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Original Article

Cephalometric Variability Among Siblings: A Pilot Study

Katharine L. Marcks, Yihong Zhao, Melih Motro, Leslie A. Will

Department of Orthodontics and Dentofacial Orthopedics, Boston University Henry M. Goldman School of Dental Medicine, Boston, MA, USA

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Main Points

- Families with at least 4 postpubertal siblings were examined cephalometrically to see if a clinically meaningful family resemblance could be identified.
- Cephalometric measurements that could indicate the need for different treatment plans were included.
- The majority of families demonstrated similarities in their cephalometric measurements.
- These measurements, however, while not statistically different had a large enough range that orthodontic treatment planning might differ for the siblings.
- Cephalometric measurements from one sibling cannot reliably be used to predict the cephalometric measurements of another sibling.

ABSTRACT

Objective: To determine whether multiple siblings resemble one another in their craniofacial characteristics as measured on cephalometric radiographs.

Methods: This study was conducted retrospectively using the Forsyth Moorrees twin sample. A total of 32 families were included, each with ≥4 postpubertal siblings, totaling 142 subjects. Only 1 monozygotic twin was included per family. Headfilms were digitized, skeletal landmarks were located, and 6 parameters that indicated sagittal jaw relationships and vertical status were measured. Diverse statistical approaches were used. Dixon's Q-test detected outliers in a family for a given parameter. Manhattan Distance quantified similarity among siblings per parameter. Scatter plots visually displayed subject's measure relative to the mean and standard deviation of each parameter to assess the clinical relevance of the differences.

Results: A total of 11 families (34.4%) had no outliers on any parameter, 13 families (40.6%) had outliers on 1 parameter, and 8 families (25%) had outliers on ≥2 parameters. We identified 29 individuals with at least 1 outlying measure (20.4%). Among these, only 2 individuals (1.4%) were significantly different from their siblings for more than 1 measurement. Although the majority of the families did not demonstrate any statistical outlier, the ranges of the measurements were clinically relevant as they might suggest different treatment. For example, the mean range of SNB (Sella-Nasion-B point) angles was 7.23°, and the mean range of MPA was 9.42°.

Conclusion: Although families are generally not dissimilar in their craniofacial characteristics, measurements from siblings cannot be used to predict the measurements of another sibling in a clinically meaningful way.

Keywords: Sibling relations, facial bones, growth, craniofacial, cephalometry

INTRODUCTION

Orthodontic diagnosis and treatment planning in adolescent patients requires an assessment of the individual's growth potential. Skeletal maturity indices utilizing hand-wrist x-rays or lateral cephalograms provide valuable information regarding the timing of the pubertal growth spurt, and population norms have historically been used as a template against which to compare an individual's growth pattern. As Harris discussed in a 1976 editorial, the usefulness of these averages as a growth prediction reference "clearly depends upon the suitability of the population used in constructing the standards as a reference group."[1] The family unit has subsequently

Corresponding author: Leslie A. Will, e-mail: willla@bu.edu

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been proposed as an appropriate and personalized benchmark by which to measure a patient's growth potential. One study[2] indicated high parent-offspring heritability of maxillofacial variables in both sagittal and vertical dimensions, which corroborates earlier findings by numerous authors[3,4] and has since been confirmed by additional studies[5] on parents and their offspring.

Despite sharing approximately half of their genes, siblings raised together often resemble each other more than statistically expected by genetics, likely due to a shared parental environment, nutritional access, illness exposure, and/or socioeconomic status, among other potential similarities. This has been described in terms of "canalizing selection" wherein potentially disparate genotypes are funneled toward similar phenotypes by the epigenetic landscape.[6] Furthermore, one study demonstrated that half-sibling groups of rodents resembled each other more with age, suggesting a temporal component to both genetic and epigenetic contributions.[7] This has been confirmed in human studies where parental-offspring craniofacial correlations show increases of 72% as children progress to skeletal maturity.[8]

Past studies have shed some light on phenotypic variability among the craniofacial measurements of siblings. A longitudinal study by Harris and Johnson[9] evaluated craniofacial and occlusal variability in 30 same-sex sibships with Class I skeletal patterns and found that craniofacial measurements were more highly correlated than occlusal measurements. These results corroborated a number of prior studies that showed a similar pattern of heritability for craniofacial variables.[10-12] It is unclear whether this correlation is dependent upon the general deviation from the ideal. For instance, King et al.[13] demonstrated that sibling correlation for occlusal variables was significantly higher in sibships with overt malocclusions than in those with ideal occlusions. This could suggest that genetic and/or epigenetic factors that predispose to a significant deviation from norms within a family may be expressed reliably—that is, there may be less intersibling variability as the overall deviant tendency increases.

There have been significant limitations to prior studies conducted on the subject of cephalometric variability among siblings. The majority of studies consider only 2 siblings per family, which provides a low number of relationships. For instance, the previously referenced study by Harris and Johnson[9] utilized only one same-sex sibling per subject and excluded skeletal discrepancies. The same is true of Saunders et al.[14] who found correlations greater than 50% in lower anterior face height, mandibular corpus length, anterior face height, and anterior mandibular height, but only included individual sibling pairs. Manfredi et al.[15] assessed sibling pairs and found a stronger correlation in vertical vs. horizontal measures, but used a subject population age 10–13, prior to the cessation of growth. This potentially ignores the longitudinal effects of genetic and epigenetic components on adult phenotypes.

The aims of this retrospective pilot study were to investigate skeletal craniofacial measurements among groups of at least 4 siblings at the completion of the growth spurt to identify which of these measurements have the strongest correlation between siblings in a family and to determine whether skeletal craniofacial measurements with clinical implications can be reliably predicted among siblings.

METHODS

This research was a pilot study conducted retrospectively using data from the Forsyth Moorrees twin study. The Boston University Medical Campus Institutional Review Board approved the protocol (H-31945). A complete screening of the repository was conducted to identify all families with at least 4 siblings in a family, including only one of a pair of monozygotic twins. In families with dizygotic twins, both twins were included. Out of the total 500 families available in the repository, a total of 46 families were identified who met these criteria.

