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Genetics of Quantitative Traits in Human: Inbreeding as an Approach of Study

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ABSTRACT To understand genetic structure of human population, population geneticists, medical geneticists and anthropologists traditionally use correlation and heritability as a method despite some limitations. The study of inbreeding effect on quantitative traits may provide a useful approach. The basic premise is that increased homozygosity is expected in inbred families that lead to a higher probability of observing recessive inheritance. So it is useful for detecting the recessive genes by studying distribution of values in different inbreeding levels. This study tries to examine the genetics of some anthropometric traits in different inbreeding levels among growing children by analyzing the changes of means and variances with inbreeding in each age and verifies existing knowledge about genetics of anthropometric traits. The uniqueness of this study is that data has been collected with the help of extended pedigree of each household of an endogamous population and compared individuals in different inbreeding levels controlling socio- economic and physical environment that can confound genetic effects of inbreeding.

INTRODUCTION

Human geneticists and molecular geneticists commonly use quantitative characters like anthropometric, physiometric as well as psychometric traits by mapping quantitative trait locus to understand the genetic architecture of human population (Mackay et al. 2009). For analyses, they mainly use correlation between relatives for estimation of components of variation due to genetic influence as well as environmental influence (Mukherjee 1984; 1996). This approach has been criticized as high correlations only suggest but do not confirm the strong genetic influence on a trait. Researchers have shown that correlations can be affected by differences in mating patterns, genetical similarity and environmental variance (Roberts et al. 1978; Mukherjee 1996). Assuming family environment as similar, it is argued that relative values of correlations between relatives of different kinds, but of the same degree, may suggest the mode of inheritance of a character (Mukherjee 1996). A heritability study tries for partial explanation of the sources of variance for a particular phenotypic trait in a particular population (Buenen et al. 2000; Jhonson et al. 2011). Heritability estimate differs even within samples as specific environmental circumstances often exert considerable moderating effects (MacCafferey et al. 2009). This approach attempts to assess the contribution of additive genetic effects to the total variability of trait. But these approaches are unable to shed light on the genotypic distribution, specific effects of genes and interaction between loci involved. Studying human mating systems like mating between blood relatives is an important approach that can elucidate genetic structure of a population as it directly affects genotypic structure of the population. As a consequence of consanguinity, inbreeding elevates the frequency of homozygotes in the offspring at the expense of heterozygotes and distributes them equally to the two homozygotes. Increased homozygosity leads to a higher probability of recessive inheritance (Cavalli Sforza et al. 2004). Thus, recessive and additive phenotypes would increase in frequency in inbred groups contributing to the phenotypic variance and that adds to genetic variability (Mukherjee 1996).

For genetic analysis, researchers commonly use changes on means as an effect of inbreeding. The change of mean would reflect the amount of overall dominance of genes affecting the traits. The direction of change should be in the opposite direction of the dominant phenotype and indicate whether the recessive alleles should have positive or negative effects. Studies of inbreeding effects on means of quantitative human character are, therefore, a very useful approach to study the genetics of those characters (Mukherjee 1984, 1996).

Significant depression on means of anthropometric traits in adults (Charlesworth and Hughes

1996; Baduruddaza 2004); increased prevalence of diastolic blood pressure, hypertension and complex diseases (Halbertstein 1999; Rudan et al. 2003; Wright et al. 2003; Badruddaza 2004) as well as psychometric test scores and school performance (Schull and Neel 1965; Baduruddaza 2004) is observed . Inbreeding depression in human beings is observed to be relatively greater in traits that are correlated with social classes which affected the rate of consanguineous marriages. Some studies have corrected the findings for a series of related factors using multiple regression analysis. Besides, the phenotypic mean is equivalent to genotypic mean (Falconer 1989) as environmental deviation values of individuals are supported to be eliminated in the formulation of mean (Mukherjee 1992). In fact, some researchers pointed about the inappropriate selection of samples for getting non- significant and opposite results. For example, the increase in stature instead of depression in the Italian conscripts can be partly attributed to exclusion of short persons in military recruitment (Mukherjee 1984). But some researchers express doubt about the observed depressions due to inbreeding without any role of environmental factors (Cavalli-Sforza et al. 2004). However, the issue of environmental influence on quantitative traits has been addressed by some Indian studies. They tried to establish genetical significance of inbreeding effects in man by studying the effects on finger, palm, and sole print patterns (Mukher-jee 1996) which are apparently not affected by environmental influences, and by measuring inbred and non- inbred individuals from same kindred or extended families who have experienced similar socio-economic and physical environment (Mukherjee 1984, 1992). In addition, these studies have been done among infants and adults of consanguineous marriage in certain ages.

Variance is an important measure in understanding the inbreeding effect. Theoretically, there should be an increase of additive variance of characters at a rate equal to inbreeding coefficient (Falconer 1989; Mukherjee 2003). The excess increase either reflects the influence of some recessive genes indicated by change of means as suggested by I.Q. scores (Badruddaza 2004) or increased environmental variance as suggested for tooth size (Rudan et al. 2003).

Increase of variance in the offspring of first cousin marriages in Japan have been found significant for stature but not on age at walking (Schull and Neel 1965). The increase of variance on inbreeding is obviously due to homozygosity of different alleles in the population and is an indication of the genotypic effect of parental consanguinity irrespective of change of mean indicating non-additive effect of genes in addition to some additive effects. Therefore, the study of the effect of inbreeding in variance of measurements has been emphasized in the present study.

