Habitual physical activity in children: the role of genes and the environment¹⁻³

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ABSTRACT

Background: Understanding the factors that contribute to physical inactivity in children is important because sedentary behavior strongly relates to metabolic disorders such as obesity and diabetes.

Objective: We aimed to quantify the genetic and environmental influences on physical activity energy expenditure (PAEE) in 100 sex-concordant dizygotic (n = 38) and monozygotic (n = 62) twin pairs aged 4–10 y.

Design: Resting metabolic rate (RMR) was assessed by using respiratory gas exchange, total energy expenditure (TEE) by using doubly labeled water, and body composition by using dual-energy X-ray absorptiometry. Structural equation modeling was used to partition the phenotypic variance into additive genetic (a²) and common (c²) and unshared (e²) environmental components.

Results: Because PAEE [TEE − (RMR + 0.1 × TEE)] depends on body weight, which is highly heritable, we tested several models: 1) after adjustment for sex, ethnicity, study date, season, and weight, a² explained none of the phenotypic variance in PAEE (95% CI: 0%, 38%), whereas c² and e² accounted for 69% (33%, 77%; P = 0.001) and 31% (23%, 39%; P < 0.001) of the variance, respectively; 2) after adjustment for the cofactors in model 1, a² explained 19% of the phenotypic variance in TEE (0%, 60%; P = 0.13), whereas c² and e² accounted for 59% (16%, 79%; P = 0.007) and 23% (17%, 31%; P < 0.0001) of the variance, respectively; 3) in models adjusted as above (excluding weight), a² explained no variance in physical activity level (TEE/RMR) (0%, 32%; P = 0.50), whereas c² and e² explained 65% (34%, 60%; P = 0.001) and 35% (28%, 45%; P < 0.0001) of the variance, respectively.

Conclusions: Our data suggest that the familial resemblance in physical activity in these children is explained predominantly by shared environmental factors and not by genetic variability. Am J Clin Nutr 2005;82:901–8.

KEY WORDS Physical activity energy expenditure, physical activity level, genetics, children, twins, doubly labeled water

INTRODUCTION

Physical inactivity is a major risk factor for complex metabolic diseases such as obesity, diabetes, and hypertension (1). Traditionally, these morbidities have been the specific burden of adulthood, but their diagnosis in the young is now increasing (2–8). Some have suggested that, as is true for adults (9), children are becoming less physically active (10, 11) and that changes in lifestyle, including declining levels of physical activity, may help explain why childhood metabolic diseases are becoming more common. Thus, because physical activity appears to track from childhood through to adulthood (12, 13), and because genetic effects are potentially more discernable at a young age, comprehending the antecedents of physical inactivity in the young is important for the prevention of inactivity and related disease at all ages.

Some investigators have proposed that the behavior of physical activity is primarily determined by genetic factors (14). Indeed, several studies have shown familial aggregation of physical activity (15–25), which suggests the potential importance of genetic factors in mediating this behavior. All of these studies have used questionnaire data, and only a few have been twin studies, the latter of which have the advantage of allowing for determination of whether familial aggregation reflects genetic effects or the shared environment. The present study of twins uses objectively assessed physical activity, measured by doubly labeled water (DLW) and respiratory gas-exchange, to quantify the role of genes and the environment in the determination of physical activity in children.

SUBJECTS AND METHODS

Subjects

From September 1993 until November 2002, 100 sex-concordant (34 male and 28 female monozygotic and 19 male and 19 female dizygotic) twin pairs were recruited for this study. From 1991 to 1998, 16 monozygotic and 8 dizygotic pairs were studied, from 1999 to 2000, 34 monozygotic and 22 dizygotic pairs were studied, and from 2001 to 2002, 12 monozygotic and 8 dizygotic pairs were studied. None of the intrapair differences

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for key variables correlated significantly with time since initiation of the study. Fifty-four monozygotic twin pairs were European American, 6 pairs were Hispanic, and 2 pairs were American Indian. Twenty-seven dizygotic twin pairs were European American, 4 pairs were Hispanic, 5 pairs were American Indian, and 2 pairs were African American. The ethnicity of the child was determined by parental report. Nineteen pairs (11 monozygotic (8 male and 3 female) and 8 dizygotic (6 male and 2 female)) lived outside of the greater Phoenix metropolitan area. There was no difference in the level of the key predictor or outcome variables between these individuals and those who lived in the Phoenix area (data not shown).

