Inheritance of Craniofacial Morphology

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INTRODUCTION

In order to make an accurate diagnosis and growth prediction the orthodontist should consider the role that genetics has played in determining the facial morphology of his patient. However, the study of the presence and significance of genetic variation in the craniofacial complex has been from a limited approach. One of the major problems which has delayed progress in the investigation of the influence of heredity is the complex nature of multifactorial inheritance. It is generally accepted that virtually all of the dentofacial characteristics that are of interest to the orthodontist are polygenic and continuously variable. Furthermore, in studying traits that are the result of polygenic inheritance it is necessary to ascertain variability.

Traditional types of cephalometric analyses, utilizing line and angle constructs and dimensions, offer quantitative information of limited value to heritability studies. Since, for example, they cross several anatomic structures and growth sites and each dimension may be influenced by changes in any or all of the structures, the conclusions from this approach must be accepted with some caution. As stated by Margolis,[29] "A small area of the skull surface may be under pure genetic control or pure environmental control or a combination of both, but unless a small area is considered, multiple, and possibly independent mechanisms may be operating, which may nullify each other and therefore make recognition or study impossible."

Several investigators[23,29] have suggested that the morphologic aspects of single bones or bone segments, as expressed by their contours traced from cephalograms, may be the best indicator of the genetic control in the craniofacial complex. While this seems a sensible approach, their results are, as yet, based on subjective and qualitative analyses.

It is the purpose of this investigation to attempt to assess genetic control in the craniofacial complex by means of rigorous quantitative analysis of bony contours. This study is limited to one craniofacial component, the mandible, as seen in lateral and posterior-anterior cephalograms of identical and fraternal twins. Hopefully, the identification of anatomic units under significant genetic influence will enable clinical orthodontists to better evaluate growth potentials by means of sibling and parent comparisons.

REVIEW OF THE LITERATURE

Orthodontic Literature

An inspection of the orthodontic literature reveals a consistent yet conservative interest in the inheritance of craniofacial morphology and/or malocclusion. Goldberg[12] reported on a study of fifteen pairs of identical twins and concluded that arch form is inherited.

The first attempt to study the heredity of malocclusion is usually credited to Iwagaki[19] (1938). He analyzed over two thousand Japanese family pedigrees to ascertain the incidence and gene frequency of mandibular prognathism. He observed that this trait was familial, although his calculations and conclusions are difficult to substantiate.

Rubbrect[40] studied prognathism in six family pedigrees and concluded that the inheritance was irregularly dominant.

Johnson,[21] in a study of skull form and dental occlusion in dogs, concluded that genetic influences condition the environmental effects on facial growth.

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Hughes and Moore[16] were among the earliest investigators to subscribe to a multiple gene concept of inheritance in the craniofacial complex. They observed that craniofacial growth and morphology is under strong hereditary control and expressed this concept in percentages of heritability between parents and siblings. The mandible and maxilla were observed to be independent. Further, in the mandible, they observed that ". . . the ramus, body, angle, alveolus and teeth are not too dependent on each other," since these features are multiple factor traits.

Wylie[50] was the first to quantify the inheritance of craniofacial features by means of measurements on cephalograms. He studied cephalograms of fifteen families, thirteen of which included like-sexed twins. While none of his lines and angles showed significant genetic variation, his study introduced quantitative techniques that were the basis for many of the later investigations.

Snodgrasse[42] concluded from his family-line study that familial records enable the orthodontist to anticipate difficulty in treatment and the prognosis for success. Lundstrom[26,27] studied fifty pairs of identical and fifty pairs of fraternal twins using measurements similar to Wylie's. By charting his results on histograms he illustrated the effect of inheritance on variability.

Stein, Kelly, and Wood[43] limited their cephalometric study of families to angular measurements only. The resulting correlation coefficients showed greater significance between sibling pairs than between parent-sibling combinations.

