REVIEW OF THE LITERATURE
An attempt had been made to review the literature of human traits. ABO blood groups with Rh factor and human genetic diseases with special reference to Brahmin, Rajput Thakur, Rathis, Lohar, Chanal and Halis caste groups. The literature was reviewed separately for the following three aspects of inheritance undertaken for the present research work:

- Human hereditary traits (morphological & behavioral)
- Human serological traits (ABO blood groups & Rh factor)
- Human genetic diseases

**Human Hereditary Traits**

There are three types of traits among human being i.e. neutral traits such as: rolling of tongue, form of hair, color of hair and the ear lobes etc. where both alleles are frequent secondly the traits under selection where one allele is frequent and the other is less frequent (hitch hicher's thumb, hair on mid digital finger, little finger bent and hand clasping) thirdly the selectivity fixed traits where one allele is significantly with high frequency (widow's peak and dimple on cheeks) is near fixation in population and other allele is selectively disadvantageous (Verma, 1996). Similarly Bhasin et al. (1987) studied the distribution of ear lobe attachment, mid-phalangeal hair, tongue rolling, hand clasping, arm folding and leg folding among 14 population groups of Sikkim. Mitra et al. (1995) studied hand clasping, leg folding, arm folding, tongue rolling and ear lobe attachment in Saryupari Brahmin of Chhattisgarh, Central India. Zheng et al. (1999) studied the distribution of hand clasping, arm folding and leg folding in the Daur population, China.
Eye colour

Eye colour is one of the several human characters, which are inherited, in a Mendelian fashion in man. Davenport (1910) studied a number of family pedigrees. He studied that brown eyes are dominant over blue eyes in the white races. There are many variation of eye colour, which may be influenced by other genes. The darker colors generally are dominant over the blue or gray, but there is considerable variation in the expression of the darker colors because of modifying genes (Winchester, 1974). Rufer et al. (1970) reported eye colour to be as polygenic trait. Nicholls (1973) reported that two of minimum three major gene pairs that control skin colour also regulate eye colour to a large extent.

Gedde-Dahl et al. (1982) reported positive relationship between brown eye colour (BEYI) and the blood groups Colton (CO), which they mapped on chromosome seven. Eiberg and Mohr (1987) studied the eye colour in a large Danish family. They found strong evidence for linkage "green eye colour" to the Lutheran-secretor system. They also found evidence for linkage of "green eye colour" to "brown hair colour". It would appear to identify a second major gene, which is present in the same region of chromosome nineteen.

Eiberg and Mohr (1996) studied 832 families from Copenhagen area for the linkage analysis. They found 80 markers in 120 segregating families and 290 markers in 5 segregated families by exclusion mapping. They obtained some indications of a locus for brown eye colour (BEY2) in chromosome 15.They also selected 45 families from their DNA bank segregating for brown eye colour. All these were tested for chromosome 15 markers. They found a strong indication of tight linkage with the DNA polymorphism and with the flanking markers. Frank et al. (2000) studied iris color and age
related macular degeneration in 306 sequential patients, 60 years of age or older. The differences in the association between iris pigmentation and age related macular degeneration reflected genetic difference in the groups. Devi (2002) reported the high heterogeneity of black eye colour in the non-tribal and homogeneity in the tribal population groups in Himachal Pradesh, India. Frudakis et al. (2003) studied human iris pigmentation in 851 individuals of mainly European descent. The results suggested that cryptic population structure might serve as a average tool for complex trait gene mapping. Verma (2003) reported wide range of phenotypic frequency of black eye colour among Brahmins (74%), Rajputs (35%) and Harijans (69%) of Shimla and Mandi districts of Himachal Pradesh. Sharma (2004) studied that the gene frequency of black eye colour was found maximum (46.8%) in Kolis and minimum (31.1%) in Brahmins of Tribal population in Shimla district (Himachal Pradesh).

Hair colour

The variation in hair colour is influenced by multiple genes. Darker hair colour genes are dominant over the genes for light hair. There seem to be two primary pigments in the hair, each of which is subjected to quantitative variation through multiple genes and multiple alleles. One of these is a black melanin, which may result in black, brown, sepia or light blonde hair with varying shades between. Upon this is superimposed another melanin pigment which may range from sandy red to yellow. Various genes influence the intensity and the quality of these pigments in such a way as to produce the wide variation in hair color that is characteristic of man (Winchester, 1974). Nicholls (1973) reported a strong correlation between the occurrence of red colour hair and freckles. His data support the hypothesis that individuals who are homozygous for gene of red hair
also possess freckles. While heterozygote have brown hair and freckles.

Eiberg and Mohr (1987) studied Danish material of normal families. These material tests for 65 marker systems. They found red hair colour as an autosomal dominant against blond hairs and as hypostatic to dark hair. They assigned a major locus for red hair linked to MNS blood groups on chromosome 4. Hair colours were considered polygenic traits in the past. The recognition of individual loci was thought to be difficult. Eiberg and Mohr (1996) reported hair colour for linkage analysis. They found new locus for brown colour (HCL3) at a locus for brown eye colour, which they mapped on different chromosome sites (15q11-15q21). They found association between brown eye colour and brown hair colour in the 45 selected families. They observed that forty-six parents were brown eye colour, forty-four had brown hair, while among forty four spouses with blue eye colour, only twenty six had brown hair colour. They also pointed out that the chromosome (15q11-15q21) region contains the gene (P or DNIO). It is the site of mutation causing type eleven oculocutaneous albinism and autosomal recessive ocular albinism. It could be a candidate gene for blue eye colour and for brown hair colour.

Rees et al. (1999) suggested a critical role for the melanocortin-1 receptor in the control of pigmentation. It was shown that this gene is unusually polymorphic in European population. Family studies suggested that these are inherited as an autosomal recessive trait. Schaffer and Bolognia (2001) reported that the melanocortin -1 receptor has been associated with physiologic variation in hair color. The MCI-R, a G protein - Coupled receptor with 7 transmembrane - spanning domains, plays a key role in
determining the type of melanin (eumelanin vs pheomelanin) that is produced within melanocytes. Pavlov (2002) studied morphological features of hairs from the head of the native population of Syria, India, Lebanon, Jordan, Yemen, Nepal, Palestine, Bahrain, Iraq and some residents of the Eastern Europe. Original information on some macro and microscopic characteristics of hair has been obtained for citizens of the above countries. Devi (2002) studied high significant differences of black hair colour in the tribal and non-tribal population groups in Himachal Pradesh. Verma (2003) studied the range of phenotypic frequency of black hair colour among Brahmins (70%) Rajputs (69%) and Harijans (77%) in Shimla and Mandi districts of Himachal Pradesh. Sharma (2004) studied that the gene frequency of black hair colour was found maximum (72.6%) in Baris and minimum (42.2%) in Lohars of Tribal population in Shimla district (Himachal Pradesh).

Van Neste and Tobin (2004) studied Hair cycle and hair pigmentation. The tight coupling of hair follicle melanogenesis to the hair growth cycle dramatically distinguishes follicle melanogenesis from the continuous melanogenesis of the epidermis. Pigment dilution results primarily from a reduction in tyrosinase activity within hair bulb melanocytes.

**Hair form**

The form of hair is dependent directly upon its shape. Straight hair is rounded, while wavy, curly, and Kinky hair shows progressive degrees of flattening. No doubt a number of genes are involved in hair form, but in the white race the evidence indicates that there is one pair of alleles which can produce the difference between curly and straight hair, with the heterozygote showing wavy hair. The kinky hair of the Negro race generally dominates over the hair form
of the white race (Winchester, 1974). The curly hair behaves as dominant and the straight hair as recessive character (Davenport, 1910). Martin (1928) studied that the uncut hair of the ulotrichous races remains short. The length varying from 8cm to 25cm. The admixtures of black vary unlikely in the Norwegian kinded with many persons affected with curly hairs (Mohar, 1932). Schokking (1934) and Anderson (1936) reported Caucasian families with many family members affected with wooly hairs, who had close familiarity with the hair of blacks. They felt that the wooly hair was different.

Hutchinson et al. (1974) distinguished dominant and recessive forms. In the autosomal dominant trait: a variable degree of tight curling is present in all hair throughout the scalp. In case of autosomal, tightly curled, fine, white or blond hair tends to be short. It is present from birth. The third type of woolly hairs is the nevus type, in which the woolly hairs are present with in well-demarcated area. These hairs are tighter than the normal hair. It has a reduced diameter. Rook and Hari (1975) reported that variation in hair form also have a polygenic basis.

