

Triambelas

Sexual dimorphism in humans is an established trend with long evolutionary history. All known hominids have exhibited skeletal and dental dimorphism to some degree (Fruyer and Wolpoff 1985). Today's humans are less dimorphic than both their hominid ancestors and the rest of the living primates with the exception of the gibbon (Griffin 2008) but they nevertheless exhibit marked morphological differences in the skeleton of the two sexes. These are associated with differential rates of maturation, increased hormonal output during puberty, and the specialization of the female pelvis towards birth and parturition. Because these ontological changes have an increased effect on the morphology of the cranium and pelvis, it is possible to sex an unknown skeleton with as high as 100% accuracy (Iscan and Kedicic 2003). Additionally, because of the effect that biology, culture, and the environment can have on bones, human skeletal remains are traditionally assessed for age at death and population affiliation, or "race". And since bones and teeth show the cumulative effect of genes and environment, osteological and dental assessment can provide insights into population structure, health, diet, lifestyle, and relationships of past cultures to each other (White 2003).

Of all the features of the human body, teeth hold a special value for the osteologist. Being the hardest part of the skeleton, teeth are likely to be preserved in

the archaeological record because of their tendency to resist chemical and physical destruction. They are thus overrepresented in paleontological assemblages and in many cases dental elements provide the only information available on extinct hominid species. Additionally teeth do not require dissection for access, are easy to measure, and are ideal candidates for quantitative analyses and statistical interpretation. Because of the enormous variation in shape and size and their adaptive significance as the agents of mastication, teeth have also become valuable tools in comparative populational and evolutionary studies as well. The latter are of particular interest to this work because teeth are used to calculate rates of heritability, i.e. the amount of genetic variation within a population at a particular time (Townsend et al 2008). And because teeth are under the effects of both genetic and environmental factors, they can be used to indicate the interaction of these two forces in phenotypical expression of variability making dentition an important component of heredity studies, both within and in-between human populations.

The importance of dentition for assessment of variability became clear very early in the theory of evolution, long before the advances of modern science allowed us to look at the bio-molecular component of inheritance. Bateson (1894) was the first to introduce teeth as serially repeated (meristic) features with differences that are quantitative rather than qualitative. Scott (1892) argued that the serial homology observed by Bateson was a result of convergent evolution and he implied

that each tooth was under independent genetic control though, of course, he lacked the mechanism to prove it. Francis Galton (1876), Darwin's half-cousin, put forth his own theory of inheritance according to which the individual is the sum of different genetic particles that vary in their form of expression with some remaining dormant during one's lifetime while some others achieved various levels of coming into being. Knowing what we know today about the complicated nature of variability in humans, it is to wonder at the creative imagination of these early pioneers of the evolutionary theory and how close they got, in various degrees of accuracy, to our own model of inheritance. For example, the well-documented variation in the bucco-lingual (BL) and mesio-distal (MS) crown dimensions of most teeth has been traditionally been interpreted as evidence for differential genetic control on different elements of the dental arcade (Garn, Lewis, and Kerewsky 1968, Potter et al 1968 and 1976, Townsend and Brown 1979).

Fisher (1918, 1922) was the first to introduce the distinction between additive (alleles or genes with similar effects) and non-additive (dominant and epistatic effects) portions of genetic inheritance and concluded that continuous variation is a result of multiple Mendelian factors rather than environmental influences. This is the point where the "nature vs. nurture" debate is introduced into studies of inheritance; from here on twin studies will become the focus of heritability assessment. Today, odontometric studies on inheritance concentrate

almost exclusively statistical analysis of crown dimensions between monozygotic (MZ) and dizygotic (DZ) twins. The assumption is that MZ twins share the exact genetic code and thus any differences in the heritability of teeth can be attributed to environmental—usually uterine or immediately post-natal—influences whereas DZ twins share only half have their genes and are subject to both genetic and environmental effects. By measuring the observed variation in features or traits, one can theoretically account for both genetic and environmental components in the phenotypic expression (Townsend et al 2008). Thus most of the research reviewed here is concerned primarily with twin or other inter-family studies.

Bachrach and Young conducted a pioneering study on twin heritability as early as 1927. They measured two categories, “heredity” and “environment” and their relative roles in tooth eruption times, dental carries, enamel hypoplasia, and normal occlusion in pairs of twins. They concluded that the observed variation was a result of both of these factors, an assertion that was further extended by Goldberg (1929) to include malocclusion as well.

