Individual Differences, Ethnicity, and Aging: What Can Gero-genetic Studies Contribute?

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Introduction

The purpose of this article is to present the value of using quantitative genetic approaches to understanding individual differences and ethnic diversity in aging. There are three major points to be discussed: 1) the difference between race and ethnicity, 2) inter-versus intra-group differences, and 3) the contribution of quantitative genetics methods to understanding individual variation within ethnic groups and differences and similarities between ethnic groups. This paper also includes a discussion of several twin studies of older African Americans.

The rapid increase in elderly across a variety of countries and cultures demands that scientists appreciate and acknowledge similarities and differences in adulthood and aging in a greater world context. Similarities across cultures provide support for the universal nature of aging that is proposed in theories of aging. Differences in aging among ethnic groups provides support for the existence of fluid and mutable dimensions. Understanding differences between ethnic groups allows scientists to identify conditions that reduce the quality of life across groups and diminish practitioners' ability to provide care necessary to optimize the later years of life for the world's aging populace.

It is important to note that the concept of ethnicity is not synonymous with race. Ethnicity involves ways of being, norms, mores, beliefs, and rituals. Ethnicity, in part, represents a behavioral dimension of aging. Conversely, race is a biological feature that typically is described in relation to physical descriptors such as skin color or facial features. In many of the past discussions concerning race, heterogeneity within race that arises from cultural influences has not been addressed. For example, the Hispanic race might include, Mexican Americans, Latin Americans, and Puerto Ricans, all of whom reflect varying historical ethnicity and levels of assimilation into the United States. While inherently these individual groups are different, by collapsing the groups under one ethnic umbrella and then comparing them to whites, important attributes within each group are lost. These distinctions are important for interpreting individual differences within and across ethnic groups. Thus, race in many

ways is too simplistic a proxy for understanding individual differences in aging among people of similar race but different ethnic backgrounds.

The second issue is the importance of intra-group studies and their relation to inter-group comparisons. Intra-group individual variability represents an important domain for gerontological research on ethnic diversity. Understanding ethnicity and aging from an individual differences perspective requires one to appreciate and understand intra-group differences. Ethnic groups vary in their beliefs, traditions, and perceptions of aging. In addition, the amount of variability observed within a culture differs from ethnic group to ethnic group. For example, Jackson (1985) notes that there is greater variability within aged African-Americans as a group than found in comparisons between Caucasian and African-Americans. This observation is likely true for various ethnic groups within the United States and across the globe.

Between-group differences observed across aged ethnic groups have arguably not been adequately modeled statistically. One reason for the lack of adequate statistical models is that for many conceptual approaches and variables of interest, the within group sources of individual variance in aging are not the same as the between-group sources of variance (for a discussion see, Whitfield & Baker-Thomas, 1999).

The challenge to scientists is how to maintain an appreciation for individual variation that characterizes aging within various ethnic groups while keeping the importance of across-group understandings of the aging process. One useful approach to understanding individual differences is quantitative genetics.

Quantitative genetics is the study of the inheritance of differences between individuals that are measured in degree (quantitative) rather than in kind (qualitative) (Falconer, 1981). The goal of quantitative genetics is the separation of the origins of individual differences into descriptive components of variance. Working under the theory of the relationships between family members (parent-child, siblings, or twins), expectations of genetic and environmental similarity are established. These expectations are used to calculate the proportions of individual variability that arise from genetic and environmental influences that impact a trait. The decomposition of genetic and environmental influences is an important initial step toward understanding individual differences in the aging process (Plomin & McClearn, 1990b; Whitfield, 1994).

Quantitative genetic approach divides individual variation into genetic, shared environmental, and non-shared environmental components of variance. Genetic variation, for purposes of this article, is the sum of the additive effects from genes influencing a behavioral or biological trait. The underlying premise of the genetic component is that multiple genes (polygenic) or genes having multiple effects (pleiotropy) (see Plomin, Defries, & McClearn, 1990a) work in an additive manner to influence a be-

havioral trait. It should be noted that genes can also act in a nonadditive manner wherein alleles interact at a single locus (i.e., dominance) or multiple loci (i.e., epistasis) (for more see, Plomin et al., 1990a; Falconer, 1981). In some age-associated diseases, such as familial Alzheimer's disease and Huntington's Chorea, dominant, single genes have been found to be responsible for these diseases. Single dominant genes are typically not the case for most aging phenomena. Dominance is reflected in intra-pair correlations when members of monozygotic twin pairs are more than twice as similar as dizygotic twin pairs.

