Genetic influences on mechanically-assessed activity level in children

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Background: Activity level is an important component of children's temperament, as well as being part of the core symptom domain of hyperactivity-impulsivity in attention deficit hyperactivity disorder (ADHD). Yet it is poorly understood, due partly to limitations on parent and teacher ratings, which are typically used as measurements of these symptoms.

Methods: We aimed to study the etiology of objectively-measured activity level across two situations, using actigraphs. A population-based sample of 463 7–9-year-old twin pairs were assessed individually both when apart undergoing laboratory-based cognitive testing and when together during a break in testing.

Results: Heritability of activity level was estimated as 24% during the test session and at 30% during the break in testing. Shared environmental influences accounted for 27% of the variance in activity level during the test session and 42% of activity level measured during the break. A genetic correlation of 1.0 indicated that the same genes influenced activity level across the two situations, justifying the use of a composite measure of the two situations. This produced a heritability estimate of 36%.

Conclusions: Objectively-measured activity level shows a moderate degree of genetic influence, with a common set of genes influencing activity level across situations. This supports the use of actigraphs as an additional source of information in studies that aim to improve phenotype definition for molecular genetic studies of activity level and ADHD.

Keywords: Activity level, actigraph, etiology, heritability, twin study, genetic effects, attention deficit hyperactivity disorder.

Abbreviations: ADHD: attention deficit hyperactivity disorder; CI: confidence interval; MZ: monozygotic; DZ: dizygotic; A: variance due to additive genetic effects; C: variance due to shared environmental effects; E: variance due to child-specific environmental effects; rA: genetic correlation; rC: shared environment correlation; rE: child-specific environment correlation.

Activity level is an important component of children's temperament, as well as being part of the core symptom domain of hyperactivity-impulsivity in attention deficit hyperactivity disorder (ADHD). Parent and teacher ratings suggest moderately strong genetic influences on activity level or symptoms of overactivity, with heritability estimates in the range of 42–72% (Thapar, Hervas, & McGuffin, 1995). The diagnosis of ADHD is similarly highly heritable, with a recent meta-analysis converging at a heritability estimate of 76% (Faraone et al., 2005). Molecular genetic studies on ADHD indicate an association with several candidate genes, including the dopamine D4 and D5 receptor genes, although the effect sizes are small (Asherson, 2004; Faraone et al., 2005; Kuntsi, Neale, Chen, Faraone, & Asherson, 2006; Li, Sham, Owen, & He, 2006). The genetic influences on ADHD are likely to be quantitative trait loci (QTLs), with multiple genetic variants of small effect contributing to one or more continuous dimensions of ADHD symptoms and behaviours, including overactivity (Asherson, 2004).

Despite the advances in genetic research on activity level and ADHD, improvement in phenotype measurement remains a critical issue (Holmes et al., 2002; Thapar, Langley, O'Donovan, & Owen, 2006). The difficulties in phenotype measurement relate partly to the reliance on parent and teacher reports on behavioural rating scales, which are subject to potential biases and often show low inter-rater agreement. Parent ratings can indicate low or even negative dizygous (DZ) twin correlations, which are not explained by additive genetic effects (Simonoff et al., 1998). Twin model fitting suggests that such low DZ correlations are likely to reflect rater bias in parent ratings (Saudino, Cherny, & Plomin, 2000; Simonoff et al., 1998; Thapar et al., 1995). Teacher reports do not show the same bias (Martin, Scourfield, & McGuffin, 2002), but may be subject to other limitations, given the limited circumstances in which they observe the child's behaviour. Teacher ratings may also be affected by teachers' conceptions of other aspects of the child, such as their academic achievement or social abilities (Goodman & Stevenson, 1989; Verhulst, Koot, & Van der Ende, 1994).