A physical activity questionnaire, completed by the parent, was used to assess average hours per week over the past year in which the child was typically engaged in sports and recreational activities requiring a greater expenditure of energy than that normally needed for daily grooming, bathing, and eating. Additional questions assessed the number of hours children engaged in sedentary activities such as napping, sleeping, watching television, and playing computer and video games. Given that the questionnaire assessed activity over the past year, it was completed on just one occasion. Parents were initially asked to indicate activities in which the child had participated >10 times in the past year. Parents were then asked to estimate the amount of time the child spent in each of these activities and to indicate the number of times the activity was engaged in each week, the number of hours per bout, and the number of months per year. From this information, we calculated the average number of hours that children spent in sports and recreational activities over the past year.

The 1 wk of study was designed to take place while the children were engaged in their usual activities and to avoid any atypical weeks such as family vacations, Thanksgiving, and Christmas. Most of the studies (~80%) took place during the summer months.

Many of the twins were recruited through review of State birth records. In 1998, we canvassed the records of the State of Arizona for information on mothers who had borne 2 same-sex children on the same day during the time period that would have yielded a study population between 4 and 10 y of age (n = ~4000). These records were then correlated with driver’s license information files from the Arizona State Department of Transportation (n = ~1400). Letters were then sent to all of these families around the state of Arizona inviting them to participate in the study. Children were also recruited from across the United States by advertisement in the newsletter of the National Organization of Mothers of Twins Clubs, over the internet, in local newspapers, with the assistance of colleagues, and by attendance at meetings of local twins’ clubs. Twins were studied together at the National Institutes of Health (NIH) Metabolic Unit in Phoenix, AZ, where the subjects arrived at 0800 after fasting overnight accompanied by one of their parents. All participants, including those from outside the Phoenix metropolitan area, stayed in Phoenix during the laboratory phase of the study. The free-living phase of the study was conducted with the children in their home environments, and urine samples from participants living outside Phoenix were shipped to the NIH on dry ice immediately after collection. Only healthy children were included, as determined by medical history and physical examination. Two pairs of twins were excluded: one pair was developmentally delayed (not reported until after the twins began the study) and one of the children in the other pair had von Hirschberg syndrome as an infant. Before participation, volunteers and their parents were fully informed of the nature and purpose of the study, and written informed consent and assent were obtained. The Institutional Review Board of the National Institute of Diabetes and Digestive and Kidney Diseases approved the protocol. All studies were conducted in accordance with the ethical standards of the Helsinki Declaration of 1975, as revised in 1983, for research in human subjects.

**Zygosity determination**

Because this study was conducted across several years, and techniques for zygosity determination during this time improved, several methods were used. In 72 pairs of twins, zygosity was determined by DNA testing of blood cell samples (50 pairs; Chapman Institute of Medical Genetics, Tulsa, OK) or buccal cell samples (22 pairs; Affiliated Genetics, Woods Cross, UT). In 18 pairs, zygosity was determined by using HLA blood typing. Blood could not be obtained in the remaining 10 pairs of twins. Thus, in these children zygosity was reported by the parents and verified by questionnaire (26). To control for the possibility that zygosity was misclassified on the questionnaire, we conducted subanalyses in which these children were excluded from the models. This did not materially affect the variance estimates (data not shown).

**Anthropometric measures**

Anthropometric measurements in all children were performed during 2 clinic admissions, 1 wk apart; the results represent the means of the 2 measurements. Height was measured while the children were not wearing shoes, and body weight was measured while the children were wearing light clothing.

