Cluster analysis of tooth size in subjects with normal occlusion

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Introduction: Tooth-size studies are important in orthodontics. Our aim in this study was to establish normative data on tooth size with a clustering method. Methods: Dental casts of 307 subjects with normal occlusion were examined. In these subjects, the tooth-size data sets in the maxilla and the mandible were clustered for men and women by using multivariate normal mixture models. This analysis clustered the data sets into groups of observations that were cohesive and separate from the other groups. The parameters were estimated with expectation-maximization procedures, and the number of clusters was selected via the Bayesian information criterion. Results: Seven heterogeneous clusters in men and 4 clusters in women were identified. This study indicated that, in normal occlusion, tooth sizes are variable. These heterogeneities in the normal occlusion group seem to have contributed to the variability found in normative data. Conclusions: The method used in this study seems to provide a more substantive design for artificial teeth and add an additional dimension in the process of diagnosis of patients. Further applications seem possible in dental anthropology by simultaneously dealing with the full dentition as a data set. (Am J Orthod Dentofacial Orthop 2007;132:796-800)

Researchers of tooth size have presented normative data with sex differences, and a review of the literature shows variations in tooth sizes between racial groups, with a suggestion of genetic influence. Traditionally, this research has been performed anthropometrically. Additionally, normative data have been used to standardize the information required for artificial tooth fabrication.

In orthodontics, disproportionately sized teeth in either arch can make it difficult to obtain good occlusion; thus, research on normal tooth size is important not only to discriminate a normal vs a malocclusion problem, but also to predict the posttreatment occlusal outcome mathematically. Sometimes, tooth size combined with a skeletal problem has been considered a cause of malocclusion. However, several aspects of malocclusion have previously been explored, such as dental arch dimensions and tooth morphology. Determining whether variation in tooth size arises from the differences between normal data and malocclusion or whether this variation is related to the original distributions has been long argued in dentistry.

The normative data previously reported are expressed with norms and variations for each tooth. However, an assessment of individual variability by using only the mean (standard) data is unreasonable because the data comparison was interpreted as the difference of means between various times for variable numbers; this is only a parallel integration of 1-dimensional individual measurements. Integration of 1 dimension is different from a multivariate, high-dimensional analysis, which can interpret all features of a data set and preserve the characteristics of the individual measurements. In this regard, model-based cluster analysis, introduced in this study, is a methodology from which unexplained variables can be upgraded into distributing specific variables; this is based on unsupervised mathematic function and is free from observer bias. Originally, cluster analysis was used to identify certain groups of observations that are cohesive and separated from other groups. Recently, this relatively new methodology has been applied to new techniques in biotechnology, such as the simultaneous monitoring of gene expression microarray data. In dentistry, a possible application of this methodology could be to classify and evaluate characteristic sets of tooth sizes for the full dentition.
MATERIAL AND METHODS

A total of 307 subjects with normal occlusion were selected from 15,836 young Korean adults through a community dental health survey, from 1997 to 2005, in Seoul, Korea. They included 188 men and 119 women with a mean age of 20.0 years (range, 17-24 years). The selection criteria were as follows: (1) Class I molar and canine relationship with normal occlusal interdigitation, (2) fully erupted permanent dentition except the third molars, (3) normal overjet and overbite (about 2-4 mm), (4) minimal crowding (<2 mm) and spacing (<1 mm), and (5) no history of previous orthodontic or prosthetic treatment. In addition, subjects with proximal caries or fillings that affected a tooth’s mesiodistal size, gross restorations, significant attrition, congenital defects, or deformed teeth were excluded. Absence of tooth anomalies of structure and development was also considered. The subjects were part of the Korean Standard Occlusion Study, which has been ongoing since 1997.14

On the dental stone casts from alginate impressions, tooth sizes were measured with digital Vernier calipers (Mitutoyo; Kawasaki, Kanakawa, Japan) under an illuminated magnifier (Otsuka Optics, Tokyo, Japan) from the central incisors to the second molars (accurate to 0.01 mm). The size of each tooth was defined as the mesiodistal width measured from its mesial contact point to its distal contact point of its greatest distance, as suggested by Moorrees et al.15

Two investigators (B.K.K. and H.Y.C.) made all measurements, and the mean data were used for the analysis. Three months after these measurements, 80 casts were randomly selected and measured twice.

The intraexaminer and interexaminer reliability coefficients were 0.9979 and 0.9963, respectively. In terms of root mean squares, the random errors were less than 0.083 and 0.111 mm, respectively.