Environmental effects are partitioned into those that are common (shared) or unique (non-shared) (see Plomin et al., 1990a). Shared environmental variation is the phenotypic variation due to subjects living in the same family, thus sharing the same environment. Non-shared environmental variation is the component of phenotypic variance that can be attributed to the environmental factors, not shared by family members, making individuals in the same family different from one another. Plomin and Daniels (1987) provide an excellent illustration of the importance of non-shared environmental variance on numerous dimensions of behavior such as personality. In addition, measurement error is included in the non-shared environmental component.

Currently, there are several quantitative genetic studies of adulthood and aging (*gero-genetic*) in this country as well as in Sweden, Denmark, Australia, Russia, and in various parts of Europe. What can these studies contribute to our understanding of ethnicity, individual differences, and aging? Gero-genetic methodology represents a "natural study" for examining how different ethnic groups produce both distinctive and common phenomena in the process of aging and the etiology of those phenomena. These methods represent a natural study because there are few phenotypes for which we can alter the actual genes that may be involved in genetic variation. However, we can study populations that have different environmental conditions to examine the influence of ethnicity on individual differences in various biobehavioral constructs of aging. These environmental influences involve more than simply socio-demographic factors such as marital status, occupation, or education. These factors would also include contextual influences such as neighborhood or national region (e.g., north vs. south), and social policies (e.g., segregation).

The cultural groups involved in the aforementioned gero-genetic studies possess distinctive attributes by virtue of their language, life-style, socioeconomic status, and historical experiences. These factors produce differences in environmental variance across ethnic groups. The difference in environmental variance can be evident in both within family and extrinsic or non-shared environmental factors.

The relative influence that environmental factors have on aged individuals within an ethnic group must also be considered within a life-span development framework. For

example, a general finding is that as we grow older, genetic factors become very important in individual variation. This finding does not (necessarily) mean that genetic variation increases with age. It may be more the point that environmental influences have less effect on the trait of interest as individuals age. For example, gero-genetic studies of cognition have found greater proportions of genetic variance compared to studies of younger adults and children (McGue & Bouchard, 1994; Pederson, et al., 1992). In later life, individuals have experienced most of the typical environmental contributors such as education and perhaps parental socioeconomic status that contribute to variability in cognitive functioning. With some of the most powerful environmental factors perhaps behind older individuals, genetic factors in later life can then evince more influence in individual differences. This is not to say that the aged cognitive system is not flexible or enhanced by environmental interventions, but in a "natural condition" (without intervention), this life-span change in the sources of individual variability appears to occur for cognitive functioning.

To grasp the significance of understanding similarities and differences between aging ethnic groups, is it important that this methodology be capable of comparing estimates of genetic and environmental influences between ethnic groups? What interpretation about aging could be drawn from differences in the genetic and environmental estimates between different ethnic groups? One plausible inference is that sociocultural influences drive differences in estimates of environmental and genetic influences between ethnic groups (Whitfield & Miles, 1995). Quantitative genetic assumptions are based on estimating 100% of the variance across individuals. The estimates of genetic or environmental influence are dependent upon the role each of these forces play in the individual variation observed. These authors propose that environmental variability is responsible for most of the differences in genetic and environmental estimates of individual differences that would arise from gero-genetic studies of individuals from different ethnic groups. Thus, the individual variation due to genetic factors within ethnic designations is assumed to be relatively similar across any ethnic groups. This is not to say that there are not allelic differences between ethnic groups. However, the identification of allelic differences between groups for complex phenotypes would require large sample sizes to obtain significant differences.