**Body composition**

Total body water, calculated from $^{18}$O dilution spaces, was used to assess body composition in all children, assuming that water is 75% of the fat-free mass in girls and 74% in boys (27, 28). Body composition was determined by using a Lunar DPX dual-energy X-ray absorptiometry (DXA), as previously described (29, 30). In 16 dizygotic and 35 monozygotic children, we were unable to perform the DXA measurements because of technical difficulties or because the child (or parents) declined to participate in this aspect of the study. For these children we used the DLW estimate of body composition. The correlation between DLW and DXA body-composition measures was $r = 0.91$ ($P < 0.0001$) in those subjects in whom both methods had been performed. In all twin pairs, with one exception, the same method for determining body composition was used in both members of the pair. Furthermore, in the subset of individuals in whom DXA had been performed, the results did not differ from those obtained when all twins were analyzed (data not shown).

**Resting metabolic rate**

After ingesting the DLW, the children rested comfortably on a bed for 10 min and then the resting metabolic rate (RMR) was measured for 20 min with a DeltaTrac Metabolic Monitor (SensorMedics Corporation, Yorba Linda, CA) as previously described (31). Children were carefully instructed about the testing procedure before the measurement began. While a parent was nearby completing a detailed activity questionnaire, the child was allowed to watch a nonviolent cartoon video during the
measurement. The RMR measurement was repeated at the return visit 1 wk later, and the results of the 2 measurements were averaged to obtain the mean of the 2 values. Carbon dioxide production (VCO₂) and oxygen consumption (VO₂) were calculated for each minute of the 20-min period during which RMR was measured, and all values were averaged to obtain the mean.

Total energy expenditure

Total energy expenditure (TEE) was measured by using the DLW method. The subjects were asked to provide 2 baseline urine samples; one sample was collected at home during the evening before the test, and the other sample was collected on arrival at the clinic. To account for differences in baseline enrichment of the stable isotopes, the subjects were asked to bring samples of drinking water as well as the baseline urine samples collected at home. If the children lived outside the Phoenix area, they were also asked to provide baseline drinking water and urine samples after arriving in Phoenix. Children were then dosed with DLW as previously described (27, 28); the dose contained 0.132 g 100% 2H₂O/kg total body weight and 2.508 g 10% H₂18O/kg total body weight (Isotec Inc, Miamisburg, OH). The dosing container was rinsed with 100 mL tap water, which was given to the children to drink to ensure complete consumption of the labeled water. Complete urine collections were made at 1.5, 2.5, and 3.5 h after dosing on day 1 and twice during a 3-h period 7 d later. The sample collected at 1.5 h was discarded because it contained urine present before equilibration. Isotopic enrichment of the 2 baseline urine samples was averaged to provide one baseline value. The disappearance rates of the 2 stable isotopes were determined as previously described (27, 28) by using a food quotient of 0.866 to determine carbon dioxide production.

Physical activity

Physical activity energy expenditure (PAEE) was estimated as follows:

\[
PAEE = TEE - (RMR + 0.1 \times TEE) \tag{1}
\]

where 0.1 \times TEE represents an estimate of the thermic effect of food (32). The following indexes of physical activity were also calculated: the physical activity level (PAL) was calculated as TEE/RMR, and TEE was adjusted for RMR, age, and sex with the use of linear regression analysis.

Statistics

The existence of a stronger correlation in monozygotic twins than in dizygotic twins provides putative evidence that genetic factors underlie the observed phenotype (33, 34). Twice the difference between the correlation in monozygotic twins and that in dizygotic twins is a crude estimate of heritability for a given trait under certain conditions, but correct estimates for heritability are provided by variance component estimation (see below).

To formally enable the partitioning of shared environmental from genetic factors, we used structural equation models (35, 36). In these models, variances and covariances are partitioned into 3 components: an “additive genetic” component (a²), which represents the total effects of multiple alleles on the phenotype; a “common environmental” component (c²), which reflects the action of environmental factors that are shared by the twinship; and an individual environmental component (e²), which reflects the action of the environmental factors unique to the individual.

In addition to the full model, which included all 3 parameters (ACE), we also fit reduced models in which the a² component, the c² component, or both components were constrained to equal 0, and models that considered a dominant genetic component (d²).

