

## **GENETIC AND ENVIRONMENTAL INFLUENCES ON INTELLIGENCE: A STUDY OF TWINS<sup>#</sup>**

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*A twin study using 30 identical (Monozygotic MZ) and 30 fraternal twins (Dizygotic DZ) was conducted to assess the role of genotype, environment, and their interaction. All the twins were males and reared together. Raven's Standard Progressive Matrices (SPM) was taken as a measure of general intelligence 'g'. Genotype x environment effect was nonsignificant. Non-iterative least square weighted analysis was applied for goodness of fit for genetic (additive genetic variance DR and dominance HR) and two environmental (within family environment E1 and between family environment E2) components. A model comprising additive genetic variance (DR) and within family environmental variance (E1) was a good fit to the data, explaining 89.80% of narrow sense heritability. However, much of the variance could be explained only by the additive genetic variance component (DR). Addition of dominance (HR) or between family environment (E2) component failed to explain rest of the variance. It is concluded that general intelligence is largely determined by the genetic factor, particularly the additive genetic variance.*

Intelligence is a phenotypic behavioral construct having both genetic and environmental substrates. The concept of general intelligence 'g' was propounded by Spearman (1904) as the quality of around general superiority or inferiority. He thought that people differed by heredity in 'g' just as they differed in height or weight. Since several tests of intellectual performance correlated closely, he postulated a hypothetical general and purely quantitative factor

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underlying all cognitive performances of any kind. It was described as the mental energy, that is, the energy available in the cortex for functioning of a group of neurons or a potential. However, the act or its success would depend upon the efficiency with which the neurons can utilize this energy. There are individual differences in average ability to profit from various types of instructions and to acquire knowledge under conditions in which instructional procedures are less than optimal. It is this general ability that defines general intelligence. Thus, intelligence is both many different things, indeed, even idiographically present within an individual, and is also in a coherent and meaningful sense one thing.

Empirical study of the genetics of intelligence is as old as other genetic studies, e.g., works of Mendel, and of Galton were published in 1860's. Despite overwhelming evidence in support of polygenic theory of genetic determination of intelligence (Bouchard & McGue, 1981; Erlenmeyer-Kimling & Jarvik, 1963; Rodger & Rowe, 1987), the findings were not stressed due to controversies (e.g., racial differences) cropped in psychology (Eysenck, 1971; Jensen, 1983). A great number of twin studies has been conducted across cultures because of the robustness of twin study design in behaviour genetics (Finkel, Pederson, McGue, & McClearn, 1995; Pedersen, Plomin, Nesselroade, & McClearn, 1992; Thompson, Detterman, & Plomin, 1993), reporting heritability from moderate (.50) to high (.80). A lone Indian study by Nathawat and Puri (1995) done on a small sample of 15 MZ and 15 DZ twins of both sexes reports very high intraclass correlation which amounts to .90 heritability. Evidence in support of genetic basis of intelligence also comes from inbreeding studies reporting depression (Aggrawal, Sinha, & Jensen, 1984; Jensen, 1983; Schull & Neel, 1965; Spuhler, 1967). Weiss (1982) using Mendelian analysis of Spearman's general factor found that it is the result of genotypes with discrete true scores of central processing time, the heterozygotes being exactly in the mean of the differences of the mean of the homozygotes. Thus, it was difficult to speak of the major locus for it as distribution between genotypic classes overlapped considerably (may be due to error of measurement or environmental influences). The reigning biometrical paradigm asserts that continuous variation implies the determination of intelligence by many genes with small effects.

Biometrical genetic analysis initiated by Fisher (1918), applied by Mather (1949) and popularized by Jinks and Fulker (1970), Jinks

and Eaves (1974), Eaves, Last, Young and Martin (1978), is the most appropriate technique to study traits having continuous variations, e.g., intelligence. The approach has been tried for personality dimensions, such as extroversion, neuroticism, and psychoticism by Eaves and Eysenck (1975, 1976, 1977). For scholastic abilities by Martin (1975), Petrill and Thompson (1993) fit phenotypic and behavioural genetic models to twin data from Western reserved project on cognitive ability temperament and scholastic achievement. Casto, Defries, and Fulker (1995) did multivariate genetic analysis of WISC-R on twins from Colorado reading project.

In view of the absence of such a study on Indian sample, the present study was conducted to assess the genetic basis of intelligence using biometrical genetic analysis. The approach offers variety of models having genetic and environmental components suitable for situations having G x E interaction or no interaction, on twin data reared together or reared apart. Thus, the interaction of genotype and environment was also tested before fitting the best model. The findings would offer an opportunity to test the generality of genetic influences across cultures on intelligence. Due to effects of different educational systems, cultural norms, greater social class differences, and different breeding patterns genetic and environmental influences may be different than seen in Western samples.