Horowitz, Osborne, and De George[15] studied fraternal and identical adult twin pairs using linear measurements on lateral cephalograms. An analysis of variance showed that highly significant hereditary variations occur in anterior cranial base, mandibular body length, total face height and lower face height.

Hunter[18] evaluated the conclusions of Horowitz, et al. His use of twenty-six linear measurements on lateral cephalograms of seventy-two like-sexed twins showed the strongest genetic component of variability for height measurements rather than for measurements of depth. Harris[14] recommended that any study of genetic variation using lines and angles requires the use of multivariate analysis in order to identify significant relationships.

Meanwhile, Curtner[6] showed the value of superimposed head films for predetermining adult faces in children by superimposing on their parents. Kraus, Wise, and Frei[23] criticized the use of line and angle constructs and facial polygons to study heredity. In their study of six sets of like-sexed triplets, superimposition of bony profiles offered the most valuable information as to genetic control of craniofacial morphology. The superimposed profiles were scored visually and subjectively for concordance or discordance and percentages calculated.

Moorrees[30] divided cephalometric tracings into a series of horizontal and vertical planes and superimposed them to note familial patterns in facial proportional relationships. Margolis,[29] in a study of sixty-eight families, divided the bony profile of the mandible and maxilla as seen in lateral cephalograms into segments, noted concordance and discordance of each segment, and then analyzed these results using the Chi-square test.

In general, several methods of investigation of the inheritance of the craniofacial complex have been identified. Early investigators (Goldberg, Iwagaki, Rubbrect, and Johnson) used little or no statistics and tried to interpret their findings in terms of simple Mendelian genetics. Wylie, Snodgrasse, Stein, Horo-

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witz, et al. used cephalometric measurements to quantify variation. Curtner, Kraus, Moorrees, and Margolis suggested morphologic superimposition.

Noyes[35] best summarized the criticism of cephalometric measurements when he declared that one ". . . can't expect an angle or plane composed of several structural units to show a high familial pattern since no genes are responsible solely for the structural units that determine these lines."

In a discussion of the work of Kraus et al., Goodman[13] observed that, "The scoring of the presence or absence of line coincidences is subjective and not readily quantifiable." Goodman also states, "Any suggestion that certain traits are regulated primarily by genetic factors are based on tenuous ground and could be profitably reexamined using newer methods."

Osborne and De George[36] had previously stated that, "Polygenic variation constitutes the greater part of genetic variation in man. The more complex the genetic and nongenetic component of variability, the more intricate become the methods of analysis."

It is on the premise that a "new method," a "quantifiable method," a "more intricate method" is needed to study the heritability of craniofacial morphology that the techniques of this investigation are based.

Environment versus Heredity

The role of genetic or hereditary factors and environmental or functional factors in determining the normal adult size and form of the face is one of the most controversial problems in orthodontics. The importance of function has been emphasized by Baker,[1,2] Landsberger,[25] Wallace,[45] Rogers,[39] Thoma[44] and many others. Much experimental evidence supports the importance of muscular action in determining the size and shape of a bone. Washburn[46] removed the temporal muscle from newborn rats and found after a few months that the coronoid process had completely disappeared. Watt and Williams[47] fed rats a rough diet requiring extra mastication and produced heavier and thicker mandibles. Wolffson[49] reduced the size of the rat scapula by removing scapular muscles. However, these experiments and others demonstrate the effect of abnormal physical stresses on growing and already developed bones. They do not clarify the role of normal stresses in normal development. The statement by Weinmann and Sicher[48] that ". . . the final shaping of the masticatory skeleton is to a great extent dependent upon muscular influences, dentition, and the growth of the tongue" is a commonly held view with little irrefutable evidence to support it.