Lateral cephalograms were obtained for each sibling at the latest available timepoint after peak pubertal growth, as verified by the cervical vertical maturation score (CVMS) and/or hand-wrist skeletal maturity index (SMI), when available. Post-peak pubertal growth was defined as CVMS IV or SMI 9. Once puberty is completed, it is considered that 85–90% of facial growth is complete. Since all siblings were at least 14 years of age, requiring all siblings to have complete growth would be impossible, since the study only took records up to age 18. A total of 14 families were excluded due to skeletal immaturity at the latest available time point for any individual which would have reduced the family size to fewer than 4 siblings.

The final sample included 32 families with a total of 142 individual siblings. Out of this, 77 (54.2%) were female and 65 (45.8%) were male. All individuals ranged from 14 to 18 years of age at the time of radiographic evaluation, and their growth assessments showed them to be after their growth spurt. Twenty-three families (71.8%) included exactly 4 siblings, while the remaining 9 families consisted of 5 or more siblings (5 with 5, 3 with 6, and 1 with 7).

The majority of sibships consisted of at least one pair of dizygotic twins (29/32, 90.6%), both of whom were included. Of these, 5 families included 2 pairs of dizygotic twins, 1 family included 3 pairs of dizygotic twins, and 2 families included a set of dizygotic triplets. The remaining 3 families (9.4%) included one monozygotic twin, so that all 4 siblings in these families were born at different times. Twelve sibships (33.3%) consisted of an even number of males and females, while the remaining 24 sibships did not. In only one instance was the entire sibship the same sex, all female.

For all families, lateral cephalograms were digitized and traced by a single operator (KM) using Dolphin imaging software (Patterson Dental Supply, Chatsworth, CA, USA). A total of 20 linear and angular parameters, including measurements of facial proportion, maxillary position, mandibular position, maxillomandibular relation, and cranial base proportion, were chosen in order to fulfill as many as possible of the following criteria: (1) inclusion in prior heritability literature, (2) widespread use in orthodontic and anthropometric cephalometrics, (3) clinical

value to treatment in orthodontics, and (4) easily distinguishable landmarks on records of varying quality. Of these 20 measurements, 6 were identified as having strong clinical relevance to growth prediction and orthodontic treatment planning due to their indication of jaw relations in the sagittal and vertical planes: facial convexity, facial axis of Ricketts, lower facial height, mandibular arc, mandibular plane angle, and SNB angle.

Statistical Analysis

Statistical analysis focused on several approaches to measuring similarities and differences among the groups of siblings, to approach the predictability of sibling measurements. Dixon's Q-test was applied to see if there were any outliers in a family for a given parameter.[16] Dixon's Q-test is defined in terms of gap/range, where the gap is defined as the larger absolute difference between the questionable subject and its 2 closest neighbors, while range encompasses the entire sibship. A sibling was called an outlier if the Q-test value was greater than a Q-critical value at 90%.[17] Manhattan distance (MD) was used to quantify similarity among siblings per parameter.[18] The data is reported in terms of minimum, maximum, mean, median, and range of MD for each family per parameter. This information is descriptive of the pattern of familial clustering, but as there is no critical value, it cannot be used to determine the significance or lack thereof. Scatter plots visually displayed a subject's measure relative to the mean and standard deviation of each parameter to assess the clinical relevance of the differences. These statistical tests did not result in measures of significance, so that no power analysis was calculated.

RESULTS

In this study, siblings were compared only within families. For the 6 major parameters, Dixon's Q-test was performed in order to determine whether any sibling was a significant outlier from the rest of their family. The results are summarized in Table 1 and detailed in supplemental Table 1, which shows a relatively narrow range of outlier variability across the 6 parameters (ranging from 12.5% to 18.7% of families). Eleven families (34.4%) did not demonstrate a single outlying sibling across any of the 6 parameters. In 13 families (40.6%), there was an outlying sibling in only a single measurement. The remaining sibships demonstrated outliers for either 2 measurements (6 families, 18.8%) or 3 measurements (2 families, 6.3%). Interestingly, in the majority of these multiple-outlier families, each measurement demonstrated a different outlying sibling. Only 2 individuals out of 142 (1.4%) were shown to be the outlying sibling in 2 different measurements, and none were the outlying sibling in 3 or more measurements.

MD was used to demonstrate similarity among siblings per parameter and is summarized in Table 2 as well as detailed in Supplementary Tables 1–7. It can be seen that the range, even within a given parameter, varied widely between families.

Intraclass correlation coefficient (ICC) was used to provide reliability estimates among 3 repeated measures. ICC was greater than 0.96 for each of the 6 major parameters, indicating excellent intra-rater reliability.

Table 1. Dixon's Q-test results, summarized

Parameter Name	Convexity	Facial Axis	LFH	Mandibular Arc	MPA	SNB Angle
# families with significant outlier	4	5	6	5	6	5
% families with significant outlier	12.5	15.6	18.7	15.6	18.7	15.6

LFH, Lower Facial Height; MPA, Mandibular Plane Angle; SNB, Sella – Nasion - B Point Angle

DISCUSSION

The familial facial resemblance has long been a topic of discussion and debate, from the notable 16th-century Spanish Habsburg family through today. A number of studies throughout the years have attempted to elucidate the contribution of genetics to craniofacial growth and development. Genetics was previously a focus because the genetic pattern of an individual was considered immutable and thought to demonstrate the underlying framework of development predictably. However, a genotype never exists in a vacuum, and as Waddington et al.[6] have discussed, the functional demands of the environment upon a genetic scaffold are responsible for producing an individual phenotype.[6]

From an orthodontic perspective, this topic has been discussed in modern literature for almost a century. Byron Hughes stated in a 1944 editorial that research has "shown development or growth to be an unfolding design of interrelated morphological and functional items. The development plan is supplied by genetic facts in which the material and technique of application is provided by nurture and environment. Each of these two areas … contributes similarities and differences … within and between individuals."[19] In the immediate biological family, where siblings can be assumed to share approximately 50% of their genetic material, it stands to reason that shared environmental factors acting upon the genetic scaffolds would produce phenotypes that are more similar than genetics alone would suggest. One study confirmed a temporal component to maxillofacial similarity, demonstrating that variability between first-degree relatives decreases over time, as environmental effects have more time to shape the individual.[8]

Table 2. Manhattan distance results, summarized

Parameter	Minimum Range	Maximum Range
Convexity	0.80	10.70
Facial Axis of Ricketts	0.27	5.52
Mandibular Arc	0.40	7.16
Lower Facial Height (Ricketts)	0.13	5.73
Mandibular Plane Angle	0.27	6.12
Sella – Nasion - B Point Angle	0.2	6.68

Indeed, sibling resemblance is a common-sense phenomenon that is encountered regularly, both in daily life and clinical practice. The fact that such resemblance within families is highly variable is also quite evident. Determining the ways in which non-twin siblings' craniofacial structures resemble each other is not merely an intellectual consideration, but a practical one as well. The application of such information would lie in whether or not same-generation first-degree relatives can be utilized to predict the future craniofacial growth pattern of an individual. This is an important and complex clinical question, one which is not likely to have a simple answer. If predictable sibling resemblance does exist, this would be highly relevant to the practice of orthodontics. Evaluation of a patient's older siblings, via records within the same practice or obtained from another orthodontist, could offer significant insight into a growing patient's future morphology and therefore aid in determining the need for early treatment and/or growth modification.