Seawall Wright (1931), a geneticist like Fisher, countermanded the latter’s assertion that heritability is a result of the small phenotypic effects exercised by multiple Mendelian factors by postulating direct inheritance of environmental factors, a position supported later on by Cavalli-Sforza and Fieldman (1973) who proposed that there exists another mode of inheritance (“cultural inheritance”)

which operates side by side with the strictly biological, DNA-based model. Tobias' (1955) study on fraternal and "identical" twins lends another voice in support of the "nurture" argument by postulating that the dental differences observed in twins are the result of differential action of environmental factors—and specifically uterine at that—after the splitting of the embryonic axis.

Garn, Lewis, Swindler, and Kerewsky (1967) hypothesized simple genetic control of sexual dimorphism in tooth size and postulated a relationship between tooth and body dimorphism in humans. To test absolute size of tooth dimorphism, the authors began their study by examining the MS dimensions in 243 Ohioans of European descent and concluded that in absolute terms the greatest dimorphism was exhibited by LP3's and LP4's; however, percentage-wise dimorphism was greatest for MS dimensions of canines and lowest for mandibular incisors. Percent-size dimorphism—the ratio of the male/female difference minus 1.00—is an important concept because Garn et al found (1967) that individual tooth size can account only for part of the overall difference between males and females and thus another indication is needed that takes into account the entirety of the dentition as a whole. In order to measure their percent dimorphism and its relationship to general tooth size in different populations, the authors next compared MD dimensions of nine groups: Caucasian Ohioans, Japanese, Aleuts, Lapps, Pima Indians, Tristanites, Javanese, Swedes, and Australian Aboriginals. In all nine groups upper canines

consistently showed highest percentile dimorphism with values up to 7.3%. However, the patterning of dimorphism varied greatly among groups, a fact that according to the authors cannot be explained by tooth size per se. They postulated that the observed differences in the patterning of dimorphism among different populations must have a genetic basis and that they represented the cumulative effects of selection for sexual dimorphism in the human species as a whole. Making the observation that this is only tenable if tooth size is heritable, Garn et al proceeded to correlate the magnitude of brother-sister dimorphism in pairs from the same family. They concluded that inter-family sibling dimorphism exhibits significant correlation with  $r$  values approximating 0.5 in most cases. Having established, in their opinion, the genetic basis for tooth dimorphism of the MD dimensions in the canines and some of the adjacent teeth among siblings and in certain populations, the authors attempted to correlate tooth and body dimorphism by examining brother-sister pairs at two separate ages, 12 and 17 years. They concluded that the correlations between tooth and body size difference were significant at a 5% level or better against the little more than 1% that should be expected in the case of a chance event. Warning against attempting to directly correlate tooth and body dimorphism in humans, the authors suggest communality of causation between axial and appendicular dimorphism and that of the MD diameters of permanent teeth. In their view, the fact that tooth and body size

difference are related variables in humans means that selection for one would result in selection for the other, and vice versa, in a 'classic' example of what Darwin called "correlated evolution (Garn et al 1967)".

Potter et al (1976) accepted genetic control of tooth size and questioned whether the differences are influenced by common or separate genetic factors and, if that is the case, which measurements are affected more. Potter and her colleagues applied multivariate analysis techniques to 28 MD and 28 BL dimensions of the permanent teeth on 43 MZ and 32 DZ twin pairs. Multivariate analysis differs from univariate in that it compares the covariance matrices for multiple variables instead of the differences in means. According to the authors, some factors that appear non-significant under univariate analysis made a significant impact under multivariate; multivariate analysis then can be considered more accurate and should be used in all odontometric studies in conjunction with more traditional univariate techniques. The results of the study showed much higher correlations of within-pair differences for DZ than for MZ twins, suggesting that a limited number of genetic factors influence these variables. The analysis of these factors offers some striking and insightful information in the nature of genetic influence on tooth size. Specifically, Potter et al postulated differential influence of genetic factors on maxillary and mandibular teeth with four major factors effecting the upper and seven major factors effecting the lower dentition. Further, these correlations were shown to be