Some of the Indian studies have clearly demonstrated that the most useful genetical analysis of inbreeding effects on quantitative traits is that of the frequency distribution (Mukherjee 2003). The change of variance without change of mean on inbreeding can be helpful but because of the uncertainty of environmental variance and sampling fluctuations the study of variance is only of secondary importance. On the other hand, the study of distribution has served as a substitute for segregation analysis for several quantitative traits as has been illustrated by appearance of bimodality or bi tangentiality (Mukherjee 1996) in a number of anthropometric traits, including menarcheal age and even skin colour grades and finger ridge count and trimodality suggesting three alleles (A Mukherjee 1985; Mukherjee 1992). The antimodes represent heterozygous of a few additive genes which would decline in frequency on inbreeding. The asymmetry in the distributions in the inbred individuals would be caused by dominant / recessive alleles in the distribution of inbred ((Mukherjee 2003).

As gene assortment occurs within a breeding unit and because caste groups are closed categories in India, the ideal unit would be a caste or breeding population for a theoretical genetical model. But most of the analyses has been done based on data from composite geographical populations, hospital sources that encompasses several different castes that are completely reproductively isolated from each other or mixed sample of different breeding units or caste groups (Reddy 1992). The socio- economic status, occupations, religious background varies from one caste to other. Moreover, the features of subdivided population can affect the maintenance of variation and the manifestation of homozygosity (Jorde 1980; Cavalli Sforza et al. 2004). These factors might have confounded the genetical effects of inbreeding. Therefore, identification of single endogamous unit is absolutely necessary to get a proper picture of inbreeding effects on traits. These problems have been addressed by taking single endogamous caste , Telaga population, for analyses with the help of extended pedigrees and compared non-inbred individuals with individuals of different inbreeding levels from same kindred or extended families who have experienced similar socio- economic and physical environment .

As non- additive genetic sources (dominance and epistasis) of variance introduce expected relationships between inbreeding and phenotypic means and variances, the effects of inbreeding on means variances have potential value in testing for non- additive genetic factors (Mukherjee 1996). Hence, this study to tries to understand the nature and mechanism of genetical effects on quantitative traits by using inbreeding as an approach in the children aged 5 to 20 years by analyzing the changes of means and variances with inbreeding in each age and verifies existing knowledge about genetics of anthropometric traits. Recessive genes are those that are manifested only in homozygote. Theoretically, inbreeding leads to increased homozygosity. So, studying of values in different inbreeding levels may help in detecting recessive genes responsible for the trait. The effect on frequency distribution of traits has also been examined on the pooled data after age correction.

DATA AND METHODOLOGY

Background of the People

The data for the present analysis have been collected from Telugu – speaking populations of Kharagpur town in Medinipur district of West Bengal, India. It was found by applying genealogical method (using pedigrees) that ancestors of the bulk of these populations had migrated through generations from Srikakulum district of Andhra Pradesh as Railway Employees since late 1880's. The rest of the Telugu–speaking populations are also the descendants of immigrants from Vishakhapatnam and East Godavari district of Andhra Pradesh. A great majority of the said population is the outcome of kin-leased migration (Das 2000). The bulk of these peoples have permanently settled here as a result of succession of employment through generations in course of expansion of the local railway workshop which has become the largest of its kind in India. There was a long tradition of consanguineous marriages among Telegu speaking populations (Das 2005). A large number of marriages among them have taken place in the Kharagpur town itself. A few families have still retained their kinship links with their ancestral home especially due to railway facilities and reduction of employment opportunities at Kharagpur in recent times.

From the analysis of extensive pedigree data collected up to five generations during field investigation, it is revealed that Telaga, a local endogamous group is most numerous out of at least 27 strictly endogamous groups among Telegu-speaking populations. Socio- economic and educational statuses within Telaga endogamous group are almost equal. Though Telagas are traditionally cultivators, a majority Telagas of Kharagpur is employed as drivers, mechanics, clerks etc. in the Railways. A few of them are owners of small shops, grocery, stationery etc. Most adult males have received technical training after middle level schooling and adult female have generally attended upper primary schools (Das 2003).

Inbreeding Levels: The primary biological effect of consanguineous marriages is the increase of inbreeding in the offspring. The closer is the consanguinity between parents, greater will be the intensity of inbreeding in their offspring. To measure the intensity, inbreeding co-efficient (F) are calculated for autosomal genes by applying Wright' path coefficient method and considering F values of common ancestors of both parents. However, for utilizing samples of reasonable sizes, the offspring of (i) unrelated parents ($F = 0.00$); (ii) relatives more remote than first cousins ($0.00 > F < 0.0625$); (iii) first cousins ($0.0625 \geq F < 0.1250$); (iv) maternal uncle: niece pairs ($F \geq 0.1250$) are grouped into successive classes ignoring variation within each level.

Anthropometric Measurements

The effect of inbreeding in physical measurements like stature (ST), sitting height (SH), bi-acromial diameter (BAD), bi-iliac diameter (BID) have been examined only in the data collected from Telaga endogamous groups to control for genetic variance as well as environmental variance, which are apparently small with Telaga population. Measurements were taken on the basis of consent of the subjects aged five to twenty years in each case after selecting subjects under various inbreeding level on the basis bilateral genealogies. To minimize the effect of environmental variance, preference was given to relatives belonging to same kindred. The results of study on boys only are presented in the paper. Anthropometric measurements were taken up to the nearest 1.00 mm using standard techniques (Weiner and Lourie 1981). The subjects were requested to remove their shoes and put on light clothes during taking measurements. The mean, variances of ST, SH, BAD, and BID in mms were calculated for each category of inbreeding.