## METHOD

### Design

Twin study design was used and every twin pair was considered as a family and the term within family environment and between family environment are used for within twin pair environment and between twin pair environment, respectively.

### Sample

The sample consisted of 30 Monozygotic (MZ) and 30 Dizygotic (DZ) male twins reared together and was obtained from villages of Krukshetra, Karnal, Kaithal, Jind, and Yamunanagar districts of Haryana State (India), on the basis of survey conducted

with the help of contacts in the area. All the MZ twins were monochorionic. The information was obtained from mothers and 'Dais' or 'midwives' who assist in deliveries and labour in villages and are well trained to examine placental vasculature. Within twins both subjects so strongly resemble to each other in physical structure, colouring, features of the face, etc., that they are frequently mistaken as one or the other even by parents. This method of zygosity diagnosis is 95% reliable to typing by blood group polymorphism (Gill, Jardine, & Martin, 1985). After selecting the MZ twins, matched DZ twin sample was selected from the same areas. Attempt was made to match the educational standard as well as background factors pairwise. Mean ages of MZ and DZ twins were 21.80%, ( $SD = 6.25$ ) and 21.50 ( $SD = 6.40$ ) years, respectively and the youngest twin was of 15 years and the eldest was of 31 years.

### Instrument

Standard Progressive Matrices (SPM) of Raven (1960) was used as a measure of general intelligence. It is a widely used culture fair test of reasoning ability of figural patterns and geometric forms which depends minimally on past learned knowledge and skills. The test consists of sixty problems arranged in five sets in an increasing order of difficulty. This test was used because of two reasons: (i) this is considered as one of the best culture fair measure of Spearman's 'g' or general ability, and (ii) it has been widely used on Indian samples.

### Procedure

Standard procedure as prescribed in the test manual was adopted for administration and scoring of SPM (Raven, Court, and Raven, 1983). There was no time limit for taking test and the instructions were given in Hindi.

## RESULTS AND DISCUSSION

The scores obtained by subjects were first of all arranged to obtain between and within variances among MZ and DZ twins, separately. Mean SPM score of MZ twin sample was 27.83 with a  $SD$  of 8.61 and  $SE = 1.11$  and of DZ twin sample was 26.00 with a  $SD$  of 8.20 and  $SE = 1.06$ .

Table 1

*Sum of squares and mean sum of squares for within and between MZ<sub>T</sub> pair*

MZ <sub>T</sub>	SS	df	MS
Between pair	4225.334	29	145.70
Within pair	227.000	30	7.57
Total	4452.334	59	

$N = 60$ ; Pairs = 30;  $\bar{X}_{spm} = 27.87$ ;  $SD = 8.61$ ;  $SE = 1.11$

Table 2

*Sum of squares and mean sum of squares for within and between DZ<sub>T</sub> pair*

DZ <sub>T</sub>	SS	df	MS
Between pair	2994.000	29	103.24
Within pair	1044.001	30	34.80
Total	4038.001	59	

$N = 60$ ; Pairs = 30;  $\bar{X}_{spm} = 26.00$ ;  $SD = 8.20$ ;  $SE = 1.06$

Since 'g' may be determined by genetic (G), environmental (E), and GE. To ascertain the GE interaction, Cochran's test of heterogeneity of variance (Winer, 1971) was used as recommended by Jinks and Fulker (1970). The test is based upon phenotypic difference within pairs. It is a ratio of maximum within twin pair variance to the total within pair variance of the sample. Neither for MZ<sub>T</sub> nor for DZ<sub>T</sub> the heterogeneity of variance was significant as 'C' for MZ<sub>T</sub> was 0.193 and 'C' for DZ<sub>T</sub> was 0.155, whereas, the 'C' required to be significant at 0.05 level of probability should be

equal to or greater than .3884 for 30 pairs. Thus the G x E interaction was nonsignificant.

Table 3

*Between and within pair variance*

Pair	Source	df	Observed MS ( $Y_i$ )	Weight ' $W_i$ ' $df/2v^2$	Components	
					$E_1$	$E_2$
MZ <sub>T</sub>	Between pair	29	145.70	.00068	1	0
	Within pair	30	7.57	.26175	1	0
DZ <sub>T</sub>	Between pair	29	103.24	.00136	1	2
	Within pair	30	34.80	.01239	1	0

Table 4

*Expected contribution of different G and E components as per non GxE and twins reared together data*

Twins	Variance	DR	Components		
			HR	$E_1$	$E_2$
MZ <sub>T</sub>	Between pair	1	.5	1	0
	Within pair	0	.0	1	0
DZ <sub>T</sub>	Between pair	.75	.3125	1	2
	Within pair	.25	.1875	1	0

The models, explaining within a between variances (Table 3) on the basis of two genetic components and two environmental components, *viz.*, additive genetic variance (DR), dominance (HR), within family environment ( $E_1$ ), and between family environment ( $E_2$ ) were applied to data on twins reared together having nonsignificant G x E interaction (Table 4). The genetic variance may be due to variation in gene dosage and/or otherwise. The expected

values for the components to explain between and within pair variance may vary from zero to one.