“identifiable and biologically meaningful” and expressed in specific dimensions of certain teeth, i.e. MD of UI1,UI2, UP3, and BL as well as MD of left and right UP3’s. Generally speaking, the MD dimensions are distributed over more factors than BL and the two dimensions of each tooth seem to be associated with different genetic factors. Interestingly enough, after having demonstrated differential genetic effect on upper and lower dentition, the authors discerned homologous effect on the two sides of the same jaw with antimeric measures on both sides being under the same genetic factors. Environmental factors were shown to affect MD and BL dimensions separately than genetic factors but with more localized effect on certain dimensions. Overall maxillary teeth were shown to be under more intense genetic control than mandibular teeth with the genetic factors affecting the MD dimensions of the upper dentition in a discriminating fashion. This pattern is suggesting differences in the degrees of evolutionary stability between the two jaws with the upper showing more intense but also more ‘conservative’ effect of genetic influences. Potter et al study confirms the complicated nature of the differential genetic effects on tooth crown dimensions as well as their interaction with environmental actors. In the words of the authors, “...correlations among tooth dimensions are primarily genetic in origin, probably attributable to pleiotropic action of either independent genes or groups of genes.”

Townsend and Brown (1978) attempted to calculate the product-moment coefficients in full sibling and half sibling pairs of Yeundumu Aboriginals. They argued that the half-sibling data would show less influence from shared environment and thus be more likely to differentiate between additive and non-additive genetic components of heritability. They found additive genetic variance to account for 64% of tooth size difference—much less than Garn's 90%--with common environmental factors accounting for 6% and influencing the BL dimensions more than the MD.

Alvesalo (1971) investigated the possible influence of sex chromosome genes on tooth size by collecting dental and genetic material from 730 subjects from the island of Hailuoto, off of the western coast of Finland. The extensive research involved gathered information on genealogies, family trees, histories of inbreeding, as well as 6,003 measurements of permanent teeth taken on stone casts. In an innovative approach Alvesalo sharpened the end points of the vernier calipers as to provide increased accuracy in measuring adjacent teeth in crowded conditions. His methodology included comparisons between the metric characters between relatives and the chromosomal distribution of the sexes. The comparison of the mean value correlation coefficients between sibling pairs of brother-sister, brother-brother, and sister-sister revealed a significantly higher correlation for sisters than for brothers (X-chromosome related) but the correlations between first cousins

pointed to Y-chromosome involvement in the genes that are affecting tooth size. From this, Alvesalo concluded that the genes affecting tooth size are situated on both X and Y-chromosomes but with different phenotypic quantities.

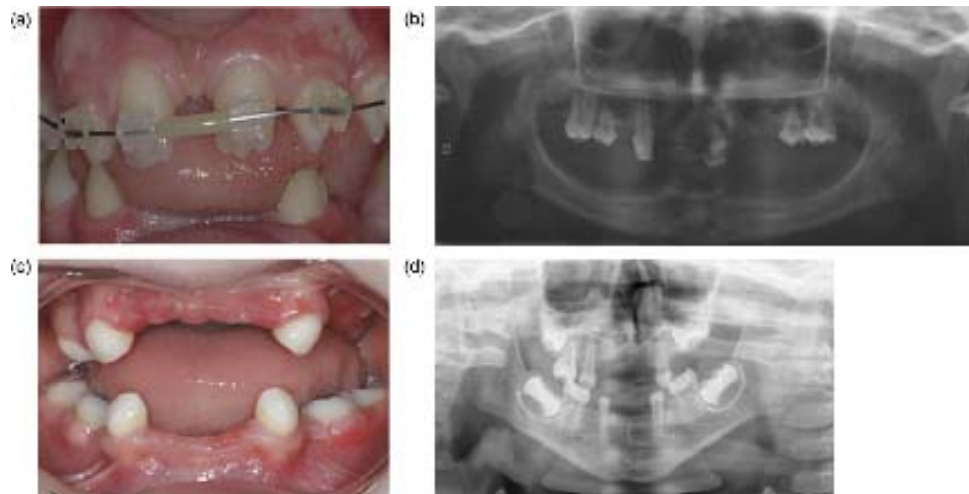
Whereas the studies mentioned so far are but a fraction of the ongoing research on human variability and inheritance through dentition, it must be clear that twin studies, as well as other familial relations, have unequivocally established at least partial genetic control in the phenotypical expression of tooth crown dimensions via the multifactorial action of independent genes or groups of genes. And since heritability is defined as the ratio of the genotypic (genetic) variance over the phenotypic (environmental) variance (Kieser 1990), the fact that traits in crown shape and size vary among populations as well as individuals is another evidence towards genetic control, i.e. if a trait is heritable by definition it involves some degree or other of genetic effect. As this fact has been established on firm basis, research on dental variation is moving towards the identification of the exact genes that are involved in the final shape and size of permanent dentition. The apparent gene pleiotropy and the complexities of the interaction between genetic (additive and non-additive) and environmental (common, unique, and other) factors make the search for a single answer in human heritability a rather futile attempt, at least for the near future. However, the continuous improvements in micro technologies, biogenetics, and DNA splicing techniques make the field of genetic anthropology a

fertile ground for ongoing research that is shedding some exciting new light into the interrelationship of biology and environmental and how these might affect human evolution.