In this study, we chose to concentrate on 6 variables that were considered to have major clinical implications for orthodontic decision making. Angular measurements were chosen over linear measurements due to the lack of reliable quality of the measuring instrument on the analog radiographs, making linear measurements less reliable. In addition, angular measurements take proportion into account and prevent similarities and differences from being determined due to size alone. The anteroposterior position of the maxilla (facial convexity), anteroposterior position of the mandible (SNB angle and mandibular arc), and vertical status of the craniofacial complex (facial axis of Ricketts, lower facial height, and mandibular plane angle) were chosen due to the reliability of the landmarks used for analysis as well as the relative constancy with age after puberty. These measurements are obviously interrelated and none of them describes anteroposterior or vertical status alone, but together give an overall description of an individual facial pattern and help to define treatment goals. In general, it would be expected that a sibling with a facial pattern distinctly different from that of their sibling would be an outlier in more than one measurement, and siblings who appear very similar would demonstrate closely related values in multiple measurements as well.

The data does show a relatively consistent percentage of families with outliers for each of the 6 parameters, with a range of 12.5–18.7% (Table 1). However, these are generally not the same families across categories, and the actual outlying sibling is not generally consistent. In 21 of 32 families (65.6%), there was a statistically significant outlying sibling in at least one measurement. Although 8 of these 21 families (38.1%) demonstrated outliers in 2 or 3 measurements, the large majority of the outliers were different siblings for each parameter. Only 2 individuals out of 142 (1.4%) were the outlying sibling in 2 separate variables (lower facial height and mandibular plane angle; mandibular plane angle and SNB angle, respectively). A further 13 families (40.6%) demonstrated an outlying sibling in only one of the 6 measurements, with no outliers in the remainder. This suggests that facial patterns are not developed as a whole, but rather a sibling can resemble their family in multiple measurements but still be an outlier in another.

The scatter plots of MD for each of the 6 parameters (Figures 1–6) offer a visual display of the values per sibling for each family. In general, a smaller mean, median, and range of MD for a given family reinforces the similarity in measurements across siblings, indicating tighter clustering. This is a subjective delineation, but important nonetheless, as some families show striking similarities across all siblings (i.e., SNB angle in family 24) and the predictability of such clustering would have important clinical ramifications. For the sake of comparison, families with clear visual similarity and who demonstrated a value for MD range below 1 standard deviation of the study population were considered to demonstrate clustering. For any given parameter, the number of families with tight clustering ranged from 3 to 6 (9.3–18.7%), whereas a relatively equivalent number of families demonstrated a significant outlier (range of 4–6 families; 12.5–18.7%; Table 1). Therefore, for a given measurement, there appears to be a similar incidence of families where all siblings resemble each other and families with a statistically significant outlier.

For each parameter, the majority of families showed neither a tight clustering of siblings nor a particular outlier. The average sibship demonstrated a relatively wide range of values across individuals for any given measurement. The distribution of sibling values in relation to published historical norms per parameter is summarized in Table 3. For any given parameter, only 18.8–31.3% of families demonstrated sibling values entirely within 1 standard deviation above or below the normal value. The majority of families, therefore, had at least one sibling with a value that would be considered significantly deviant from the mean. Of these, the majority of families (43.8–62.5%) demonstrated a consistent direction of abnormality, that is, positive or negative values in relation to the mean. However, some families (3.1–9.4%) had at least one sibling with values greater than 1 SD in both the positive and negative direction, indicating vastly different facial patterns that would likely require significantly different orthodontic treatment objectives. Around 12.5–18.8% of families included at least one sibling with a value greater than 2 SD from the mean. In multiple instances, 2 or even 3 sibling values per family fell more than 2 SD from the mean. These families were no more likely to demonstrate a statistically significant outlier than families without such a deviant sibling. However, almost all families with at least 1 sibling more than 2 SD from the mean also included at least 1 sibling within the normal range, that is, within 1 SD. Such a wide range of values despite the absence of a statistical outlier implies a relative continuum across siblings and therefore emphasizes the significant variability possible within a single family.

Many studies have looked at heritability from parents to offspring,[20] and this narrow-sense heritability has often been the primary focus of much of the orthodontic literature concerning craniofacial variability. It is possible that sibships with greater variability in craniofacial measurements came from parents with distinctly different measurements between them, while sibships with less variability had parents who more closely resembled each other. However, Saunders et al.[14] demonstrated that the midparent value explains more of the variation of the offspring than the value from either parent alone. This is