Mortimer (1985) gave a discussion of differential diagnosis of unruly hair. Ormerod et al. (1987) reported a family in which 6 members of 3 sibs and 2 generations. They show unusual form of woolly hair. The woolly and normal hair was intimately interspreaded throughout the scalp. They also found 20-38% of the hairs were abnormal in the several family members.

Taylor (1990) reported that a family with 10 affected individuals in 4 generations with an instance of male-to-male transmission. The length of the hair on the vertex varies from 5cm to 10-12cm. In rare cases the hair attain a length of 14cm, but the hair never gets long.
Rosen et al. (1994) studied premature of hair graying as a risk marker for Osteopenia. Although the pathophysiology of melanin depletion in hair follicles is unknown, genetic factors regulate the expression of this trait. Birch et al. (2001) studied 377 women aged 18-99 years for hair density, hair diameter and the prevalence of female pattern hair loss. Hair density in women is distributed as a normal variable indicating that it is a multifactorial trait. Devi (2002) reported the high heterogeneity of curly hair in the non-tribal regions and homogeneity in the tribal population groups of Himachal Pradesh, India. Verma (2003) reported the distribution of this trait among Brahmins (13%) Rajputs (21%) and Harijans (9%) in two districts of Himachal Pradesh. Sharma (2004) showed that the gene frequency of strait hair was found maximum (58.1%) in Sunars and minimum (50.4%) in Turis of Tribal population in Shimla district (Himachal Pradesh).

**Hair on mid-digit**

The presence of hairs on mid-digit are dominant character over the absence of hair on mid-digit. The growth of hair on the middle joint of the fingers is an interesting human characteristic. Mid-digital hair may occur on fingers in various combinations. It is most common on the ring finger; next comes the ring finger plus the middle finger; next comes the ring finger, plus the middle finger, plus the little finger; and least common is hair on all four fingers. A multiple allele hypothesis has been proposed to account for the inheritance of these combinations. This hypothesis assumes the presence of hair on all four fingers as dominant to its presence on three; on three, in turn, dominant to its presence on two; two dominant to one; and one dominant to none (Winchester, 1974).
Sastry (1975) studied the middle phalangeal hair in some South Indian populations. The study of middle phalangeal hair on a sample of some 5000 non-related subjects of both sexes and different, age groups, representing 11 South Indian populations, had shown very limited sex and age variability. Most of the groups tested showed genetic homogeneity. Singh and Goel (1975) studied mid-phalangeal hair among khatris and Baniyas of Patiala, India. In a majority of subjects (53.73% in males and 46.35% in females) mid-phalangeal hair appears to be completely absent. The highest frequency of this trait was found in the combination III - IV and, when considering individual digits, on IV (around 50%).

Bhanwer et al. (1981) studied 156 males and 63 females belonging to the Ramgarhia community, an endogamous group of Punjab. The mid-digital hair was absent in 67.34% of females and 64.74% of males. Sethuraman et al. (1982) studied distribution of middle phalangeal hair in the two groups of Srivaishnava Brahmins of Tirupati (south India). 400 adult unrelated individuals of both sexes were studied from two groups of Srivaishnava Brahmins residing in Tirupati. The occurrence of middle phalangeal hair was predominantly manifested on the III, IV, and V digits of both hands in the two sexes of Vadagalai and Tengalai groups. Tengalai males showed high frequency of presence of mid-phalangeal hair (39%) than Vadagalai males (37%). Among the females the frequency was (36%) in Tengalai and (34%) in Vadagalai groups. Sex differences were not statistically significant in both the groups. Populations of Mongoloid affinity seems to have a marked increase in the frequency of individuals without mid-phalangeal hair and the present Srivaishnava Brahmin sample reflected such a similar tendency.
Malik et al. (1988) studied mid-phalangeal hair and other trait among Jats of Haryana (India). Comparison of Haryanvi Jats and Jat Sikhs suggest that though the two castes, to a large extent are reproductively isolated, they have parallel development and ethnic relationship. Vona and Porcella (1989) studied middle phalangeal hair distribution in a Sardinian population. Data relating to middle phalangeal hair among unrelated individuals of both sexes born and living in Sardinia were presented. The occurrence of middle phalangeal hair is generally manifested on the 3-4-5 digits of both hands in the two sexes. The observed sex differences are statistically non-significant. The Sardinian sample seems to have a marked decrease in the frequency of individuals with mid-phalangeal hair with regard to Mediterranean and other European populations.

Luna (1989) studied distribution of middle phalangeal hair in a population of the south of Spain. The presence or absence of middle phalangeal hair had been studied in an Andalusian population sample. This sample consisted of 245 students from Granada (128 males and 117 females). The frequencies of middle phalangeal hair are similar to those obtained in the Basque population, which shows the lowest frequencies so far reported. The most affected finger is the ring finger; the least affected one is the fore-finger.

Yadav and Gupta (1992) studied distribution of middle phalangeal hair (4.7%-54.7%) in Jats population of Haryana, India. Dharap et al. (1995) studied 200 Malay subjects (100 males and 100 females) from patients attending out patient Clinics of Hospital USM, Kelantan, Malaysia to find out the incidence, density and direction of hair on the dorsum of phalanges of the hand. Mid phalangeal hair was present in 48% of males and in 33% of females studied. Comparisons with presence of mid-phalangeal hair in other
populations showed that Malays are ethnically similar to other Asiatic populations.

Dharap et al. (1996) studied distribution of hair on the dorsum of the phalanges of the hand in a Chinese population. 302 Chinese subjects (134 males and 168 females) randomly selected from the residents of Kota Bharu, Malaysia. The frequency of middle phalangeal hair distribution in Chinese falls between that in Malays and in Japanese that is probably explained by the fact that all these three racial groups originate from Asia. The study revealed that though Chinese females had less digital hair on the hands than Chinese males yet they showed a much larger variety of digital hair distribution than males. Borthakur et al. (1997) studied the Dalu of Meghalaya. The results of the present study are compared with other populations in order to assess the group differences or similarities. The present Dalu sample stand significantly apart from most of the population under investigation. Verma (2003) studied the distribution of presence of hair on mid-digit among Brahmins (50%) Rajputs (56%) and Harijans (48%) in two districts of Himachal Pradesh. Sharma (2004) reported that the dominant gene frequency was found maximum (17.8%) in Turis and minimum (5.5%) in Rehars.

Widow's peak

In widow's peak, the front line of hair project down in the middle of forehead (Winchester, 1974). It is inherited as an autosomal dominant character. Lata and Singh (1986) studied the frequency of individuals showing smooth hairline. The frequency of widow's peak phenotype gene is higher in males than in females. Nath and Devi (1998) studied the hairline of Kaibartas of Assam. A comparison is made with other castes and tribes of North-East India and Kaibartas are showing intermediate position among Caucasoid
and Mongoloid groups. Devi (2002) showed a mixed pattern of heterogeneity and homogeneity for different alleles of widow's peak in the tribal and non-tribal population groups of Himachal Pradesh. Verma (2003) reported the phenotypic frequency of widow's peak among Brahmins (15%) Rajputs (30%) and Harijans (16%) in two districts of Himachal Pradesh. Sharma (2004) reported that the frequency of widow's peak was found maximum (43.3%) in Rehars and minimum (20.8%) in Kolis.

**Ear lobe attachment**

The continuous variation in the size and form of the ears and their position in the head indicate multiple gene inheritance. A few ear characteristics seem to variation in single gene. Free ear lobes seem dominant over attached ear lobes, but there is variation in the degree of freedom of those, which are not attached. (Winchester, 1974). The different types of ear lobes were studied by Hilden (1922). Srinivasan and Mukherjce (1975) studied ear lobe attachment among Tamil Brahmans in relation to cultural and ethnic affiliations. This trait showed a high degree of homogeneity in Tamil Brahmans. They appear to be closest to the Bengali Brahmans and differ significantly from other Brahman populations, with respect to earlobe. Bhasin et al. (1986) studied frequency distributions of earlobe attachment for different population groups from Himachal Pradesh, North India, namely Pangwalas. Transhumant Gaddis (Brahmans, Rajputs and scheduled castes) and settled Gaddis (Brahmans, Rajputs and scheduled castes). An attempt had been made to compare the results of the present study with in and between these groups as well as with results of other reports from different population groups of India and Asia.
A number of studies on ear lobe attachment had been reported among various populations from India (Bhasin and Khanna, 1992). The frequency of attached ear lobes is 35.8% in Jats of Haryana, India (Yadav and Gupta, 1992). Mian et al. (1994) studied frequency distribution of ear lobe attachment for different ethnic groups (Balochs, Rajputs; Syeds, Pathans, Araeen and Jats) for Pakistan (Southern-Punjab).

