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# Genetic and Environmental Influences on Playing Video Games

Toqa Hassan

College of Communication and Information, Kent State University, Kent, Ohio, United States of America

**ABSTRACT**

In this study, I use a representative survey from the German Twin Family Panel ($N$ = 5,472) to examine the extent to which genetic and environmental factors account for time spent playing video games on personal computers and gaming consoles. Results show that genetic variation among twins explains a non-trivial amount of variation in video game play. Through ACE modeling techniques, I find that between 25% to 39% of the total variance in time spent playing video games can be attributed to shared genetic traits with the remainder explained by shared environmental factors (e.g., parenting and culture) and environmental attributes unique to individuals. This study and its findings provide a starting point for future genetic and neurological research on video game use and effects.

According to the annual report of the German Games Industry Association (2022), Germany's video game trade association, nearly 6 in 10 Germans play video games. Similarly, two thirds of Americans play video games on a weekly basis (Entertainment Software Association, 2022). Recent researchers (Johannes et al., 2021) collaborating with game companies in the United States found that time spent playing video games is positively related to players' overall well-being and specifically, players' social well-being (Bowman et al., 2022). In addition to gaming time, video games and virtual reality have the potential to improve psychological outcomes and reduce violent and negative behaviors (Bowman et al., 2020).

In analyzing gaming time, Johannes et al. (2021) found that the relation between playing time and well-being were associated with gamers' needs for satisfaction and motivation. Hartmann and Klimmt (2006) suggest that individuals select and use games due to a variety of factors including individual factors, such as motivation and personality, as well as neurobiological factors as suggested by Weinstein and Lejoyeux (2015). Researchers have also linked time spent playing violent video games to differences in specific genes that regulate neurotransmitters such as serotonin (Nikkelen et al., 2014), but the

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**CONTACT** Toqa Hassan ✉ thassan@kent.edu College of Communication and Information, Kent State University, 334 Franklin Hall, 550 Hilltop Dr, Kent, Ohio 44242-0001, United States of America

overall genetic contribution to individual differences in time spent playing video games, violent or otherwise, remains understudied.

This study examines the degree to which broad genetic and environmental factors explain variation in time spent playing video games on personal computers and game consoles. Generally, screen time has been shown to have varying positive and negative effects depending on the users (Browne & Walden, 2020), the content viewed, the medium, and the context (Domingues-Montanari, 2017). This study particularly focuses on gaming time since it can consistently capture gameplay intensity across individuals regardless of physiological or gaming differences and preferences such as game content, mode, or platform.

Secondary twin data from the German Twin Family Panel is analyzed through ACE modeling techniques to produce heritability estimates for both types of gaming, which indicates how much trait variation in a population can be attributed to genetic variation between individuals (Lockyer & Hatemi, 2018). The results suggest that genetic traits account for substantial variation in time spent playing video games on both game consoles and personal computers. The findings indicate that variation in time spent playing video games is partly due to variation in genetic differences as well as environmental factors.

## Motivations for Media Selection

Media selection theories like uses and gratifications (Blumler & Katz, 1974; Rubin, 2009), selective exposure (Klapper, 1960), and mood management (Zillmann, 2000) have proposed psychological, cognitive, and emotional mechanisms for differences in media selection (see, Oliver, 2002). Although such seminal theories are comprehensive of psychological and behavioral explanations of media use, they consider media behaviors to be heavily shaped by the social environment. Moreover, they do not account for the biological origins that might impact human behavior. For example, Ferguson and Dyck (2012) proposed to retire the General Aggression Model since it does not account for genetic and neural interaction effects with the environment to influence aggressive behavior. In addition, Sherry (2001) and Weber et al. (2008) argue for a paradigm shift toward a truly neurophysiological approach that measures the etiology of media and communication behaviors.

A more recent framework, the differential susceptibility to media effects model (DSMM), suggests that media use and selection are fundamentally dependent on three inter-related groups of traits: dispositional, developmental, and social (Valkenburg & Peter, 2013). While social and developmental traits include social and cultural characteristics that make individuals susceptible to media use, the present study focuses on the DSMM's dispositional traits. Within the DSMM, dispositional traits include individual differences

that are stable across the lifespan such as cognition, personality, and temperament (Valkenburg & Peter, 2013).