Statistical analysis

Tooth sizes in the maxilla and the mandible were described separately for men and women, and comparisons were made between the sexes with 2-sample t tests. All reported P values were based on 2-sided levels of significance. All analyses were performed with software (SAS Institute, Cary, NC).

All tooth sizes in the maxilla and the mandible were clustered based on multivariate normal mixture models in men and women, respectively. To be specific, the density of tooth sizes y, say f(y), is approximated by a multivariate normal mixture distribution

\[ f(y) = \sum_{k=1}^{G} f_k(y|\theta) \]

where \( f_k \) and \( \theta_k = (\mu_k, \Sigma_k) \) are the density and the parameters of the k component in the mixture, and \( \tau_k \) is the probability that an observation belongs to the k component (\( \tau_k \geq 0; \sum_{k=1}^{G} \tau_k = 1 \)).

Here, each mixture component is considered as a cluster, and the membership of an individual is the mixture component that maximizes the probability \( f(y|\theta)/\sum_{k=1}^{G} f_k(y|\theta) \). Given tooth sizes \( y = (y_1, y_2, \ldots, y_n) \), we estimated the parameters of the mixture model, \( \theta \) and \( \tau \), to maximize the likelihood function

\[ L_{MIX}(\theta_1, \ldots, \theta_G; \tau_1, \ldots, \tau_G|y) = \prod_{i=1}^{n} \sum_{k=1}^{G} \tau_k f_k(y|\theta), \]  

by expectation-maximization procedures16 and the number of clusters \( G \) was selected via the Bayesian information criterion, which is the value of the maximized log likelihood with a penalty for the number of parameters in the model, and it allows comparison of models with differing numbers of clusters.17 For details on model-based clustering, refer to Fraley and Raftery.12

Finally, mixture components were confirmed as clusters by the density clustering algorithms for finding local maxima of the estimated multivariate normal mixture density.18,19 The iterative expectation-maximization methods also compute a matrix \( z \) so that \( z_{nk} = f_k(y|\theta)/\sum_{k=1}^{G} f_k(y|\theta) \) is an estimate of the conditional probability that an observation \( y_i \) belongs to cluster \( k \). We, therefore, selected the cluster \( k \) so that it maximizes \( z_{nk} \) for each observation \( y_i \).

RESULTS

The Table gives the descriptive statistics for tooth sizes in men and women with normal occlusion. In men, the mean values in both the maxilla and the mandible were significantly larger than those for women (\( P < .001 \)).

Figures 1 and 2 show the results of the density clustering analysis of tooth size in the maxilla and the mandible, respectively. The number of clusters, \( G \) in equation [1], was determined as 7 in men and 4 in women based on the Bayesian information criterion.

Seven kinds of clusters were selected in men. There were 2 clusters with tooth sizes greater than the mean tooth size, 4 clusters with tooth sizes smaller than the mean tooth size, and 1 cluster that crossed from greater to smaller tooth sizes with the maxillary first premolar as the midpoint. Variation between clusters in the maxilla was small except for the maxillary second molar. On the other hand, cluster variation in the mandible was greater than in
the maxilla including canines, first molars, and second molars (Fig 1).

In women, however, there was less variation in the tooth-size cluster pattern, with only 4 clusters. There was 1 cluster with tooth sizes greater than the mean tooth size, 2 clusters with tooth sizes smaller than the mean tooth size, and 1 cluster that crossed from greater to smaller tooth size. There was great variation in the sizes of the maxillary and mandibular central and lateral incisors between the clusters. For the maxillary first premolar, there was little variation in the mean value for all clusters (Fig 2).

**DISCUSSION**

In dentistry, “normal value” is of the utmost importance as a standard for diagnosis, treatment planning, and posttreatment evaluation. However, to interpret certain variations in what we call normal, a unit of scatter, such as standard deviation, is introduced simultaneously with the normal value. The concept of variation compels us to think of it as existing outside the normal signal. But there are always considerable standard deviations in a set of normative data for tooth sizes. However, this variation can be a diversely mixed signal, which we cannot detect as a real signal but only as noise. In this respect, individual variation is not always variation from what we call normal; it might be simply a variation of normal range, for which we have no ready explanation. Again, variance and standard deviation are not really errors; they are simply variations that we cannot explain. The more explanatory variables that are introduced—to the extent that they really do explain variance—the smaller the unexplained error, or variance, will be. The starting point of this study was the hypothesis that we can find a specific signal from complicated noises and that unexplained signals can be interpreted by mathematic modeling that is composed of multivariate and high-dimensional structures. The use of this method has become much easier now because of enormous developments in computer science. The results of this study discriminated some heterogeneous data sets in the normal occlusion group, and this could explain the variance in the normative data.