Yadav et al. (1994) studied the distribution of ear lobe attachment among eleven endogamous groups of Haryana. They found highest incidence of attached ear lobe in Brahmins (63.5%) and lowest in Saini (20.71%). They found inter-sex differences in Ahirs to be non-significant among all the groups. Several inter-group comparisons showed statistically significant differences. They obtained frequency variation for this trait (20.71 - 63.5 %) falls with in the range of north-west Indian population i.e. between 7.47% in Gujjar (Malhotra and Bhanu, 1976) and 66.6% in Brahmins (Bhasin and Gupta, 1974). There is a significant difference in the total material indicating a heterogeneous distribution of traits among eleven endogamous groups.

Nath and Das (1995) had studied the ear-lobe attachment among Kaibartas of Assam. They found that the frequency of ear-lobe attachment is high in kaibarta males than to females, but statistically sex differences are not significant. Various studies reported from Assam observed that the frequency of attached ear lobe is high among Kaibartas than to Baishya (24.20%), (Das and Deka., 1960), Kumar (18.90%), (Das and Ghosh., 1970), Brahmins, Kalita and Keot 20.60%, 22.22% and 18.10% respectively, (Das and Sharma.. 1968). This shows the intermediate position between population groups with Caucasoid and Mongoloid affinities.
Reddy and Reddy (1997) studied the ear lobe attachment in Andhra Pradesh. The paper reports the morphological variation of ear lobe types among the two Madigo groups belonging to the same sub-caste of Gampadhompti Madigas: Madigas at Cuddapath District (MDCDP) and Madigas of Chittor District (MDCTR). The proportion of persons with attached earlobe is lower in MDCDP (26.22%) than in MDCTR (38.79%), with highly significant sex difference in the latter group. The overall incidence of the trait of attached earlobe of the pooled Madigas is relatively lower than in other population. Parvatheesam and Babu (1997) reported great variation in the incidence of free ear lobes in Andhra. The highest frequencies were recorded in Pattu Sali and lowest in Nayi Brahmins, (Bhasha, 1980).

Ear lobe attachments among five endogamous groups of Haryana were studied. These groups were Bishnoi, Bazigar, Gadia Lohar, Dhobi and Labana Sikh. The frequency of attached ear lobes varied from 57% to 43%. The highest frequency was observed in bazigar and lowest in Dhdbi. Sex difference was found to be significant in Bishnoi and Gadia Lohar and nonsignificant among Bazigar, Dhobi and Labana Sikh. The inter-caste differences were found to be significant only among Bazigar-Dhobi and Dhobi-Labana Sikh. There was a non-significant difference in total population indicating a homogeneous distribution of this trait among the five endogamous groups under report (Yadav et al., 1997).

Yadav et al. (1998) studied the ear-lobe attachment among four endogamous groups of northwest India, viz., Jat, Kathri, Brahmin and Kashmiri Sunni Muslim. The frequency of attached ear lobes varied from 62% to 42%. The highest frequency was observed in Khatri and lowest in Kashmiri Sunni Muslims. The inter-caste differences were found to be significant among Jat-Kathri, Jat-Sunni...
Muslim, Kathri-Brahman, Kathri-Kashmiri Sunni Muslim. There was no significant difference in total population indicating homogenous distribution of this trait among the four endogamous groups.

The distribution of ear lobe attachments has been reported among 4 endogamous groups of northwest India viz. Bawria, Dakaut, Khatik and Meena. The incidence of attached earlobe was lower than that of free earlobe in all groups. The frequency of attached earlobe varied from 16% (Dakaut) to 24% (Bawaria). The inter caste differences as well as difference in total population were found to be non-significant. The distribution of this trait is homogeneous among the four endogamous groups (Yadav et al., 2001). The frequency of attached earlobe varied from 7.47% in Gujjar (Malhotra, 1976) to 66.69% in Brahmin (Bhasin et al., 1992). The frequency of attached ear lobe is more in Meos (56.58%) then Sunni Muslims (53.18%) of Haryana (Yadav and Singh, 2002). Devi (2002) showed a mixed pattern of heterogeneity and homogeneity for free ear lobe in the tribal and non-tribal population groups of Himachal Pradesh. Verma (2003) studied the frequencies of free ear lobes varied from 53% in Brahmins to 69% in Harijans of two districts of Himachal Pradesh. Sharma (2004) reported that the frequency of free ear lobes was found maximum (49.5%) in Sunars and minimum (39.6%) in Rajputs.

Polydactyly

Polydactyly is the presence of extra fingers and toes. The extra digit may be appended to the little finger or toe, or it may be attached to the thumb or the big toe. The condition is inherited as a dominant with variable expressivity (Winchester, 1974).
Tosti et al. (1992) studied doubled nail of the thumb, a rare form of Polydactyly. Bifid thumb is a rare manifestation of Polydactyly. The trait is autosomal dominant, but the expressivity is highly variable.

Zguricas et al. (1999) reported that polydactyly is the most frequently observed congenital hand malformation with prevalence between 5 and 19 per 10000 live births. It can occur as an isolated disorder, in association with other hand/foot malformations, or as a part of a syndrome, and is usually inherited as an autosomal dominant trait.

Qin et al. (2003) reported genetic analysis of a Chinese pedigree with congenital synpolydactyly. Syndactyly is a limb malformation that shows a characteristic manifestation in both hands and feet. This condition is inherited as an autosomal dominant trait with reduced penetrance. Clinical presentation, in general, was complete or partial webbing between 3rd and 4th fingers. The result demonstrated that synpolydactyly locus in the Chinese Han population was in the region of chromosome 2q 31 - q 32 but a different causal gene could be involved. Sharma (2004) reported the frequency of polydactyly among Brahmin (2.8%), Thakur (8.8%), Rajput (0.4%). Sunar (3.9%), Baris (0.7%) and none cases (0%) were reported in Lohar, Rehar, Turis and Kolis.

**Rolling of tongue**

The shape and size of the tongue respond to so many different genes, it is not possible to isolate many defects of individual genes. The ability to roll tongue in to "u" shape depends upon a dominant gene (Winchester, 1974).
Sturtevant (1940) reported that the ability of rolling up the lateral edges of the tongue is conditioned and is at least partially inherited. This ability may be due to single dominant gene. Hsu (1948) described the ability to fold up the tips of the tongue as a recessive trait.

Liu and Hsu (1949) reported independence of the two traits. The cloverleaf tongue (ability to fold the tongue in a particular configuration) may be yet another distinct trait (Whitney, 1950). Matlock (1952) studied thirty-three pairs of identical twins and observed seven pairs were discordant. He concluded that tongue rolling is not entirely hereditary; it is inherited as a simple dominant allele. Sturtevant (1965) cited a finding of high frequency of discordance in monozygotic (MZ) twin. He reported little genetic basis for the traits. Hereditary factors strongly influence tongue-rolling ability (John, 1970).

Reedy et al. (1971) concluded from twin studies that hereditary factors strongly influence tongue-rolling ability. From the additional twin studies, Martin (1975) reported that the degrees of genetic influence on tongue rolling ability must be slight. It is polygenic in nature, if occurring at all. He excluded genetic determination by showing that the frequency of concordance is the same in monozygotic twin pairs.

Hernandez (1980) reported that the ability to roll tongue in males (63.7%) and (66.84%) of female in Barcelona. He also found association with ability to move the ears in males. Cruz-Gonzalez and Lisker (1982) studied inheritance of tongue rolling ability in 77 families with a total of 293 children. The lack of ability to roll the tongue was less conclusive due to difficulties in communication between the examined individuals and the examiners.
Mitra et al. (1986) studied the incidence of tongue rolling and tongue folding among the Oraons of twenty-four Paragnas. Altogether 200 unrelated individuals: 112 males and 88 females were considered. It was observed that the frequency of tongue rollers and tongue folders are higher in both the sexes of this group. Pentzos- Daponte (1986) studied tongue rolling and tongue curling in a total of 77.63 individuals from Thessaloniki and its surroundings, representing a sample of the population of Northern Greece. The statistical analysis of the data indicated significant sex differences concerning tongue rolling.

Fry (1988) studied tongue rolling ability of 948 undergraduates at the Ohio State University. Among the 403 men included in the final sample, 77.4% could roll their tongues, where only 62.7% of the 491 women could do so.

Azimi - Garakani and Beardmore (1989) studied Tongue-rolling phenotypes and geographical variation in the United Kingdom. The distribution of tongue-rolling phenotypes in a sample (n=477) of undergraduate students of the University college of Swansea (U. K.) was studied. The birthplaces of these students were also recorded. England was divided into six areas, and Wales was left as an area on its own. The data suggested that those students who came from North-east were more non-rollers, which may be due to mixture with Scandinavians. Borthakur et al. (1997) studied the tongue rolling and tongue folding of the Dalu of Meghalaya. They reported that the present Dalu sample stand significantly apart from most of the population under investigation.