Age Estimation: Age estimation of all individuals occurring in pedigrees has been checked by birth or school certificates as well as by genealogical checks for cross checking for younger individuals from 5 to 25 years. In some cases, reference to the important events, horoscopes, physical observation has also been considered.

Comparison of Mean Values of Measurements in Different Inbreeding Levels

For a preliminary detection of inbreeding effects on means of measurements, the consistency in the trend of change of means in each yearly age group has been considered allowing for a small number of sampling fluctuations. However, one-tailed t-test for decline of the mean with inbreeding has been applied for comparison between high and low inbreeding categories in each age group in each sex for each of the measurements.

The change of mean with inbreeding has been studied to examine the non-additive (dominant recessive) effects of genes controlling the traits defined in the following formula:

$$M_F = M_o - 2F\,\Sigma dpq$$

where M_F and M_o are mean values in the absence and presence of inbreeding at the level F respectively, p and q are allele frequencies ($p + q = 1$) and d the phenotypic value of the heterozygote measured from the mid value between two homozygotes at a locus, and Σ denotes summation over the involved loci assumed to be mutually additive. Thus, the change of mean would reflect an amount of overall dominance of genes affecting the trait, $\Sigma d \neq 0$ (Falconer 1989).

To examine the consistency of decline of mean values with inbreeding, the percentage of inbreeding depression has been estimated in each of the three levels of non-zero F from the mean value of F = 0.

Comparison of Variance and Squared Coefficient of Variation of Measurements

To the extent an anthropometric character is determined by pairs of genes, there should be a linear increase of additive variance at a rate equal to the inbreeding coefficient F and also an increase of variance for non-additive gene for most of the gene frequency (Falconer 1989). Thus, variance should generally increase due to the genetic effects of inbreeding even if there are no dominance / recessive effect of genes. The assumption of linear effect of inbreeding may not always be obtained due to factors like selection, if not epistasis (Mukherjee 1984). It may not, therefore, be possible to test the increase of variance for any specific expected value in the present study. Secondly, it has been noted that variance is more sensitive sampling fluctuation than mean. Therefore, any trend of increase of variance would suggest genetic effects of inbreeding on the measurements concerned.

The change of variance of measurements with inbreeding has also been examined in each yearly age in each sex. To eliminate the effect of difference in mean values on the variances between inbreeding levels, $(CV)^2$ determined by the following formula has also been compared between different inbreeding levels.

$$(CV)^2 = (S/M \times 100)^2$$

where, S is standard deviation of measurement concerned; M is mean value of the measurement.

Comparison of Frequency Distribution of Measurements

Age Correction of Measurements: The effects of growth on the measurements have been eliminated by converting the mean values for each age for each inbreeding level into the grand mean of individuals at the age of 20 years combining all inbreeding level in each sex separately. For this purpose, the difference of the mean value in a particular age from the grand mean at 20 years has been added to each individual of the same sex to each individual of the same sex. It is worthwhile to mention that the age corrected mean for each age in a particular level of inbreeding turned out to be equal to the mean at 20 years of age in that inbreeding level. This would suggest the representative nature of the sample in spite of their small size.

The frequency distribution and variance of the age corrected measurements has been examined for each level of inbreeding in each sex to find out the effect of autosomal inbreeding on the measurements independent of age changes. The purpose of the analysis has been to test the hypothesis of increment of variance with inbreeding as has been already observed in individual ages.

The distribution of age corrected measurements is graphically represented to observe any segregation of homozygotes due to inbreeding. Frequencies of some measurements are displayed in tabulated form to determine the modes and anti-modes where possible.

Test of Bimodality: As inbred distributions of some traits appear to show bimodality the significance of such a trend is verified by obtaining Penrose's formula (1951) D / S index,

where D = (Mean of the higher mode – Mean of the lower mode)

S = mean of standard deviations of the two modes.

A half of the frequency at the anti-mode has been attributed to each modal distribution following Penrose. An index value of below 2 is not taken as an indication of bimodality and that of above 3 is taken as a dependable evidence of genotype distribution between the modes, as the mis-classification or overlapping is only about 5 per cent (Penrose 1951).

The bimodality and the asymmetry of the modes have been compared between different levels of inbreeding for different measurements in order to examine the mode of additive or non-additive action of genes concerned.

Problem of Sample Size: Scientists generally in favour of significant mean differences between different levels of inbreeding for recognizing inbreeding effects on biological traits. However, since the statistical significance is a function of sample size, very large samples would be needed for obtaining significant mean changes on inbreeding. This is because the expected average inbreeding effects on means within human populations are usually small in magnitude (Falconer 1989).

But large samples for different degrees of inbreeding, controlling genetical and environmental variances within a mating group are unrealistic (Mukherjee 1996). The sample sizes cannot be indefinitely enlarged for comparisons between breeding size and area of marriages within populations. There are concentrations of consanguineous marriages in clusters of villages surrounded by other within several endogamous populations (A. Mukherjee 1985). Against this backdrop, small sample sizes are obligatory in the present series of analyses of the effects increasing levels of inbreeding in boys in each annual age.

