in the formation of diseases or, more generally, the functions of genes that direct our metabolism (Ulucan et al. 2015).

The rightful priority of genetics is hereditary diseases. While it is a known fact that people face diseases due to genetic reasons, it is obvious that genetics is not the only reason. In addition to genes, the environment also has an effect on diseases. Likewise, when trying to explain human behavior, it is not possible to talk about genetic basis only. In addition to genetics, environmental influences also affect behavior. Still, the relationship between genes and diseases is easier to understand than the relationship between genes and behavior. Although the relationship between genes and diseases is so clear and understandable, the relationship between genes and behaviors is quite complex. The reason for this is summarized in the book titled Genetics and Human Behavior: Ethical Terms published by the Nuffield Council on Bioethics in 2002 (Kennedy, 2002):

- More than one genetic factor being effective on the behavioral trait,
- These genetic factors can interact with each other,
- The existence of non-genetic (environmental) effects on traits as well as genetic factors,
- These environmental effects are in interaction with each other,
- Genetic factors can affect the effect of environmental factors (this is called gene-environment interaction),
- On the contrary, environmental factors can affect the effect of genetic factors,
- Genetic and environmental factors can be effective at the same time (this is called gene-environment correlation),
- The protein produced from a gene can be modified and thus differentiated in its function,
- The fact that the effects of our genes can differ over time, because our genes do not have a permanent and unchanging effect on our brain and body.

Behavioral genetics has shown that genetic differences are an important component of differences in all behavioral traits. In 1991, Turkheimer and Irwing Gottesman mentioned in their study that the universal effect of genes on behavior is the first law of behavioral genetics. After that, Turkheimer mentions three laws for behavioral genetics in his article published in 2000 and summarizes these laws as follows:

1st Law: All human behavioral traits are inherited.
Law 2: The effect of growing up in the same family is smaller than the effect of genetics.
3rd Law: A significant part of the differences in complex human behavior cannot be explained by genetic or parental factors.

Chabris et al. (2015) talk about adding a fourth law to behavioral genetics in their work. According to this, “A typical human behavioral trait is related to a large number of genetic variants, each of which constitutes a very small part of behavioral change.” The authors' thesis is based on molecular genetic studies that directly measure DNA variation.

Similar study methods are observed in the investigation of genetic causes of phenotypic traits. Phenotype refers to all the typical characteristics of an individual that are observable and measurable and come from their genes. For example, features such as hair color, IQ level, eye color are phenotypic features (Kennedy, 2002). In the

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Dictionary of Genetic Terms published by the Turkish Society of Hematology in 2013, the phenotype is defined as "the appearance of an organism, depending on its genetic structure and the effect of external factors". Phenotypic traits can be expressed as features such as the appearance, development, physical characteristics and behaviors of the individual. Carey defines the phenotype as the characteristics or traits observed in the individual. Features such as height, weight, intelligence, memory and extraversion are phenotypic features (Carey, 2002).

3. STUDY METHODS IN BEHAVIORAL GENETICS

3.1. Quantitative Genetic Methods

Quantitative genetic theory offers some insights into how traits of different selective importance should be inherited. Quantitative genetic methods are a collection of methods that examine the effects of genetic and environmental factors on variations in some behavioral characteristics that can be measured quantitatively among individual groups and use statistical methods in this direction. Her research subjects are twins, adopted individuals and families. It is not specifically studied with genes and its findings do not refer to a gene or environmental factor. The heritability estimates they reveal in their results belong to a group, not an individual. In addition, heritability estimates obtained by these methods are useful in understanding the relative contribution and interrelationship of different effect types (Kennedy, 2002). Quantitative genetic analyzes are used to address questions about the evolution of behavior and physiology's interrelationships. This approach is complementary to both studies of individual, inter-population, and inter-species variation, as well as studies of experimental manipulation of physiological capacity or the effects of hormonal levels on behavior (Garland, 1994).

Behavioral genetic studies are basically divided into quantitative and molecular genetic methods. While quantitative genetic methods, which are called population genetics in some sources, help to determine the contribution of genetic factors to the etiology and the inheritance pattern of diseases, cytogenetic and molecular genetic studies provide the determination of the locations of genes on the chromosomes (gene mapping) (Arısoy, 2004). In molecular genetic studies, it is aimed to determine the genes that affect the heritability of a certain phenotype and, if this phenotype is a disease, to determine why the gene in question shows abnormal behavior (Arısoy, 2004).

