# No Evidence for Sex-Linked or Sex-Limited Gene Expression Influencing Spatial Orientation

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Scores of 83 pairs of twins and their parents on the Cubes Comparison Test have been analyzed to test competing hypotheses about the origin of individual differences in spatial orientation. Models allowing for polygenic sex-linked or sex-limited gene expression show no improvement in fit over the simple autosomal additive polygenic model. However, individual environmental influences  $(E_1)$  account for twice as much variance in males as in females.

KEY WORDS: spatial ability; sex linkage; sex limitation; sex differences.

### INTRODUCTION

Spatial ability entails visualization and mental transformation of two- and three-dimensional images. Although there is still disagreement about the mental processes involved in spatial tasks (McGee, 1979; Guttman and Shoham, 1982), at least two spatial factors, spatial visualization and spatial orientation, have been consistently found in factor analytic studies since the 1930s (French, 1951; Michael *et al.*, 1957; McGee, 1979). Visualization requires that an object be mentally transformed into components for manipulation, whereas the whole figure is manipulated in spatial orientation (Ekstrom *et al.*, 1976).

Of particular interest is the cause of sex differences on spatial tests. Although sex differences in spatial ability account for less than 5% of the population variance (Hyde, 1981), it is consistently found that males are

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superior to females on tests having a high visuospatial component and that this inequality is particularly marked in the tails of the distribution (Maccoby and Jacklin, 1974; Harris, 1978). On a number of tests, only 20 to 25% of females reach or exceed the average performance of males (Bock and Kolakowski, 1973; Harris, 1978; Bock, 1973). One hypothesis of the superior spatial skill of males is that an X-linked recessive gene enhances spatial ability (Stafford, 1961; Thomas and Jamison, 1981; but see also McGee, 1981), while competing hypotheses propose sex limitation of gene expression (Peterson, 1973; cited by Bock, 1973) or differences in sex role conditioning (Sherman, 1967). Although single-gene models for traits as complex as this are naive and evidence purporting to demonstrate the existence of a major gene can arise simply as an artifact of the distribution of test item difficulties (Eaves, 1983), it is possible that polygenic X-linked or sex-limited gene expression might account for some of the variance in spatial ability.

We have analyzed scores from a test of spatial orientation in balanced pedigrees of twins and their parents, using the method of pedigree analysis described by Lange  $et\ al.$  (1976). They confined themselves to estimation of additive and dominant genetic components. Others have used the flexibility provided by the approach to test for genotypes  $\times$  age interaction and to fit path models for cultural transmission to family data (Eaves  $et\ al.$ , 1978). Here we take advantage of this flexibility to test for the effects of polygenic sex-linked or sex-limited gene expression and hence to distinguish between hypotheses concerning the origin of differences in spatial ability.

## **METHOD**

# Sample and Measurements

The Cube Comparisons Test (French *et al.*, 1963), a test of three-dimensional spatial orientation, was administered as a timed group test. It consists of 42 items, each presenting a pair of drawings of cubes with distinctive markings on the visible faces. The subject is told that no single cube can have two faces with the same markings and is asked to decide which pairs can be different rotations of the *same* cube and which must represent *different* cubes. The score is taken as the number of items answered correctly in 4 min. The test has been used in a number of studies, each of which has identified a clear spatial orientation factor (Ekstrom *et al.*, 1979). It is one of a battery of tests whose split-half reliabilities are reported as in excess of 0.70 (Ekstrom *et al.*, 1979). Data were available for 83 pairs of twins aged 13–19 years [20 monozygotic (MZ) males, 12 MZ females, 14 dizygotic (DZ) males, 17 DZ females, 20 DZ opposite

			Progeny	
	Sex	linkage	Sex limitation	
Statistic	Female	Male	Female	Male
Total variance	$\frac{1}{2}D_{\mathrm{Rr}}$	$D_{x}'$	$\frac{1}{2}D_{RF} + E_{1F} + E_{2F}$	$\frac{1}{2}D_{\rm RM} + E_{\rm 1M} + E_{\rm 2M}$
Covariance				
MZ	$\frac{1}{2}D_{\mathbf{R}_{\mathbf{x}}}$	$D_{x}$	$\frac{1}{2}D_{\mathrm{RF}} + E_{\mathrm{2F}}$	$\frac{1}{2}D_{\rm RM} + E_{\rm 2M}$
DZ same sex	$\frac{3}{8}D_{\mathbf{R}_{X}}$	$\frac{1}{2}D_{x}{}'$	$\frac{1}{4}D_{\rm RF} + E_{\rm 2F}$	$\frac{1}{4}D_{\rm RM} + E_{\rm 2M}$
Parent-offspring				2111
On female parent	$\frac{1}{4}D_{\mathrm{Rr}}$	$\frac{1}{2}D_{xx}'$	$\frac{1}{4}D_{\mathrm{RF}} + E_{\mathrm{2F}}$	$\frac{1}{4}D_{\rm RMF} + E_{\rm 2M}$
On male parent	$\frac{1}{2}D_{xx}'$		$\frac{1}{4}D_{\mathrm{RMF}} + E_{\mathrm{2MF}}$	$\frac{1}{4}D_{\rm RM} + E_{\rm 2M}$
DZ opposite sex		$D_{xx}'$		$+E_{2MF}$