Parvatheesam and Babu (1997) studied the tongue rolling traits obtained from adult male and female between Rajaka residing in Vishakhapatnam city (Andhra Pradesh). They found that the ability
of tongue rolling into "u" shape is less in male and more in female. The tongue rolling incidence among Andhra caste ranges (43.64%) in Srivaishnav Brahmins and 78.21% in Nayi Brahmins, while tongue folding is 7.10% in Kapu and 38.43% in Madigo, Reedy (1984), Seethuraman et al. (1978), Naidu, (1974) and Shammen (1980). Devi (2002) reported that the ability of tongue rolling was heterogenous in the tribal and homogenous in the non-tribal population groups of Himachal Pradesh. Bulliyya (2003) studied that the incidence of tongue rolling trait is more frequent in females (35.6%) than in males (27.2%) among Vannekula Kshatriya of Andhra Pradesh. Verma (2003) reported that the ability of tongue rolling into "u" shape was homogenous among Brahmins (78%), Rajputs (75%) and (76%) Harijans of two districts in Himachal Pradesh. Sharma (2004) reported that the ability of tongue rolling into "u" shape was found maximum (46.5%) in Baris and minimum (28.6%) in Kolis.

Hand clasping

Hand clasping is thought to have a Mendelian mode of inheritance. Lutz (1908) reported that when the hands are closed naturally, most people would put the same thumb either left or right upper-most every time. He concluded that the trait was under genetic influence, if not simple Mendelian control. Ferronato et al. (1974) and Lai and Walsh (1965) reported little or no evidence for genetic component in hand clasping from different family relationship. The manners of hand clasping were shown by twin studies to have no genetic basis (Martin, 1975).

Bhasin and Gupta (1974) reported the right type of hand clasping values (40%) in Rajputs of Himachal Pradesh and (72%) in Jats of Punjab (Bansal, 1968). Singh and Goel (1975) studied hand clasping among Khatris and Baniyas of Patiala India. It was noticed
for hand clasping, that R—type appears to be more frequent in Khatris and L-type in Baniyas.

Srinivasan and Mukherjee (1975) studied hand clasping among Tamil Brahmans. These traits showed a high degree of homogeneity in Tamil Brahmans. They appear to be closest to the Bengali Brahmans. Kobyliansky et al. (1978) studied the comparative analysis of hand clasping in four groups of adult Israeli males indicates a significant similarity between the groups. They observed that right hand clasping predominated at all, but in the central European groups left hand clasping were predominated. Right hand clasping predominated in adult Israel Jewish males of East European Origin (N = 562), Middle Eastern Origin (N = 191), North African Origin (N=163) while left hand clasping predominated in Central European Origin (N = 165).

It was observed that the frequency of right and left types makes nearly 50% in all age groups (Paliukhov, 1980). Forrai and Bankovi (1983) studied adult Hungarian monozygotic and diazygotic pairs for hand clasping, arm folding and tongue curling. They found positive correlation between hand clasping type and handedness.

Arrieta et al. (1985) reported hand clasping and arm folding in males and females of the Basques and results were compared with other Spanish populations. Hand clasping had been analyzed in 286 males and 455 females of the Basques. The association between right hand clasping and left arm folding shows strong correlation. Pentzos - Daponte (1986) studied hand clasping in a total of 7763 individuals from Thessaloniki and it's surrounding, representing a sample of the population of Northern Greece. The frequencies under study were compared with data from the literature. Mitra et al. (1986) studied the hand clasping among the Oraons of twenty-four paragnas.
Altogether two hundred unrelated individuals—hundred twelve males and eighty-eight females were studied. It is observed that the frequency of R/L type of hand clasping is more or less equally distributed in both the sexes. Association between hand clasping, tongue rolling and tongue folding do not show any significant results.

Yadav et al. (1994) studied the distribution of hand clasping among eleven endogamous groups of Haryana. They had reported the incidence of right type of hand clasping higher than left type of hand clasping in all the caste groups except the Kumhars. They observed lowest frequency of right type in the Rajputs (6%) and the highest in the Kumhars (49.03%). All intersex comparisons were found to be non significant. There was no statistically significant difference. Therefore this trait had homogeneous distribution in Haryana population. Mitra et al. (1995) reported R/L type of hand clasping (58.15%) in Saryupari Brahmin of Chhattisgarh, Central India.

Parvatheesam and Babu (1997) reported the distribution of hand clasping between Rajaka, a washer man caste of Andhra Pradesh. They observed that the frequency of right type is more in males than in females. Yadav et al. (1997a) studied the distribution of hand clasping among five endogamous groups of Haryana. The right-handed individuals were prominent in all the groups. The frequency of R-type handedness varies from 93% in Bazigar to 88% in Bishnoi. They further studied the distribution of hand clasping among seven endogamous groups of Haryana. It was concluded that all inter-group comparisons founded to be non-significant. The distribution of hand clasping in Haryana is homogeneous.

The hand-clasping trait was studied among four endogenous groups of northwest India, viz., Jat, Khatri, Brahman and Kashmiri
Sunni Muslim. The incidence of R-type hand clasping was higher in all groups. The frequency of R-type was highest in the Jat (72%) and lowest in Khatri (43%). The intercaste differences among Jat-Khatri, Jat-Brahaman and Khatri-Kashmiri Sunni Muslims are found significant. It was non-significant among other castes. The result indicating the heterogenous distribution of this trait (Yadav et al. 1998).

Reiss (1999) reported that about 55% of the populations are left hand claspers, 44% are right hand claspers and remaining 1% is different. Familial data suggested that hand clasping may be under genetic control. Although the data is not fit any recessive or dominant Mendelian model. The environmental influences are also evident. Both monozygotic and diazygotic twins show a low concordance. Right right, right-left and left-left pairs in monozygotic and diazygotic twins are in binomial distribution. Zheng et al. (1999) studied hand clasping in the Daur population, China. They reported right type hand clasping 45.87%. There are some relation between hand clasping and arm folding.

Yadav et al. (2001) studied the distribution of hand clasping among 4 endogamous groups of north west India viz., Bawaria, Dakaut, Khatik and Meena. The frequency of R type hand clasping was highest in Meena (52%) and lowest in Khatik (46%). Both the differences in total population and intercaste were found to be no significant. The distribution of this trait is homogeneous. The frequency of R type hand clasping was 40% in Rajput (Bhasin et al., 1992) to 75% in Gadia Lohar (Yadav et al., 1997a). Yadav and Singh (2002) reported the distribution of hand clasping in Meos and Sunni Muslims (Haryana). The frequency of R-type hand clasping is higher than L-type in both Meos and Sunni Muslims. Chi-square value for
two groups is found to be non-significant indicating homogeneous distribution of this trait. Devi (2002) reported that the incidence of left thumb over right thumb was heterogenous in the tribal and homogenous in the non-tribal population groups of Himachal Pradesh. Verma (2003) reported homogenous distribution of this trait (R/L hand clasping) among Brahmans (52%), Rajputs (58%) and (46%) Harijans of two districts in Himachal Pradesh. Sharma (2004) reported that the dominant (R/L hand clasping) gene frequency was found maximum (24.4%) in Brahmans and minimum (16.7%) in Thakurs.

Arm folding

Arm folding is thought to have a Mendelian mode of inheritance. The incidence of right arm over left arm is dominant trait against left arm over right arm. The frequency of R type arm folding was 31.90% in Gaddi (Bhasin et al., 1992) to 72% in Sunar (Yadav et al., 1997a). Yadav and Gupta (1992) reported that the frequency of R-type more than L-type among Jat individuals of Haryana. Mitra et al. (1995) studied L/R type arm folding (58.93%) in Saryupari Brahmin of Chhattisgarh, Central India. Yadav et al. (1997b) reported that the incidence of R-type folding showed lots of variation among five endogamous groups of Haryana. The highest frequency was observed in Bishnoi (53%) and lowest in Bazigor (41%). Yadav et al. (2001) studied the distribution of arm folding among 4 endogamous groups of north west India viz., Bawaria, Dakaut, Khatik and Meena. The frequency of R type arm folding was highest in Khatik (60%) and lowest in Dakaut (36%). Zheng et al. (1999) reported right type arm folding 49.50% in the Daur population, China. There are some relation between hand clasping and arm folding. Similar result were shown by different researcher in
Haryana and other north-west India (Yadav et al., 1998 and Yadav et al. 2000).