3.1.1. Family Studies

Family studies were designed to investigate whether relatives with a particular trait increase the chance of having it and to compare it with relatives who do not. Family studies show that the trait has a familial basis, with the increase in the proportion of this trait among relatives of individuals with a particular trait. Researchers estimate the similarity of biological relatives in the family by calculating the correlation coefficient of the trait in question. Zero correlation indicates no similarity, while positive correlation indicates similarities in this trait among relatives. In the case where the correlation coefficient is 1, the similarity has reached the maximum point, and in this case, it can be easily said that this feature has a familial basis. However, it cannot be said to be purely genetic (Kennedy, 2002). The similarity between family members arises as a result of the effects of both genes and the shared environment. That is, inheritance is necessary but not sufficient on its own (Sherman et al. 1997).

3.1.2. Adoption Studies

Adoption studies are studies on humans and animals that stand out in the evaluation of various traits. The earliest studies have been on cognitive abilities; however, today, adoption studies are mostly focused on in psychopathology and physical characteristics (Yates, 2011). Studies on adoption are important in determining predisposition to a disease and in evaluating prenatal and postnatal factors (Ersan & Abay, 2001). Adoption studies are very important to explain the differences in behavior, personality and psychopathology, because in this study, the biological family is examined for genetic basis and the parent family is examined for environmental effects. In other words, the correlation between the adopted children and the adoptive parents and the correlation between the adopted children and the biological parents give the relative interaction of genetics and environment on the behavior studied. Basically, any similarity between the adopted child and the biological parents will reflect the influence of genetic factors, while the similarity between the adopted child and the adoptive parents will

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reflect the influence of environmental factors (DiLalla, 2004).

3.1.3. Twin Studies

After accepting the existence of genetic and environmental effects in human behavior, one of the most preferred methods in the field of behavioral genetics has been twin studies. These studies are important in terms of understanding the behaviors of monozygotic and fraternal twins and revealing the interaction of genetics and environment with the different behavior examples exhibited by individuals, while their genetic structures are exactly the same, especially in monozygotic (MZ) identical twins. According to Turkheimer (2000), twin studies are a remarkable method in examining the intimidating interaction of genes and environment in the formation and development of personality and behavior.

Twin studies do not show which gene is specifically affected by the relevant phenotype trait or a particular gene, but rather give the percentage of the variance explained by the genes. Because, assuming that identical and fraternal twins have similar environmental characteristics for the respective phenotype, heritability will depend on the difference in correlation between monozygotic and fraternal twins (Chew et al. 2011).

3.2. Molecular Genetic Methods

In traditional behavioral genetic studies, the genetic and environmental effects on individual differences in measuring family relationships and the impact of these relationships on individuals in families are tried to be estimated using quantitative techniques that analyze behavioral variability among family members (for example, twins) according to the degree of genetic relationship. In more recent studies, molecular genetic techniques have been used to analyze the relationship between behaviors and specific genes (Moore and Neiderhiser, 2014).

3.2.1. Linkage Analysis

Before the advent of modern molecular genetics, researchers did not have effective tools to pinpoint the genes underlying a trait. Linkage analysis, based on the matching of chromosomes, was one of the methods used by researchers before modern molecular genetics (Baker et al., 2004). In linkage studies, the genetic traits of interest are not directly observed but are inferred from what is known about chromosomal recombination. In such studies, data on a limited number of genes are used to make inferences about many nearby genes based on the idea that genes that are close together on a chromosome stay together. Although genes of interest are never observed, information about them can be obtained from observable genes (Markon, 2010). The method, in the most general sense, is based on testing the coexistence of a gene whose localization is sought and a genetic determinant whose localization is known between generations (Arısoy, 2004).

3.2.2. Candidate Gene Studies

It has more widespread use for behavioral genetic studies. In the simplest terms, in these studies, it is essential to compare a group of people (experimental group) who show a certain behavior characteristic with a group of people who do not have this characteristic (control group) (Kennedy, 2002). In other words, association studies focus on a single gene that has already been isolated as a candidate gene (hence also known as candidate gene studies). Through these studies, researchers try to determine whether variation in alleles of this gene is statistically related to variation in a particular trait. The DNA of each individual is genotyped to see which allele is present in the genetic location examined, and it is tried to determine that any allele is seen more frequently in the individuals in the experimental group, unlike the individuals in the control group (Baker et al., 2004).

3.2.3. Microarray Analysis

Microarray analyzes provide a powerful and increasingly popular field of study for studying changes in gene expression at large scale. This field enables simultaneous monitoring of changes in gene expression for several thousand or tens of thousands of genes. A single microarray experiment provides gene expression information not only about individual genes, but also about the collective behavior of gene compounds. The resolution of this common behavior also facilitates the study of biological events that have been impossible until now (Hariharan, 2003).