While the DSMM (Valkenburg & Peter, 2013) does not explicitly include genetics as dispositional traits, the DSMM does recognize the possible influences of genetics on media behaviors (Piotrowski & Valkenburg, 2015). Research grounded in the DSMM has found indirect genetic effects on media selection and susceptibility (see, Piotrowski & Valkenburg, 2015). The only study guided by the DSMM with a focus on genetic dispositions and their link to gaming is Nikkelen et al.'s (2014) study on media violence exposure among children with attention-deficit/hyperactivity disorder (ADHD). The researchers used Valkenburg and Peter's (2013) disposition-content congruency hypothesis to estimate the extent to which genetics as individual differences influence exposure to violent media, including television, DVDs, and video and computer games.

Nikkelen et al. (2014) demonstrated that differences in 5-HTTLPR, a region of the 5-HTT gene that regulates how the brain processes excess serotonin, contributed to variation in the use of violent media, including video games, and subsequent ADHD-related behaviors among children. Other empirical research has also shown links between genetic disposition and media use. Focusing on time, Browne and Walden (2020) found that the CHRNA4 gene impacts time spent viewing information online. The CHRNA4 gene plays a major role in tolerance, reward, and the modulation of dopamine (Han et al., 2011). The influence of this gene on information search was found to vary by gender, age, frequency of internet use and years of internet experience (Browne & Walden, 2020), all of which are considered which are dispositional and developmental traits in the DSMM.

It is important to note that both Browne and Walden's (2020) and Nikkelen et al.'s (2014) studies used the candidate gene approach where one gene previously associated with a personality trait, whether the CHRNA4 gene or the 5-HTT gene, is particularly examined. A limitation of candidate gene studies is that their results have widely not been replicable (Harden & Koellinger, 2020; Pasche & Yi, 2010). That is, there are no specific genes nor set of genes that moderate media use. Instead, it is likely that interactions between the human neurophysiological nature and the external environment moderates media behavior (Sherry, 2004), also known as gene-environment interaction (Lockyer & Hatemi, 2018).

Moreover, in Border et al.'s (2019) review of the effects of 18 genes on depressive behaviors, findings suggest that previous main effects or interaction effects of these genes on depression were false positives. These results are likely due to the small effect sizes of individual genes on expressed behaviors, or in other words, behaviors and traits are polygenic in that they are influenced by thousands of genes, with small effects (Harden & Koellinger, 2020). Additionally, Harden and Koellinger (2020) conclude that many candidate

gene studies used underpowered sample sizes. As such, Border et al. (2019), along with Harden and Koellinger (2020), call for abandoning the candidate gene approach and using more advanced molecular genetics approaches such as genome-wide association studies. Nonetheless, no other research in the communication nor other social science disciplines has explored the possible effects of genetics as biological individual differences on video game behaviors except for Nikkelen et al.'s (2014) study.

Although these two studies are examining the possible impacts genetics might have on expressed media behaviors, communication biology research using genetic data and twin study approaches is still developing in its early stages. Twin studies, especially those with large sample sizes and more statistical power (Martin et al., 1978), have an advantage to candidate-gene studies in that they measure the effects of both genetics and the social environment on behavioral traits. Sherry (2004) along with other scholars (Ferguson & Dyck, 2012; Lockyer & Hatemi, 2018; Plomin, 2018) call for research that acknowledges and measures both genetic and environmental effects on behaviors. As such, twin studies are used to disentangle the genetic from environmental influences and proportion the impacts of each on a certain behavior, like playing video games.

While Sherry (2001) calls for bio-behavioral research to investigate the etiology of media use, media and communication scholars have not thoroughly investigated the genetic effects on media use and more specifically, video games. Weber et al. (2008) highly encourage media research that is grounded in neurophysiological and biological influences to understand human behaviors. As such, researchers have examined video game addiction from a communication neuroscience perspective (Craighead et al., 2015), using rewarding video game stimuli with fMRI studies to understand cognitive control and neuropsychological processes (Huskey et al., 2018a) and examine task difficulty and flow processes (Huskey et al., 2018b). Despite the advance in cutting-edge communication neuroscience work, research on media behavioral genetics and their influences is still in its early stages, especially on video game selectivity and use.