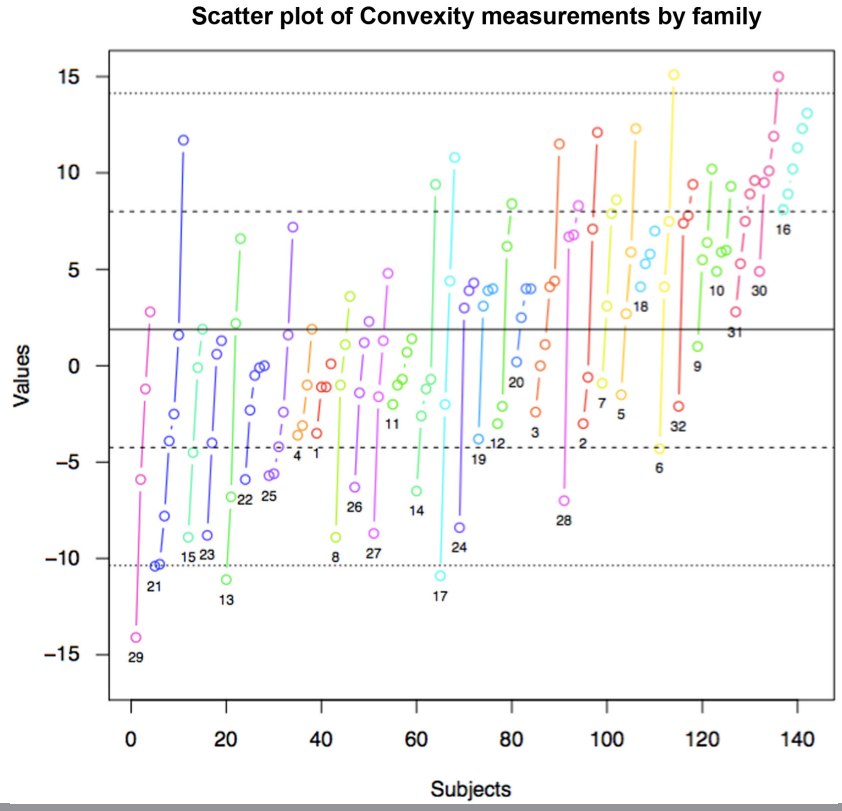

Figure 1. Facial convexity—individual sibling data points grouped according to family. The solid line represents the published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

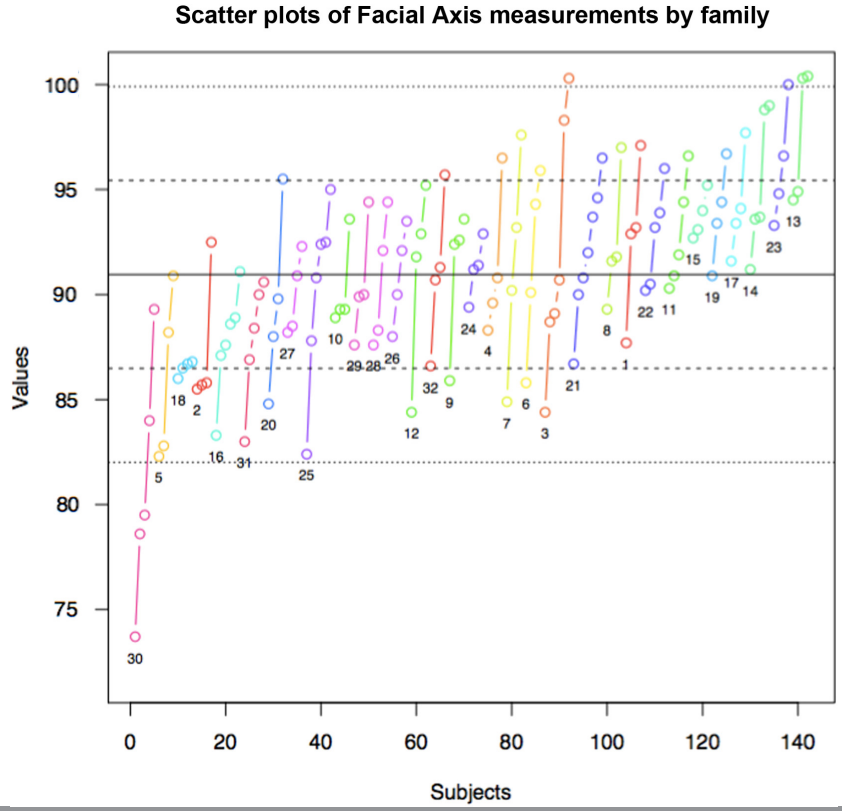

Figure 2. Facial axis of Ricketts—individual sibling data points grouped according to family. The solid line represents the published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

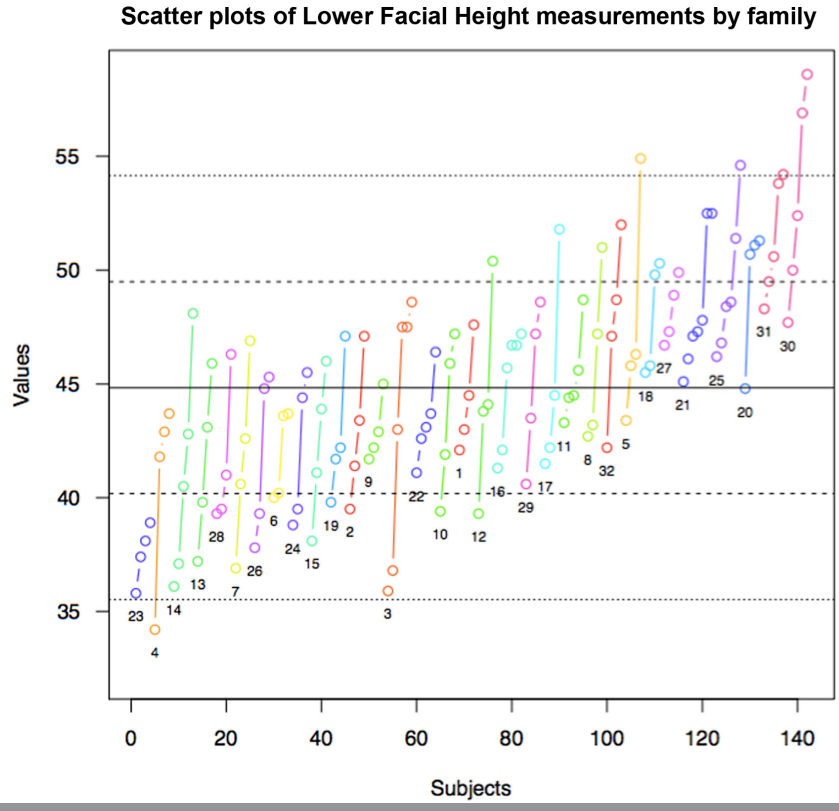

Figure 3. Lower facial height—individual sibling data points grouped according to family. The solid line represents the published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