Hence, the analyses have to depend more on the general consistency of results in different subsamples (like different ages, for example) rather than on significance of results that can some times occur by chance, for assessing the reliability of the findings.

RESULTS AND DISCUSSION

Inbreeding Effect on Means of Measurements

Change of Means in Each Yearly Age Group: There is a declining trend of mean values of all the physical measurements under study with inbreeding even in rather small samples in each yearly age group from 5 to 20 years in boys, except for a few cases of small sampling fluctuations (Tables 1-3). The reduction of means with inbreeding is found to be significant at 5% level of probability in even small samples in each yearly age-group more often in boys and in older age group than in younger. This reinforces the hypothesis of lowering of means for physical measurements in each age in years with increase of inbreeding which would indicate recessive effects of involved genes for the traits under study (Das 2005).

Data revealed that the frequency of exceptions to the rule of 'inbreeding depression' is higher in the lower level of inbreeding than in higher degrees. The amount of percent inbreeding depressions also tend to be generally higher in post adolescent boys than in pre adolescent boys for most of the measurements with a few exceptions especially for BAD, BID (Tables 1-3).

In High and Low Inbreeding: Moreover, sampling fluctuations, causing exceptions to the rule of 'inbreeding depression' occur more often in the lower levels of recognized inbreeding ($0.00<F<0.0625$) than in higher levels ($F \geq 0.0625$) of inbreeding in all ages of Telaga boys.

Table 1: Mean (m) and depression percentage (d) of stature (in mm) in Telaga boys of different levels of inbreeding in comparison with non-inbred boys

Age (in years)	*0.000*		$0.000 < F < 0.0625$			$0.0625 \leq F < 0.1250$			$0.1250 \leq$		
	n	*m*	*n*	*m*	*d*	*n*	*m*	*d*	*n*	*m*	*d*
5	15	1055.00	5	1037.40	1.67	6	1017.83	3.52	9	1013.89	3.90
6	16	1076.25	7	*1082.43	-	7	1076.14	0.10	8	1073.87	0.11
7	12	1156.92	6	1140.17	1.45	10	1114.40	3.67	9	1112.00	3.88
8	18	1211.44	8	1206.62	0.40	12	1203.67	0.64	13	1199.85	0.96
9	21	1231.05	5	1226.00	0.41	8	1224.87	0.50	13	1218.92	0.98
10	17	1301.71	6	1298.17	0.27	7	1288.71	1.40	13	1276.31	2.35
11	19	1374.37	7	1365.00	0.68	6	1351.33	1.68	10	1341.00	2.43
12	20	1445.80	6	*1455.00	-	6	1443.50	0.16	10	1436.20	0.66
13	15	1483.80	7	1482.57	0.08	9	1480.44	0.23	11	1464.54	1.30
14	20	1549.25	6	*1566.50	-	7	*1560.73	-	10	1547.90	0.80
15	15	1608.53	6	1582.67	1.61	8	1576.37	2.00	10	1562.70	2.85
16	16	1625.19	7	1604.00	1.30	7	1601.86	1.44	10	1595.90	1.80
17	15	1647.33	5	1614.20	2.01	7	1605.57	2.54	10	1603.60	2.65
18	13	1656.69	6	1622.33	2.07	8	1611.12	2.75	10	1610.80	2.77
19	11	1668.36	6	1627.83	2.43	6	1615.33	3.18	8	1615.37	3.18
20	10	1678.00	5	1641.00	2.21	6	1633.17	2.67	8	1628.00	2.98

*increased mean from only F = 0.00 n=sample size

Source: Das 2005

In fact, such exceptions to the rule of mean reduction with inbreeding not observed when all individuals with low inbreeding ($0.00 < F < 0.0625$) are compared with those with high inbreeding ($F \geq 0.0625$) in each age group (Das 2005).

In Younger and Older Boys: It is revealed that the amount of percent inbreeding depression tends to be higher in post adolescent boys than in younger children for ST, SH with a few exceptions especially for BAD, BID measurements. This reduction of mean appears to be significant and consistent. This supports the observation of higher inbreeding depression in post adolescent period than in earlier age groups for those traits (Das 2005). Furthermore, there is no apparent exception to the rule of reduction of mean with inbreeding in higher age groups except in some cases for BAD, BID measurements. This finding is also observed in other studies (Mukherjee 1984; Rudan et al. 2003). It appears that inbreeding effect causing reduction tends to stronger with age especially after puberty and that heritability increases with age during grow-

Table 2: Mean (m) and depression percentage (d) of sitting height (in mm) in Telaga boys of different levels of inbreeding in comparison with non-inbred boys