In fitting these models, it was assumed that genetic factors are perfectly correlated in monozygotic twins, whereas dizygotic twins are assumed to have 50% of their alleles in common; it is further assumed that common environmental factors are perfectly correlated (ie, r = 1.0) in twins, regardless of zygosity. To fit these models, the variance components were estimated by using PROC MIXED in SAS (SAS Institute Inc, Cary, NC), and the parameters a², c², and e² were expressed as a proportion of the total variance. The likelihood ratio test was used to test the hypothesis that a given variance component was 0. For these tests, all P values were one-sided, and α was set at 0.05. CIs for each parameter were calculated by using a systematic exploration of the likelihood surface (37).

To determine the most parsimonious model for the present data, models were refit with exclusion of components (a², c², and e²) that did not contribute significantly (P < 0.05) to the full model. If the genetic variance was retained but the common environmental variance was not, a further test was performed to determine whether there was a significant dominance component (d²) to the genetic variance. These dominant genetic factors are assumed to be perfectly correlated in monozygotic twins and to have a correlation of 0.25 in dizygotic twins.

In addition to the variance components described above, mixed models included fixed effects to adjust for the potential confounders of age (y), sex (0 = male pair, 1 = female pair), ethnicity (European American versus other), season (summer versus other), and study date (days since the study began). Structural equation models were also adjusted for other putative influences. For example, when PAEE was the phenotype of interest we adjusted this model for body weight, because excess weight may predispose sedentary behavior and may also be determined by genetic factors. When RMR was the phenotype of interest, we adjusted this model for fat-free mass, the primary determinant of resting energy expenditure in mammals. To minimize the possibility that confounding by body mass could explain our observations for energy expenditure variables, we chose to adjust for body composition as a covariate rather than to express energy expenditure per unit body mass. This was because energy expenditure expressed per unit body mass is highly correlated with body mass.

RESULTS

Participant characteristics stratified by zygosity (n = 100 pairs) are shown in Table 1. Thirty-four monozygotic and 19 dizygotic twin pairs were male. Dizygotic twins were older (P < 0.001) and therefore had a tendency (P > 0.05) to be taller and heavier and to have a higher RMR and PAEE than did the monozygotic twins (Table 1). In unstratified univariate models, weight was strongly correlated with RMR (r = 0.79, P < 0.0001), TEE (r = 0.89, P < 0.0001), PAEE (r = 0.71, P = 0.0001), and PAL (r = 0.48; P < 0.0001). Twin-twin univariate correlations stratified by zygosity for a variety of body composition and energy expenditure variables are shown in Table 2. Correlations for monozygotic twins were higher than those for dizygotic twins for measures of body composition, TEE, and RMR (P < 0.05).
All dizygotic twins were concordant for sex. Mixed models were used accounting for the nonindependence of observations within twinships, adjusted for age, study date, season, ethnicity, and sex. All dizygotic twins were concordant for sex.

The results of structural equation modeling for body-composition and energy expenditure variables are shown in Table 3. There was no statistically significant difference in the variance of any of these variables by zygosity ($P > 0.1$). The results in Table 3 indicate that models containing familial effects, both genetic and common environmental, fit far better than did those with only an effect of the individual environment (determined by comparing the ACE with the E model) for all variables. Further analyses indicated that genetic effects accounted for most of the variance in body composition, with estimates for $a^2$ ranging from 82% to 90%, and the comparison of the ACE with the CE model indicates that inclusion of the genetic effect gives a significantly better fit to the data. On the other hand, the effects of the common environment were not significant (ACE versus AE model). Further adjustment for PAEE, which is known to influence body composition, only modestly affected the estimate of $a^2$. Because similar results have been reported in other studies, the remainder of this section will focus on the heritability of energy expenditure phenotypes.

**Resting metabolic rate**

In the structural equation models (Table 3), initially adjusted for study date, ethnicity, season, and sex, additive genetic factors explained most of the variance in RMR (79%; $P < 0.0001$), whereas the shared environment accounted for none of this variance, and the unshared environment accounted for the remaining variance (21%; $P < 0.0001$).

To assess the heritability of RMR independent of body weight, which is the main determinant of resting energy expenditure, we also adjusted our models for this covariate. In these models, the variance explained by additive genetic factors was much lower than that with the preceding model (3%; $P = 0.45$), whereas the shared environment explained 26% ($P = 0.007$) and 26% ($P = 0.0001$) of the model variance ($P < 0.0001$).