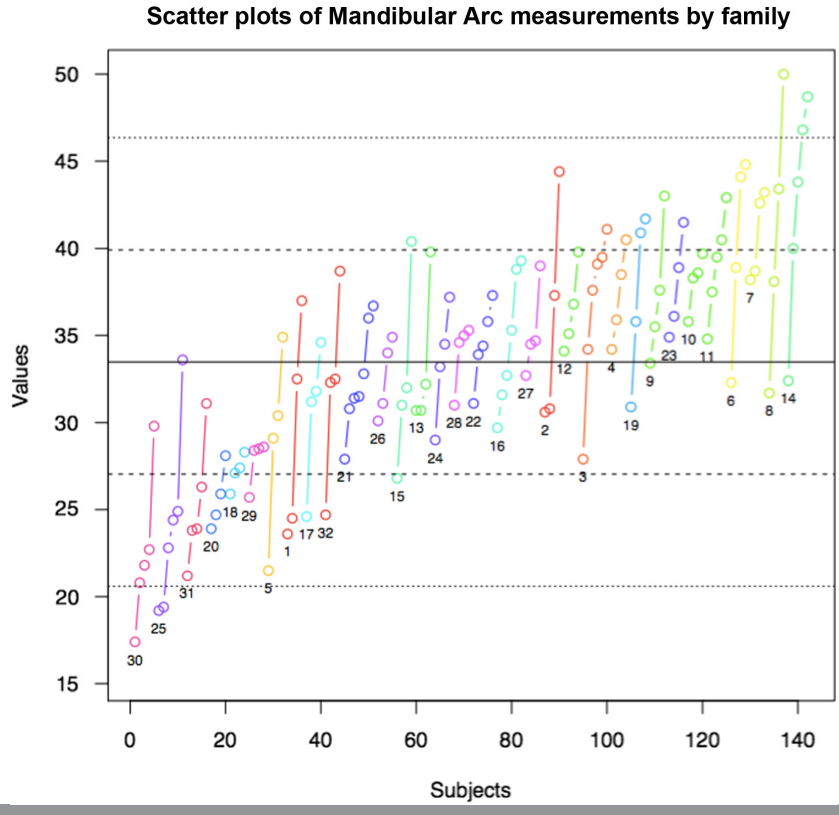

Figure 4. Mandibular arc—individual sibling data points grouped according to family. The solid line represents the published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

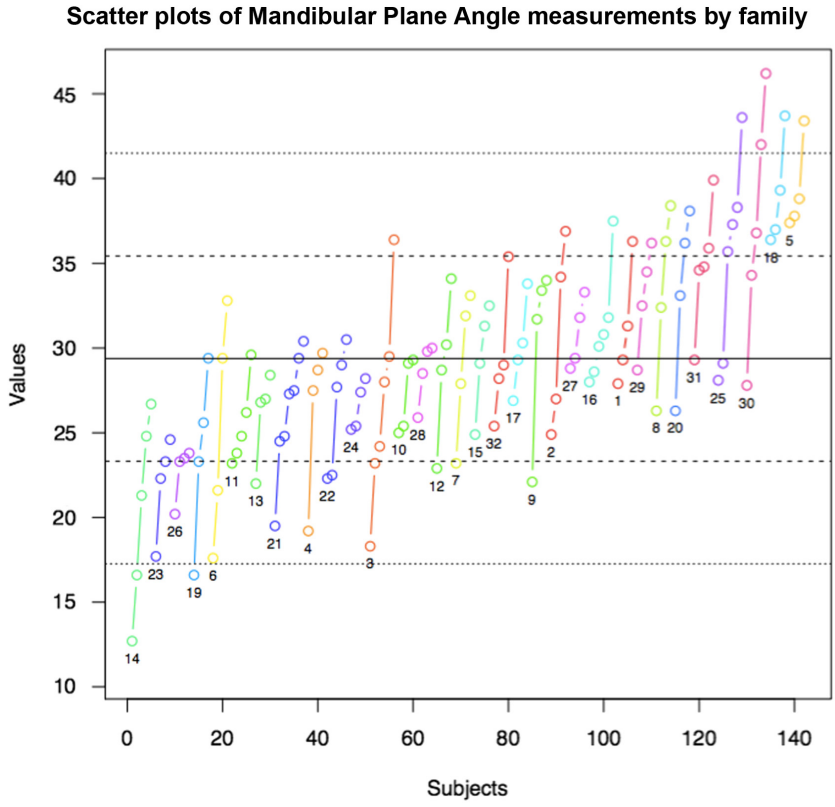

Figure 5. Mandibular plane angle—individual sibling data points grouped according to family. The solid line represents the published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

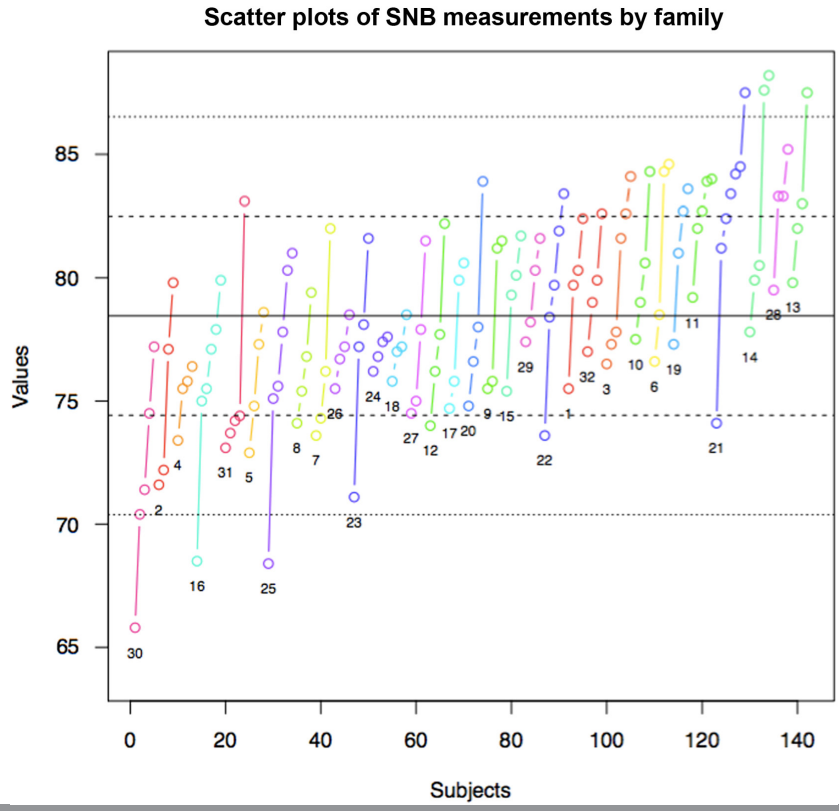

Figure 6. SNB angle—individual sibling data points grouped according to family. The solid line represents published population mean. Dashed and dotted lines represent 1 and 2 standard deviations from the mean, respectively.