Actigraphs provide an alternative, or additional, method for measuring activity level by the direct recording of an individual's body movements. They record the cumulative intensity and frequency of movement, during a specified time, in an objective and quantifiable way. Actigraphs can be worn on any
part of the body, although most commonly in studies of childhood activity they are worn on the ankle, wrist or trunk. Actigraph measurements correlate positively across situations (Saudino, Wertz, Gagne, & Chawla, 2004) and around .3 with parent reports of activity level taken from the Colorado Childhood Temperament Inventory (Dane, Schachar, & Tannock, 2000; Saudino, Wertz, Gagne, & Chawla, 2004). Although such correlations vary for different scales and raters (Dane et al., 2000; Eaton & Yu, 1989; Saudino, Wertz, Gagne, & Chawla, 2004), they indicate a similar degree of phenotypic overlap to that seen between teacher and parent ratings; and their inclusion in studies of ADHD may therefore provide a more complete characterisation of the disorder. Research on children with ADHD using actigraphs indicates good discrimination between ADHD and comparison groups (Inoue et al., 1998; McGrath, Handwerk, Armstrong, Lucas, & Friman, 2004; Teicher, Ito, Glod, & Barber, 1996), although this can be dependent on circumstances, with situations requiring greater self-regulation having the most discriminatory power (Dane et al., 2000; Porrino et al., 1983). Discrimination between ADHD and control groups has been reported with sensitivity and specificity of over 75% (Inoue et al., 1998) and actigraph data have indicated an activity level 25–30% higher in children with ADHD than those without (Porrino et al., 1983). The measures are also sensitive to changes in motor activity following drug treatment (Konrad, Gunther, Heinz-Gutenbrunner, & Herpertz-Dahlmann, 2005).

Despite the potential importance of actigraph data as bias-free measurements of activity level, few methodologically strong twin studies have investigated the overall extent of genetic influences on actigraph-measured activity level in children. An early study suggested a heritability of around 10% based on twin correlations (Plomin & Foch, 1981), but used pedometers which may not be sensitive to subtle changes in activity. Subsequent research, which used actometers on a sample of approximately 60 twin pairs, suggested a higher heritability estimate, in the range of 40%, in infancy and early childhood (Saudino & Eaton, 1991). This study also suggested a role for common environment, indicating a different pattern of variance components from that usually seen in twin studies of ADHD symptoms using standard behaviour rating scales, which often show no significant role of shared environment (Faraone & Doyle, 2000). It is uncertain how accurately this estimate reflects the heritability of activity level in older children, given that activity level is more unstable during infancy than later on in childhood (Keenan & Wakschlag, 2002), reflecting the transitory motor development of the child (Eaton & Yu, 1989; Saudino & Eaton, 1991). However, an analysis of actometer data obtained during a testing session on 225 adult twin pairs indicated a similar heritability of 40%, but no contribution from shared environment (Spinath, Wolf, Angleitner, Borkenuau, & Riemann, 2002).

The investigation of heritability is important for molecular genetic studies, which require measures that are maximally sensitive to the underlying genetic liability and thus as free from bias as possible. Inconsistencies across molecular genetic studies seeking to identify candidate genes for ADHD and associated symptoms, including activity level, may relate in part to inconsistencies in phenotype definition, but also to the power of linkage and association studies to detect what is likely to be many genes of small effect (Asherson, 2004). An initial molecular genetic study using actigraph data was encouraging in this respect, in suggesting an association between the DRD4 risk allele (exon three 7-repeat) and increased activity among children with ADHD (Langley et al., 2004), but understanding the similarities and differences in the genetics of activity level across situations may help explain inconsistencies across studies that assess activity level in different situations. The importance of composite scores in reducing error variance in phenotype measurement and in maximising sensitivity to genetic factors has been recently highlighted (Kuntsi, Rogers et al., 2006).

To address the lack of previous data on the extent of genetic influences on objectively-measured activity level in middle childhood, we aimed to investigate this with a sample of 486 twin pairs between the ages of 7 and 9. We further aimed to investigate potential differences in the etiology of activity level in two different situations – a structured laboratory-based test session and an unstructured break session – and whether data from these two situations could be justifiably combined for further analyses. The children wore the actigraphs on waist and leg, and both the intensity and number of movements were measured.

**Methods and materials**

**Sample and procedure**

Participants are members of the Study of Activity and Impulsivity Levels in children (SAIL), a study of a general population sample of twins at age 7–9. The sample was recruited from a birth cohort study, the Twins’ Early Development Study (TEDS; Trouton, Spinath, & Plomin, 2002), which had invited parents of all twins born in England and Wales during 1994–96 to enrol. Despite attrition, the TEDS families continue to be representative of the UK population with respect to parental occupation, education and ethnicity (Spinath & O’Connor, 2003). Zygosity has been determined using a standard zygosity questionnaire, which has been shown to have greater than 95% accuracy when compared to zygosity status determined by genotype data (Price et al., 2000).