**Leg folding**

It was reported that when the legs are folded naturally most people will put the same leg either left or right – upper most every time. The incidence of right leg (R-type) over left leg is dominant trait against left leg over right leg (L-type). It was considered that the trait was under genetic influence, if not simple Mendelian control (Lutz. 1908). Yadav and Gupta (1992) reported that the frequency of R-type more than L-type among Jat individuals of Haryana. Yadav et al. (1997b) reported that the incidence of R-type folding showed lots of variation among five endogamous groups of Haryana. The highest frequency was observed in Bazigar (87%) and lowest in Gadia Lohar (58%). Zheng et al. (1999) reported right type leg folding 72.28% in the Daur population, China. Similar results were shown by different researchers in Haryana and other northwest India (Yadav et al.; 1998, Yadav et al.; 2000 and Yadav et al., 2001).

**Serological traits (ABO blood groups and Rh factor)**

The discovery of blood groups and the simple mode of inheritance initiated various studies elucidating the phenomenon of blood group polymorphism and their linkage with other genetic traits (Greenwalt, 1997). The ABO and Rh (D) blood groups are the two most thoroughly investigated genetic markers of human population. Genetic basis of blood groups was given by Bernstein (1925). He reported that A, B, O blood types are due to their alleles at a single locus near the tip of the long arm of chromosome nine. These alleles are designated as I^a, I^b, I^o (I designated the gene iso-haemoglobin). The person with blood group AB have genotype I^a, I^b, while those of
blood group O possesses genotype 1°, 1°. Therefore $I^a$ and $I^b$ are dominant over 1°. Individual with alleles $I^a$, $I^b$, express phenotypic characters associated with both of the $I^a$, $I^b$ alleles, therefore AB type are said to be co dominant. The frequencies of the ABO blood types vary from population to population. Among Caucasians (Londoners), the frequencies are O (48%), A (42%), B (8%) and AB (1%). Among Chinese, the frequencies are O (34%), A (31%). B (28%) and AB (7%) (Hartl, 1983). Individuals of blood group A have antigen 'a' on the surface of red blood cells, while those of blood group B have antigen 'b' on their red blood cells. In blood group AB, both the antigens a and b are present, but in blood group O, both these antigens are absent (Winchester, 1963).

Landsteiner and Levine (1927) discovered another set of red blood cell antigens, which is responsible for the MN blood groups. It is very different from the ABO blood groups. Landsteiner and Weiner (1940) discovered a most important and well-publicized blood group Rh factor they observed that 85% persons carried Rh factor (+antigen). Rh+ condition depends on a dominant, autosomal gene and double recessive condition result in a Rh-individual. The symbol Rh comes from the first two letters of the species name of the monkey (Macacus rhesus). The presence of Rh+ substance is due to dominant alleles at a locus on the short arm of chromosome 1. The dominant allele is denoted by D and the recessive allele is denoted by d. The DD and Dd genotypes are phenotypically Rh+, whereas dd genotype is Rh-.

Mitra (1936) and Boyd (1939) reported that in all mongoloid people blood group A is more prevalent than B and the incidence of blood group O is also very high. In some tribes blood group O is
more than A and the AB blood group is least in all the mongoloid tribal people.

Mathew (1959), Jolly et al. (1960), Srivastava and Shukla (1963), Sehgal et al. (1966), Singh and Ojha (1967) and Singh et al. (1997) have studied the distribution of ABO blood groups and allele frequencies for Hindu and Muslim soldiers, donors in Varanasi district. They reported that the O allele was more frequent than B and A alleles. The investigation of blood groups ABO from Sultanpur was found to be in genetic equilibrium. Tiwari (1972) studied the definite pattern in the distribution of ABO blood groups in the population of Himalayas. This hilly tract of India, running from Jammu and Kashmir in the west to Arunachal Pradesh in the east. The frequency of blood group B is higher than that of blood group A among scheduled caste. In Garhwal Himalayas among scheduled caste populations, the frequency of blood group A has been consistently higher than that of blood group B (Kaul, 1953; Tiwari and Bhasin, 1968).

Bhatia et al. (1976) conducted Genetic studies among endogamous groups of Saraswats in Western India. Three groups of Saraswat Brahmans in Western India and a group of Goan Catholics ethnologically related to Saraswats were studied for various genetic markers. Saraswats have higher A than B with an Rh (D) - negative incidence ranging from 10 to 17%. Genetic relationship between Goan Catholics and Chitrapur Saraswats confirms the ethnological and historical evidence of relationship between the two groups.

Negi (1977) studied that in all the systems of blood groups; ABO system has been on the largest in number among the Indian population. All populations of north-western India show a preponderance of B and A blood Groups. Undevia et al. (1978)
reported a population genetic study of the Vania Soni in Western India. A total of 267 blood samples from persons belonging to the Shrimali Vania Soni Caste group in Gujarat state, Western India, had been analyzed for 6 blood groups. On the basis of individual genetic markers the Vania Soni appear not to be genetically differentiated in any remarkable way from other Hindu populations in Western and Northern India.

Bernhard (1980) studied the distribution of ABO blood groups and the Rh factor (D) in different native ethnic groups (Kafirs, Kalash, Chitrali) in the Hindukush region of Afghanistan and Pakistan. Kaur et al. (1980) studied biochemical polymorphism in members of the Gaddi tribe of Himachal Pradesh. The genetic traits reported here included ABO blood group and antigen Dd. The frequencies of genes p, q and r for the ABO system were 0.212, 0.290 and 0.428.

Papiha et al. (1980) conducted genetic studies among Kanet and Koli of Kinnaur district in Himachal Pradesh, India. Data are presented on serological and electrophoretic variants of 18 systems of red cells in 228 individuals belonging to a scheduled tribe (Kanet) and a scheduled caste (Koli) of Kinnaur district. Differences in gene frequencies clearly indicated biological distinction in the local population.

Ramesh et al. (1980) conducted genetic studies on the Chenchu Tribe of Andhra Pradesh, India. A total of almost 200 members of a tribal group, the Chenchu from the Mahabubnagar and Kurnool districts of Andhra Pradesh, have been tested for electrophoretic variation in a number of red cell enzyme systems. The former population has also been tested for ABO, MN and Rh blood group systems.
Kaur et al. (1981) studied the distribution of ABO blood groups and antigen Dd-reactivity in three populations from Punjab, North India. The frequencies in Jat Sikhs, Khatris and Balmikis were 17-30%, 21.90% and 19.44% for antibodies against antigen Dd. The frequencies for the alleles A, B and O of the ABO system were 0.216, 0.239 and 0.545 in Jat Sikhs, 0.238, 0.320 and 0.442 in Khatris, and 0.196, 0.274 and 0.530 in Balmikis. These tests showed these populations to be in Hardy-Weinberg equilibrium. Sehajpal et al. (1981) studied the distribution of ABO blood groups among Ramgarhias and Ramdasias of Punjab. Frequencies for the A, B and O genes were found to be 0.1711, 0.2566 and 0.5723 in Ramdasias, and 0.1737, 0.2960 and 0.5303 in Ramgarhias. In all 13 Rhesus-negative individuals were encountered.

Bhasin et al. (1981) studied Geographic and ethnic distribution of genetic markers in India. The result of blood group, serum protein group and enzyme group typings, on a sample of 101 Jains, a population group in the area around Delhi, was presented. He observed the relatively high frequency of blood group gene A. Empana and Jouveneaux (1982) studied the ABO blood groups from Congo to determine the gene frequencies. They found that the blood group O has a high frequency and the frequency of group A is close to that of the B blood group.

The equality to Hardy-Weinberg equilibrium is improved if a typical B allele is assumed to exist along with the A1, A2, B and O genes in the ABO system. This typical B allele accounts for 37% or so of the total B gene frequency in both Brazilian whites and blacks Palatnick and Shull (1986).

Mitchel and Eslick (1988) reported that there is no association between the phenotypes of the two systems but the distribution of the
HP* 1 (heptoglobins) allele varied among ABO blood groups and the
difference between those who had blood group O and the other ABO
groups in combination was significant. Blavy (1986) reported the
ABO blood groups, sub-groups of A and gene frequencies in
Senegalese subjects. He showed an important frequency of the gene
A and B (0.7042), the frequencies of the genes A1 and A2 gene are
respectively (0.1248 and 0.0223). Veerraju (1988) conducted a
genetic study of the Konda Kapu tribe of Coastal Andhra Pradesh,
South India. Phenotype and gene frequencies of two blood group and
four red cell enzyme systems were examined. The gene frequencies
for these systems in Konda Kapu indicated the middle range values
for Andhra Pradesh tribal populations, excepting the Rh (D) system,
where extreme range value was found. Balgir and Sharma (1988)
studied the ABO and Rhesus blood groups in the Hindu and Muslim
Gujjars of Northwestern India. The study showed that the Muslim
Gujjars differ significantly from their counterpart, the Hindu Gujjars.