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3.2.4. Knockout Studies

In this technique, researchers disable a gene in stem cells using modern laboratory techniques. They then insert this gene into an embryo in a female's uterus. Once the puppies have grown and matured, they examine the germ cells (sperm and egg cells) to see if there has been any development in the modified stem cells. These germ cells are used to breed mice to create a mouse strain that lacks the target gene. As might be expected, these studies are not performed on humans (Baker et al., 2004).

3.2.5. Genome Wide Association Studies

GWAS aims to discover the genetic factors underlying phenotypic traits. In other words, GWAS examines the relationship between phenotypes and genetic variations or genotypes within the entire genome. The main purpose of GWAS is to identify or select the most appropriate SNPs that distinguish one individual from another or contribute to phenotypic differences between individuals (Utkin and Utkina, 2017).

4. GENOMARKETING AND EXAMPLES

After neuromarketing, which measures the neural activity of consumers in response to various products or advertisements through biometric measurement methods such as fMRI or EEG, companies are now looking for ways to target their customers based on genetics. Because while it is possible that differences in brain activity are affected by developmental or environmental factors, there is ample evidence to suggest that some of these differences are due to genes. Important steps have been taken in order to carry out similar studies through behavioral genetic research, and thanks to the knowledge of the genetic basis of human phenotypic characteristics, the development of personalized marketing strategies has begun to be paved. Although the ethical debates continue, the messages in the commercials of the companies show that the methods and practices in neuromarketing, neuroscience and marketing, which they are influenced by the evidence, are also used in the field of marketing with an interdisciplinary approach. Genomarketing is the new marketing discipline in which researches go one step further after neuromarketing.

Genomarketing is the application of genetic techniques to marketing in order to analyze and understand the behaviors promoted by variants of a particular gene towards an advertisement or product (Taveras, 2022). In advertising, it can be used to measure how effective a campaign is in persuading a potential consumer, and it is also a good research method for perceiving the desire and impulse to buy in the target consumer when they see an advertisement in question. Genomarketing can be used in advertisements or campaigns that will receive an immediate response about the product, regarding the customer's first reaction to a product. Likewise, this will help to understand what the triggers of the product or advertisement are that make consumers want to buy.

Advances in molecular genetics are leading to the exponential growth of the direct-to-consumer genetic testing industry. The private sector seeks to obtain the genetic data of its target audience and to develop personalized marketing strategies in all production and marketing processes. The first example was set by the music service Spotify in 2018, when it called for the genetic data of its 217 million users to be uploaded. The company argued that uploading genetic data to the system would allow it to create playlists that "match their genetic lineage" (Hassan 2018). Then, Mexico's national airline reported that it aspires to collect genetic data from its customers through its "DNA Discounts" campaign. The most important point of the campaign is the announcement that customers will benefit from discounted prices if they have "Mexican DNA" at the end of the DNA test (Vora, 2019). These actions mark a new era in which both consumers and companies have access to information that was rarely accessible until recently.

National genome projects are not limited to Mexico. The UK has set up a public initiative called BioBank and has started collecting large-scale genetic data from its people (Bycroft et al. 2018). National genome projects are also found in other countries, including Sweden and Singapore (Swede, Stone, and Norwood 2007).

A new market has started to be mentioned in the collection and storage of genetic data. Through the direct-to-consumer genetic testing (DTC-GT) marketplace, consumers deposit saliva samples in personalized DNA kits,

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which are sent to laboratories for genomic analysis. The reasons for consumers to have DNA testing in this process range from a desire to uncover forgotten family histories to assessing genetic susceptibility to diseases. However, the genetic data obtained is also extremely productive for the development of personalized strategies in terms of marketing. A byproduct of the growing DTC-GT market is the accumulation of huge genetic datasets. Industry leaders such as AncestryDNA and 23andMe encourage consumers to participate in surveys that explore everything from dietary habits to personality, laying the groundwork for linking numerous independent variables with genetic data (Farr, 2020). It could be predicted that it would be difficult for companies in the DTC-GT market to make millions of dollars by producing DNA kits. However, if the genetic data obtained is made available to companies, the size of the pie can be estimated. A good example would be that 23andMe, one of the leading companies in the industry, authorized access to its data to the pharmaceutical company GlaxoSmithKline with a $300 million deal (Brodwin, 2018).