### *Video Game Motivations*

Video games are unique in that they are interactive rather than passive media such as television, movies, and books (Granic et al., 2014). Video games are also different from other interactive media, such as social media, which are becoming highly-gamified platforms (Hristova et al., 2020). Unlike social media, video games have a predesigned narrative that can be interrupted and changed by players as they advance through the game's levels (Lee et al., 2006). Weber et al. (2014) explain that interactivity in video games can be explained in three levels. First is player input such as keystrokes that elicit output by the game with changes

to the position of the on-screen characters and the game environment (Weber et al., 2014). The second and third levels explain the concept of sequential game episodes that contribute to the game's narrative (Weber et al., 2014). Specifically, users play to get through the stages of a game to win and reach the end of a story (Weber et al., 2014). Video games are also interactive in that players choose which game to play based on when to play and who to play with (Weber et al., 2014). Raney et al. (2006) also suggest that selectivity based on game features such as title, design, storyline, and other features contribute to video game interactivity.

As such, the use and selection of video games can be understood through the process of allocating the necessary effort, time, money, and energy (Klimmt & Hartmann, 2006; Wang et al., 2018) to seek out enjoyment and express emotional responses (Oliver, 2002; Oliver & Raney, 2011). Players go through several "well-considered and intentional" processes (Klimmt & Hartmann, 2006, p. 134) to ensure that the chosen game, the device used, and the cognitive demands of a game meets their satisfaction and entertainment needs. As a result, video games can transport players (Oliver et al., 2018) to different realms by evoking a variety of emotions and reactions (Bowman et al., 2020) that further motivate more dedication and time committed to playing. Aspects of a game, such as responsiveness, competitiveness, and rewards, motivate players to continue playing for long durations (Klimmt & Hartmann, 2006).

From an evolutionary perspective, researchers have attempted to understand how certain behaviors have evolved into play behaviors over time. For example, Steen and Owens (2001) suggest that using entertainment media may tap into cognitive functions related to unconscious and conscious play systems from early human development. Huskey et al. (2017) suggest that play is an innate trait fundamental to human cognition. Additionally, Huskey et al. (2017) explain that variations in playing behaviors and abilities are due to biological factors, such as natural selection. Ohler and Nieding (2006) propose that gaming can be explained by preexisting play behaviors that are stable within human nature despite the changing forms of play over time. Despite this longstanding evolutionary research on video games, the present study is the first to investigate the genetic foundations of video gameplay using a behavioral genetics approach.

While research has primarily examined the social and psychological factors that motivate video game choice and play, Nikkelen et al. (2014) is the only study that briefly links genetic disposition with video game use. Additionally, Nikkelen et al.'s (2014) and Browne and Walden's (2020, 2021) work strongly suggests that other biological factors such as neurological and genetic factors predispose media use and selection. While researchers have examined the genetic dispositions related to media use, the origins of video game behaviors from a behavioral genetics perspective are yet to be investigated. Therefore, the goal of this study is to begin exploring the underlying biological motivational factors influencing game use and effects by starting with genetic traits using the classic twin study design.

### *Twin Studies in Communication*

Genetic traits are assumed to influence almost all psychological characteristics (Harden & Koellinger, 2020), and have been shown to explain differences in communication traits and behaviors, as suggested by recent twin studies. Specifically, twin research shows evidence for the heritability of media behaviors, such as political discussion (York, 2019), traditional and digital media use (Kirzinger et al., 2012; Miller et al., 2012), social media use (Ayorech et al., 2017; York, 2017), problematic internet and phone use (Deryakulu & Ursavaş, 2014, 2019; Vink et al., 2016), and news use (York & Haridakis, 2020). Analyzing and comparing twins' behaviors allows for the disentanglement of genetic influences from environmental influences (Knopik et al., 2016). Twin studies can identify the influences for expressed behaviors and whether behaviors are espoused due to heritability or factors of the social environment. While they can identify influences of expressed behaviors, twin studies do not use observed variables to understand the specific genetic and environmental influences. In other words, using a twin study approach will not indicate if any specific genes are related to video game behaviors, nor will they explain how certain aspects of the environment might affect players' gaming patterns.

Quantifying the latent genetic contribution to individual differences in time spent playing video games is an important first step in identifying a biological basis for gaming behavior. Heritability can help explain why individuals express different behaviors despite experiencing the same social environment (Lockyer & Hatemi, 2018). Since immediate family members are physically similar due to sharing an average of 50% of their DNA, with identical twin-siblings sharing 100% of their DNA, it is expected that observable behavioral similarities would exist as well.