**Total energy expenditure**

Initial assessment of variance components included adjustment for age, ethnicity, study date, season, weight, and sex. In these models, additive genetic factors explained 19% of the phenotypic variance in TEE ($P = 0.13$), whereas shared and unshared environmental factors accounted for 59% ($P = 0.007$) and 38% ($P < 0.0001$) of the variance, respectively (Table 3). Because TEE is the sum of PAEE, RMR, and the thermic effect of food, we also adjusted our models for RMR (but not body weight). In this model, genetic factors explained 28% ($P = 0.10$) of the variance in TEE, whereas the shared and unshared environment explained 46% ($P = 0.04$) and 26% ($P < 0.0001$) of the variance, respectively.

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**Table 2**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Monozygotic twins</th>
<th>Dizygotic twins</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>($n = 62$ pairs; $n = 124$ individuals)</td>
<td>($n = 38$ pairs; $n = 76$ individuals)</td>
</tr>
<tr>
<td>Body weight (kg)</td>
<td>$0.93^2$</td>
<td>$0.60^2$</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>$0.83^2$</td>
<td>$0.29^2$</td>
</tr>
<tr>
<td>Fat mass (kg)</td>
<td>$0.89^2$</td>
<td>$0.31^2$</td>
</tr>
<tr>
<td>Fat-free mass (kg)</td>
<td>$0.95^2$</td>
<td>$0.78^2$</td>
</tr>
<tr>
<td>RMR (kcal/d)</td>
<td>$0.87^2$</td>
<td>$0.51^2$</td>
</tr>
<tr>
<td>TEE (kcal/d)</td>
<td>$0.85^2$</td>
<td>$0.66^2$</td>
</tr>
<tr>
<td>PAEE (kcal/d)</td>
<td>$0.87^2$</td>
<td>$0.76^2$</td>
</tr>
<tr>
<td>PAL</td>
<td>$0.78^2$</td>
<td>$0.80^2$</td>
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</tbody>
</table>

$^1$ RMR, resting metabolic rate; TEE, total energy expenditure; PAEE, physical activity energy expenditure; PAL, physical activity level (TEE/RMR).

$^2$ Twinships were compared by using the chi-square test for dichotomous traits or the t test for age and study date; for other continuous traits, mixed models were used accounting for the nonindependence of observations within twinships, adjusted for age, study date, season, ethnicity, and sex. All dizygotic twins were concordant for sex.

$^3$ Significantly different from monozygotic twins, $P < 0.05$.

$^4$ Unadjusted $t \pm SD$ (all such values).
and 31% (shared and unshared environment explained 69% (p < 0.001) of the variance, respectively). Notwithstanding our observations here, it is quite possible that the predominance of the shared environment constrains the extent to which genetic factors predisposed children in the present study and elsewhere to be physically active. Moreover, adjustment for body mass, which attenuates the heritability of PAL, because this is a commonly used index of physical activity and represents TEE/RMR. In structural equation models adjusted for age, study date, ethnicity, and sex, additive genetic factors explained none of the variance in PAL, whereas the shared and unshared environment explained 65% (p = 0.001) and 35% (p < 0.0001) of the variance, respectively (Table 3).

The estimates for the most parsimonious model for each trait are shown in Table 4. For all of the body-composition traits and for RMR without adjustment for weight, the common environmental variance was not significant and was, thus, left out of the model. A significant dominance component was observed for weight and for fat mass without adjustment for PAEE. For most of the energy expenditure traits, with the exception of PAEE adjusted for body weight, the most parsimonious model included the common environmental, but not the genetic, variance.