IMPORTANT-Teeth are on the verge of becoming the first ever part of the human skeleton that we might actually be able to demonstrate ACTIVE selection by evolutionary forces and we might be able to detect the process on gene freakin' level! This is absolutely HISTORIC, on par with the discovery of the atom or something like that. Just imagine the implications. Population studies then become even more important because we might be able to apply our knowledge from twin studies and modern populations ACROSS time/space continuum of human evolution!! Mesial maxillary dentition appears to be more 'refused' with more genetic and less environmental action. Canines most dimorphic, i.e. retain primitive characteristics in a sense (canines are the most dimorphic in non-human primates as well). It fits with Falconer's (1967) observation that "characters more closely connected with fitness would display lower heritabilities", i.e. be slower to change. Tooth size and stature not correlated in humans (Perzigian 1981, Wolpoff 1985), however Leutenenegger and Kelly (1977) demonstrated correlation between tooth/body size in anthropoid primates; tooth and phalanx dimorphism are not correlated (Anderson and Thompson 1973), i.e. teeth as a meristic trait are under

independent effect from factors. Reduction of dentition then not a result of secondary selection? Brace's PME and resulting "enzymic inefficiency". Hmm. Then dentition not subject to selection? Wolpoff (1969, 1971) contends that structural reduction would be accompanied by increased variability which befits with extant variation in tooth size. Leutenegger argued that this is an unfounded *inter alia* inversion by Wolpoff of a previous statement by Simpson (1953) that reduction due to direct selection will not be accompanied by increase in variability. I wish these guys could agree, I'm gonna have to do it all on my own ☺

Tooth anomalies Besides twin studies, research is also conducted on the genetics that cause tooth anomalies. Experiments with mice have identified deficiencies in



**Fig. 1 - Dental phenotypes associated with an autosomal form of hypohidrotic ectodermal dysplasia (HED), linked to EDAR mutation. Clinical phenotype associated with a 10-year-old boy including ectopic (agenesis of maxillary permanent incisors and maxillary lateral incisors) and conical-shaped canines (a). A panoramic radiograph (b) of another patient (7 years old) with autosomal HED shows mandibular agenesis and maxillary oligodontia. There is agenesis of the primary right central incisor, lateral incisor, left canine and first primary molar with presence of only one dysmorphic permanent right central incisor and permanent first molars (b). Clinical (c) and radiographic (d) appearance of another patient (1/2 years old) with an autosomal dominant form of HED. Agenesis of maxillary and mandibular primary incisors, first molars and second maxillary right primary molars evident. There is also agenesis of all permanent teeth, except for the permanent maxillary and mandibular first molars.**

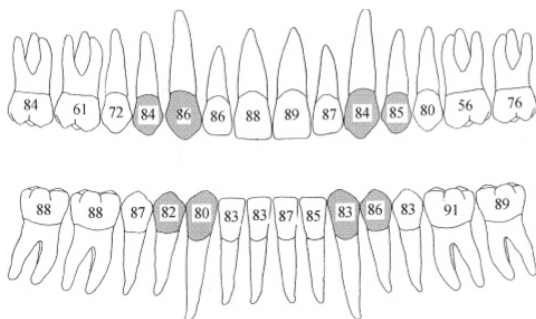
Figure 1: Examples of tooth anomalies linked to EDAR mutation (from Townsend et al 2008).

protein production of a specific gene as responsible for the two most common tooth anomalies, more teeth (supernumerary) or less teeth (hypoplasia) than the normal number. According to the data from these studies the culprit is a signaling molecule, Ectodysplacin A (EDA) that is present at the locus Xq12-q13.1 of the ectodysplacin gene ED1. Alteration in tooth number occurs when there is a disruption between EDA, its receptor EDAR, or the intracellular adaptor protein EDAR-binding death domain adaptor EDARADD that is associated with apoptotic, or “shedding” role (Townsend et al 2008). Though much is still under debate, it has been proposed that