Proponents of the hypothesis that heredity is the primary determinant of the form and size of the jaws include Jansen,[20] Brash,[4] MacMillan[28] and Brodie.[5] Murray[33] showed that the general form of the cartilaginous skeleton in higher vertebrates is determined by factors inherent in the rudiment. In addition, the capacity for self-differentiation possessed by skeletal rudiments when isolated in culture has been clearly demonstrated by Fell,[9] and Fell and Conti.[10] Murray also indicated that special mechanical conditions are not necessary for the differentiation or the continued activity of osteoblasts or for the initiation and continuation of osteogenesis. Sissone[41] states, "Under normal circumstances intrinsic factors are of overwhelming importance in determining the form of bones. The motive power is inherent in the tissue which, given a normal environment, will develop according to a genetic template."

Then again, whenever differences of opinion arise, certain individuals will choose a compromise course such as that stated by Baume,[3] "The course of any osteogenesis during foetal life lies in

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heredity and during functional life in the functional muscular influence. During the time of growth, heredity and function overlap in their task as bone producing and bone forming elements."

The investigation of any anatomic model, when studied in convenient subsets, might provide the researcher with the specificity of information needed to reconcile this controversy.

Sample

The sample used in this study consisted of lateral and posterior-anterior cephalograms of seventy pairs of like-sexed twins, where one half were diagnosed as monozygotic (MZ) and one half as dizygotic (DZ). Zygosity was determined serologically on the basis of ABO, MN, Rh, Kell, Duffy, and secretor reactions. In addition, comparisons of the iris of the eye, the color and type of hair, finger and palm prints, and dental morphology were used to corroborate the serological classification.

Even with the most thorough of regimes, some errors in zygosity determination are inevitable. However, as Goodman[13] has pointed out, the mistake of classifying identical twins as fraternal, or the converse, if random with respect to the variable of interest, would minimize the probability of detecting differences, and any findings that were significant must therefore exist despite the classification techniques and not because of them.

The thirty-five MZ twins included fifteen female and twenty male pairs. The DZ twins consisted of twenty-two female and thirteen male pairs. The ages of the twins ranged from 11.8 years to 21.1 years, with a mean age for females of 16.5 years, and a mean for males of 16.3 years.

Method

Cephalometric Procedure

All cephalograms used in this study were taken with a rotating anode x-ray source and Thurow cephalostat. The source-film distance was 5 feet and the midsagittal plane to film distance was 7.5 inches.

The tracings were drawn on frosted acetate and, where double images of bone contours appeared on the lateral cephalograms, only the *left* side was traced. Complete tracings were made of the lateral headplates, while only the mandible was traced from the P-A cephalograms.

The tracings of the mandibular profiles were divided into separate curved segments by the construction of a baseline for each segment. The following cephalometric landmarks were used as defined by Krogman and Sassouni:[24] Articulare (Ar), Menton (Me), Pogonion (Pog), and Infradentale (Id). The following contours may be identified, with their baselines drawn between the starting and end-points of the curve (Figs. 1 and 2):

Lateral Cephalogram

1. Posterior border of ramus — from articulare to a point where a tangent constructed through articulare contacts the posterior border of the ramus (ramal plane).
2. Gonial angle — from the tangential point of the ramal plane to the tangential point of a line drawn through menton tangent to the lower border of the mandible (mandibular plane).
3. Lower border of mandible — from the tangential point of the mandibular plane to menton. This curve is further divided into an antegonial notch and a subsymphyseal contour.
4. Labial contour of symphysis — from x-point to menton, where x-point is taken as the most posterior point on the anterior symphysis from a line drawn between infradentale and pogonion.
5. Lingual contour of symphysis—from y-point to menton, where y-point is taken as that point where a line through x-point, parallel to the

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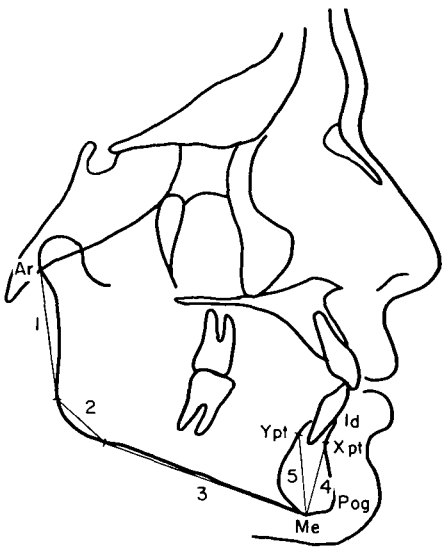

Fig. 1 Demarcation of mandibular contours - lateral cephalogram.