Twin studies allow for identifying how much of the variation in time spent playing video games is attributed to genetic and environmental factors. In this paper, I use twin study data to estimate the extent to which latent genetic and environmental factors contribute to time spent playing video games. Parental controls on environmental (Wang et al., 2018) and cultural factors (Eklund, 2015) are expected to contribute to differences in gaming behavior. Additionally, it is also expected that latent genetic traits will contribute to differences in video game play, given research suggesting that genes influence all phenotypes (Harden & Koellinger, 2020), these exact estimates of variance are unclear. Therefore, I pose the following question:

(1) To what extent do genetic variation and environmental variation contribute to differences in time spent playing video games?

## Method

The study uses data from the German Twin Family Panel (TwinLife) by the GESIS – Leibniz Institute for Social Sciences (Diewald et al., 2020). TwinLife is a longitudinal study that began with the goal of creating a probability-based sample of twins from all regions of Germany (Mönkediek et al., 2019). TwinLife focuses on the social and psychological development of twins in society and is used to investigate psychosociological theories through behavioral genetic analyses (Hahn et al., 2016) like the classic twin design. TwinLife began interviewing twins in 2014 and follows up with the same twins and their families every other year for face-to-face interviews and conducts computer-assisted phone interviews in consecutive years (Krell et al., 2020). The first wave of the TwinLife project included four age cohorts starting with cohort 1 having twins born in 2009 and 2010 (Krell et al., 2020; Mönkediek et al., 2019). Those born in 2003 and 2004 are in cohort 2. Cohort 3 includes twins born in 1997 and 1998. Finally, twins born "between 1990 and 1993" are in cohort 4 (Lang et al., 2019, p. 2). This data is publicly available upon request through the GESIS Institute (Diewald et al., 2020) and continues to be updated and published as more interviews are conducted.

### *Classic Twin Design*

Twins are valuable study participants in estimating the genetic and environmental influences for a specific expressed behavior, such as gaming time. The biological factors and the social environments of twin pairs, although latent and unobserved in twin studies, allow for strong assumptions to be made regarding the genetic relatedness among identical and fraternal dyads (Plomin, 2018). After birth, identical and fraternal twins are assumed to share nearly the same environmental circumstances, for example, those associated with being reared in the same household (Derks et al., 2006). Twin studies rely on these assumptions to estimate how much individual variation in an expressed media behavior, specifically video game use, can be traced back to genetic and environmental factors (Knopik et al., 2016). However, it is important to note that twin studies cannot direct us to which aspects of genetics or features of the social environment contribute to the variation in behavior (Hatemi et al., 2010).

To investigate the effects of genetic traits on variation in time spent playing video games, survey items assessing time spent on computer games and game consoles were analyzed through correlations and ACE structural equation modeling (Knopik et al., 2016; Medland & Hatemi, 2009; York, 2020). While twin correlations can be indicative of genetic influence, they alone cannot be used to identify the extent to which gene and environmental aspects explain differences in behavior. ACE is therefore used as a type of latent structural

model that uses information known about biological twins to determine the amount of variance in a behavior that is attributed to unobserved genetic and environmental factors. An ACE model has three latent factors in which twins' shared additive genetic traits are represented by latent factor A, common environment by factor C, and unique environment by factor E. With A, C, and E being latent variables, claims cannot be made about specific additive genes contained in A, specific components of the common environment in C, nor aspects of the unique environment in E. The ACE model only decomposes the total variance in an observed trait, specifically gaming time, by latent factors. For further ACE model technical specifications and mathematical proofs see, Neale (2009).

## Participants

In line with Martin et al.'s (1978) recommended twin sample size of 600 twins or more, the twin sample used for this study includes over 5,000 twins. Additionally, twin participants ($N = 5,472$) in this study are unique in that they are twins from three different birth cohorts, providing responses from different age groups (see, Table 1). These cohorts provide information on behavior throughout the developmental transitions from childhood to adolescence to young adulthood (Hahn et al., 2016). Twins between ages 12–27 ($M = 18.55$, $SD = 4.9$) were asked about their average time spent playing games on personal computers and gaming consoles. Identical twins make up 45.36% of the sample ($n = 2,482$) while fraternal twins ($n = 2,990$) make up 54.64% of the sample. Zygosity was not specified for three twin-pairs in the sample and thus, these pairs were excluded from the analysis. Importantly, "only same-sex and no opposite-sex dizygotic twins were sampled for TwinLife" (Lang et al., 2019, p. 839). Female twins make up 54.04% of the sample, while male twins make up 45.96%. A full list of demographic characteristics for identical and fraternal twins is shown in Table 1.