Malik and Singhrol (1992) studied the blood group ABO and
Rh (D) in hundred twenty unrelated individuals belonging to both the
sexes of the kamar tribal population of Raipur district in Madhya
Pradesh. The observed gene frequencies for ABO locus are 0.3428
for A, 0.2763 for B and 0.3809 for O. The Rh (D) negative group is
observed to be present in this study. Koley et al. (1992) reported the
distribution of the ABO among the Brahmins, Bania, Kshatria,
Kayasth, Shudra and Muslim from central India. No significant
differences have been found in the distribution of both these blood
markers among the six studied populations. Genetic data on two
polymorphic systems, namely A1A2BO and Rhesus, were studied on
Gujjars and three Dogra population groups- Brahmans, Rajputs s and
Ramdasias of Jammu district. Distribution of these markers does not
show any difference among three Dogra population groups, though Gujjars are little different (Bhasin and Khanna, 1992).

Mandal and Kumar (1992) studied the distribution of the A1A2 BO and AB (D) blood groups among five caste populations of Uttar Pradesh. Both these blood systems are in the genetic equilibrium in the present sample and their gene frequencies are well within the ranges observed for other North Indian populations. Walter et al. (1992) reported sixteen tribal populations from Orissa, M.P and Maharashtra for the polymorphic blood group Systems A1A2 BO, MNs, Rhesus, Kell, Duffy and Diego. The heterogeneity in the distribution of haplotype and allelic frequencies respectively is partly considerable. It is supposed that this is due to the operation of several micro evolutionary factors, such as genetic drift, social and geographical isolation and gene flow.

Walter et al. (1992) studied the five-caste population (Brahmins, Rajputs, Khatris, Mahajans, and Kambohs) from Chamba (H.P) and sanaur village near Patiala (Punjab), for the distribution of red cell enzyme polymorphism. The genetic heterogeneity among these caste populations was analysed. Genetic distance analysis showed the existence of a clear distance pattern: Brahmans and Rajputs as well Khatris and Mahajans are found in different subclusters forming one coherent cluster, whereas Kambohs are deviating obviously from this cluster. These analyses affect the regional and social differentiation of the five caste groups and substantiate the importance of endogamy for emergence and maintenance of genetic diversity is man.

Gene diversity and genetic structure of tribal populations of Andhra Pradesh (India) have been analysed. The infralocation coefficient of gene diversity was estimated at 96% of the total,
whereas the intertribal within and between-regional gene diversities were found to be only 1.90%, 0.95% and 1.43% respectively. The tribes of the plains exhibit the least gene diversity, apparently because of higher gene flow among them. The contribution of loci with intermediate gene frequencies in intertribal and regional gene diversity was found to be higher than for loci with extreme allelic frequencies. Forces like selection, gene flow and drift also influence the diversity depending upon the nature of the locus (Murty et al. 1993).

Mesa et al. (1994) studied unrelated blood donors (226), whose 4 grandparents were born in the study area, were tested for blood group markers (A1A2Bo, Rh). Comparison suggests a certain degree of genetic variation between the populations of these two valleys. The Sierra de Gredos can thus be considered a biological barrier limiting the gene flow between the valleys. Choudhury et al. (1994) studied blood groups in the district of Bankura with special reference to tribals. Distribution of ABO blood groups was studied in 4301 subjects, both tribals and non-tribals of Bankura district in, West-Bengal. It was observed that group 'O' blood was found in most cases and group 'AB' was seen in least number of cases. There was no significant difference in distribution of blood groups between the tribals and non-tribals.

Mitra et al. (1995) have investigated the Saryupari Brahmins of Chhattisgarh for the distribution of ABO blood groups and Rh factors. They found the frequency of group O slightly dominant (38.91%) and statistical analysis show that the population is in genetic equilibrium. The gene frequency exhibited $r > q > p$ pattern. Kaur et al. (1995) studied consecutive sib pair samples according to maternal phenotype for segregation deviations of ABO system.
Approximately 60% of the sibs shared the same phenotype. The sub-samples of pair born to A, B and O mothers of the total sib-sib matrix had perfect harmony with the expected segregation. Both AO and BO mother segregated preferentially in favour of A and B groups.

Onde and Kence (1995) reported the gene frequencies of A, O and Rh, which was subjected to spatial auto-correlation analysis. Significant spatial auto-correlation co-efficient was observed for each gene in the first distance class. They also suggested marked decrease in genetic similarity in relation to geographic distances. Scheil and Strunz (1995) studied the ABO allele frequency from the administrative area of Koln and North Rhine-West Phalia. They observed the B allele relatively in high frequencies (>0.0800) on both sides of the river Rhein in the eastern parts of the area and it is separated from the Koln region by a region of lower B frequencies in Aachen region. The O allele shows relatively low and the B allele relatively high frequencies in the eastern and south-eastern parts of the region. Fukumori et al. (1995) found the frequencies of ABO genotypes in Japanese blood donors with A and B phenotypes (AA=19.8%), (AO=80.2%) and (BO =87.2%). Papiha et al. (1996) studied the variability of genetic markers of 9 blood groups in 11 populations from 3 districts, Chamba, Kangra and Kinnaur of Himachal Pradesh. The analysis indicated that geographic proximity; random inbreeding and admixture mainly affected local differentiation.

Choudhary and Malik (1997) reported the distribution of ABO and Rh (D) blood groups among the Khasas (Rajputs)- a scheduled tribe of Jaunsar Bawar area of Utter Pradesh in Dehradun district. The observed allelic frequencies at the ABO locus were: 0.2653 for
A. 0.2613 for B and 0.4734 for O. No Rh (D) negative subject was detected. Yadav et al. (1997) studied the ABO and Rh (D) blood group systems, among five endogamous groups of Haryana viz. Bishnoi, Bazigar, Gadia Lohar, Dhobi and Labana Sikh. There was a preponderance of B allele over the A allele except Bazigar in which the incidence of A allele (0.356) was higher than B allelic incidence (00.274). However the value of total group comparison revealed a heterogeneous distribution. The incidence of blood group Rh (D) negative varies from 1% in Bazigar to 8% in Gadia Lohar.

The frequency of Rh-negative blood group in Damman region was found to be 9.18%. The gene frequency for D was calculated as 0.7. (Al Sheikh et al., 1998). The heterozygosity indices of the population (0.554-0.573) for ABO and (0.410-0.499) for Rh. According to him heterozygosity in this population was higher than average heterozygosty in total population of Ukraine as a result of intensive migration and prevalence of heterolocal marriages over homolocals (Mukhin. 1999).

Bulliyya and Ramachandraish (1999) studied the frequency distribution of ABO and Rh (D) blood groups among Vennekula Kshatriyas, an endogamous caste population of Andhra Pradesh in South India. They observed that the most frequent blood group was O followed by B, A and AB. The allelic frequencies of ABO system vary widely among endogamous caste population of Andhra Pradesh. Sidhu (1999) studied the frequency of blood group B is highest as compared to O, A and AB in the Balmiki Harijans and Khatik Harijans of Punjab. She compared them with other castes of the state viz. Bazigars, Gujjars, Sansis, Harijans and Chamars, only the Gujjars showed significant difference both with the Balmiki Harijans and Khatik Harijans.
The different ethnic groups (Aryan, Mughal, Syed, Jat, Rajputs, Baloch and Pathan) are not significantly different from one another with regard to distribution of Rh blood group allele and also from the average allele frequencies (A=0.23, B=0.33, 0=0.47), except for the Pathan ethnic group (A=0.35, B=0.47, 0=0.27). Southern district of Rahim Yar Khan (A=0.12) and the Northern district of Sahiwal (A=0.19). The population of Sahiwal and Muzaffargarh yield significantly different allele frequencies at the Rh locus. They observed significant difference in the frequencies of the ABO alleles between rural and urban population but these population are not significantly different from one another concerning the allele frequencies at the Rh locus (Mian and Farooq, 1999).

Nath et al. (2000) studied the distribution of the ABO and Rh blood groups among the Adi (mixed) tribal population of Arunachal Pradesh. The prevalence of blood group frequencies, A>B>0>AB, was fairly similar to that of their Mongoloid stock from South China. The Rh -ve was remarkably low. Pramanik and Pramanik (2000) studied the blood group distribution in Nepalese students. The blood groups A=34%, B=29%, AB=4% and 0=32.5% and the frequency of Rh^+ve =96.66% and Rh^-ve =3.33%. They found that the frequencies of ABO and Rhesus blood groups vary from one population to another.