Age (in years)	*0.000*		$0.000 < F < 0.0625$			$0.0625 \leq F < 0.1250$			$0.1250 \leq$		
	n	*m*	*n*	*m*	*d*	*n*	*m*	*d*	*n*	*m*	*d*
5	15	549.80	5	546.20	0.65	6	536.17	2.48	9	534.89	2.71
6	16	556.00	7	552.71	0.59	7	550.14	1.05	8	547.75	1.48
7	12	605.92	6	580.50	4.19	10	565.90	6.60	9	563.78	6.95
8	18	633.06	8	621.25	1.87	12	619.67	2.11	13	606.85	4.14
9	21	636.33	5	630.20	0.96	8	+630.50	0.92	13	624.77	1.82
10	17	654.53	6	643.33	1.71	7	641.57	1.98	13	641.46	2.00
11	19	669.74	7	666.14	0.54	6	660.67	1.35	10	658.10	1.74
12	20	713.15	6	*717.67	-	6	710.33	0.39	10	709.20	0.55
13	15	745.20	7	741.71	0.47	9	738.78	0.86	11	730.81	1.93
14	20	776.15	6	*779.33	-	7	772.43	0.48	10	770.50	0.73
15	15	806.87	6	796.33	1.31	8	791.62	1.89	10	778.00	3.58
16	16	823.62	7	810.43	1.60	7	805.29	2.23	10	802.10	2.61
17	15	834.87	5	828.00	0.82	7	811.29	2.82	10	809.10	3.09
18	13	841.00	6	833.83	0.85	8	818.87	2.63	10	816.10	2.96
19	11	847.00	6	837.50	1.12	6	829.33	2.09	8	821.12	3.06
20	10	853.10	5	840.20	1.51	6	832.33	2.43	8	826.00	3.18

*increased mean from only F = 0.00 +increased mean from next lower class of F.

n = sample size *Source :* Das 2005

Table 3: Mean (m) and depression percentage (d) of bi-acromial diameter (in mm) in Telaga boys of different levels of inbreeding in comparison with non-inbred boys

Age (in years)	*0.000*		*0.000 < F < 0.0625*			*0.0625 ≤ F < 0.1250*			*0.1250 ≤*		
	n	*m*	*n*	*m*	*d*	*n*	*m*	*d*	*n*	*m*	*d*
5	15	215.60	5	211.40	1.95	6	202.67	6.00	9	197.78	8.27
6	16	220.31	7	*222.14	-	7	215.00	2.41	8	205.75	6.61
7	12	230.17	6	*235.17	-	10	226.80	1.46	9	222.78	3.21
8	18	254.67	8	249.50	2.03	2	+251.50	1.24	13	245.54	3.59
9	21	256.90	5	254.60	0.90	8	+255.37	0.60	13	249.23	2.99
10	17	278.59	6	268.33	3.68	7	267.71	3.91	13	260.54	6.48
11	19	287.21	7	278.57	3.01	6	280.67	2.28	10	275.60	4.04
12	20	304.00	6	301.83	0.71	6	297.33	2.19	10	293.71	3.38
13	15	317.73	7	311.00	2.12	9	308.11	3.03	11	301.45	5.12
14	20	331.95	6	326.50	1.64	7	323.14	2.65	10	318.3	4.11
15	15	343.27	6	340.33	0.86	8	337.75	1.61	10	327.00	4.74
16	16	350.19	7	346.43	1.07	7	341.14	2.58	10	337.70	3.57
17	15	356.40	5	352.60	1.07	7	349.00	2.08	10	343.80	3.54
18	13	360.46	6	356.83	1.01	8	354.37	1.69	10	348.50	3.32
19	11	365.27	6	362.00	0.90	6	359.00	1.72	8	352.37	3.53
20	10	368.40	5	365.40	0.81	6	361.17	1.96	8	356.50	3.23

*increased mean from only F = 0.00 +increased mean from next lower class of F.
n = sample siz*e*
Source: Das 2005

ing period (Buenen et al. 2000; Tanner and Israelsohn 2007). One possibility is that environmental variations in the rate of growth before adolescence might overwhelm the inbreeding effect on change of means before adolescence.

Some exceptions in low inbreeding level to the general rule of reduction mean in different traits with inbreeding might be attributed to enhanced genetical selection (Mukherjee 2003). The mechanism of such selection can provide evidence by studying changes in variance and distribution of the traits in the inbred groups.

Inbreeding Effect on Variance of Measurements

In Yearly Age Groups**:** The variance generally tends to increase with high inbreeding in each age in years for each of the measurements in the present data. But the comparison of squared coefficient of variation $(CV)^2$ in four different levels of inbreeding indicates a wavy nature of the change in its value rather than a direct linear increase with inbreeding. Most often there is rather a reduction of variance or $(CV)^2$ in the lowest level of non-zero F followed by an increase with further rise of inbreeding level even though that increase may not also be always, linear with steady rise (Tables 4-6). The underlying trend of non-linear change of variance with inbreeding might be suspected to conform to the earlier suggestion of an initial fall and subsequent rise of variance in adults in a number of human populations, reflecting the possible effect of interaction of enhanced selection with inbreeding (Mukherjee 2003).

A critical comparison of changes in $(CV)^2$ in previous Indian and non-Indian data have suggested a consistency of initial reduction of its value in low inbreeding followed by its increase in high inbreeding in adult populations. This phenomenon has been interpreted as an indication of enhanced selection against small size of body measurements (Mukherjee 1984). The present result may also be tentatively attributed to such an enhanced selection to cause non-linear deviation in the progress of increase in variance with inbreeding.

However, as the sample size of each age in years is rather small and variance is relatively more sensitive to sampling errors, it would be rather premature to confirm that phenomenon of non-linear change of variance with inbreeding for each age in the present data. It is more relevant to note that even the small samples of each yearly age-group does not provide any evidence against the inbreeding effect of increase in variance for any of the measurements studied. In theory, increase of variance with inbreeding is expected for traits controlled by additive genes and / or non-additive genes with wide ranges of genes frequencies (Falconer 1989).