## Measures

Video game time is reported by each twin through four survey questions. The survey asks two questions about computer games and two questions about

**Table 1.** Demographic Characteristics.

| | Identical Twins | Fraternal Twins |
|---|---|---|
| Sex | 2,482 (45.36%) | 2,990 (54.64%) |
| Male | 1,106 | 1,409 |
| Female | 1,376 | 1,581 |
| Age | $M = 19.07$ ($SD = 4.97$, 12–27) | $M = 18.11$ ($SD = 4.89$, 12–27) |
| German Born | 2,389 (96.25%) | 2,884 (96.45%) |

N = 5,472 twin pairs (2,482 identical, 2,990 fraternal).

game consoles. For computer and online games, participants were asked, "How long do you spend, on average, per day with the following devices or activities? Please indicate how much time you spend on ... computer games (also online) ... hours per day (school and workdays)" (Diewald et al., 2020, p. 242). For weekend days, they were asked "How long do you spend, on average, per day with the following devices or activities? Please indicate how much time you spend on ... computer games (also online) ... hours per day (weekends)" (Diewald et al., 2020, p. 244).

The same two questions were asked regarding gaming consoles. Questions inquiring about game consoles provided examples of devices, such as Nintendo, Xbox, and PlayStation (Diewald et al., 2020). Each twin provided hourly estimates for weekdays and weekend days. These items are recorded as continuous variables. Prior to the analysis, hours per weekday and weekend day were summed and used to generate a single continuous variable that accounts for the total number of hours spent playing video games per week. Of note, self-reported time is a complicated measure since it is players' perceptions of how long they spent playing (Scharkow, 2016). Additionally, time may be perceived to pass more quickly when activities are more entertaining, leading to miscalculations of self-reported time (Xu & David, 2018). I discuss possible limitations with time-based self-report measures in the final section of this article.

### *Zygosity*

Zygosity is a dichotomous variable that indicates whether each participant was part of a genetically identical or fraternal twin pair. Martin et al. (1978) suggest that twin studies with accurately reported zygosity are more statistically powerful than twin studies without reported zygosity. In cohorts 1 and 2 of the TwinLife project, parents were asked to report their twins' zygosity (Mönkediek et al., 2019). In cohorts 3 and 4, the older twin cohorts, twins self-reported their zygosity. Cheek swabs were also taken from a subsample of the twin pairs ($n$ = 328) to validate accuracy in parent- and self-reported zygosity classification (Hahn et al., 2016). Results from the DNA samples suggest a 97% correct classification from parent-reported zygosity and 96% correct classification from twins' self-reported zygosity (Lenau et al., 2017).

### *Analytical Procedures*

The *OpenMX* package (Boker et al., 2020) is used in R (R Core Team, 2022) to retrieve the ACE estimates. Specifically, the *OpenMX* script from Maes (2016) is used to model latent influences on the observed univariate continuous variable, time reported playing video games. To identify the ACE model, covariances for latent factors representing additive genetic traits (A) were constrained at 1.0 for identical twins, since identical twins share 100% of

their DNA, and 0.5 for fraternal twins, as they share, on average, 50% of their DNA (see, Medland & Hatemi, 2009; Verweij et al., 2012). Covariances for the common environmental factor (C) were constrained at 1.0 under the assumption all twins were reared together within the same household. The last component (E) accounts for experiences unique to each twin and is freely estimated. This is because nonshared unique experiences represented by (E), such as, theoretically, each twin having a unique friend, is assumed to contribute to phenotypic variance in addition to twins' shared genes and shared environment (Medland & Hatemi, 2009).

ACE models make use of likelihood ratio tests to identify the most parsimonious and best-fitting model (see, Medland & Hatemi, 2009; York, 2020). In twin studies, nested models within the ACE model can be compared by constraining "one or more of the variance components in the larger model" to zero (Knopik et al., 2016, p. 359). As such, if the AE or CE models, with either C or A constrained to zero respectively, lead to an equivalent likelihood ratio value, then the nested model is the better and more parsimonious fit (Medland & Hatemi, 2009). However, if dropping a parameter, A or C, worsens model fit as indicated by a chi-squared test of significance, the full ACE model is considered the most parsimonious (Knopik et al., 2016; Medland & Hatemi, 2009; Verweij et al., 2012). Only the best-fitting models are interpreted in the analysis that follows. For the ACE model R scripts adapted from Maes (2016) to analyze time spent playing computer and console games, see Hassan (2022).[1]