Falusi et al. (2000) reported the micro differences of genetic markers of ABO and Rh blood groups between the ethnic groups in the ABO and Rh blood group systems. They observed the frequencies of 0=0.7068, A=0.1490, B=0.1443 and Rh (D) =0.8150 blood groups. The phenotypic frequencies of the blood groups are in agreement with Hardy-Weinberg equilibrium expectations but in two zones, North -West (Hausa-Fulalni) and Platean (Birom) was thought to be due to a high frequency of blood group AB. Galushkin et al. (2001)
reported the high allelic frequencies for blood group B and the rare incidence of individuals with Rh negative phenotype from three tribes (Torguts, Derbets and Buzavas) of the Valga's Kalmy Koyrats. They found genetic affinities exist between the Derbets and Buzars, but population differs significantly from Torguts.

Goicoechea et al. (2001) reported four of the five Chaco tribes exhibit good genetic homogeneity, but the Ayoreo are somewhat different. Chaco has a distinct biological as well as cultural and economic region, which would be considered in evaluations of genetic variability among South American Indians.

Yadav et al. (2001) studied the ABO and Rh (D) blood groups among 4 endogamous groups of Northwest India viz., Bawaria, Dakaut, Khatik and Meena. The frequency of A allele ranges from 0.122 to 0.270, that the B allele varies from 0.246 to 0.349 and O allele ranges from 0.400 to 0.571. The frequency of d allele varies from 0.200 to 0.282 and that of D allele ranged from 0.718 to 0.859. The inter-caste comparison showed nonsignificant differences. However, the total group comparison revealed heterogeneous distribution.

Naidu et al. (2002) studied Genetic Markers in Sishta Karanam Population, Andhra Pradesh, India. The population exhibited the phenotypes, O, B, A and AB and the gene frequencies in the decreasing order of predominance 0>B>A>AB respectively. The frequency of the AB phenotype is the highest when compared to the other caste populations of Andhra Pradesh.

The distribution of A1, A2, B, O and Rh (D) blood groups has been reported in Meo and Sunni Muslims belonging to Haryana. The frequency of A allele was slightly higher in Meos (0.400) and that of
B allele was low (0.020) in comparison to other populations of Haryana. In Meos the gene frequency of Rh (D)+ is 0.701 and that of Rh(D)- is 0.299. The frequency of d allele was found higher in Meos (0.363) than in (0.299) Sunni Muslims (Yadav and Singh, 2002). Pandey et al. (2003) studied the distribution of ABO and Rhesus blood groups among seven endogamous populations of the Koshi Zone, Bihar (India). The phenotypic and allele frequencies show considerable differences between these populations. Verma and Varma (2005) studied the distribution of ABO and Rh (D) blood groups among Brahmin, Rajput and Harijan population groups of Shimla district in Himachal Pradesh, India. The frequency of A allele ranges from 0.157 to 0.243, that of B allele varies from 0.158 to 0.252 and O allele ranges from 0.538 to 0.648. The frequency of d allele varies from 0.173 to 0.265 and that of D allele ranged from 0.735 to 0.827.

Pattanayak (2006) studied the distribution of A1A2BO and Rh blood groups among the Rajputs of Mussoorie, Uttarakhal. The frequency of A1 is highest with a percentage frequency of 38.54% and that of Rh+ is 94.63%. Krithika et al. (2006) studied the distribution of ABO blood groups among three little known subtribe of the Adi tribe, the Panggi, Komkar, and Pandan, of Arunachal Pradesh, India. Blood group O was the predominant group in the Komkar and Padan, whereas group A was the predominant group in the Panggi. Blood group AB was found to be the least frequent group in all three studied populations. The populations showed significant differences in blood group A (43% in Panggi, 23% in Komkar and 18% in Padam) and O (33% in Panggi, 54% in Komkar and 61% in Padam).
**Human genetic diseases**

Human genetic diseases are the aspect of human genetics that is concerned with the relationship between heredity and disease. In recent years there have been a great increase in appreciation of the importance of genetics in understanding diseases of man. Different diseases can be categorized on the basis of genetic factors involved in their causation. A number of diseases are heterogeneous in cause and multifactorial in their underlying gene basis e.g. diabetes and hypertension (Hartl, 1983).

Diabetes and hypertension are multifactorial diseases and both environmental and hereditary factors are equally involved in their causation. The affected genes responsible for these two diseases are very low in their frequency, as compare to the non-effective one. These diseases are move prevalent due to environment factors such as diet, etc. rather than their appearance due to inheritance Verma (1998). Many defects of the nervous system may actually have their origin in variation in other system, such as endocrine. A few mental disorders can even be traced to a single gene such as Amaurotic idiocy, Huntington’s cholera, epilepsy etc. (Winchester, 1967). There are several forms of therapy for genetic diseases: Substrate restriction by elimination diets, Supply of the substance that cannot be synthesized. Avoidance of drugs, Elimination from the body, Competitive inhibition, Enzyme induction, Enzyme repression, Co-factor supplementation, Replacement of defective tissue, Preventive therapy, Surgical therapy (Mc Kusick, 1978).
Hypertension

Hypertension is by far the most common form of disease and affects both sexes equally. It has been estimated that heredity plays an important role in hypertension. If both parents have hypertension, the incidence of the disease in children is about 45% and if one parent has hypertension than incidence is 30% (Guyton, 1971). Like many other characteristics, hypertension is greatly influenced by environment, but its tendency to reoccur in families strongly suggests an heredity background. It was concluded from an extensive study made in Germany that the predisposition for the development of high blood pressure is inherited as a dominant trait (Winchester, 1974). Role of heredity in the development of Hypertension in man was first suggested by Bauer (1968) and Mckusick (1960). Platt (1959) proposed that the pattern of inheritance may be a result of single gene with complete dominance for essential hypertension. This hypothesis was supported by Morrison and Morris (1959).

Schull et al. (1970) and Boyle (1970) found tendency for darker skinned negroes to have high blood pressure than light skinned individuals. Krieger et al. (1965) studied northeastern Brazil population, but he did not find any correlation between white and black population. The black population has significantly greater incidence of high blood pressure as compared to white population of United States at all ages. Gardon and Devile (1966), Longford et al. (1968) and Lennard and Glock (1955) found differences of blood pressure in the black and white population due to exposure to environmental stress. Miall et al. (1967) was the first to point out that change in blood pressure in related to previous history rather than the age. Boyle (1970) has reported the relationship of blood pressure among black in the age group over 65 year. He observed
significant relationship between blood pressure and skin colour in Negroes.

Charles et al. (1974) showed a significant relationship of sex to blood pressure. They observed that male had high blood pressure than female of the same age. Gutmann and Benson (1971) studied that many environmental factor are either known or are suspected to affect blood pressure. Even mild hypertension conventionally (90-140 mm Hg) for the diastolic pressure is viewed as a major public health burden (Labarthe, 1986). Cheng et al. (1995) found evidence for a major gene affect for diastolic blood pressure with age. These studies suggested that the hereditary resistance for blood pressure changed with time. The age decreases the expression of major gene at older age. Rice et al. (1991) studied the heterogeneity in systolic blood pressure to non-heredity and heredity environments. Province et al. (1989) examined longitudinal familial correlation for systolic blood pressure measured in the East Boston. It increased from about zero at birth to maximum of about 40% at age 30 and then declined to zero at 90.

Partha et al. (1995) studied two contrasting population i.e. Marwaris of Calcutta and Hindu middle caste agriculturists of Digha. They observed the prevalence of hypertension among Marwaris (17%) in over ten fold higher than among the agriculturist (1.42%) Tsutsu, et al. (1991) observed that both systolic and diastolic blood pressure were not at hypertensive levels in the patient with insulinoma. But according to Morrish et al. (1990) hypertension is significant in insulin dependent diabetes.

Verma (1998) calculated the allelic frequency data for hypertension in fifteen families for two successive generations. It was inferred, that the disease was more prevalent due to
environmental factors such as diet, etc. rather than appearance due to inheritance. Devi (2002) reported that 48.5% individuals of non-tribal and 19.5% individuals of tribal population were affected with hypertension in Himachal Pradesh. Feng et al. (2004) studied linkage analysis of ordinal traits for pedigree data. The blood pressure for hypertension was reported to be dichotomized or measured by a quantitative trait. Gu et al. (2004) studied Genetic susceptibility Loci for essential hypertension and blood pressure on chromosome 17 in 147 Chinese pedigrees of Han population. The results demonstrated that a 70 cM interval region flanked by D 175 8.31 (7cM) and DI 75938 (15cM) is suggestively linked with hypertension. Sharma (2004) reported the distribution of hypertension in Brahmins (0.69%), Thakurs (3.65%), Rajputs (0.84%), Bari (5.2%), Lohar (3.7%) and Turis (1.75%) of Tribal population in Shimla district (Himachal Pradesh).