The genetic data obtained at the end of all these efforts range from the relationships between gene and individual differences (MacArthur et al. 2017; Mills & Rahal 2019; Visscher et al. 2017), coffee or tea preference (Taylor, Smith, & Munafò 2018), adventurism (Karlsson). Linnér et al. 2019), schizophrenia (Egan, Goldberg et al. 2001), eating disorder (Mikołajczyk et al. 2010) and harm avoidance (Hashimoto et al. 2007). All these studies are studies that pave the way for genomarketing.

5. SOME EXAMPLES OF USE OF GENETIC DATA IN MARKETING

The global beauty and cosmetics industry has grown tremendously over the years and its marketing strategies have diversified. Considering the idea that marketing strategies should also be personalized when it comes to personal care, the use of genetic data in cosmetic products will not be surprising. Some research on the use of personal data, especially in the marketing of personal care products, seems important. For example, Shimomura et al. (2008) examines the relationship between hair type and genetics. To identify a gene involved in controlling hair texture, genetic linkage analysis was performed in six Pakistani families with autosomal recessive woolly hair (ARWH; OMIM 278150), and all six families showed linkage to chromosome 13q14.2–14.3. In all examples, pathogenic mutations were discovered in P2RY5, a nested gene encoding a G protein-coupled receptor and residing in intron 17 of retinoblastoma 1 (RB1). The researchers' findings suggest that disruption of 2RY5 underlies autosomal recessive hair formation, revealing a new gene involved in the broader determination of hair texture in humans.

Another study that can benefit from the marketing of personal care products for hair care is related to male pattern baldness. Pirastu et al. (2017) were able to identify 71 susceptibility loci that could explain 38% of the risk of male pattern baldness with the help of GWAS technology. The study, conducted with over 70,000 male participants, presents the results of a genome-wide association study that identified 71 independent replicated loci, 30 of which were novel. Showing that many of these loci contain pathology-related genes and highlight the pathways and functions underlying baldness, the researchers were able to identify and amplify a large number of new loci that, along with previously identified ones, could explain a large part of the predicted inheritance.

6. THE TIGHT RELATIONSHIP BETWEEN THE MAOA GENE AND MARKETING

Dopamine receptor genes are known to be closely related to human behavior. The investigation of the basis of financial decisions using molecular genetic methods has been studied not only with dopamine receptor genes but also with many different genes and polymorphisms. One of the genes considered in such studies is the MAOA gene. The MAOA gene provides instructions for making an enzyme called monoamine oxidase A. Specifically, monoamine oxidase A is involved in the breakdown of the neurotransmitters serotonin, epinephrine, norepinephrine, and dopamine. Signals transmitted by serotonin regulate mood, emotion, sleep and appetite. Epinephrine and norepinephrine control the body's response to stress. Dopamine transmits signals within the brain to produce smooth physical movements. Mutations in the MAOA gene cause monoamine oxidase A deficiency. The condition affects almost exclusively males and is characterized by mild intellectual disability and behavioral problems that include outbursts of aggression and violence (ghr.nlm.nih.gov). From this point of view, it would not be a surprise to find the causes of aggressive risk-taking, overconfidence, and biases such as self-attribution in

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financial decision-making behavior and accordingly over-trading, bearing excessive transaction costs and decreasing returns in the MAOA gene (Güngör, 2020).

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Mutations in the MAOA gene cause monoamine oxidase A deficiency. The condition affects almost exclusively males and is characterized by mild intellectual disability and behavioral problems, including aggressive and violent outbursts (Brunner et al. 1997).

Researchers think that an excess of certain neurotransmitters, particularly serotonin and norepinephrine, may impair the affected person's ability to control their impulses, leading to aggressive outbursts. Some studies suggest that decreased monoamine oxidase A activity alters the development of certain regions of the brain, which may contribute to intellectual disability and behavioral problems in people with monoamine oxidase A deficiency (Bach et al. 1988; Caspi et al. 2002; Chester et al. 2015; Huang et al. (2004; Kuepper et al. 2013; Brunner et al. 1993; Piton et al. 2013; Reif et al. 2012).

In the field of marketing, it is known that the personal characteristics of customers are extremely important in terms of marketing strategies. The MAOA gene is also a gene that may be widely used in marketing in terms of its relationship with personal characteristics. There are many studies linking MAOA u-VNTR on cognition, emotional arousal, and brain function during personality tests (Fan, Fossella et al, 2003; Meyer-Linderberg, Buckholtz et al., 2006; Buckholtz et al., 2008).