Table 3. Distribution of sibling values by published norms per parameter

	Convexity	Facial Axis	Lower Facial Height	Md Arc	Md Plane Angle	SNB Angle
≤1 SD						
# families	6	7	7	10	9	10
% families	18.8	21.9	21.9	31.3	28.1	31.3
≤2 SD unilateral						
# families	18	19	20	17	16	14
% families	56.3	59.4	62.5	53.1	50.0	43.8
≤2 SD bilateral						
# families	3	2	1	1	1	2
% families	9.4	6.3	3.1	3.1	3.1	6.3
>2 SD						
# families	5	4	4	4	6	6
% families	15.6	12.5	12.5	12.5	18.8	18.8

Families are classified into the category occupied by the sibling with the most deviant value. Unilateral indicates the presence of one or more siblings with values $1 < x \leq 2$ SD in only one direction (positive or negative) from the mean. Bilateral indicates one or more siblings with values $1 < x \leq 2$ SD in both directions from the mean.

contrary to a finding by Nakasima et al.[21] who demonstrated high parent-offspring correlation in families with severe Class II or Class III malocclusions. In any respect, from a practical sense, the skeletal and dental measurements of the parents are unlikely to be available to the orthodontist in the same manner that a previously treated siblings may be. Our primary objective was to determine whether siblings can be utilized in a predictive manner in the absence of parental data. For this reason, we determined that parental measurements would not be included in this study.

Prior studies have demonstrated a possible difference in heritability between sexes. Johannsdottir et al.[2] studied craniofacial variability within an Icelandic population and found that males generally showed stronger heritability to their mothers than their fathers, whereas females were affected by both parents equally.[2] We did not differentiate between sexes in this study, as it would have significantly reduced the number of effective siblings per family. However, of the 31 total instances of a statistically significant outlying sibling, in only 4 of these cases (12.9%) was the outlying sibling the sole member of one particular sex within the family. In other words, it does not appear that females are more likely to be significantly different from their male siblings as compared to their female siblings, and vice versa. This is in agreement with the findings of the landmark study by Saunders,[14] which demonstrated a high correlation between siblings regardless of sister-sister, sister-brother, or brother-brother pairings, with brother-sister correlations slightly higher in general.

The present analysis was undertaken as a pilot study in order to assess the predictive value of evaluating multiple siblings in a family. There are several limitations to this study. The sample size was limited to the Forsyth Twin Study data and the number of siblings per family contained therein. We felt that post-pubertal status was important, as it eliminated a significant source of variability that was a limitation in prior literature. The sample size was greatly limited by the presence or absence of records for each sibling at a time point after skeletal maturity was achieved, as numerous additional families (and additional siblings per family) were discarded due to study termination prior to maturity of the youngest siblings. Furthermore, although our sample size of siblings per family is larger than similar studies of this nature[5,9,12] the sample itself consists of a relatively homogeneous Caucasian population. The generalizability of the findings at the national level should be made with caution due to the relatively small size and representativeness of our sample.

An additional limitation is the use solely of two-dimensional images for skeletal measurements. Although these measurements were chosen with regard to their relevance in treatment planning, the use of soft tissue measurements would also contribute to significant information toward detecting family resemblance. Furthermore, the use of three-dimensional images would give a clearer idea of family resemblances; however, the lack of availability of 3-D growth samples prevented us from doing this.

A third limitation pertaining to the measurements chosen for this study involved the configuration of the cephalostat machine used to obtain the lateral cephalograms. A metal rod in the cephalostat was present at a level that prevented the identification of anatomical porion. Therefore, we were unable to use any cephalometric measurements involving Frankfort Horizontal, which utilizes porion, despite the wide use of this reference plane in the orthodontic and anthropologic literature.

From a statistical perspective, one limitation of Dixon's Q-test is that it can only detect a single outlier. In situations where the largest gap between sibling values occurs in the middle of the ordered data, such as when there are 2 distinct clusters of sibling values, the Q-test can produce a false positive despite the lack of a single outlying sibling. In order to mitigate this, the Q-test results were manually checked against the data in order to distinguish true positive outliers from false positives.

CONCLUSION

The present study offers the following insight into the concept of sibling resemblance from a craniofacial perspective:

- Only a small percentage of sibships demonstrated appreciable clustering for any given measurement, and these families were no more likely to show clustering for any other measurement, despite the relative interrelatedness of the variables studied. This runs counter to what we often think as clinicians.

- On the contrary, families with a statistically significant outlier for one variable also had an outlying sibling in a second or third variable 38% of the time. However, with the exception of 2 instances, it was not the same individual who deviated from their siblings in more than one parameter.
- The vast majority of sibships demonstrated neither appreciable clustering nor a significant outlier, and the range of values for these families generally spanned at least 2 standard deviations from the established means.

Therefore, although the majority of families are generally not statistically dissimilar from one another in their craniofacial characteristics, we conclude based on this study that measurements from siblings cannot reliably be used to predict the measurements of another sibling.

Ethics Committee Approval: This study was approved by the Ethics Committee of Boston University Medical Campus University. Number: 71306642-050.01.04.

Informed Consent: An informed consent form was signed by all the patients/parents involved in the study.

Peer-review: Externally peer-reviewed.

Author Contributions: Concept – M.M., L.A.W.; Design – Y.Z., M.M., L.A.W.; Supervision – L.A.W.; Data Collection and/or Processing – K.L.M., L.A.W.; Analysis and/or Interpretation – Y.Z., M.M., L.A.W., K.L.M.; Literature Review – K.L.M.; Writing – K.L.M., M.M., L.A.W.; Critical Review – Y.Z., M.M., L.A.W.

Declaration of Interests: The authors have no conflicts of interest to declare.