**Table I.** The Contribution of Additive X-Linked and Sex-Limited Gene Action to the Covariances Derived from Twin-Family Data<sup>a</sup>

sex] and their parents. The data and the sample have been described in detail elsewhere (Jardine and Martin, 1983).

## Genetic-Environmental Models

We distinguish between environmental variation specific to the individual  $(E_1)$ , which includes errors of measurement, and those environmental factors which are shared by members of the same family but differ between families  $(E_2)$  (Jinks and Fulker, 1970).  $D_{\rm R}$  is the genetic variation due to the additive effects of autosomal genes in the absence of assortative mating and  $H_{\rm R}$  is the variation due to dominance at autosomal loci affecting the trait. The contributions of these terms to the expectations for covariances between relatives are well known (e.g., Eaves  $et\ al.$ , 1978, p. 295).

To these expectations can be added terms arising from polygenic additive variation due to X-linked genes. In females there are three possible genotypes with respect to an X-linked gene pair A-a, namely, XAXA, XAXa, and XaXa, with contributions to the mean phenotype of  $d_x$ ,  $h_x$ , and  $-d_x$ , respectively. In males, only two genotypes are possible, XAY and XaY, which make contributions of  $+d'_x$  and  $-d'_x$ . Assuming that  $d_x \neq d'_x$ , the expected covariances between relatives can now be elaborated as shown in Table I (Mather and Jinks, 1982, p. 299). Note that this is a model for polygenic sex linkage in which a large number of

<sup>&</sup>lt;sup>a</sup>  $D_{R_x} = \sum 4uvd_x^2$ ;  $D_{x'} = \sum 4uvd_{x'}^2$ ;  $D_{xx'} = \sum 4uvd_xd_{x'}$ ; u =the frequency of the increasing allele; u + v = 1;  $D_{RM} = D_R$  effect for males;  $D_{RF} = D_R$  effect for females;  $D_{RMF} =$ the covariance of additive genetic effects in males and females; and similarly for  $E_1$  and  $E_2$ .

polymorphic loci of small and equal effect on the trait and in linkage equilibrium with each other are posited on the X chromosome.

If there is sex-limited expression of autosomal genes such that loci contributing to variation in males are different from those in females or the same loci are being expressed in both sexes but with different effect (i.e., sex limitation is operating), then the contributions of the three genotypes AA, Aa, and aa to the mean phenotype are  $d_{\rm m}$ ,  $h_{\rm m}$ , and  $-d_{\rm m}$  in males and  $d_{\rm f}$ ,  $h_{\rm f}$ , and  $-d_{\rm f}$  in females. The new expectations for covariation between relatives are now calculated as shown in Table I. The expectations for twin data have been calculated previously to include the effects of sex limitation (Eaves, 1977; Clark et al., 1980), and here the expectations of parent-offspring covariances have also been expanded to include such effects.

The power of our small study to detect genetical nonadditivity is negligible (Martin *et al.*, 1978) so dominance terms have been omitted from the expectations for sex-linked and sex-limited inheritance in Table I.

# Fitting Models to Balanced Pedigrees

Lange et al. (1976) give an expression for the log-likelihood of an observed pedigree assuming multivariate normality. For a given pedigree of n individuals, we define a vector of observed scores  $\mathbf{x}$ , and a corresponding vector of expected scores  $\mathbf{\mu}$ . The expected covariance matrix of individuals in the predigree is  $\mathbf{\Sigma}$ . The elements of  $\mathbf{\Sigma}$  will depend on the relationships between members of the pedigree and on the causal model assumed for the trait under study.

For a given  $\mu$  and  $\Sigma$ , the log-likelihood of obtaining the pedigree of individuals with observed scores x is

$$L = \frac{1}{2} \ln |\Sigma| - \frac{1}{2} (x - \mu)' \Sigma^{-1} (x - \mu) + \text{constant.}$$

The joint log-likelihood of obtaining p pedigrees is the sum of the log-likelihoods of the individual pedigrees. Estimation involves the selection of parameters which maximize the joint likelihood of observing the given set of predigrees. We have minimized -L using a powerful and efficient Fortran subroutine for unconstrained optimisation (EO4JAF) from the commercially available Numerical Algorithms Group (1981) library. Standard errors of the estimates were obtained not by use of the algebraic differentials given by Lange  $et\ al.$  (1976) but by numerical differentiation at the minimum and inversion of the resulting Hessian matrix.