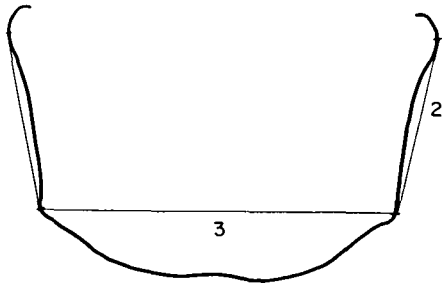

Fig. 2 Demarcation of mandibular contours - P-A cephalogram.

mandibular plane, crosses the posterior symphyseal contour.

P-A Cephalogram

1. Lateral border of right ramus—from the most lateral point on the contour of the right condyle to the point where a tangent through the condyle point contacts the gonial angle.
2. Lateral border of left ramus—from the most lateral point on the contour of the left condyle to the point where a tangent through the condyle point contacts the gonial angle.
3. Frontal curvature of mandible — from the gonial tangential point on the right to the gonial tangential point on the left.

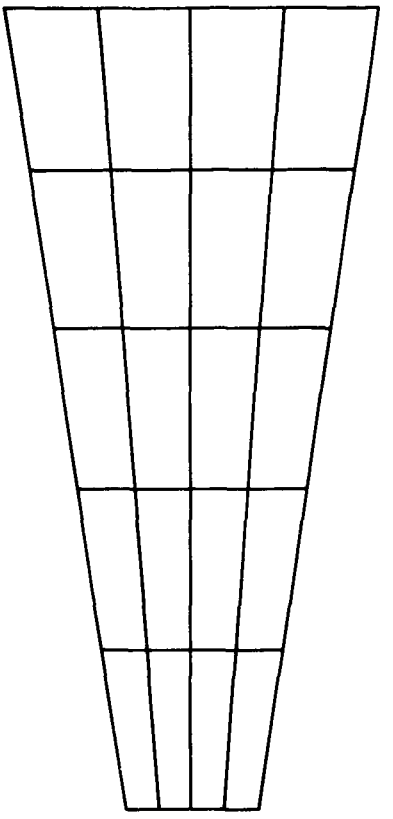

Fig. 3 Portion of template used to divide each contour into equal parts.

Digitization

After partitioning, each contour, except the gonial angle, was divided into eight equal parts by means of a template (Fig. 3). The baseline of each contour was superimposed on, or parallel to, one of the horizontal lines such that the end-points of the curve were located on the outermost vertical lines. The inner vertical lines then divided the curve into halves, quarters, etc., and marks were made on the curve at the points of intersection. Because of its size, the gonial angle contour was only divided into four equal parts (Fig. 4). The lower border of the mandible was further divided into an antegonial notch and a subsymphyseal contour by arbitrarily designating the first three divisions of the curve as representing the

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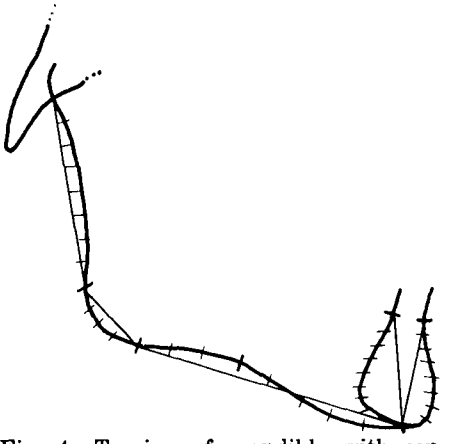

Fig. 4 Tracing of mandible with contours divided and ready for digitization.

area of the antegonial notch, while the last five points on the curve delineate the contour below the symphysis.