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Supplementary Table 1. Dixon's Q-Test results

Family #	Convexity	Facial Axis	LFH	Mandibular Arc	MPA	SNB Angle
1	0.667	0.553	0.564	0.597	0.595	0.609
2	0.510	0.957*	0.487	0.514	0.600	0.598
3	0.511	0.478	0.488	0.477	0.381	0.500
4	0.527	0.695	0.800*	0.413	0.790*	0.700
5	0.464	0.628	0.748	0.567	0.767*	0.439
6	0.433	0.426	0.919*	0.528	0.513	0.725
7	0.505	0.417	0.430	0.780*	0.475	0.690
8	0.632	0.675	0.482	0.361	0.504	0.491
9	0.489	0.844*	0.636	0.563	0.807*	0.900*
10	0.750	0.915*	0.513	0.641	0.860*	0.544
11	0.412	0.397	0.574	0.333	0.531	0.583
12	0.728	0.685	0.568	0.526	0.518	0.549
13	0.508	0.915*	0.379	0.835*	0.750	0.584
14	0.635	0.654*	0.442	0.466	0.336	0.683*
15	0.407	0.480	0.380	0.618	0.553	0.619
16	0.260	0.487	0.610*	0.365	0.600*	0.570*
17	0.410	0.590	0.709	0.660	0.507	0.695
18	0.414	0.625	0.833*	0.500	0.603	0.481
19	0.885*	0.431	0.671	0.472	0.523	0.587
20	0.605	0.533	0.908*	0.524	0.576	0.648
21	0.457	0.337	0.635*	0.364	0.459	0.530*
22	0.610	0.466	0.509	0.452	0.634	0.490
23	0.475	0.507	0.516	0.424	0.667	0.581
24	0.898*	0.514	0.731	0.512	0.667	0.429
25	0.434	0.429	0.381	0.604*	0.426	0.532
26	0.570	0.382	0.733	0.604	0.861*	0.433
27	0.526	0.585	0.500	0.683	0.533	0.514
28	0.895*	0.559	0.757	0.837*	0.634	0.667
29	0.485	0.647	0.463	0.931*	0.507	0.500
30	0.455	0.340	0.413	0.573	0.353	0.404
31	0.368	0.513	0.542	0.485	0.500	0.870*
32	0.826*	0.484	0.500	0.543	0.640	0.482

*indicates Q-score greater than Q-critical value at 90%

Supplementary Table 2. Convexity—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	1.20	2.80	1.80	1.60	1.60
2	7.60	10.93	8.83	8.40	3.33
3	4.26	10.06	5.71	4.54	5.80
4	2.53	4.47	3.10	2.70	1.93
5	5.67	9.93	7.43	7.07	4.27
6	7.60	13.20	10.27	10.13	5.60
7	4.77	7.43	5.55	5.00	2.67
8	4.87	10.13	6.60	5.70	5.27
9	3.37	6.37	4.75	4.63	3.00
10	1.50	3.70	2.22	1.83	2.20
11	1.28	2.15	1.70	1.63	0.88
12	6.57	8.03	7.08	6.87	1.47
13	8.90	11.83	10.35	10.33	2.93
14	4.45	12.15	6.74	4.80	7.70
15	5.07	8.00	6.13	5.73	2.93
16	1.90	3.06	2.42	2.36	1.16
17	9.37	15.30	11.92	11.50	5.93
18	1.13	1.93	1.53	1.53	0.80
19	2.87	7.47	4.03	2.90	4.60
20	1.77	3.30	2.15	1.77	1.53
21	6.55	17.25	9.09	8.45	10.70
22	2.03	5.18	2.80	2.20	3.15
23	4.90	8.10	5.82	5.13	3.20
24	4.53	12.13	6.50	4.67	7.60
25	4.38	10.46	5.86	4.98	6.08
26	3.73	7.00	4.73	4.10	3.27
27	5.47	10.20	7.23	6.63	4.73
28	5.13	14.27	7.67	5.63	9.13
29	7.20	12.67	9.23	8.53	5.47
30	3.13	6.73	4.52	3.58	3.60
31	2.60	5.03	3.44	3.15	2.43
32	3.97	10.30	5.82	4.50	6.33

Supplementary Table 3. Facial axis of Ricketts—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	3.23	6.70	4.75	4.53	3.47
2	2.37	6.83	3.52	2.43	4.47
3	5.42	10.06	7.33	7.02	4.64
4	3.13	6.93	4.30	3.57	3.80
5	4.67	6.47	5.20	4.83	1.80
6	4.77	7.63	5.75	5.30	2.87
7	5.23	8.77	6.85	6.70	3.53
8	2.63	6.10	3.88	3.40	3.47
9	2.63	6.97	3.88	2.97	4.33
10	1.57	4.43	2.35	1.70	2.87
11	2.45	4.72	3.22	3.08	2.27
12	3.97	8.90	5.58	4.73	4.93
13	3.77	4.03	3.85	3.80	0.27
14	3.25	5.08	4.16	4.53	1.83
15	1.13	1.93	1.40	1.27	0.80
16	2.12	5.36	3.03	2.28	3.24
17	2.27	4.67	3.17	2.87	2.40
18	0.33	0.67	0.43	0.37	0.33
19	2.27	3.93	3.07	3.03	1.67
20	4.17	7.97	5.65	5.23	3.80
21	2.88	6.23	3.95	3.48	3.35
22	2.30	4.05	3.00	2.98	1.75
23	2.83	5.10	3.65	3.33	2.27
24	1.23	2.43	1.78	1.73	1.20
25	3.78	9.30	5.25	4.40	5.52
26	2.53	3.87	3.10	3.00	1.33
27	2.17	3.10	2.45	2.27	0.93
28	3.53	5.07	4.03	3.77	1.53
29	2.30	5.23	3.42	3.07	2.93
30	5.25	10.35	7.32	6.38	5.10
31	2.68	5.98	3.66	3.08	3.30
32	3.23	6.17	4.65	4.60	2.93

Supplementary Table 4. Lower Facial Height—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	2.33	4.40	3.00	2.63	2.07
2	3.20	5.67	4.13	3.83	2.47
3	5.58	8.78	6.67	6.02	3.20
4	3.53	8.60	4.93	3.80	5.07
5	4.00	9.73	5.83	4.80	5.73
6	2.37	2.50	2.42	2.40	0.13
7	4.00	6.87	5.33	5.23	2.87
8	4.10	6.63	4.82	4.27	2.53
9	1.33	2.73	1.77	1.50	1.40
10	3.93	5.60	4.57	4.37	1.67
11	1.65	4.25	2.40	1.93	2.60
12	3.80	8.00	5.60	5.30	4.20
13	4.00	5.87	4.90	4.87	1.87
14	4.43	8.98	5.94	5.28	4.55
15	3.57	5.57	4.42	4.27	2.00
16	2.30	4.38	2.95	2.50	2.08
17	4.20	9.07	5.53	4.43	4.87
18	2.93	3.27	3.07	3.03	0.33
19	2.60	5.87	3.73	3.23	3.27
20	2.30	6.23	3.32	2.37	3.93
21	2.42	4.85	3.40	2.95	2.43
22	1.60	3.78	2.34	1.75	2.18
23	1.27	2.33	1.67	1.53	1.07
24	3.87	4.60	4.17	4.10	0.73
25	2.64	6.32	3.73	3.52	3.68
26	4.33	5.33	4.67	4.50	1.00
27	1.60	2.27	1.87	1.80	0.67
28	2.83	6.37	3.75	2.90	3.53
29	3.90	5.83	4.62	4.37	1.93
30	4.45	6.85	5.74	5.58	2.40
31	2.55	3.73	3.22	3.35	1.18
32	3.80	7.07	5.17	4.90	3.27