Simultaneous equations were generated to try three models for goodness of fit. These are: (1) Assuming HR and  $E_2$  as zero and DR and  $E_1$  as parameters; (2) Assuming  $E_2$  as zero, and DR, HR, and  $E_1$  as parameter; (3) Assuming HR as zero, and DR,  $E_1$  and  $E_2$  as parameters (Table 5).

Table 5

*Expected values of different components in three models*

Models		Components			
		DR	HR	$E_1$	$E_2$
Model I	DR + $E_1$	125		1	
		$\pm 21.60$		1	
Model II	DR + HR + $E_1$	161.88	-65.88	7.21	
		$\pm 85.80$	$\pm 148.22$	$\pm 1.91$	
Model III	DR + $E_1$ + $E_2$	123.78		7.12	1.64
		$\pm 26.66$		$\pm 1.90$	$\pm 16.77$

Table 6

*Test of Goodness of Fit Model-I*

Pair	Source	Observed $MS(Y_i)$	Expected $MS(EY_i)$	$Y_i - EY_i$
MZ <sub>T</sub>	Between pair	145.76	132.69	13.01
	Within pair	7.57	7.11	0.46
DZ <sub>T</sub>	Between pair	103.24	101.29	1.95
	Within pair	34.80	38.51	-3.71

Total =  $\chi^2 W_i(Y_i - EY_i)^2$  0.3459;  $df = 2$ ; nonsignificant.

The first model with two parameters yielded the values of  $DR = 125.58 (\pm 21.60)$  and  $E_1 = 7.11 (\pm 1.90)$ . Narrow sense heritability with these two parameters ( $1/2 DR/1/2 DR + E_1$ ) was found to be 0.898 (Table 5). Therefore, the similarities in twins reared together showed similar phenotypic intelligence due to additive genetic variance to the tune of 89.80%. Within family environmental variance ( $E_1$ ) was quite small due to similar rearing environment. Test of goodness of fit for discrepancy in observed and expected mean square ( $\chi^2 = .3459$ ,  $df = 2$ ,  $p < .90$ ) supports the model as there was no deviation if variance was explained only by  $DR$  and  $E_1$  (Table 6). Hence, the model was best fit and suitable. The addition of  $HR$  in Model-II and of  $E_2$  in Model-III as parameters (Table 5) was not appropriate because of inflated standard errors ( $HR = 65.8 \pm 148.22$ ,  $E_2 = 1.64 \pm 16.77$ ). Any other model whether genetic or environmental could not be tried as obtained  $E_2$  and  $HR$  terms were not reliable. Thus, the model that fits the phenotypic intelligence is genetic one in comparison to environmental and that too with additive rather than dominance component.

It is important that in this study no  $G \times E$  interaction was found. A common belief is that  $G \times E$  interaction has a modulating role, it does not need to be sizable. One of the reason that  $G \times E$  was not significant may be due to matching, because the elements of sample were drawn from the same background factors. It has been further validated in within and between family environmental indices. One of which is found to be in a very low proportion (Table 5). In order to have  $G \times E$  interaction, there is a prerequisite of range freedom in  $G$  as well as  $E$  components. Owing to weak,  $E$  component much of the variance could be explained on the basis of genetic component comprising two parameters which may be responsible for 89.8% of the variance - the additive genetic variance and the dominance. The gene dosage seems to determine genotype value reliably with standard error being less than 20%. Thus, as the gene dosage would increase the genotype value of the trait would also increase. The stability of the predictive aspect of additive genetic value on the trait's genotype value depends on another genetic parameter, i.e., dominance ( $D$ ). When the dominance component was induced in the model it turned out to be a bogus parameter being negatively loaded and standard error in multiplicative value. The inclusion of between family environment ( $E_2$ ) in place of dominance failed to make a change in the earlier



model. Even otherwise it was a weak and unreliable parameter (Table 5).

Casto, DeFries, and Fulker (1995) in a study using WISC-R on twin children, applied multivariate genetic analysis. They reported goodness of fit for the full model and attributed 50% of the phenotypic variance due to additive genetic effects. The inflated additive genetic effect in the present study may be due to the measure of intelligence employed, as SPM saturates higher on 'g' than Wechsler's scales.

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