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Families on the TEDS register were invited to take part if they fulfilled the following SAIL project inclusion criteria: twins’ birthdates between 1 September 1995 and 31 December 1996; lived within feasible travelling distance of the Research Centre (return day trip); ethnic origin white European (to reduce population heterogeneity for molecular genetic studies); recent participation in TEDS, as indicated by return of questionnaires at either 4- or 7-year data collection point; no extreme pregnancy or perinatal difficulties (15 pairs excluded), specific medical syndromes and chromosomal anomalies (two pairs excluded) or epilepsy (one pair excluded); not participating in other current TEDS sub-studies (45 pairs excluded); and not on stimulant or other neuropsychiatric medications (two pairs excluded).

The current analyses focus on data obtained following contact with the first 1230 suitable families on the register. Of these, 672 families agreed to participate, reflecting a participation rate of 55%. Actigraph data were obtained for 486 families and, of the 972 participants, data from twenty-two individual children were subsequently excluded (thirteen children with IQs below 70, three children due to epilepsy and one child due to each of the following: obsessive-compulsive disorder, neurofibromatosis, hyperthyroidism, dyspraxia, severe autism and on stimulant medication for ADHD). In addition, data from 108 participants were lost due to mechanical failure and data from a further six participants were subsequently excluded due to difficulties during test sessions that inappropriately affected the data (e.g., playing with the actigraph). The final sample consisted of 836 children: 325 identical (monozygotic, MZ) twins (data for 150 complete twin pairs), 253 same-sex non-identical (dizygotic, DZ) twins (data for 113 complete twin pairs) and 258 opposite-sex DZ twins (111 complete twin pairs). The data for the remaining 89 ‘singleton’ twins were also used for model fitting in the structural equation modelling (see Neale et al., 2006). The mean age was 8.51 (SD = .42). Parents of all participants have given informed consent and the study was approved by the Institute of Psychiatry Ethical Committee.

The families visited the Research Centre for the assessments. The laboratory-based test session involved the administration of a short-form IQ test and several theory-driven experimental tasks (for further details see Kuntsi, Rogers et al., 2006). Two testers assessed the twins simultaneously in separate testing rooms. Halfway through the testing session there was a 25-minute unstructured break, during which the children were together with their parents in the reception atrium of the Research Centre. The testers were present during this time, but children were allowed to complete their own activities, or wander around and explore the area. The total length of the testing session, including breaks, was approximately 2.5 hours.

Measures

Actigraph measurements. The children wore two actigraphs that were slightly larger than a watch (MTI Health Services, version 323, Health One Technology). One was worn on the dominant leg (established by asking which leg they would kick a ball and walk up the stairs first with) and one on the waist. MTI actigraphs have been shown to have the least variability across units and the highest reliability compared to other personal motion sensors (Welk, Schaben, & Morrow, 2004). They contain accelerometer technology, which not only records the number of movements, but also the magnitude. The actigraph data output was set to readings per minute (total number of movements and the cumulative magnitude for each minute), measured in gravitational acceleration (G) units. This acceleration is then digitised and band limited to .25–2.5 Hz, which was selected to detect normal human activity, while rejecting motion from other sources. In all analyses, we obtained an average reading by dividing the number of movements and the cumulative frequency by the number of minute readings; this removed the effect of time, as some children spent longer on some conditions, or in the whole test session, than others.

Analyses

The structural equation-modelling program Mx (Neale 1997) was used to conduct the genetic analyses. Models were fitted to age- and sex-standardised scores, using raw data analysis. Participants with incomplete data were included in the analyses as Mx provides a method for handling incomplete data by using raw maximum likelihood estimation, in which a likelihood statistic (−2LL) of the data for each observation is calculated. This implies that there is no overall measure of fit (such as a $\chi^2$-value with corresponding $p$-value for the number of degrees of freedom, as obtained by fitting directly on observed variance–covariance matrices). Instead, with raw data, there are relative measures of fit: by comparing the −2LL and degrees of freedom of our models with the −2LL and degrees of freedom of the saturated model (where the maximum number of parameters is estimated to describe the correlational structure between variables), a $\chi^2$ fit index is obtained. The degrees of freedom for this test is equal to the difference in degrees of freedom of the two models (M.C. Neale & Cardon, 1992). A $\chi^2$-difference test can be performed to compare the fit of nested models. For non-nested models, the Akaike’s information criteria (AIC) values are used to compare the fit of alternative models. Low (ideally negative) AIC values indicate less difference between the observed and predicted covariances and therefore better fit (Williams & Holahan, 1994). A difference in AIC between two models of less than
2 suggests substantial evidence for both models; a difference between 3 and 7 indicates that the higher AIC model has considerably less support; a difference of more than 10 indicates that the higher AIC model is very unlikely (Wagenmakers & Farrell, 2004).