In Pooled Age-corrected Data: To reduce the effect of small sample fluctuation, the variance of measurements in different degrees of inbreeding has been recalculated on age-corrected

Table 4: Variances (V) and Squared Coefficient Variation (CV)^2 for stature among Telaga boys of different ages in different levels of inbreeding

Age (in years)	*0.000*		$0.000 < F < 0.0625$		$0.0625 \leq F < 0.1250$		$0.1250 \leq$	
	V	$(CV)^2$	*V*	$(CV)^2$	*V*	$(CV)^2$	*V*	$(CV)^2$
5	217.60	1.95	397.05	3.69	326.48	3.15	447.43	4.35
6	925.19	7.99	1652.25	14.10	1265.84	10.93	1447.10	12.55
7	765.75	5.72	1277.60	9.83	1762.64	14.19	2126.89	17.20
8	1194.92	8.14	2261.23	15.53	2466.73	17.03	4115.98	28.59
9	2012.62	13.28	698.8	4.65	2141.10	14.27	2579.30	17.36
10	1006.45	5.94	1027.81	6.10	1601.06	9.64	2534.99	15.59
11	2422.44	12.83	1373.43	7.37	2087.89	11.43	2323.60	12.92
12	2136.96	10.25	3451.67	16.30	1501.25	7.21	6749.76	32.73
13	952.69	4.33	2613.39	11.89	2290.69	10.45	3644.97	16.99
14	1584.09	6.60	1204.92	4.91	2655.06	10.90	3209.49	13.39
15	1118.12	4.32	2056.55	8.21	1905.48	7.67	2180.61	8.93
16	1255.53	4.75	1300.57	5.05	1600.69	6.24	2378.29	9.51
17	1077.96	3.97	1559.36	5.98	1625.96	6.31	2121.04	8.25
18	363.60	1.33	1266.23	4.81	1737.35	6.69	2386.16	9.20
19	1468.05	5.28	1236.47	4.67	1948.89	7.47	4811.23	18.44
20	527.20	1.87	1744.00	6.48	1247.81	4.68	2973.25	11.22

measurements (by converting each individual to that expected at 20 years of age). The increase of sample size by this method appears to have reduced the sampling error in estimated variances. There is, if fact, no exception to the general rule of increase of variances of each measurement with each step of increasing degree of inbreeding in the boys (Table 7).

Inbreeding Effects on Frequency Distribution of Measurements

The frequency distributions of each age corrected measurements in the pooled samples of boys with different levels of inbreeding (Figs. 1-3) appear to indicate a trend of segregation of homozygotes on both sides in increased frequency and in both ends of the distribution. There is apparent decrease of the frequency in the middle range of the range for traits under study which tends to be enhanced with increase of inbreeding as argued by others (Mukherjee 1996). This would suggest the location of heterozygotes in near the middle of the range. The clear modal distribution in some traits indicates involvement of a few genes and alleles otherwise distribution of genotypes would overlap instead of forming modes. Different studies have shown that modes are more distinct in high inbreeding than low level of inbreeding suggesting at least a few major genes clearly segregate on inbreeding (Mukherjee 1984, 1996).

Table 5: Variances (V) and Squared Coefficient Variation (CV)^2 for sitting height among Telaga boys at different ages in different levels of inbreeding

Age (in years)	*0.000*		$0.000 < F < 0.0625$		$0.0625 \leq F < 0.1250$		$0.1250 \leq$	
	V	*(CV)2*	*V*	*(CV)2*	*V*	*(CV)2*	*V*	*(CV)2*
5	149.76	4.96	157.36	5.27	151.14	5.25	06.32	17.69
6	304.625	9.85	211.06	6.94	194.98	6.44	859.19	28.63
7	424.57	11.57	408.92	12.13	308.69	9.64	1181.73	37.19
8	883.38	22.04	410.94	10.65	1055.89	27.49	891.56	23.67
9	707.65	17.47	306.16	7.71	1291.50	32.49	1135.72	29.09
10	444.84	10.39	500.22	12.09	466.81	11.34	1313.33	31.92
11	1285.03	28.65	501.55	11.30	523.56	11.99	593.29	13.70
12	473.93	9.32	1911.23	37.11	1290.23	25.57	1928.36	38.33
13	363.23	6.54	758.21	13.79	1222.62	22.41	1832.33	33.76
14	286.33	4.75	1196.23	19.70	1772.53	29.71	1124.85	18.95
15	485.98	7.46	522.22	8.23	1230.985	19.64	938.2	15.11
16	722.485	10.65	357.10	5.44	809.92	12.49	1146.69	17.82
17	367.05	5.27	368.00	5.37	726.78	11.04	894.09	13.66
18	438.46	6.20	289.47	4.16	809.855	12.08	914.69	13.73
19	289.45	4.03	203.25	2.90	467.22	6.79	1393.85	20.67
20	130.09	1.79	287.36	4.07	371.89	5.37	1095.00	16.05

Table 6: Variances (V) and Squared Coefficient Variation $(CV)^2$ for biacromial diameter among Telaga boys of different ages in different levels of inbreeding