A statistical example of this approach to study the environmental contribution to group differences is presented in an article by Carmichael and McGue (1995), who reported a cross-sectional study of body mass index (BMI) in a sample of adult twins. Using twins from 18-81 years of age and creating three age groups, they examined whether the relative influence of genetic and environmental factors on BMI, height, and weight differed across the life-span. They found that genetic variance remained stable while non-shared environmental variance increased with age. This scenario resulted in decreases in heritability with age for each of the measures being driven by increases

in extrinsic idiosyncratic influences. While this study did not compare ethnic groups, it does demonstrate how this approach could provide important insights into similarities and differences in sources of individual variation across groups.

An example of how environmental differences might produce ethnic differences in a phenotype is provided by Whitfield, Grant, Ravich-Scherbo, Marutina, and Ibatoullina (1999). They compared data from Russian twins to results from Swedish twins on forced expiratory flow. Forced expiratory flow is a useful predictor of remaining life in older adults (e.g., Burrows, 1990; Tager, Segal, Speizer, & Weiss, 1988). In both samples, the affects of age, gender, height, and smoking were partialled out of FEV, and quantitative genetic analyses were conducted.

The results indicated that there were differences between the Swedish and Russian studies in the relative contribution of genetic and environmental factors to FEV. The proportion of variance on FEV that was attributable to genetic factors was 57% for the Swedish subjects compared to 28% for the Russian subjects. In addition, shared environmental influences were not important in the Swedish sample but accounted for nearly half of the variance in the Russian sample. This example highlights the possible differences between ethnic groups that may arise in cross-cultural quantitative genetic studies.

Twin Studies of African Americans

Toni Miles and her colleagues have conducted the Black Elderly Twin Study (BETS) (Miles, Ferner, Goldberg, & Meyer, 1994). The BETS was designed to gain a better understanding of the genetic contribution to physical frailty among older African American and Caucasian populations using both epidemiologic and quantitative genetics methods. The BETS used date of birth, race, and characteristics of the health insurance claim number (HIC) from Medicare records to identify potential pairs for study. Separate strategies were developed for finding potential male and female pairs. The BETS project's most important contributions to date have been establishing the feasibility of an algorithm to identify a national cohort of older African American and Caucasian twins from the Medicare enrollment files (Goldberg, et al., 1997) and the identification of genetic and environmental influences on physical frailty (Miles, 1997).

Another registry of twins that contains African-Americans is the Vietnam Veterans twin registry (Eisen, True, Goldberg, Henderson, & Robinette, 1987). This registry is an excellent source for a quantitative genetic study of adult African-Americans, although it has the limiting characteristics that it consists only of men and the twins in this sample are young on average compared to most gerontological studies.

One of the most recent African American twin studies is the Carolina African Ameri-

can Twins Study of Aging (CAATSA). CAATSA is designed to examine health and psychosocial factors in older adult African American twins between 50 and 85 years of age. The variables include measures associated with chronic illness (hypertension, cardiovascular disease, arthritis), health behaviors, personality, stress, and memory.

The study design is a classical twin design extended to include siblings and singletons so the impact of familial dynamics and shared environmental influences might be better estimated. The location for this study was derived in part from the estimates from BETS that indicated that North Carolina had one of the highest estimates of African American twin pairs over 65 years of age. Using birth records from 19 counties in North Carolina with high concentrations of African American births between 1913 and 1950, we have developed a registry with the names of over 6200 twin pairs. We locate twins using information from web based white pages, a credit bureau, and voter registration records. With three counties remaining to be searched, we have over 1300 names of twins.

An example of a possible extension of quantitative genetic research could be the study of alcohol use in African-Americans by employing a classical twin study. An advantage of using twins over siblings or other pairs of relatives is that comparisons are made between genetically related individuals that have experienced developmental events during similar time periods. However, given the relatively low rate of births that are twins (although this is higher in African-Americans than other ethnic groups in the United States) (Segal, 1990), a twin study of African-Americans might require a data collection site that is densely populated with African Africans such as done in CAATSA or using a national population based sample such as in the BETS.