**Mental retardation**

The role played by heredity in mental retardation would appear to be due to a number of genes in most cases. Therefore, there are some marriages between persons of inherited sub-normal mentality that result in children of normal intelligence because of gene-segregation. Likewise, normal or even superior parents may occasionally produce children who inherit mental retardation because of this gene segregation (Winchester, 1974).

Franceschini et al. (1996) studied mental retardation syndrome caused by a microdeletion on the long arm of chromosome 7 in 77 patients from 11 Italian Pediatric Dysmorphology - Genetics Unit. Jain et al. (1998) studied prevalence of fragile X (A) syndrome in mentally retarded children at a genetics referral centre in Delhi, India. Of 1206 children with mental retardation 360 (29.8%) boys
fulfilled defined clinical criteria to be screened for fragile X syndrome by chromosomal studies. Hirose and Mitsudome (2003) reported mental retardation as heterogeneous syndromes based on dysfunction in the brain. Some 50 monogenic Causes of Mental retardation had been found in genes localized on the X chromosome. Kumar et al. (2004) studied Genetic analysis of primary microcephaly in Indian families. Patient with primary microcephaly, an autosomal recessive trait had mild to severe mental retardation without any other neurologic defects. Sharma (2004) reported that the frequency of mental retardation was 0.75% in Baris and 0.69% in Brahmins.

Over 750 known genetic causes of mental retardation have now been identified. These can be single gene disorder, polygenic, chromosomal and mitochondrial. The two main causes of mental retardation are environmental (60%) and genetic (40%). Chromosomal disorders leading to mental retardation include Downs syndrome, trisomy 13 and 18, fragile X etc. of all chromosomal disorders, trisomy 21 or the Down syndrome in the most common 'inherited' cause of mental retardation, with a frequency of 1 in 800 to 1000 newborns and the risk increases with increases maternal age (Gulati and Wasir, 2005). Chromosome abnormalities are the single most common cause of mental retardation in humans (Gopalrao et al. 2005).

**Diabetes mellitus**

It is one of the common diseases which result from endocrine disturbance persons with this disease produces an insufficient amount of insulin in the pancreas and sugar metabolism is defective as a consequence. Excess sugar accumulates in the system and is excreted in the Urine. Diabetic coma and death may result if proper
treatment is not administered. A predisposition to become diabetic seems to be inherited as a recessive, but the development of the disease may be avoided if the intake of carbohydrate foods is moderate (Winchester, 1974). The two different types diabetes mellitus are; one is juvenile diabetes that usually but not always begins in early life and other is maturity onset diabetes that usually begins in later life. Heredity plays an important role in the development of both these types of diabetes. The juvenile type is usually rapid in onset and seems to result from hereditary predisposition to development of antibodies against the beta cells thus causing autoimmune destruction of these cells. It can be due to possible destruction of beta cells by viral diseases and possibly simple degeneration of these cells. The maturity onset diabetes seems to result from degeneration of beta cells as a result of more rapid aging in susceptible persons (Ahluwalia, 1985). The other reasons for their frequent appearance can be environmental such as diet, stress and strain etc. (Verma, 1998). Diabetes Mellitus (DM) is a chronic disorder resulting from a number of factors in which an absolute or relative deficiency of insulin or its function occurs. It is projected that by the year 2025, India alone would have 57 million diabetics mainly of type 2 diabetes constituting 90% of the diabetic population (Rani et al., 2005).

Ledermann (1955) reported that molecular genetics of maturity-onset diabetes of the young (MODY) is an important and informative autosomal dominant disease that account for 25% of all type-2 diabetes. Lee et al. (1990) has found in their study that the number of diabetes increases with age. However, the hypertension was not associated with age in the diabetic patients. Reballo et al. (1990) reported that diabetes becomes more multicomplcicated over the age of 50 years. Rewers and Hamman (1995) studied that
hereditary clustering and twin studies have a genetic component for type 2 diabetes. The incidence of type 2 diabetes between the Oji-Cree of sandy lake in Northern Ontario is 40%, which is 6 times higher than the general Canadian population. Harris et al. (1997) and King et al. (1998) referred diabetes mellitus to a diverse group of metabolic diseases that are characterized by high plasma glucose concentration. According to Todd (1999) type 1 diabetes, previously called “Juvenile-onset” or “Insulin dependent” diabetes mellitus (IDDM) is characterized by the failure of insulin secretion by pancreatic beta cells due to autoimmune destruction. According to Busch and Hegels (2001) the complexity of type 2 diabetes in related to various factors, such as genetic heterogeneity interactions between genes and the modulating role played by the environments.

Rao (2002) studied dietary patterns and glucose intolerance among rural Indian populations. Of the Indian dietary habits it was difficult to identify any specific dietary pattern to relate with diabetes. Van Tilburg et al. (2003) studied Variance - component of obesity in type 2 diabetes that confirmed Loci on Chromosomes 1q and 11q. Genotype data were obtained from 5b2 individuals from 178 families from the Breda study - cohort. The Locus on Chromosome 1 had been implicated in diabetes and locus on chromosome 11 in diabetes and obesity. Misra et al. (2004) reported a high prevalence of insulin resistance in postpubertal Urban Asian Indian Children that was associated with excess body fat, abdominal adiposity, and excess truncal subcutaneous fat. Primary prevention strategies for coronary heart disease and diabetes mellitus in Asian Indians should focus on the abnormal body composition profile in childhood. Sharma (2004) reported the distribution of diabetes mellitus in Brahmins (1.38%), Thakurs (2.19%), Rajputs (0.4%), Sunar (1.96%),
Rehar (7.14%) and Turis (1.75%) of Tribal population in Shimla district (Himachal Pradesh).

**Epilepsy**

Epilepsy is characterized by sudden seizures known as epileptic fits, which in the most extreme form run to unconsciousness and muscular spasms. Some persons have the disease in a milder form in which the fits are minor. Brain injury is known to be an environmental agent that can induce the onset of epilepsy, but the majority of cases arises without such injury and has a hereditary basis. A great advance in understanding the disease has been made possible through the use of the electroencephalograph, a machine which records the electrical brain waves. Sufficient studies have been made to indicate that the irregular waves are inherited as a dominant trait. All persons who show the irregularity are potential epileptics and those who do not show the condition lack some other factor, either a modifying gene or some environmental factor required for the expression of epilepsy (Winchester, 1974).

A hereditary component to epilepsy has been suspected since the time of Hippocrates. Sushruta too in the Indian system of medicine-Ayurveda, emphasizes the role of hereditary influences in epilepsy. These diseases, however, are few and account for only 1% of all epilepsies. The role of genetics in not only restricted to epilepsy type but also influences various aspects of pharmacotherapy. (Tripathi and Jain, 2002). Lo Nigro et al. (2003) studied Genetic heterogeneity in inherited spastic paraplegia associated with epilepsy. This trait was inherited as an autosomal dominant trait. Patterson et al. (2003) studied clinical characteristics and inheritance of idiopathic epilepsy in Vizslas. It was concluded that idiopathic epilepsy in Vizslas appeared to be primarily a partial
on set seizure disorder that was inherited as an autosomal recessive trait. Hirose and Mitsudome (2003) reported epilepsy as heterogeneous syndromes based on dysfunction in the brain and closely associated it with mental retardation. Monogenic causes of about 30 epilepsy syndromes were reported to be transmitted as an autosomal trait. Combi et al. (2004) reported evidence for a fourth Locus for autosomal dominant nocturnal frontal lobe epilepsy. The involvement of the three Loci in the pathogenesis was investigated in 12 unrelated Italian families. The data strongly suggested that ENFL1, ENFL2, ENFL3 were minor Loci for the disease. Sharma (2004) reported none cases of epilepsy among different caste groups in the Tribal areas of Shimla district in Himachal Pradesh.

Epilepsy is a chronic neurological condition characterised by recurrent and unprovoked seizures, affecting 1% of people worldwide. Epilepsy can have many causes, including brain injury, poisoning, head trauma or stroke; and these factors are not restricted to any age, group, sex or race. A small proportion of epilepsy subtypes are inherited as single gene ('Mendelian') traits. In the remaining cases, the etiology is complex, arising from the contribution of multiple genetic and non-genetic factors (Ganesh and Singh, 2005).