Information about the precision of parameter estimates and their explained variance in Mx was obtained by likelihood-based confidence intervals (CIs) rather than by standard errors. In this method a parameter is progressively moved away from its maximum likelihood estimate in either direction, while the other model parameters are optimised, until the difference in fit, distributed as a chi-square with one degree of freedom, is significant. For 95% CI the .05 level of significance is approximately 3.84 in each direction (M.C. Neale & Miller, 1997).

Univariate genetic analyses. The logic behind quantitative genetic analyses of twin data has three parts. First, MZ twins share all their inherited parental chromosomes and are therefore genetically identical, whereas DZ twins, like ordinary full siblings, share on average only half of their parental chromosomes and therefore 50% of inherited genetic variation. For shared environmental influences MZ and DZ twins are expected to correlate to the same extent. As such, when the similarity of MZ twins is greater than the similarity of DZ twins, this indicates a genetic contribution to the behaviour being measured. In model fitting, this yields a significant variance component called for additive genetic variance (A). Second, if only genetic influences were involved, the behaviour of MZ twins’ should be twice as similar as DZ twins’. If, however, MZ twin pairs are less than twice as similar as DZ twin pairs, this indicates that environments the children share in common have enhanced their similarity. In model fitting, this yields a variance component called C (common or shared environmental variance). Third, if MZ twins, despite sharing all their genes, are not perfectly identical in their behaviour, this indicates that experiences unique to each twin have reduced the twins’ behavioural similarity. In model fitting, this yields a variance component called E (child-specific environmental variance, which, since it also includes measurement error, cannot be omitted from any model).

The full genetic ACE model is fitted first. Then, to attain the most parsimonious model, parameters which do not significantly contribute to the fit of the model are dropped. The AE and CE models are nested within the full ACE model (i.e., subsets of free parameters in these models are contained in the full model). The results from the univariate analyses on the two situations separately are used to inform model choice for the bivariate analyses that were conducted across the two situations. However, parameter estimates are based on those from the bivariate model due to its increased power (Schmitz, Cherny, & Fulker, 1998).

Bivariate genetic analysis. Bivariate genetic analysis allowed us to investigate whether the same genetic and environmental factors influence activity across the two situations. In bivariate twin analysis, MZ and DZ correlations are compared across traits: that is, one twin’s scores on a trait are correlated with the co-twin’s scores on another trait. Here, the two traits represent the two different situations: one twin’s activity level in the laboratory is compared to his/her co-twin’s activity level in the break. If cross-trait twin correlations are greater for MZ than for DZ twins, this implies that genetic factors contribute to the phenotypic correlation across traits. A genetic correlation \( r_g \) indicates the extent to which genetic influences on one trait overlap with those on another trait (regardless of their individual heritabilities); correlations can similarly be estimated for shared environment influences \( r_e \) and for child-specific environmental influences \( r_c \). Based on the individual heritability of each trait, and the estimated genetic correlation, the extent of the shared genetic influence on the variance in phenotypic correlation can be estimated. Using each situation (the laboratory-based test session and the break in testing) as a separate trait, we fitted a correlated factors model (Neale & Cardon, 1992). In a correlated factors solution both traits have separate A, C and E influences and the correlations across these influences are estimated.

Results

A composite activity measure

A principal components analysis showed that one major factor accounted for 76% of the variance between the two measurements, for the intensity of movements taken on the leg and on the waist (Eigenvalue = 1.52). No other factors were extracted, as their Eigenvalues were below 1. Seventy-six percent of the variance in each actigraph measurement was explained by this one factor. As such, neither of the measurements contributed significantly to a unique aspect of activity level and we therefore combined both measures into a single composite score. Over the whole session, including the laboratory-based testing and the break, the two actigraph measurements were significantly correlated at \( r = .52 \) (\( p < .001 \)). A single composite actigraph score for each session was created by taking an average of the two actigraph measurements.