Summary

As we learn more about aging in this country and in others, there are distinctive cultural influences that need to be considered in the study of majority and minority populations. Of equal importance is appreciating individual differences among these groups and considering conceptual and methodological approaches that highlight the variation that exists among these groups of aging people.

Accounting for the individual variation and appreciating the cultural influences that contribute to differences provides a better understanding of why people experience aging differently within and across ethnic groups. While this approach can provide useful *initial* insights into aging, prospective studies should combine other individual differences approaches so that specific mechanisms involved in non-shared environmental variance can be identified. Advances in conceptual and methodological approaches can be gained from merging different research strategies. The bridging of such strategies will better inform us how genetic **and** environmental interventions

can contribute to enhancing the lives of aged individuals.

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References

Carmichael, C. M. & McGue, M. (1995). A cross-sectional examination of height, weight, and body mass index in adult twins. Journal of Gerontology, 50A, 237-244.

Eisen, S., True, W., Goldberg, J., Henderson, W., & Robinette, D. (1987). The Vietnam Era Twin (VET) registry: Method of construction. Acta Geneticae Medicae et Gemellalogiae, 36, 61-66.

Falconer, D. S. (1981). Introduction to Quantitative Genetics. New York, Longman.

Goldberg, J., Miles, T. P., Furner, S., Meyer, J. M., Hinds, A., Ramakrishnan, V., Lauderdale, D. S., Levy, P. S. (1997). Identification of a cohort of male and female twins aged 65 years or more in the United States. American Journal of Epidemiology, 145(2), 175-183.

Jackson, J. J. (1985). Race, national origin, ethnicity, and aging. In R. H. Binstock and E. Shanas (Eds.), Handbook of Aging and Social Sciences. (pp 264-303). New York: Van Nostrand-Reinhold.

McGue, M., Bouchard, T., Iacono, & Lykken, D. T. (1993). Behavioral genetics of cognitive ability: A lifespan perspective. In R. Plomin & G. McClearn (Eds.), Nature, Nurture, & Psychology. (pp.59-76). Washington D.C.: A P A.

Miles, T. P. (1997). Population-based, genetically informative sample for studies of physical frailty and aging: Black elderly twin study. Human Biology, 69(1), 107-120.

Miles, T., Ferner, S., Goldberg, J., & Meyer, J. (1994). Black Elderly Twin Study: Mail and telephone pilot survey. Gerontologist (Special Issue), 34, 217.

Pedersen, N. L., Plomin, R., Nesselroade, J. R. & McClearn, G. E. (1992). A quantitative genetic analysis of cognitive abilities during the second half of the life span. Psychological Science, 3, 346-353.

Plomin, R., & Daniels, D. (1987). Why are children in the same family so different

from one another? Behavioral and Brain Sciences, 10, 1-16.

Plomin, R., DeFries, J. C., & McClearn, G. E. (1990a). Behavior Genetics, (2nd ed.). New York: W.H. Freeman.

Plomin, R., & McClearn, G. E. (1990b). Human Behavioral Genetic and Aging. In J. E. Birren & K. Warner Schaie (Eds,) Handbook of The Psychology of Aging, (pp. 77). San Diego: Academic Press.

Segal, N. L. (1990). The importance of twin studies for individual differences research. Journal of Counseling and Development, 68, 612-622.

Whitfield, K. E. (1994). The use of quantitative genetic methodology to gain insights into the origins of individual differences in later life. Experimental Aging Research, 20(2), 134-143.

Whitfield, K. E., & Baker, T. A. (1999). Individual differences in aging among African-Americans. International Journal of Aging and Human Development, 48(1), 73-79.

Whitfield, K. E., Grant, J. D., Ravich-Scherbo, I., Marutina, T., & Ibatoullina, A. (1999). Forced expiratory volume: A cross-cultural comparison. Experimental Aging Research, 25(3), 255-266.

Whitfield, K. E. & Miles, T. P. (1995). Studying ethnicity and behavioral medicine: A quantitative genetic approach. In J. R. Turner, J. K. Hewitt, & L. R. Cardon, Behavior Genetic Approaches in Behavioral Medicine, (pp. 201-213). New York: Plenum Press.