## **RESULTS**

We found significant differences in sex and generation means for the Cube Comparisons Test. Males performed significantly better than females and twins performed significantly better than parents. Consequently, in all models we have estimated separate means for the mothers, fathers, and male and female twins. Within these four groups no significant correlations with age were found.

We first fitted an "empirical" model, devoid of any theory, against which we might judge the fit of the various environmental and genetic models. Different means and variances were allowed for female and male twins, mothers, and fathers. Separate correlations were also allowed for the five twin groups (MZ female, MZ male, DZ female, DZ male, DZ opposite sex) as well as four separate parent-offspring correlations depending on the sex of the parent and the child. Estimates of all these parameters, their standard errors, and their significance are shown in Table II. It should be noted that since these are maximum-likelihood estimates, the correlations and their variances are adjusted for the fact that the same individual contributes to several correlations.

The estimated correlations are not in accord with simple sex-linked transmission of spatial orientation. In the presence of X linkage and in the absence of other sex-influenced transmission, one predicts a higher father-daughter (fd) than father-son (fs) correlation and a higher mother-son (ms) than mother-daughter (md) correlation, i.e.,

$$r_{\rm ms} = r_{\rm fd} > r_{\rm md} > r_{\rm fs}$$

Opposite-sex pairs of siblings (bs) should show less similarity than pairs of sisters (ss), with the correlations between pairs of brothers (bb) intermediate between the two, i.e.,

$$r_{\rm ss} > r_{\rm bb} > r_{\rm bs}$$

(Mather and Jinks, 1983, p. 300). Neither the parent-offspring nor the sibling correlations are in the expected order. The fact that two of the five twin correlations and all of the parent-offspring correlations are nonsignificant and that the correlation of DZ males is nearly twice that of MZ males indicates sampling difficulties. Nevertheless, the almost-zero father-son correlation (0.02) suggests that there may be some information concerning sex linkage in the data. It is still, therefore, of interest to see which of the various models allowing for autosomal, sex-limited, and sex-linked inheritance is most compatible with the data, although discrimination among them may be difficult with such a small sample.

Table II. Results of Fitting an "Empirical" Model in Order to Obtain Maximum-Likelihood Estimates of Means, Variances, and Familial Correlations for the Cube Comparisons Test

Statistic	Estimate	SE
Mean		
Female twin	20.19	0.83
Male twin	23.36	0.94
Mothers	15.95	0.57
Fathers	20.90	0.74
Variance		
Male twin	59.75	9.57
Female twin	44.46	7.59
Mothers	26.89	4.17
Fathers	45.36	7.04
Correlation		
Spouse	-0.06	0.11
MZ female	0.60**	0.17
MZ male	0.33*	0.18
DZ female	0.16	0.28
DZ male	0.57**	0.17
DZ opposite sex	0.23	0.19
Mother-son	0.17	0.11
Mother-daughter	0.18	0.13
Father-son	0.02	0.12
Father-daughter	0.18	0.12
Log-likeliho	od = -778.16	

<sup>\*</sup> 0.01 < P < 0.05.

Results of model fitting are shown in Table III. Models including the effects of assortative mating were not fitted since the marital correlation was nonsignificant (r = -0.06). A test of the absolute goodness of fit of the model is cumbersome with this approach, but it is possible to compare alternative hypotheses by the likelihood ratio criterion (Elston and Stewart, 1971). We shall judge all our models against the fit of the empirical model which has 18 parameters. The degrees of freedom for chi-square are then 18 less the 4 for the means (which must be estimated for each model but which are not tabled since they hardly vary) and the number of variance components estimated.

We first fit an  $E_1$  model which assumes that all variation is specific to the individual. Both the  $E_1E_2$  and the  $E_1D_R$  models (2 and 3) provide significant improvements in fit over model 1, twice the difference in likelihoods yielding chi-square values for 1 df of 11.60 and 13.78, respectively. The inclusion of additional parameters results in only trivial

<sup>\*\*</sup> P < 0.001

Table III. Results of Model Fitting: Parameter Estimates, Their Standard Errors, and Their Significance and A Comparison of the Fit with that of the "Empirical" Model Are Given