Log transformations were applied to the composite scores (optimised minimal skew through the lnskew0 command in Stata version 9.1) to normalise skewed distributions. The composite scores were also regressed for age and sex, as required for the quantitative genetic model fitting.
Genetic analysis

For both the test session and the break in testing composite actigraph scores, MZ correlations were higher than DZ correlations (Table 1), indicating a genetic influence on activity level. The correlations for both MZ and DZ twins also indicated that shared environmental effects influenced AL scores in both situations. Exploratory univariate analyses on data from the two situations separately indicated that the ACE model was the best-fitting model in each case.

Bivariate genetic analysis between the laboratory-based test session and the break in testing

The phenotypic correlation between activity during the test session and activity during the break in testing was .57. The higher MZ than DZ cross-twin cross-trait correlations indicate genetic contribution to the phenotypic correlation (Table 1). A full ACE bivariate model was fitted to the data (Table 2). For the test session composite actigraph score the proportion of variance accounted for by A (95% confidence intervals in brackets) was 24% (5–49%), by C 27% (5–44%) and by E 49% (40–59%). For the break composite actigraph score the proportion of variance accounted for by A was 30% (12–50%), by C 42% (24–57%) and by E 27% (22–35%). The genetic correlation was 1.0, indicating that 100% of the genes influencing activity during the test session also influenced activity during the break. The shared environment correlation was .6 and the child-specific environment correlation was .44.

The parameter estimates from the bivariate model allow us to estimate the genetic contribution to the phenotypic correlation. This is obtained by multiplying the square root of the heritability of the activity level during test session (√.24) by the square root of the heritability of the activity level during a break in testing (√.30) by the genetic correlation between the two traits (1.00). Thus .27 (.50 * .55 * 1.00) is the genetic contribution to the phenotypic correlation, which indicates that 48% (.27/.57 * 100) of the phenotypic correlation is due to genetic influences. Of the remaining 52% of the phenotypic correlation that was not due to genetic effects, 36% was accounted for shared environmental influences and 16% by child-specific factors (including possible measurement error).

Univariate genetic analysis on a composite score of the whole session

Given that the bivariate analysis between the two situations indicated shared genetic etiology, a further univariate analysis was run on a composite score of the two situations (an average of the readings taken during the test session and the break).

For this new, full composite score, MZ correlations were higher than DZ correlations (Table 1), indicating a genetic influence. The high correlations for both MZ and DZ twins also indicate a shared environmental contribution.

Four genetic models were fitted to the data: ACE, AE, CE and E. An ACE model provided the best fit (Table 2). The proportion of variance (95% confidence intervals in brackets) accounted for by A was 36% (17–56%), by C 39% (21–55%) and by E 25% (20–32%).

Discussion

We demonstrated significant additive genetic influences on objectively-measured activity level in middle childhood. The analysis indicated that during

![Table 1: Within-pair Pearson correlations: composite actigraph measure for activity during laboratory-based test session and break in testing, and a full composite of the two situations](attachment:table1.png)

Table 1: Within-pair Pearson correlations: composite actigraph measure for activity during laboratory-based test session and break in testing, and a full composite of the two situations

<table>
<thead>
<tr>
<th></th>
<th>Twin 1 test session</th>
<th>Twin 1 break</th>
<th>Twin 1 full composite</th>
<th>Twin 2 test session</th>
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<td>Mean (SD)</td>
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<td>733.28 (498.76)</td>
<td>350.94 (216.69)</td>
<td>140.36 (150.64)</td>
<td>751.31 (504.72)</td>
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<td>Mean (SD)</td>
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<td>752.67 (587.16)</td>
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*Composite of the whole session.

*Prior to transformation.
both the laboratory-based test session and the break in testing the effects on sibling similarity were due to both genetic influences (24% and 30%) and shared environmental influences (27% and 42%); however, during the break in testing shared environment played a greater etiological role. This is the first study, to our knowledge, to investigate the etiology of activity level across two situations, as well as being the largest twin sample to date to use actigraphs. The break-period findings are similar to those from the earlier twin study of infants and toddlers, which used actometer measurements in similar circumstances (the twins were together and undergoing self- or parent-directed activities; Saudino & Eaton, 1991, 1995). The test session findings, in turn, more closely correspond to findings from the study with adults, where measurements were based on activity during individual test sessions (Spinath, Wolf, Angleitner, Borrenau, & Riemann, 2002), in that shared environment contributes somewhat less to the etiology of activity level.