The X and Y coordinates of each point on each curve were recorded by means of a D-MAC DIGITIZER. This machine reads the coordinates of each point to the nearest tenth of a millimeter, and these data are recorded on cards through a direct linkage to a card punch. Each curve was positioned on the digitizer so that the starting points were identical and the baselines superimposed (end-points of each curve always had the same Y-coordinate).

Statistical Procedure

The data, in the form of X and Y coordinates for each point on each of the nine segments and punched on IBM cards, were inspected by special programs prepared for the 360-67 IBM computer.

The over-all design was to compare intrapair differences in the MZ sample with intrapair differences in the DZ sample. Basically, two methods were used to measure and compare differences in morphology:

1. The vector of differences, di, between twins j and k at the i*th* coordinate pair is given by the Euclidean measure:

$$di = \sqrt{(Xij - Xik)^2 + (Yij - Yik)^2}$$

The application of this mathematical procedure for each comparable point on the comparable curve of each twin pair produces a set of numbers showing the intrapair vectors of differences. Comparison of MZ and DZ mean intrapair differences was performed using a *Multivariate Analysis of Variance.*[38] This program is especially useful because it permits the investigator to perform univariate or multivariate analyses of variance or covariance with the freedom to specify any combination of dependent variables and covariates.

This procedure was carried out twice, once on the original data, and once on a new set of coordinate points created by making each curve pair the same size and measuring and testing only differences in shape. The method used to factor out size differences in each pair of curves was to multiply each coordinate of each point on the second curve by the factor

$$\frac{Xn_1}{Xn_2},$$

where Xn_1 is the X-coordinate of the last point on curve 1 and Xn_2 is the X-coordinate of the last point on curve 2. This changes the location of each point on the second curve so as to maintain its original shape while making the X-coordinates the same as the comparable points on the first curve. The second twin of each pair, as determined by alphabetical order of their first names, was consistently the observation to be changed. This meant that some curves were expanded and some were contracted among the nine curves that described the mandible within one individual to match the size of the curves of the co-twin.

2. The *difference in area* between each pair of curves, after size differ-

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TABLE I

MULTIVARIATE ANALYSIS OF VARIANCE
COMPARISON OF MEAN INTRAPAIR MZ AND DZ VECTORS OF DIFFERENCES (ORIGINAL DATA)

Contour	U-Statistic	D.F.			Approximate F-Statistic	D.F.	
1. Posterior border of ramus	0.7709	8	1	68	2.2655*	8	61
2. Gonial angle	0.9469	4	1	68	0.9116	4	65
3. Antegonial notch	0.9061	3	1	68	2.2792	3	66
4. Sub-symphyseal	0.8365	5	1	68	2.5019*	5	64
5. Labial symphysis	0.8927	8	1	68	0.9163	8	61
6. Lingual symphysis	0.7684	8	1	68	2.2985*	8	61
7. Lateral border of ramus (right)	0.7796	8	1	68	2.1554*	8	61
8. Lateral border of ramus (left)	0.8402	8	1	68	1.4507	8	61
9. Frontal curvature of mandible	0.5983	8	1	68	5.1192**	8	61

* Significant at .05 level.
** Significant at .01 level.

ences were eliminated, was then calculated by a method of numerical integration. According to *Simpson's Rule*:

$$A = \frac{\triangle}{3}(Y_1 + 4Y_2 + 2Y_3 + 4Y_4 + \ldots Yn),$$

where A = area, $\triangle$ = the increment between points as measured along the baseline, and Y is the Y-coordinate of each point plotted on the curve. Since the X-coordinates of each pair of points on the two curves were the same, this formula was used with each Y value in the equation representing the difference in Y-coordinates between comparable points on the curves. The area A, therefore, was a measure of the residual area between the two curves when the first and last points were superimposed.

Comparison of MZ and DZ intrapair differences for area was examined by means of an *Analysis of Variance* (F-test) to test the hypothesis: Ho: $u_1 = u_2$.