### DISCUSSION

The purpose of the present study of 100 twin pairs was to determine the extent to which objectively assessed free-living physical activity in children is attributable to genetic factors. Measures of body composition in this study were highly heritable, as has been shown in other studies. However, once weight is accounted for, genetic factors are modest determinants of the tendency to move around and expend energy. By contrast, the shared environment is an important determinant of physical activity, with ≈70% of the variance in this phenotype attributable to this factor. Notwithstanding our observations here, it is quite possible that the predominance of the shared environment constrains the extent to which genetic factors predisposed children in the present study and elsewhere to be physically active. Moreover, adjustment for body mass, which attenuates the heritability of PAL, because this is a commonly used index of physical activity and represents TEE/RMR.
estimate for physical activity, may not be necessary if physical activity is more proximal to genetic factors other than obesity. However, this is presently unknown.

TEE is the sum of RMR, the thermic effect of food, and PAEE. Of these subcomponents, between-person variability in energy expenditure can be explained in several ways. For example, genetic variability on energy metabolism pathways causing decreased proton uncoupling and mitochondrial biogenesis could result in a lower rate of local energy metabolism (39). Although the between-person variability in energy expenditure per unit weight is not related to body mass (40, 41), the propensity for movement, even in persons of similar body size, varies greatly from one person to the next (42). Owing to this, it is rational to express PAEE relative to body weight, at least from the perspective of disease prevention in societies where activity is primarily load-bearing. Although physical activity adjusted for weight (ie, movement) can be presented in several ways (eg, PAL or TEE adjusted for RMR), these methods overestimate movement in children, whereas PAEE adjusted for weight does not (38, 43).

On the one hand, genetic contributions to physical activity may be more readily detectable in children than in adults. This is because levels of physical activity during childhood are more variable than in adulthood, sub-clinical and clinical disease increases with age, and non-genetic environmental influences on physical activity, such as the need to work in sedentary occupations, is less. Alternatively, behavior is plausibly governed more directly by others (eg, parents and teachers) in childhood than in adulthood, and this could restrict the expression of genetic effects.

Importantly, although the study of genetics of physical activity in children is appealing, the capacity for self-perception and self-appraisal at this age is limited (20, 44–46), and the array of volitional activities that results in marked increases in energy expenditure is extensive (10). Thus, the need for precise and objective measurements of activity is likely to be greatest in the pediatric setting.

The possibility that physical activity in humans may be partly attributable to genetic factors is supported by several lines of evidence. Numerous studies, including some in twins, have examined the heritability of physical activity–related behaviors (16–25). Heritability estimates for leisure-time physical activity and sports participation are reported to range from 0.09 to 0.63 and from 0.40 to 0.77, respectively. One of these studies reported a considerable shared environmental component (23), although most other studies did not partition this component from the genetic component. Human overfeeding studies have shown that caloric excess is directly related to increased spontaneous physical activity (47), which indicates a role for biological feedback mechanisms in this behavior. Loos et al (48) used these observations as a basis to study associations between single nucleotide polymorphisms in the hypothalamically expressed Melanocortin-4 receptor (MC4R) gene and physical activity in adults from the Quebec Family Study. In the same population, Simonen et al identified associations with physical activity and a single nucleotide polymorphisms in the dopamine D2 receptor gene (DR2R) (49), and subsequently performed a genome-wide linkage scan (15), with the purpose of identifying loci affecting physical activity. Modest evidence of linkage was found for physical inactivity on several chromosomes, but none of these linkage points corresponded with the regions to which the MC4R or DR2R gene map. Elsewhere, associations have been reported between free-living physical activity and variation in genes, including the angiotensin-converting enzyme (50), calcium-sensing receptor (51), and the aromatase (52) genes. Although suggestive, none of these results provide definitive evidence that genetic factors predispose activity levels in humans.
All of the above-referenced studies used subjective approaches (eg, questionnaires, diaries, and interviews) to assess self-reported leisure-time physical activity or sports participation. The main limitations of self-reported estimates of PAEE are that they are unreliable and lack validity (53). Even when the sample size is large, which to some extent counters the effects of measurement error, several forms of bias persist. Although heritability estimates for memory, self-perception and self-explanation, which could theoretically confound the relation between genetic factors and self-reported physical activity, may generally be low, other factors, which could differentially relate to genotype, may persist. For example, obesity has strong genetic antecedents (54) and obese people tend to overestimate their level of activity (55). Therefore, it is plausible that heritability estimates for physical activity may be more prone to confounding, in this example by obesity genes, when derived through self-reported methods than through objective approaches.