## Results

### Twin Correlations

Table 2 shows the correlations within identical and fraternal twin pairs for time spent playing video games on a personal computer or a game console. The results show Pearson correlations were stronger for identical twins $r_{IDEN}$ (1155) = 0.60, $p < .001$, in the context of playing video games on a computer compared to fraternal twins $r_{FRAT}$ (1396) = 0.41, $p < .001$. Regarding playing on a game console, identical twins also had stronger correlations $r_{IDEN}$

**Table 2.** Twin Correlations for Playing Video Games on Computer and Gaming Consoles.

|  | Twin Correlations | |
|  | Identical Twin Pairs | Fraternal Twin Pairs |
| --- | --- | --- |
| Computer Games | .60* | .41* |
| Game Console | .50* | .28* |

N = 5,472 twin pairs (2,482 identical, 2,990 fraternal). Both video game items were continuous variables reporting hours spent playing per week ranging from 0 hours to 24 hours.
*$p < .001$

(1155) = 0.50, $p < .001$ than fraternal twins $r_{FRAT}$ (1396) = 0.28, $p < .001$. In both cases, the correlations for identical twins are stronger than those of fraternal twins, which is a preliminary indication of genetic influence on differing video game playing behaviors.

## *Univariate Genetics Analyses*

Raw correlations alone, however, cannot determine the degree to which genetic variation in the sample contributes to individual variation in time spent playing video games. The ACE model results in Table 3 estimate the extent to which both latent genetic and environmental factors contribute to variance in time spent playing video games. Specifically, the table shows estimates for the additive genetic factor ($a^2$), common environment ($c^2$), and unique environment ($e^2$). Each of these estimates represents the proportion of phenotypic variance that is attributable to the latent factor.

Additionally, the likelihood ratio test statistics, the $-2$ log likelihood ($-2LL$), Akaike Information Criterion (AIC), the Bayesian Information Criterion (BIC), and the chi-square ($\chi^2$) tests are used to determine if the ACE model is better fit than the nested AE and CE models (Hatemi et al., 2009). The AIC and BIC are ideally used to compare models that have the same parameters but are not nested in one another (Acock, 2013), in this case the AE and CE models. Verweij et al. (2012) suggests that the model with the lower AIC is the best fit and that nested models with higher $-2LL$ indicate a worse fit. Additionally, the chi-square test explains if the difference in $-2LL$ is significant (Verweij et al., 2012). Finally, having significant p-values for the nested AE and CE models indicates that they are not more parsimonious than the ACE model (Verweij et al., 2012). Based on these criteria, the ACE models for both computer games and console games are chosen as best fitted and most parsimonious models.

Table 3 shows that additive genetic traits ($a^2$) accounted for 25% of the variance in playing computer games and 39% of the variance in playing time

**Table 3.** Univariate ACE Estimates for Time Spent Playing Video Game.

|  | Model | $A^2$ | $C^2$ | $E^2$ | $-2LL$ | AIC | BIC | $\chi^2$ | $p$ |
|---|---|---|---|---|---|---|---|---|---|
| *Computer Games* | ACE | 0.25 | 0.31 | 0.44 | 22,088.69 | 11,576.69 | $-19,546.90$ | Base | - |
|  | AE | 0.58 | - | 0.42 | 222,125.27 | 11,611.27 | $-19,518.24$ | 36.58 | 0.00 |
|  | CE | - | 0.50 | 0.50 | 22,111.57 | 11,597.57 | $-19,531.94$ | 22.89 | 0.00 |
| *Game Consoles* | ACE | 0.39 | 0.09 | 0.52 | 19,870.18 | 9358.18 | $-21,765.41$ | Base | - |
|  | AE | 0.50 | - | 0.50 | 19,873.18 | 9359.18 | $-21,770.34$ | 2.99 | 0.00 |
|  | CE | - | 0.38 | 0.62 | 19,909.99 | 9395.99 | $-21,733.53$ | 39.80 | 0.00 |