Findings

The results of the multivariate analysis of variance on the vectors of differences before size differences were removed are shown in Table I. The same test, with size differences removed, is shown in Table II. The multivariate analysis of variance program prints a U-statistic together with three parameters labeled degrees for freedom for each contour. This statistic can be used to test the hypothesis that the model parameters for a given contour is zero. Since the distribution for U-statistics are not readily available, an approximate F-statistic is computed to test the same hypothesis. The U-statistic test performs the same function as the F-test of the univariate analysis.

It should be noted that the within group variation for nonsignificant variables was comparable to that of the significant measurements. The multivariate analysis after size differences were removed resulted in the deletion of the posterior border of the ramus as a significant contour, and the addition

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TABLE II

MULTIVARIATE ANALYSIS OF VARIANCE
COMPARISON OF MEAN INTRAPAIR MZ AND DZ VECTORS OF DIFFERENCES (SIZE DIFFERENCES REMOVED)

Contour	U-Statistic	D.F.	Approximate F-Statistic	D.F.
1. Posterior border of ramus	0.8154	7 1 68	2.0055	7 62
2. Gonial angle	0.9818	3 1 68	0.4070	3 66
3. Antegonial notch	0.9650	3 1 68	0.7973	3 66
4. Sub-symphyseal	0.8564	4 1 68	2.7254*	4 65
5. Labial symphysis	0.7173	7 1 68	3.4903**	7 62
6. Lingual symphysis	0.7662	7 1 68	2.7020*	7 62
7. Lateral border of ramus (right)	0.7919	7 1 68	2.3273*	7 62
8. Lateral border of ramus (left)	0.7357	7 1 68	3.1818**	7 62
9. Frontal curvature of mandible	0.7582	7 1 68	2.8250*	7 62

* Significant at .05 level.
** Significant at .01 level.

of the labial symphysis and the lateral border of the left ramus. Those contours showing significant differences between MZ and DZ samples, both before and after size was removed, included the subsymphyseal contour, lingual symphysis, lateral border of the right ramus, and the frontal curvature of the mandible.

The mean intrapair differences in area and the corresponding analysis of variance for each contour is shown in Table III. This test was used only on curve pairs with size differences removed. Those contours which showed a significant difference between MZ and DZ intrapair comparisons included the posterior border of the ramus, lingual symphysis, right and left lateral borders of the ramus, and frontal curvature of the mandible.

Discussion

The purpose of this study was to quantify measurable qualitative traits and to ascertain to what extent the variability of these traits is genetically determined. By confining the measurement of morphology to definable anatomic units or subsets, one would hope to have an opportunity for greater insight into the inheritance of morphologic variation.

In this investigation the definition of an anatomic unit was based on geometrical constructions with the partitioning of contours occurring at areas of curve inflection. If one were to assume that a change in curvature of a bone profile from concave to convex or vice versa is the result of corresponding changes in the local cellular processes of bone deposition and resorption, then there exists a biological as well as a geometrical, and hence mathematical, basis for the method of division of the bony contours.

According to Enlow,[8] the mandible represents many localized growth sites; these include the posterior border of the ramus and its buccal and lingual surfaces, the gonial angle, antegonial region, mandibular body and the chin. Therefore, the division of a given bone,

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TABLE III

INTRAPAIR DIFFERENCES IN AREA AND ANALYSIS OF VARIANCE (F-TEST)

Contour	(N = 35) Mean Intrapair Difference MZ	S.D.	(N = 35) Mean Intrapair Difference DZ	S.D.	F-Ratio
1. Posterior border of ramus	15.69	(8.66)	25.23	(17.27)	8.53**
2. Gonial angle	18.74	(16.32)	17.97	(19.67)	0.03
3. Antegonial notch	8.46	(5.57)	7.51	(6.19)	0.46
4. Sub-symphyseal	31.93	(21.63)	37.35	(25.83)	0.91
5. Labial symphysis	11.10	(8.51)	13.46	(6.37)	1.72
6. Lingual symphysis	19.34	(10.38)	34.89	(20.72)	15.75**
7. Lateral border of ramus (right)	30.72	(18.24)	43.53	(21.34)	7.29**
8. Lateral border of ramus (left)	28.72	(16.15)	46.59	(23.95)	13.40**
9. Frontal curvature of mandible	360.12	(272.89)	508.82	(365.42)	3.72*