Although an explanation of tooth-size diversity has been attempted with a coefficient of variation for each tooth, the diversity of tooth sizes can be interpreted better with the tooth-size interrelationship (communality) that is shown by correlation matrices. The mean correlation coefficient of tooth-size communality has been reported to range from 0.43 to 0.60.

The results of this study in Table 1 and 2 show that most clusters had a relatively uniform tendency to have larger or smaller teeth than the mean tooth size; this can be explained by tooth-size communalities. On the other hand, the cluster that crosses from greater to smaller tooth sizes could be explained by the relatively low communalities that reached, at best 0.36, in squared terms; this could not be fully explained by tooth-size communality.

Sexual dimorphism in tooth size is well known, particularly in the canines. The results of this study, shown in the Table, agree with previously reported results of sexual dimorphism. The sexual dimorphism of these Korean subjects was similar to that of subjects of northwestern European ancestry.

<table>
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<tr>
<th>Jaw</th>
<th>Tooth</th>
<th>Mean</th>
<th>SD</th>
<th>Range</th>
<th>Mean</th>
<th>SD</th>
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*Significant sex differences in tooth sizes (P < .001).
women. The diversity of the clusters number in men can be partially explained by the sexual dimorphism of tooth-size communality. Sisters are known to be more alike than brothers in developmental timing, and intra-individual tooth-size correlations are consistently higher in sisters. These findings suggest an X-linked inheritance of tooth size. However, the sexual dimorphism in canine size partially suggested Y-chromosome involvement. Although the larger tooth-sized cluster in women had similar tooth sizes when compared with the smaller tooth-size cluster in men, canine size in women was explicitly smaller than in men (data not shown). This study and previous investigations all suggest both genetic and environmental control of tooth sizes. In men, developmental timing is more extended than in women; this increases the opportunity to be influenced by environmental factors, which in turn can increase the diversity of later developing teeth—e.g., the second molars. The second molar was previously reported to have the highest correlation coefficient with body size. In Figure 1, the second molar in men showed the most variability in tooth size, and this phenomenon contributed to the greater number of clusters in men.

The normative data sets obtained from this study have several advantages when compared with data usually expressed as means and standard deviations. First, a data set that is much closer to the true values can be obtained. This is because no person exists in reality with tooth sizes that exactly correspond to the mean values. Similarly, for example, it is difficult to find a person with teeth larger or smaller than 1 SD. Therefore, it is possible to obtain a more variable tooth-size data set for artificial tooth fabrication that is
much closer to reality. However, because of the limitations of this study, further studies are required to find the tooth-size data sets best suited for each facial and arch form. In addition, in reporting the inherent heterogeneity in subjects with normal occlusion, we propose that arch and facial skeletal forms, rather than tooth size, play greater roles in causing malocclusion.

Second, the methodology also conforms better to other studies—eg, racial comparisons. In contrast to previous studies in which data from each tooth were integrated, we found several representative clusters that express the characteristics of individual teeth simultaneously. By comparing the patterns and numbers of clusters, the differences in characteristics associated with tooth size in a population can be studied.

Third, the final occlusion after orthodontic treatment is planned during the initial diagnosis and treatment planning by using, for example, the Bolton tooth analysis. When the ratio is high, it can mean that the maxillary tooth sizes are small, but it can also imply that the mandibular teeth are small. If, through this study, in which actual tooth sizes were studied clinically, we can group patients into the most suitable clusters, wouldn’t it mean that we can make a better choice regarding for each patient? Similarly, by detecting the type of a tooth-size cluster when only a few teeth have erupted, wouldn’t it be easier to predict the size of unerupted teeth than using a preexisting mixed-teeth have erupted, wouldn’t it be easier to predict the type of a tooth-size cluster when only a few

CONCLUSIONS

The tooth-size data sets were clustered via multivariate normal mixture models, and 7 heterogeneous clusters in men and 4 clusters in women were identified. Thus, our findings in this biometric study discriminated a wide range of normal variations in tooth sizes in subjects with normal occlusion. These heterogeneities seem to have contributed to the variability of normative data, with various implications. For example, the various tooth-size data sets in normal occlusion could add an additional dimension in the process of diagnosis of a patient, and they might be taken as basic information for artificial-tooth fabrication. Although this study was made in a Korean population, which is a single ethnic group, the classification methodology that was attempted could be expanded to other ethnic groups.

REFERENCES