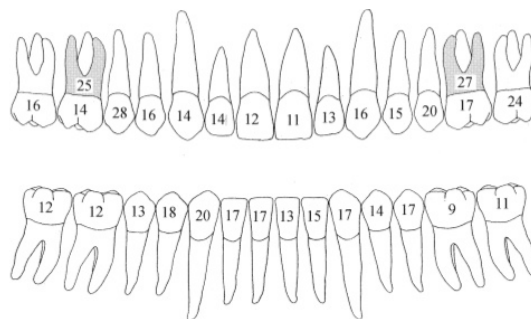
overexpression of EDA or its receptors in field mice results in supernumerary teeth, i.e. the appearance of an extra molar, albeit reduced in size and altered in shape. The insinuation here is that there is some malfunction in the apoptotic process that should have resulted in the “programmed death” of the genes responsible for the extra ‘molars’. In humans, mutation of ED1 at the Xq12-q13.1 locus has been linked to Hypohidrotic Ectodermal Dysplasia, an extreme form of oligodontia that causes a highly abnormal and distorted arcade in children (Townsend et al 2008).

Dempsey and Townsend (2001) collected data on 149 pairs of MZ and 149 pairs of DZ twins of European descent, aged 7 to 62 years, in order to determine interaction of genetic and environmental factors in tooth size heredity. By using different statistical models (variance and covariance, modeling of means, and models of genotype-by-environment,  $G \times E$ , interaction) as well as univariate and multivariate analysis, they detected additive genetic and unique environmental variation on the crown size of most teeth. In contrast to previous studies however, Dempsey and Townsend found supporting evidence for common environmental factors on MD and BL dimensions of UM1. In another finding, they detected non-additive genetic variation in the MD dimensions of maxillary canines and P3's. According to ‘traditional’ evolutionary theory, genes related to selective fitness tend to display non-additive genetic control-also in accordance with Falconer's (1967) “low heritabilities”. This has significant implications because it might indicate

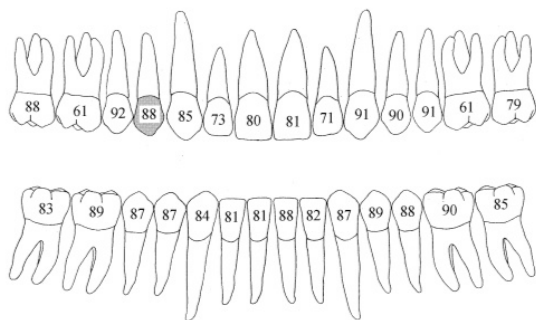
selective pressures on canines and P3's either at the present or recent human evolutionary past. Besides the obvious evolutionary insinuations that maxillary canine dimorphism can bear on comparative population studies, the apparent



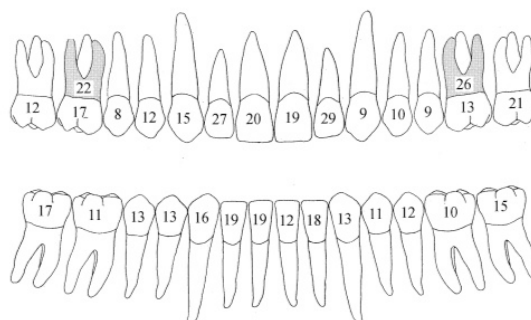
**Fig. 2** Heritability of MD diameter. Unshaded teeth, additive genetic variance (narrow heritability); shaded teeth, additive + non-additive genetic variance (broad heritability).



**Fig. 4** Environmentality of MD diameter. Unshaded region, unique environmental variance; shaded region, common environmental variance.



**Fig. 3** Heritability of BL diameter. Unshaded teeth, additive genetic variance (narrow heritability); shaded teeth, additive + non-additive genetic variance (broad heritability).



**Fig. 5** Environmentality of BL diameter. Unshaded region, unique environmental variance; shaded region, common environmental variance.

Figures 2-4: Heritability of tooth dimensions (from Dempsey and Townsend 2008).

regularity of sex-based differences encountered in human canines is increasingly utilized within the forensic/legal context that often deals with identification of severely destroyed skeletal remains of individuals due to violent crime or destructive acts of nature making thus the canines “the key tooth for personal identification (Kaushal et al 2004)”.