* Significant at .05 level.
** Significant at .01 level.

i.e., the mandible, into subsets, although defined mathematically, may bring the investigator closer to a biologic model whereby discrete control of individual sites of growth is ascertainable.

The use of a twin study is the traditional and appropriate method to examine the inheritance of morphologic variation. With reference to the twin study method, Osborne and De George[36] have stated, ". . . this method constitutes the most efficient approach for appraising the heredity-environment problem in man, particularly with respect to complex or multifactorial inheritance." Twins derived from a single ovum (MZ) have identical genetic endowments or a coefficient of genetic relationship of 1.0. Double ova twins (DZ) have the same genetic similarity as ordinary full siblings with an average coefficient of genetic relationship of 0.5. Twin studies are based on the idea that MZ twin differences are due to environmental influences alone, while DZ twin differences are due to heredity as well as environment. Ideally, comparison of MZ and DZ intrapair differences should demonstrate whether or not the measurements employed define a measurable genetic component of variability in the twin sample studied. It is usually assumed that environmental variables are distributed at random and act equally on the two kinds of twins. There are, however, certain biases that have been recognized in twin studies.

Gates[11] says there is a possibility of a third type of twin in which the ovum divides before fertilization and each part is fertilized by a different sperm. Such twins are maternally monozygotic and paternally dizygotic.

Newman, Freeman, and Holzinger[34] believe that differences in blood supply due to unequal blood exchange between foetuses sharing a common placenta often cause MZ twins to differ more in size than do DZ twins. On the other hand, Price[37] states that fraternal twins may experience intrauterine vascular anastomoses due to placental fusion and thereby increase concordance.

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It appears that most biases or errors entering into twin studies tend to make it more difficult to identify differences. However, as long as these errors are randomly distributed between the MZ and DZ samples, statistical inferences may be made with validity.

The findings of this study would seem to indicate that whether heredity or function is the primary determinant of the form and size of the masticatory skeleton depends on what part of that skeleton is under consideration.

The gonial angle and the antegonial notch, contours #2 and #3, are the only areas to show no significance in any test between MZ and DZ mean intrapair differences. This may indicate that functional mechanisms, i.e., environmental factors, have had more influence in these areas than inherited factors. Indeed, both the masseter and internal pterygoid muscles insert in the area of the gonial angle. Possibly even more important, the gonial angle and antegonial notch profiles have been reported to be dependent on the strength of mastication during childhood (Keen[22]) as well as on the amount of tooth wear (Murphy[32]).

Contours No. 6, No. 7, and No. 9, the lingual symphysis, lateral border of the right ramus, and frontal curvature of the mandible (P-A view) are the only variables with significant values in all tests. These profiles, therefore, give evidence for the predominant effect of genetic control. It is interesting that the first two of these contours are sites of muscle insertion, the masseter muscle inserting on the lateral surface of the ramus, while tongue and hyoid muscles attach to the lingual symphysis. This would tend to indicate that the presence of a muscular attachment on a bone surface does not necessarily interfere with the mechanism of genetic control of the morphology of that surface.

The lateral border of the left ramus, contour #8, should probably be included with those contours showing a dominance of genetic control. Only the multivariate analysis before size was factored out did not show highly significant values for this area. It should be pointed out at this time that the removal of size as a factor was for the purpose of eliminating size differences between fraternal twins (and between identical twins according to Newman, Freeman and Holzinger) as well as for the purpose of eliminating the distortion in length of vertical profiles on P-A cephalograms due to small variations in head positioning. Apparently this last factor did have enough effect on the original data for contour #8 to mask significant findings until the size differences due to distortion were eliminated.