The main limitation of twin studies is that assumptions are required about the correlation of genetic and environmental factors within twins to construct the variance components. When these assumptions are not met, the ability to adequately test genetic hypotheses falters. A second point for consideration is that the generalizability of data from twin studies depends on how representative the wider population the study subjects are in behavioral, genetic, and anthropometric characteristics. The present study was not population-based, and no data were available from comparably recruited singletons; therefore, the extent to which the present findings are generalizable to other children is difficult to assess. However, when analyses were restricted to those of European American ethnicity or to those from the Metropolitan Phoenix area, results were similar to those reported here. This suggests, at least, that inclusion of individuals from varied ethnic backgrounds or different geographic areas does not markedly influence our findings. The potential for differential participation is also difficult to assess. If, for example, dizygotic twins who participated in the study were more similar than dizygotic twins who did not participate, then this could artificially lead to a higher estimate of the effect of the common environment than if an unbiased sample had been analyzed. There were some differences between monozygotic and dizygotic twins in variables such as ethnicity and age, a finding that suggests the potential for differential self-selection. However, models in which we adjusted for these covariates produced very similar estimates to models in which there was no adjustment. Furthermore, if differential self-selection was a general phenomenon, one might expect to observe a large common environmental effect for measures of body composition as well as for physical activity, but this was not the case.

A further potential limitation of the present study is the possibility that aspects of the study design could have led to an overestimation of $\hat{c}^2$ and an underestimation of $\hat{a}^2$ (relative to the values that would be obtained if all subjects had been studied on the same day and had the same travel schedules). However, when analyses were undertaken only in children who lived within the Metropolitan Phoenix area, the variance estimates were unchanged, suggesting that studying children who did not reside locally was not a major limitation of the experimental design. Last, the present study did not include twins who were reared apart or who had a same-age adopted sibling; therefore, it was not possible to fully distinguish additive from dominant genetic effects in the presence of a common environmental effect. Thus, the present estimates of $\hat{a}^2$ may be confounded somewhat by dominant genetic effects and vice versa.

Although the findings of the present study suggest that physical activity (ie, movement) is unlikely to be strongly determined by genetic factors in children, such as those studied here, it is possible that the genetic predisposition toward physical activity is attenuated by a strong effect of the shared environment; in the present study, large proportions of the phenotypic variance in PAEE and TEE are explained by this factor. This is important because it indicates that sedentary behavior in children, which is becoming a widespread problem and contributes to premature morbidities such as obesity and diabetes, is modifiable. However, behavioral modification is difficult and will likely require a change in attitude toward physical activity by those who influence the lifestyles of children, both within the family and in the community as a whole (56). Thus, it would not be surprising if, in populations in whom these phenotypes were less constrained by the environment, one observed a more marked genetic effect on activity levels in children. Similarly, the extent to which genetic factors are distinguishable from shared environmental factors may vary depending on the age of the subjects studied. This is because the behavior of younger children is likely influenced to a greater extent by others than is the behavior of older children and adults. This is an additional potential explanation for why in previous adult studies a strong genetic predisposition to physical activity has frequently been reported.

In summary, the findings from the present study indicate that once weight is taken into account, the propensity to be physically active is determined largely by aspects of the environment that are shared by siblings. This likely includes the attitudes and actions of family members and the school and recreational environment. Further studies are required to identify the particular aspects of the shared environment that exert the greatest influence on the behavior of physical activity. In the meantime, because physical activity is important in preventing metabolic diseases, improving all aspects of the shared environment is a necessary objective if the pandemic of childhood obesity and related metabolic disturbances that lies to the fore in industrialized nations is to be averted.

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PWF and R.L.H statistically analyzed and interpreted the data. ER and ADS designed the experiment and collected and helped interpret the data. ITH helped design the experiment, helped collect the data, and analyzed the DLW samples. DBA, WCK, and PAT helped interpret the data and provided significant advice and consultation. All authors contributed to the writing of the paper, critiqued the intellectual content of the manuscript, and approved the final submission. No conflicts of interest were declared.

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