Fan, Fossella et al. (2003) compared the allele associated with better behavioral performance and the allele associated with poor performance, and found more activation in the anterior cingulate cortex in individuals with the allele associated with better performance. Meyer-Linderberg, Buckholtz et al., (2006) studied the neurobiological factors contributing to violence in humans and examined the allelic variation in the monoamine oxidase A (MAOA) gene as well as the MRI brain imaging technique. As a result of the study, it was determined that the low expression variant was associated with an increased risk of violent behavior, decreased reactivity of regulatory prefrontal regions, and significant limbic volume reduction during emotional arousal when compared with the high expression allele. Buckholtz et al. (2008) focused on Monoamine Oxidase A (MAOA), which encodes a key enzyme for monoamine metabolism associated with temperament and antisocial behavior. Results showed that men with the low expression variant exhibited reduced amygdala activation and increased functional connectivity with the ventromedial prefrontal cortex (vmPFC). In addition, it was stated that stronger functional connectivity was predictive of an increase in harm avoidance scores and a decrease in reward dependence scores, and the role of MAOA was also important here.

It is clear that we will come across similar studies more frequently in the literature. One of the most prominent of such studies, conducted through the use of behavioral genetic research methods, is a study that started its own advertising campaign in internet search engines. The study with an important result, known as the MAOA-Card, was done by De Neve and Fowler (2009). In the broadest sense, the study showed that a functional polymorphism in the MAOA gene is associated with credit card borrowing behavior. In a study by De Neve and Fowler (2009), which began self-advertising as the MAOA-Card, there are results suggesting that people with a particular low-yield variant of the monoamine oxidase A gene are significantly more likely to have credit card debt. Accordingly, having one or both of the MAOA alleles increases the probability of having credit card debt by 7.8% and 15.9%, respectively. At this point, if genetic data is used during customer segmentation, it would be very wise to make credit card campaigns to people with a low yield variant in the MAOA gene.

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Finally, there are many studies between gambling addiction and high-risk financial choices and MAOA. In studies on the neurobiological basis of economic risk taking, studies in which the MAOA gene, which is thought to be closely related to aggressive behavior, is considered in terms of risk-taking behavior in financial decisions, has generally been discussed together with gambling addiction. In addition, games of chance are considered as a variable in such studies, since they involve very high risks despite a very high and low probability of winning return.

Perez de Castro et al. (2002), the MAOA-uVNTR polymorphism 3- and 4-copy alleles were found to be the three most common variants, and the allelic frequency of the 3-copy allele was found to be higher in the experimental group with gambling addiction and lower in the control group. This result is a remarkable result in the marketing strategies to be made about the marketing of games of chance.

Zhong, Israel et al. (2009) discussed together with MAOA, games of chance and the behavior of taking out insurance, which are unlikely to win and can be called risky ventures. Despite the high risk-prone behavior of people in games of chance, on the other hand, the findings of the researchers, who describe buying insurance as a handicap, show that people with the high activity (4-repeat) allele of the MAOA gene are more likely to engage in risky ventures when compared to people with the low activity (3-repeat) allele. There is a tendency for people with the 4-repeat allele to buy less insurance. This can be seen as an important result in insurance marketing.

7. CONCLUSION

Future discoveries in the field of behavioral genetics will undoubtedly have to take seriously the interaction of genetics with the environment to influence behavior, genetic variations, and trauma during and after birth. But until recently, marketing researchers have largely neglected the influence of genetics on consumer behavior. However, there is a clear need for studies that aim to evaluate the utility of genetic tools for the advancement of marketing theory and practice, adopt behavioral genetic methods and eliminate ethical concerns.

Many genetic basis of phenotypes of interest to marketers have been described recently. Research in related fields points to genetic influences on many traits that are central to consumer behavior theory and practice. The most obvious common feature in these studies is the behavioral genetic methods used by the researchers. Behavioral geneticists use more readily available measurements as scales for traits that are difficult to measure. This is an approach that shows that genetic discovery increases its statistical power (Rietveld et al., 2014). Genetic research of consumer behavior could similarly benefit from such an approach.

Behavioral genetics research typically focuses on identifying variants that have causal effects on a target trait and measuring the variance they explain. However, many marketing applications of genetic data do not depend on whether genetic variants are indeed causally related to a trait, but rather whether they are more informative than other readily available metrics. In other words, genetic associations carry information useful for identifying consumer segments and reaching the target consumer.

Marketing practices such as segmentation and targeting often rely on identifying people at the extremes of a trait's distribution, as opposed to explaining variance in the general population. For example, a marketer interested in mobile phone marketing is interested in reaching customers willing to pay to buy a luxury class mobile phone, not heterogeneity in mobile phone usage trends. At this point, Miller et al. (2012) revealing possible relationships between cell phone usage habits and genetics should be seriously examined.

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