The remaining contours, 1, 4 and 5, show a random distribution of significant values with the resultant impression that genetic and environmental factors are interacting without either dominating. The posterior border of the ramus, contour #1, is an area of attachment for both the internal pterygoid and masseter muscles and its vertical dimension is influenced by condylar growth. The subsymphyseal contour may have a functional component due to the attachment of the platysma and digastric muscles. It has also been described as undergoing functional morphologic changes during the transition from sucking to chewing (Murphy[31]). The labial symphysis, contour #5, is void of muscular attachment. However, it has been asserted that the chin is a function of speech, tongue musculature, facial musculature, or even masticatory musculature. DuBrul and Sicher[7] claim that, "The laying down of the 'chin button' bone is a result of the external pterygoids pulling medially and loading the jaw especially heavily in forceful chewing closure."

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The results of this study seem to show, as Baume has stated, there is an overlap in effect between genetic and environmental factors with certain areas showing a dominance of one factor over the other. Significant values for comparisons of MZ and DZ intrapair differences for bony contours under direct influence of muscle pull may indicate that the response of bone to functional demands is itself under genetic control.

Clinical Inferences

It is routine practice in many orthodontic offices to examine, if only cursorily, the parents and siblings of the patient for the purpose of aiding in diagnosis and treatment planning.

Some authors have observed that certain types of malocclusion seem to predominate within a particular family group. Nevertheless, more recent investigators, aware of the polygenic nature of inheritance of dentofacial traits as well as the multifactorial etiology of malocclusion, have stressed a cautious approach to parent and sibling comparisons.

The variation between related individuals is often of such magnitude to limit any meaningful clinical applications. However, if certain areas within the craniofacial complex are shown to be predominantly genetically controlled (such as the ramal and symphyseal areas in this study), comparisons of these features within a family begin to provide a realistic basis for patient evaluation.

It is suggested that the assessment of growth potential, requiring higher correlation coefficients than are normally found in sibling comparisons, might be made with greater confidence if limited to those dentofacial characteristics under prevailing hereditary influence.

This study does not represent a refinement of cephalometric techniques, but rather a new approach to the investigation of the inheritance of the craniofacial complex.

Specifically, this paper would suggest that the cephalometric approach based on other than "small" anatomic units cannot be further refined or interpreted. It is not the number of measurements or variables that determine biologic relevance, but the nature of the measurement itself. The advantage of the method presented in this study is the quantification of morphologic units and their relatively small size. The investigation of these units, as though they were independent, permits the study of the morphology of any anatomic structure in a series of orderly, unbiased observations. The observation of the mandible or any other morphologic component will result in the optimal opportunity to denote specific variance and/or all the accumulative variation over a given area. This approach yields a new opportunity to interpret genetic effects on craniofacial variability and thus all of its clinical applications.

Summary and Conclusions

The purpose of this investigation was to determine to what extent the variability of bone morphology is genetically determined. The data consisted of thirty-five pairs of MZ and thirty-five pairs of DZ like-sexed twins. Tracings of the mandible, as seen on lateral and posterior-anterior cephalograms, were divided into nine separate contours and quantified using an X-Y digitizer. The method of statistical testing included multivariate and univariate analysis of variance of vector and area differences between curve pairs.

From the findings the following conclusions are drawn:

1. Analysis of small unit areas, representing local growth sites, reveals different modes of control within the same bone.
2. The variability of the lingual sym-

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physis, lateral surface of the ramus, and frontal curvature of the mandible is predominantly genetically determined.

3. The variability of the gonial angle and the antegonial notch areas is predominantly environmentally determined.
4. The posterior border of the ramus, subsymphyseal contour, and labial symphysis are controlled by a combination of genetic and environmental factors.
5. The response of bone to functional demands may itself be under genetic control.
6. Clinical applications of family comparisons should be most reliable if limited to those areas within the craniofacial complex identified to be under genetic control.

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