Age (in years)	*0.000*		*0.000 < F < 0.0625*		*0.0625 ≤ F < 0.1250*		*0.1250 ≤*	
	V	*(CV)2*	*V*	*(CV)2*	*V*	*(CV)2*	*V*	*(CV)2*
5	52.51	11.31	61.84	13.82	140.89	34.30	157.66	40.14
6	40.71	8.39	286.98	58.15	164.57	35.61	287.44	67.87
7	36.14	6.82	137.14	24.79	163.76	31.85	251.28	50.62
8	78.89	12.16	119.25	19.16	625.25	98.81	319.01	52.91
9	217.32	32.92	150.64	23.23	343.98	52.76	273.87	44.10
10	142.01	18.31	82.22	11.43	781.63	109.08	303.48	44.70
11	354.69	42.98	706.53	91.04	335.89	42.65	429.24	56.52
12	257.9	27.91	153.14	16.80	534.89	60.52	987.21	114.45
13	83.80	8.29	567.43	58.66	262.54	27.65	605.89	66.65
14	151.45	13.75	314.92	29.55	571.55	54.75	497.21	49.08
15	145.33	12.34	239.89	20.72	314.94	27.62	877.6	82.05
16	253.41	20.68	241.68	20.15	234.69	20.17	724.81	63.55
17	163.57	12.88	172.64	13.89	209.14	17.17	311.16	26.33
18	271.94	20.93	189.14	14.85	262.73	20.92	543.05	44.70
19	90.57	6.79	137.67	10.50	184.33	14.31	506.73	40.81
20	178.24	13.13	221.44	16.58	295.47	22.65	409.75	32.23

Table 7: Variances of age corrected measurements among Telaga population of Kharagpur, West Bengal, India

Measurements	*0.000*		*0.000 < F < 0.0625*		*0.0625 ≤ F < 0.1250*		*0.1250 ≤*	
	Variance		*Variance*		*Variance*		*Variance*	
	m	*f*	*m*	*f*	*m*	*f*	*m*	*f*
Stature	1305.01	1300.62	1606.99	1589.75	1828.09	1701.62	3007.77	2059.06
Sitting Height	544.51	597.42	573.39	976.41	882.64	657.13	981.65	1408.59
Bi-acromial diameter	226.92	301.00	322.67	252.16	484.33	255.08	555.46	602.86
Bi iliac Diameter	149.39	269.15	199.72	458.66	578.78	628.13	644.55	878.23

m = male, f = female

There is a clear antimode in the distribution of stature in the inbred samples of boys with a trend of decreasing frequencies at the antimode with rise of inbreeding level (Mukherjee 2003). Similarly, antimodes are located in the distribution of BAD and HC (graph not shown) in the boys with the highest level of inbreeding (F ≥ 0.1250). The values of Penrose's D/S test con-

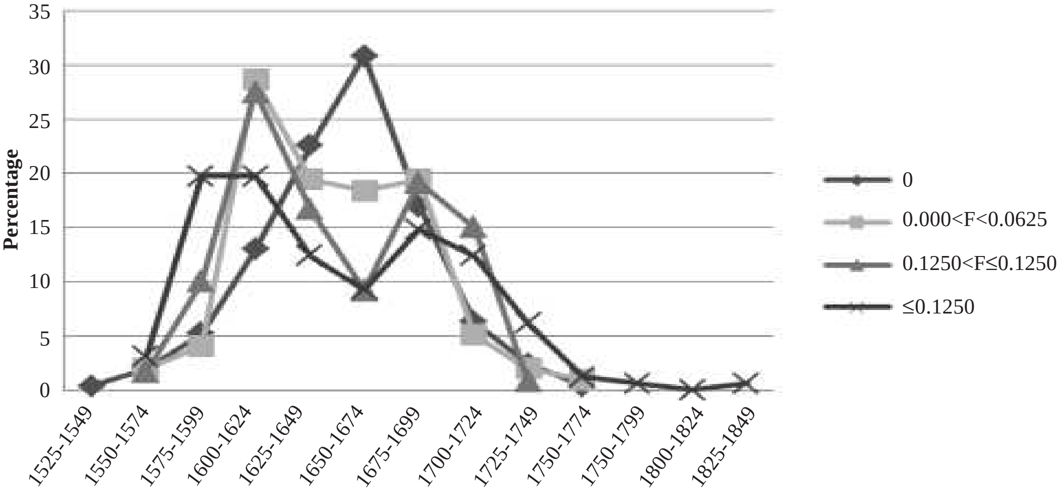

Fig. 1. Frequency distribution of stature of boys in different inbreeding levels

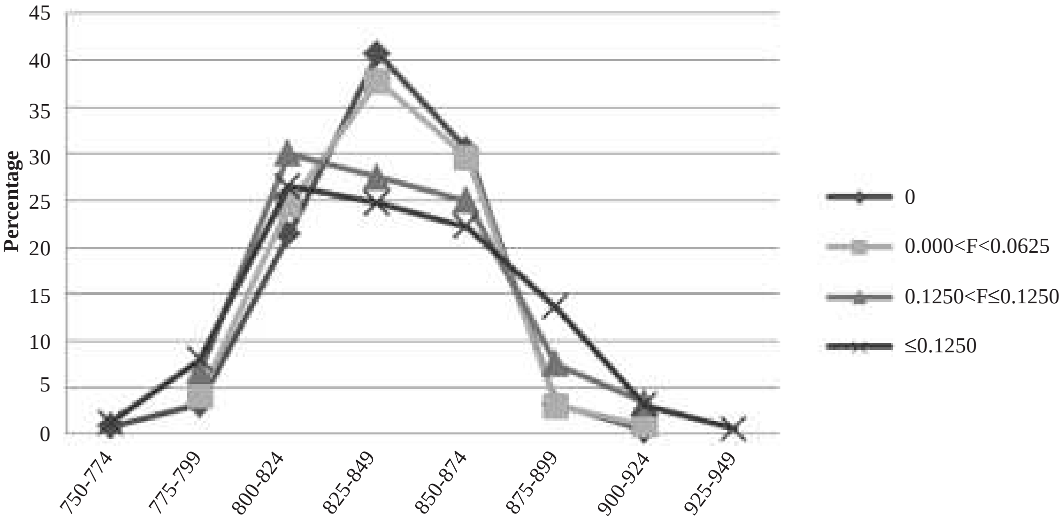

Fig. 2. Frequency distribution of sitting height of boys in different inbreeding levels

firm the significant bimodalities on the distributions of these measurements at least in some levels of inbreeding (Table 8). This would confirm involvement of a few additive autosomal genes in the variation of concerned traits.