We further demonstrated, by a genetic correlation of 1.00, that the same genes are involved in activity level in the two different situations. The phenotypic correlation between activity measured in the two situations was .57, of which 48% was accounted for by shared genetic influences, 36% by shared environment influences and 16% by child-specific environmental influences (plus possible measurement error). The finding that the same genes contribute to activity level across the two situations is important for the design and interpretation of molecular genetic studies that use directly observed activity measures. Yet the findings also indicate the important role of the environment during, in particular, unstructured activities that involved both members of a twin pair. We therefore conclude that differences in activity level between situations are in general likely to be due to environmental factors.

Given the finding of a shared genetic etiology for activity level across the two situations, we further combined the data into a single composite score. Previous analyses on cognitive data from the SAIL sample have indicated the potential of composite scores in maximizing sensitivity to genetic factors through improving reliability (Kuntsi, Rogers et al., 2006). The overall activity level composite score indicated a genetic contribution of 36%, a shared environmental contribution of 39% and a child-specific environmental contribution of 25%. Overall, the data support the potential usefulness of the activity-level full composite score for molecular genetic analyses.

This study was conducted at a Research Centre to control for potential confounding variables and hence ensure comparability of the assessment situation across twins and families. Although this is not a ‘naturalistic’ setting, it does resemble a classroom setting (i.e., controlled task situation), where high activity is often most problematic and where actigraph discrimination between ADHD and control groups has been most successful (Dane et al., 2000; Porrino et al., 1983). The comparison of the laboratory-based session with the break session enabled an investigation of differences in etiology of activity across situations. However, a more detailed investigation of situational determinants of differences in activity level is an important direction for future research. A limitation of actigraphs may be noted to be the loss of data due to mechanical failure. However, the accuracy of the data in representing the phenotype itself may increase power to counteract this. Finally, it may be noted that two and a half hours is a relatively short time to obtain actigraph data, given that momentary or unrepresentative influences may not have had time to be averaged out; yet one study showed that actigraphs best distinguished between ADHD and control groups in the first 10 minutes of recording (Inoue et al., 1998), and much laboratory-based cognitive and other ADHD research is also conducted under similarly brief conditions.

These findings also have implications for animal research. Although activity level is currently the most commonly cited reason for defining an animal model of ADHD (Johansen & Sagvolden, 2004), little is known about the genetic mechanisms involved in the regulation of activity level in animals. It seems likely that the same genetic influences on activity level will be found across different tasks situations; nevertheless, some data do indicate genetic differ-

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<td></td>
<td></td>
<td>-4.00</td>
</tr>
<tr>
<td>2. CE</td>
<td>2166.56</td>
<td>827</td>
<td>14.65</td>
<td>4</td>
<td>&lt;.006</td>
<td>12.65</td>
<td>1</td>
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<tr>
<td>3. AE</td>
<td>2168.92</td>
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<td>.002</td>
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<td>9.01</td>
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<tr>
<td>4. E</td>
<td>2359.96</td>
<td>828</td>
<td>208.05</td>
<td>5</td>
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<td>206.05</td>
<td>2</td>
<td>&lt;.001</td>
<td>198.05</td>
</tr>
</tbody>
</table>

Note: The AE, CE, and E models were compared to the full ACE models. Best fitting model indicated in bold. \( -2LL \) = Likelihood Statistic. AIC = Akaike’s information criteria.
ences between activity level during exploratory phases in novel situations, when compared to stable baseline activity level in habituated situations such as home cage observations (Johansen, Aase, Meyer, & Sagvolden, 2002). For this reason further research in human participants should also focus on the potential for genetic differences that might arise during different types of tasks and situations.

The findings of a moderate degree of genetic influence on activity level and of a common set of genes that influence activity level across situations support the use of actigraphs as an additional source of information in studies that aim to improve phenotype definition for genetic studies of ADHD. In future work on this sample we will investigate associations with specific risk genes. The report by Langley et al. (2004) of an association between actigraph-recorded activity level and the DRD4 gene suggests promise for the inclusion of actigraph measurements in molecular genetic studies.

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