More recent population-specific odontometric studies confirm the dimorphic expression of canine size in human groups and underlie the need for continuation of data collection, especially in populations with little or no previous dental research such as the sample from the Davis Farm burial sites. Iscan and Kedici (2003) conducted a dental study on the MD dimensions of 100 dental (50 males and 50 females) students from the Universities of Ankara and Istanbul. According to the authors, modern Turkish populations are of particular interest because they represent the cumulative result of increased gene flow into the area from many directions and over a long period of time. Their results showed accuracy in sex determination based on dentition between 66-84% with the MD measurements for canines of both jaws contributing the most significant model with 77% accuracy. Interestingly, and in contrast with Potter et al (1976), Iscan and Kedici (2004) did not detect any significant difference between tooth size of the two jaws and confirmed an increased contribution to sex discrimination by the teeth of the posterior dentition. However, they did not elaborate on whether posterior dentition

shows higher additive or environmental influence leaving that particular aspect of dentition in modern Turks open to further research.

Acharya and Mainali (2008) conducted stepwise discriminant analysis on the BL and MD teeth dimensions of 31 men and 22 women from Nepal and concluded that while the BL dimensions seem to have contributed >77% of the dimorphic difference vs. 64.2% for the MD, the MD dimensions of mandibular canines were the overall most differentiated measurement followed by the MD dimensions of the UP3's.

Significant dimorphism in the dimensions of mandibular canines was also confirmed in a sample of 60 N. Indians (30 males and 30 females) who took part in a study conducted by Kaushal et al (2004). The authors constructed a Mandibular Canine Index given by the ratio of the MD crown width of the mandibular canine defined as the greatest width between contact points with the adjacent teeth)/inter-canine distance defined as the maximum distance between the tips of either side canines of the lower jaw. The mean value of males and females was then used to construct a Standard MCI for the entire population defined as  $[M_m \text{ MCI (SD)} + M_f \text{ MCI (SD)}]/2$ . The Std. MCI has obvious utility in that unidentified individuals with surviving mandibular canines can have their measurements taken and then compared to the Std. MCI to see whether they are likely to belong in the population or not.

NOTE: It is tempting to start thinking about Std. MCI indexes for past populations. But since the Std. MCI is made up of two sample means, the male and female samples from which the means are extracted must be representative of the male and female components of the population. This is rarely the case with skeletal samples found in an archaeological or bioarchaeological context. For example, is the handful of skeletons found at Catal Hayuk in now-days Turkey enough to reconstruct the Std. MCI for the entire estimated population in Late Neolithic Anatolia ca. 7000 BC? Even a statistical novice such as myself knows the answer is a big no. Additionally, one must consider taphonomic and/or cultural bias: would a hypothetical burial of 80 males tell us something about the Std. MCI of the respective population they came from? At the absence of any female data the answer is again no. From the above it seems that Std. MCI indexes are better constructed for modern populations or for populations for whom the male and female samples are ascertained to be representative of total size of said population.

Regardless, Kaushal et al concluded that the MCI is useful in predicting sex in N. Indians by as much as 75%. This is graphically depicted in Figure 5 below: the

Parameters	Sex	Mean	±S.D.	CoefficientofVariation	't' Stat	'p' value	Significance
Inter Canine Distance	Male	25.87	1.25	4.84	2.538	<0.006	HighlySignificant
	Female	25.07	1.19	4.77			
Right Canine Width	Male	7.22	0.28	3.87	7.772	<7.38x10 <sup>-11</sup>	HighlySignificant
	Female	6.69	0.25	3.83			
Left Canine Width	Male	7.29	0.29	4.00	7.621	<1.32x10 <sup>-10</sup>	HighlySignificant
	Female	6.69	0.32	4.83			
Right MCI	Male	0.28	0.01	3.57	9.719	<7.69x10 <sup>-11</sup>	HighlySignificant
	Female	0.26	0.01	3.74			
Left MCI	Male	0.28	0.01	4.61	4.088	<6.76x10 <sup>-5</sup>	HighlySignificant
	Female	0.26	0.19	5.27			

Figure 5: MCI of N. Indians, Kaushal et al (2004)

coefficient of variation is an indication of the statistical significance of the differences between the variables and as we can see it is very high for all measurements taken. Kausal et al concluded that the MD measurement of the mandibular canine exhibited highest percentage of sexual dimorphism of all teeth, 7.954% for the right and 8.891% for the left canine. Additionally, the authors draw parallels with studies conducted earlier on the role of the sex chromosomes on tooth size (Garn et al 1967, Alvesalo 1971) since they too attribute canine size to the possible control of enamel built up (the component most responsible for the final size of the tooth) by the Y-chromosome while dentine is controlled by the X-chromosome.