Although the antimode is not always appar-

Table 8: Significant D/S values confirming bimodality of some (age corrected) measurements in the inbred males with non-zero F among the Telaga populations of Kharagpur, West Bengal, India

Traits	*F*	*Higher mode*		*Lower mode*		*D/S*
		M_1	S_1	M_2	S_2	
Stature	0.1250 ≤	1712.4	25.7	1612.4	7.7	5.99
	0.1250 <F≤0.0625	1639.8	17.9	1516.7	22.5	7.58
	0.0625 <F<0.000	1641.8	23.1	1516.0	23.1	5.47
Bi-acromial Diameter	0.1250 ≤	340.7	14.1	289.7	12.7	3.81
Head Breadth	0.1250 ≤	134.9	5.1	124.6	2.7	2.64
Head Circumference	0.1250 ≤	513.2	11.9	472.2	9.5	3.81

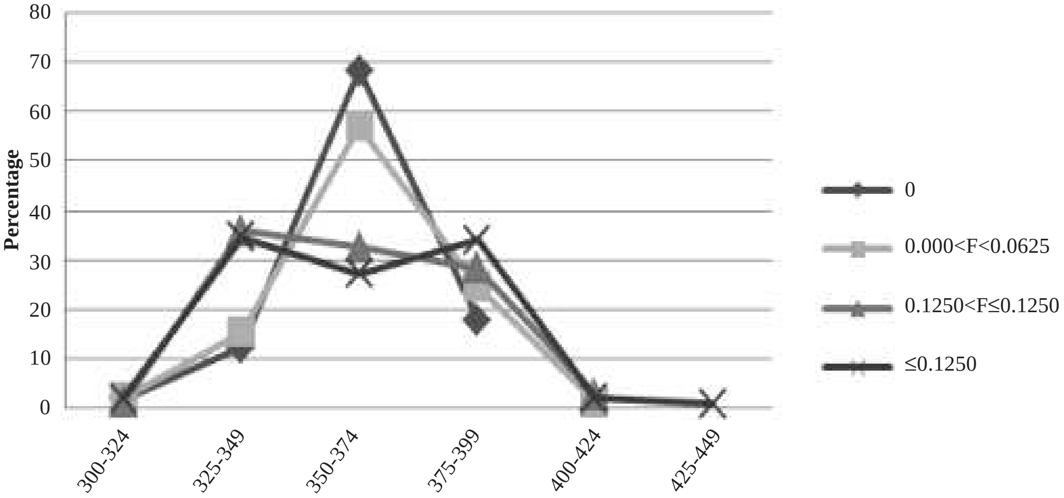

Fig. 3. Frequency distribution of biacromical diameter of boys in different inbreeding levels

ent in all the traits studied there is a general trend of gradual decline of frequency of the modal class accompanied by increase in the frequencies of the lower and higher values on the both sides of the modal class and often the extreme values on both ends of the distribution with the rise of inbreeding level as observed by others (Mukherjee 1996). This may be interpreted as an underlying process of increase in segregation of homozygotes of genes with both negative and positive effects on the quantitative characters. There is also a greater increase in the frequency of the lower values of the measurements with rise of inbreeding. This may be explained by some autosomal recessive genes with negative effects conforming to the already observed decline of mean values with inbreeding in addition to the additive genes reflected in the heterozygosity of individual in the middle of the range of values. Alternatively, the genes controlling the traits could be incompletely dominant/recessive in their effects.

CONCLUDING REMARKS

The results of the present study attempts to indicate that inbreeding effects occur independently of hereditary and environmental differences between parents of consanguineous and non- consanguineous marriage considering a well- defined endogamous population matched with similar socio-economic and physical background. It amply clarifies the phenomena of reduction of mean measurements with autosomal inbreeding in all ages including the period of childhood and adolescence, although such effects may be more marked and more consistent in older ages from adolescence onwards in males. The effect of autosomal inbreeding on variances of body measurements can also be observed with relatively less consistency due to inadequate size of samples for each age in each level of inbreeding and also environmental selection in each variance. The hypothesis of a bimodal distribution suggesting the occurrence of a few genes with additive effects and increased frequency of the lower mode indicating recessive effects of alleles are also confirmed in the age corrected data for body measurements in the Telaga population. The above observations elucidate the nature and mechanism of genetic effects of inbreeding on certain quantitative traits in human by analyzing resultant phenotypes in different levels of inbreeding. This approach is easy, less expensive and non-laboratory based than the current approach of mapping quantitative trait locus analyses. This approach definitely shed light in understanding inheritance of quantitative traits in human being and provides a direction of further research at the population level.

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