N = 5,472 twin pairs (2,482 identical, 2,990 fraternal). ACE models are followed by their nested AE and CE models. Model fit is indicated by the likelihood ratio test. Best-fitting models are in bold. $A^2$ = additive genetic traits, $C^2$ = common environment, $E^2$ = unique environment. Estimates for $A^2$, $C^2$, and $E^2$ represent the proportion of variance explained by the influences of additive genetic traits, common environment, and unique environment. $-2LL$ = $-2$ times the loglikelihood. AIC = Akaike Information Criteria. BIC = Bayesian Information Criteria. $\chi^2$ = Chi-squared. $p$ = p-value. *OpenMx* was used with Maes (2016) syntax to estimate observed continuous variables.

on game consoles. The common environment ($c^2$) accounted for 31% of the variance in computer games and only 9% in playing on game consoles. The remaining variance is attributed to non-shared unique experiences influencing individual twins to play video games. For gaming time, the unique environment ($e^2$) accounted for 44% of the variance in computer games and 52% of the variance in playing on game consoles. To answer RQ1, genetic traits account for between one- and two-thirds of the variance in time spent playing video games, with the remainder explained by environmental factors.

It is important to note that these heritability estimates are similar to heritability estimates measured in other twin studies looking at expressed media variables. For example, Ayorech et al. (2017) found between 25% to 39% of the total variance in online media use to be attributed to shared genetic traits. While Kirzinger et al. (2012) found that shared genetic traits contribute to 24% to 36% of the total variance in computer use and 9% to 39% in television use. Additionally, York and Haridakis (2020) found that between 4% to 59% of the total variance in news use was attributed to shared genetic traits.

## Discussion

A central question of interest to communication researchers concerns how individual background characteristics result in differences in media selection, use, and ultimately effects. The findings of this study show that genetic traits are a root source of between-person differences in video game use. Importantly, the results show that latent genetic traits are just as influential as social and environmental factors, such as parents and culture, when it comes to video game behaviors, specifically, time spent playing. These findings may also imply that more proximal influences, such as pleasure-seeking and emotions (Bowman et al., 2020; Oliver & Raney, 2011), related to dispositional characteristics may be more specifically and fundamentally based in genetic factors, rather than only the social, neurological, and psychological origins of emotion (Weber et al., 2008). That is, while parents cultivate the common environment that children share in the home and demonstrate learned behaviors to their children, they also pass their genetic makeup to their biological children (Knopik et al., 2016), which is espoused in their behaviors and social experiences.

While common environmental factors and unique experience factors still affect variation in time spent playing video games, the findings emphasize the importance of genetics as individual differences in understanding reasons for media selection. One goal of the DSMM is to explain why and how our unique differences affect our media susceptibilities and selection decisions. This study's findings provide further empirical evidence for the significance of dispositional characteristics in the DSMM (Valkenburg & Peter, 2013),

which consist of stable individual differences, like personality, cognition, and genetic traits, that consistently affect media selection across the lifespan.

Moreover, the results raise questions about the conceptual boundaries of the dispositional traits in the DSMM. What were once considered foundational dispositions, such as personality characteristics, may actually be more proximal to behavior yet still grounded in genetic and neurobiological differences. Research has already demonstrated the genetic foundations in the biological and neurological origins of emotions (Denes, 2015), personality (see, Plomin, 2018), intelligence (Savage et al., 2018), and temperament (Browne & Walden, 2020, 2021). Therefore, it may be more theoretically useful to specify ultimate-causal and proximate-causal dispositions, particularly as the cost of advanced genotyping techniques decline and new methods of linking genes to behavior become available (Ayorech et al., 2016).

Future studies could also use genetically informative approaches to look at the etiology of video game use and how video games relate to other behaviors such as aggressiveness, violence, and addiction. For example, it is possible that some players "are predisposed to use violent media" which further stimulates their aggressive behaviors (Valkenburg & Peter, 2013, p. 223). Genetically informative research designs, such as twin studies and DNA-based approaches could be used to unpack directional relationships between trait aggression and violent video game selection. However, not all video games are the same nor are the players and their reasons for playing. Another perspective might examine the genetic and biological associations related to game selection specific to game genre, platform preference, motivations to play (Klimmt & Hartmann, 2006), and game anticipated effects (2015).