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Model					1	Estimate					$\chi_2$	đť
-	$E_1$ ,	44.32***									34.44	13
2	$E_1$ ,	36.97***	$E_2$ ,								22.84	12
3	$E_1$ ,	30.01**	$D_{\mathrm{R}}$								20.66	12
4	$E_1$ ,	30.01** 30.01** + 5.96	$E_2$ ,	0.00	$D_{\mathrm{R}},$	28.15					20.66	11
Ŋ	$E_1$ ,	27.17**	$D_{ m R},$		$H_{\rm R}$ ,	19.76					20.10	Ξ
9	$E_1$ ,	27.46***	$E_2$ ,		$D_{\mathrm{R}}$ ,	0.00	$H_{\mathrm{R}},$	41.46			19.52	10
7	$E_1$ ,	26.56***	$D_R$ ,	8.96	$D_{\mathrm{R}_{\mathrm{c}}}$	10.57	$D_x'$ ,	20.02*	$D_{xx}'$ ,	11.09	12.96	6
<b>∞</b>	$E_{1m}$ ,	39.08***	$E_{1\mathrm{f}},$		$D_{\mathrm{R}_{\mathrm{m}}},$	27.34*	$D_{ m R_f}$	30.96**	$D_{\mathrm{Rmf}}$ ,	30.20*	11.90	6
6	$E_{ m lm},$	38.17*** ±5.80	$E_{ m lf},$	± 5.49 19.97*** ± 4.30	$D_{\mathrm{R}}$ ,	± 13.22 29.75*** ± 8.71		H 12.70		13,01	11.94	Ξ

\* 0.01 < P < 0.05. \*\* 0.001 < P < 0.01.

\*\*\* P < 0.001.

improvement over these models. Furthermore, when all three parameters  $(E_1, E_2, D_R)$  were fitted,  $E_2$  approached its lower bound of zero, while  $D_{\rm R}$  remained unchanged (model 4). Consequently in subsequent model fitting  $E_2$  parameters were omitted. However, estimates of  $D_R$  and  $E_2$ are highly negatively correlated, and it is difficult to partition variation between these two effects when both are present, particularly with small sample sizes (Martin et al., 1978). It is also difficult to detect dominance with twin data since estimates of  $H_R$  are confounded with  $E_2$  effects (Martin et al., 1978) and negatively correlated with  $\hat{D}_R$ . We see in models 5 and 6 that  $\hat{H}_{R}$  failed to reach significance in either model, and so it was also omitted in further model fitting. In model 7 additive sex-linkage terms are added to  $E_1$  and the autosomal additive genetic parameter, while in model 8 separate terms are allowed for male and female  $E_1$  and additive genetic contributions. There is little to choose between these two models. although the sex-limitation model results in a slightly greater improvement. Additionally, only one of the genetic parameters is significant in the sex-linkage model, while all estimates are significant in the sex-limitation model. If the genes affecting a trait in males are different from those acting in females, then  $\hat{D}_{Rmf}$  is expected to be zero (Eaves et al., 1978). However, if the genes acting in males and females are the same but they produce effects on different scales in the two sexes, then the correlation between the effects,

$$r_{\rm DRmf} = D_{\rm Rmf} \cdot (D_{\rm Rm} \cdot D_{\rm Rf})^{-1/2},$$

is expected to be 1. The estimate of the correlation between additive gene effects in males and females is 1.04, suggesting that there is no difference in gene effects between the sexes. In fact, if we only allow different  $E_1$  effects for males and females but constrain the  $D_R$  effects to be the same, this (model 9) represents a significant improvement of fit over the  $E_1D_R$  model ( $\chi_1^2 = 8.72$ , P < 0.01). The empirical model (Table II) is not significantly better than this final model ( $\chi_{11}^2 = 11.94$ ) and so the  $E_{1m}E_{1f}D_R$  model appears to provide the most parsimonious description of our data.

## DISCUSSION

There is no evidence for the importance of either X-linked or sexlimited gene effects as causes of individual differences in spatial orientation. This is in accord with a similar lack of support for sex-linked effects on spatial ability reported by other workers in recent years (e.g., Bouchard and McGee, 1977). However, performance on the Cubes Comparison Test appears to be much more affected by individual environmental influences in males than in females (the variation due to  $E_1$  in males is almost twice that in females). It is possible that social stereotyping restricts the range of environmental circumstances available to females to improve spatial skills and that this accounts for both their lower mean and their lower variance. However, doubtless other rationalizations of our findings could be made and it is curious that any such environmental influences are of an individual nature rather than being shared by cotwins. More probably an explanation is to be found in the psychometric properties of the test (Eaves, 1983). There were inconsistencies in the pattern of sibling and parent-offspring correlations, and the possibility that our results are due to some artifact of sampling cannot be ruled out.

Nevertheless, the foregoing analysis provides an example of a rigorous hypothesis testing approach which is needed to discriminate among the hypotheses advanced to explain individual differences in spatial ability. Obviously, the sample size in the present study is not large, but it is not known what size is necessary to distinguish with given power between the models applied here to data of this design (Loehlin, 1984). Before further work is attempted in this area, power calculations similar to those by Martin *et al.* (1978) for autosomal polygenic models fitted to the classical twin study should be performed.

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