Social Science Research 43 (2014) 184–199

Contents lists available at ScienceDirect

Social Science Research

journal homepage: www.elsevier.com/locate/ssresearch

# What can we learn from twin studies? A comprehensive evaluation of the equal environments assumption

Jacob Felson

*William Paterson University, 300 Pompton Road, Wayne, NJ 07470, United States*

ARTICLE INFO

*Article history:*
Received 13 August 2012
Revised 30 September 2013
Accepted 11 October 2013
Available online 22 October 2013

*Keywords:*
Behavior genetics
Twin studies
Equal environments assumption

ABSTRACT

Twin studies are a major source of information about genetic effects on behavior, but they depend on a controversial assumption known as the equal environments assumption (EEA): that similarity in co-twins' environments is not predictive of similarity in co-twin outcomes. Although evidence has largely supported the EEA, critics have claimed that environmental similarity has not been measured well, and most studies of the EEA have focused on outcomes related to health and psychology. This article addresses these limitations through (1) a reanalysis of data from the most cited study of the EEA, Loehlin and Nichols (1976), using better measures, and through (2) an analysis of nationally representative twin data from MIDUS using more comprehensive controls on a wider variety of outcomes than previous studies. Results support a middle ground position; it is likely that the EEA is not strictly valid for most outcomes, but the resulting bias is likely modest.



## 1. Introduction

Over the last four decades, behavior geneticists have found evidence that genes influence nearly all human behavior (Turkheimer, 2000; Freese, 2008). For outcomes like personality and educational attainment, researchers have found that the explanatory power of genes exceeds that of parental socialization (Rowe, 1995; Harris, 1999; Nielsen, 2006) (but see Nielsen and Roos, 2011). Conclusions such as these strike at the core of the sociological perspective, which maintains that the causal power of cultural forces far exceeds the causal power of genes. Although an increasing number of sociologists have integrated behavior genetic perspectives into their work (Guo and Stearns, 2002; Nielsen, 2006; Guo et al., 2007; Freese, 2008; Adkins and Vaisey, 2009; Conley et al., 2013), the idea that genes have a major influence on social behavior has not yet entered into the mainstream sociology curriculum. It is probably safe to say that many, if not most, sociologists remain skeptical that the effects of genes on social behavior are strong enough to warrant a fundamental shift in outlook.

Whether this skepticism is warranted depends to a large extent on the validity of twin studies, which provide much of the evidence for the importance of genetic effects on social behavior.[1] In the classic twin study (CTS), data are collected from monozygotic (MZ) twins, who are virtually identical genetically, and from DZ twins, who share about 50% of their segregating genes on average.[2] Similarity on a given trait is estimated, typically via correlation, for the MZ twins and for the DZ twins. When the correlation between outcomes of co-twins is higher among MZs than among DZs, a genetic effect on the outcome is inferred.

A key point of contention here is that genetic effects derived from twin studies may be biased upward if MZ co-twins share more similar environments in a way that induces greater similarity between co-twins on the outcome in question (Horwitz et al., 2003; Joseph, 2010; Conley et al., 2013). Although it is well-known that MZs experience more similar

*E-mail address:* felsonj@wpunj.edu

[1] Evidence for genetic effects also comes from adoption studies and from molecular genetic studies, both of which I discuss later.

[2] Segregating genes are genes that vary within the human species.

0049-089X/$ - see front matter © 2013 Elsevier Inc. All rights reserved.
http://dx.doi.org/10.1016/j.ssresearch.2013.10.004

environments than do DZs (Holmes, 1930; Wilson, 1934; Mowrer, 1954; Smith, 1965), there is little evidence that environmental similarity contributes to similarity in outcomes (Kendler et al., 1993; Conley et al., 2013). For this reason, behavior geneticists have generally held that twin studies are unbiased by environmental similarity between co-twins. This assertion is known as the Equal Environments Assumption (EEA), and it is disputed by critics who argue that the measurement of environmental similarity suffers from low validity and low reliability (Pam et al., 1996; Horwitz et al., 2003; Richardson and Norgate, 2005; Joseph, 2010).