Supplementary Table 5. Mandibular Arc—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	7.13	10.13	8.03	7.43	3.00
2	6.77	11.50	7.98	6.83	4.73
3	4.00	10.40	5.56	4.76	6.40
4	2.97	4.30	3.58	3.53	1.33
5	4.90	9.97	6.92	6.40	5.07
6	5.90	10.30	7.12	6.13	4.40
7	2.97	3.37	3.15	3.13	0.40
8	7.87	12.27	10.03	10.00	4.40
9	3.90	7.50	5.15	4.60	3.60
10	1.40	3.07	2.00	1.77	1.67
11	2.78	5.30	3.84	3.28	2.53
12	2.47	4.47	3.13	2.80	2.00
13	3.53	8.60	4.80	3.53	5.07
14	5.78	12.43	7.88	6.73	6.65
15	4.87	10.47	6.97	6.27	5.60
16	3.88	5.84	4.81	4.80	1.96
17	3.53	7.93	5.10	4.47	4.40
18	0.90	1.70	1.25	1.20	0.80
19	5.30	8.57	6.25	5.57	3.27
20	1.80	3.27	2.30	2.07	1.47
21	2.57	5.30	3.64	2.88	2.73
22	2.03	4.25	2.86	2.38	2.23
23	3.13	4.87	3.77	3.53	1.73
24	3.17	5.97	4.32	4.07	2.80
25	4.30	11.46	6.01	5.08	7.16
26	2.57	3.23	2.88	2.87	0.67
27	2.17	5.03	3.18	2.77	2.87
28	1.57	3.97	2.22	1.67	2.40
29	1.00	2.80	1.47	1.03	1.80
30	3.58	9.13	5.34	3.83	5.55
31	3.10	7.30	4.46	3.70	4.20
32	4.73	9.80	7.03	6.80	5.07

Supplementary Table 6. Mandibular Plane Angle—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	3.47	6.80	4.53	3.93	3.33
2	6.40	8.20	7.20	7.10	1.80
3	5.64	11.76	7.55	6.14	6.12
4	3.90	9.43	5.45	4.23	5.53
5	2.33	5.40	3.17	2.47	3.07
6	7.67	10.33	8.90	8.80	2.67
7	4.63	7.77	5.62	5.03	3.13
8	5.33	9.40	6.70	6.03	4.07
9	4.53	10.93	6.23	4.73	6.40
10	2.67	2.93	2.77	2.73	0.27
11	2.20	5.10	3.04	2.55	2.90
12	4.23	8.10	5.85	5.53	3.87
13	2.20	5.40	3.23	2.67	3.20
14	5.55	9.65	7.24	6.73	4.10
15	3.27	6.07	4.17	3.67	2.80
16	2.68	7.64	3.85	3.18	4.96
17	2.63	4.97	3.62	3.43	2.33
18	3.20	6.13	4.03	3.40	2.93
19	5.03	9.50	6.78	6.30	4.47
20	4.97	9.50	6.42	5.60	4.53
21	3.08	7.82	4.30	3.65	4.73
22	3.68	5.13	4.58	4.98	1.45
23	2.63	5.70	3.62	3.07	3.07
24	1.67	2.20	1.83	1.73	0.53
25	5.26	9.90	7.11	6.78	4.64
26	1.27	3.33	1.83	1.37	2.07
27	2.30	3.30	2.65	2.50	1.00
28	1.80	3.53	2.27	1.87	1.73
29	3.17	5.70	4.08	3.73	2.53
30	6.53	12.03	8.90	7.83	5.50
31	2.98	7.00	4.50	3.25	4.03
32	3.60	7.87	5.13	4.53	4.27

Supplementary Table 7. SNB Angle—Manhattan distance

Family	Min.	Max.	Mean	Median	Range
1	2.50	5.30	3.55	3.20	2.80
2	4.37	6.17	4.92	4.57	1.80
3	3.34	4.94	3.85	3.64	1.60
4	1.10	2.50	1.55	1.30	1.40
5	2.73	4.00	3.27	3.17	1.27
6	4.60	5.87	4.97	4.70	1.27
7	3.43	7.30	4.52	3.67	3.87
8	2.23	3.97	2.88	2.67	1.73
9	3.80	4.00	3.90	3.90	0.20
10	2.80	5.27	3.67	3.30	2.47
11	1.68	3.95	2.30	1.98	2.28
12	3.23	6.23	4.35	3.97	3.00
13	2.90	5.90	4.02	3.63	3.00
14	4.53	6.75	5.70	6.25	2.23
15	2.37	4.97	3.28	2.90	2.60
16	3.18	8.58	4.49	3.44	5.40
17	3.33	4.07	3.63	3.57	0.73
18	0.97	1.83	1.38	1.37	0.87
19	2.67	5.13	3.43	2.97	2.47
20	3.50	7.43	4.78	4.10	3.93
21	3.08	9.77	4.63	3.37	6.68
22	3.33	7.25	4.62	3.88	3.93
23	3.80	7.87	5.40	4.97	4.07
24	0.67	1.07	0.80	0.73	0.40
25	4.00	9.56	5.39	4.60	5.56
26	1.17	2.03	1.58	1.57	0.87
27	3.30	5.70	3.98	3.47	2.40
28	1.90	4.43	2.85	2.53	2.53
29	2.10	2.97	2.45	2.37	0.87
30	3.88	7.58	5.38	4.65	3.70
31	2.68	9.25	4.14	2.80	6.57
32	2.17	3.97	2.95	2.83	1.80