It is important to note that this study has a number of limitations, with some owing to the nature of secondary data analysis. For example, future researchers should consider using alternative measures of video gameplay. Twin respondents were all asked to self-report the average amount of time they spent playing video games on weekdays and weekend days, which could lead to measurement error related to poor recall, social desirability, and overestimating (Xu & David, 2018). Future researchers are encouraged to collaborate with game companies to obtain accurate play behavior, as demonstrated in Johannes et al.'s (2021) study. Although the time-use self-reports have shown reasonable accuracy in some previous studies (see, Browne & Walden, 2020; Ridley et al., 2006), daily diaries or application-based trackers may also more accurately document gaming time (Burnell et al., 2021; Ernala et al., 2020). In addition to gaming time, original surveys of twins could also differentiate between the plethora of video game factors such as game content and experiences. Participants can be asked specific game-related questions, such as preferred medium and genre, actions expressed during playing such as playing alone or with friends (Eklund, 2015; Wang et al., 2018). Such measures were not available in the secondary data.

Another limitation owing to the twin study approach is that they cannot make specific assumptions about certain genetic or environmental factors to explain heritability estimates. With this limitation in mind, it is important to discuss the differences in the heritability estimates found from the analysis. Since twin studies do not observe, analyze, or manipulate specific genetic or environmental factors, they can only estimate the extent to which observed variances between twins, who are individuals that share the least amount of biological variance, can be attributed to variation in genetic and environmental components (Plomin et al. 2016). Additionally, while the results of this study show variation in genetic traits to broadly explain differences in time spent playing video games, twin studies rely only on latent variables. Thus, they are not designed to show which specific genes are influential (Lockyer & Hatemi, 2018), nor which observed aspects of the environment affect expressed behaviors. Although this is a limitation, quantifying the extent to which variation in genetics and the environment contribute to variation in a behavioral trait presents a starting point, since aspects of both will always be present and are likely to affect behaviors (Lockyer & Hatemi, 2018).

Another limitation of twin studies is the reliance on monozygotic twins because they are known to share more similar post-natal environments (Martin et al., 1997). However, Martin et al. (1997) also suggest that identical twins' environments are also partly due to their genetic identity and the similar responses and experiences they receive from those environments. Ideally, twin research would focus on identical twins separated at birth, a very rare phenomena (Knopik et al., 2016), to better explain heritability estimates and variation in environmental factors. Fortunately, more advanced technology is available to better understand how expressed behaviors are influenced in part by genetics at the biological level. It is worthwhile to use molecular genetic approaches (Ayorech et al., 2016), such as genome-wide association studies (GWAS) to investigate full-genome associations with video game behaviors. GWAS could confirm the heritability estimates found in this study held at the level of DNA, as well as advance understanding of specific gene-brain mechanisms for behavior. While the twin study approach presents various limitations to our full understanding of behaviors related to playing video games, this study should be viewed as a gateway to understanding biological influences on gaming.

## Conclusion

This study investigated the heritability of playing video games using a representative sample of biological twins from the German Twin Family Panel. The aim was to identify the extent to which genetic and environmental factors impact time spent playing video games. The findings of the study are important for several reasons. First, all identical twin correlations were stronger than fraternal twin correlations for time spent playing video games.

Having higher similarities within identical twin-pairs is a sign that genetic factors influence video game behavior along with social and environmental factors. Specifically, the results indicate that genes contribute between 25% and 39% to variations in time spent playing video games, while shared environment among twins contributes to only 9% to 31%. Second, this is ample evidence that individual differences, specifically biological and genetic differences, have an impact on the variations in video game behaviors in addition to parental and cultural influences. While the results cannot direct us to genetic causes for the variation in time spent playing video games, they lay the foundation for future investigations on the genetic factors of video game use, gaming effects, and gamepl related expressed behaviors. If the amount of time spent playing video games is influenced by genetic factors, then variations in other video game behaviors should be explored such as motivations to play, game choice, and the psychological effects of playing.

## Note

1. The two R scripts adapted from Maes (2016) and used for the analysis of time spent playing video games on computers and game consoles can be found on the study's OSF page: https://osf.io/tukcn/?view_only=855b62cc54204b35bcd026968b24ac49

## Author Note

Toqa Hassan M.A. studies parent-child media use decisions and behaviors, with a focus on video game selection.
    I have no known financial and non-financial competing interests to disclose.

## Disclosure Statement

No potential conflict of interest was reported by the author.

## ORCID

Toqa Hassan 🆔 http://orcid.org/0000-0002-5376-1239

## Data availability statement

The data described in this article are openly available in the Open Science Framework at https://doi.org/10.1080/15213269.2023.2165504.

## Open scholarship

This article has earned the Center for Open Science badge for Open Data. The data are openly accessible at https://osf.io/tukcn/?view_only=855b62cc54204b35bcd026968b24ac49.

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