This paper evaluates the EEA in a comprehensive manner and improves on previous research in at least three ways. First, I address concerns about reliability of measurement by estimating the reliability for each measure of environmental similarity that I use and considering how random error in measurement affects the results. Second, I address concerns about validity by measuring environmental similarity in a more comprehensive way than previous researchers have done. Third, unlike previous analyses which generally focused on a small number of outcomes within a particular subfield, in my main analysis, I examine a wide range of outcomes. By examining a range of disparate outcomes within a single dataset, I am able to discern whether environmental confounding of genetic effects is greater for some types of outcomes than it is for others.

The article is organized as follows. First, I explain why the results of twin studies are still worth debating today in an era of molecular genetics. Next, I review the rationale by which researchers make inferences about the effects of genes based on comparisons of monozygotic (MZ) and dizygotic (DZ) twins. Then I review previous research that has tested the equal environments assumption for specific traits. Included in this review is a reanalysis of data used in the most cited evaluation of the EEA, Loehlin and Nichols (1976). Finally, I test the EEA with respect to a variety of outcomes using a nationally representative sample of twins.

## 2. Why focus on twin studies in an age of molecular genetics?

In the classic twin study, phenotypic variation is parsed into environmental and genetic components. Some argue that this approach is no longer sensible in light of recent discoveries indicating that genetic effects are much more complex and contingent than previously believed (Charney, 2012). Though it was once thought that particular genetic variants (i.e. SNPs) might individually have a substantial impact on variation in complex phenotypes, a search has revealed very few strong, replicable effects (Manolio et al., 2009; Chabris et al., 2012). In addition, research has shown that heritability is not only about DNA; aspects of the biochemical system that regulate genetic expression, known as the epigenome, are also heritable (Charney, 2012). In light of these findings, why is it useful to validate an assumption underlying twin studies?

One reason it is important to evaluate the EEA is to help understand why estimates of genetic effects from twin studies are large when the effects of any particular SNP are small (Manolio et al., 2009). Part of the answer seems to be that the effects of genetic variants, while individually small, cumulate into larger effects. Using data on hundreds of thousands of SNPs identified in DNA samples from several thousand people, researchers have found more direct evidence for substantial genetic influence. They have found that the proportion of shared SNPs among a group of people correlates with phenotypic variation in that group on a variety of traits such as general intelligence (Davies et al., 2011; Chabris et al., 2012), policy preferences, education (Benjamin et al., 2012), neuroticism and extraversion (Vinkhuyzen et al., 2012). To some extent, this evidence supports the overall conclusion of twin studies that genes exert non-negligible effects on complex behaviors. On the other hand, estimates of cumulative genetic influence using molecular-level data have tended to be substantially lower than the corresponding estimates from twin studies. For example, a recent estimate of the proportion of variance in educational attainment explained by genes from twin studies was 0.35, whereas the corresponding estimate from molecular-level data was 0.16 (Benjamin et al., 2012). What accounts for the discrepancy? Since the SNP data that was collected did not capture all genetic variation, it is possible that studies using data at the molecular-level underestimate the effects of genes. Alternatively, twin studies may overestimate genetic effects due to violations of the EEA. A comprehensive examination of the EEA can help resolve this question.

## 3. Estimating heritability from twin studies

Before reviewing previous research on the EEA, I explain how twin studies can provide estimates of genes' explanatory power for a given trait provided that the equal environments assumption is valid. I consider a simple model in which there is no effect of assortative mating and no gene-environment interaction. The analysis begins by estimating correlations between co-twins on the trait of interest separately for MZ and DZ pairs. Because MZ twins share 100% of their genes and DZ twins share on average 50% of their segregating genes, co-twin correlations ($r_{MZ}$ and $r_{DZ}$) can be decomposed into a heritability component ($h^2$) and a shared environmental component ($c^2$), as shown in Eqs. (1) and (2). If the equal environments assumption (EEA) is true, then $c^2_{MZ} = c^2_{DZ}$ and $h^2$ can be estimated easily by subtracting Eq. (2) from Eq. (1).[3] If on the other hand the EEA is false, then $c^2_{MZ} \neq c^2_{DZ}$ and estimates of $h^2$ will tend to be biased upward in twin studies.

[3] Estimation of heritability and shared environmental effects is usually accomplished with a structural equation model, but the logic of those models is analogous to the logic of the simpler models shown here.