

Genetic and environmental components of vertical growth in mono- and dizygotic twins up to 15–18 years of age

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ABSTRACT

Objectives: To determine the additive genetic and environmental contributions to the vertical growth of craniofacial structures.

Materials and Methods: The sample consisted of 64 untreated monozygotic (44 male, 20 female) and 61 untreated dizygotic twins (32 male, 29 female). Lateral cephalograms taken at 15 and 18 years of age were traced to analyze the sella-nasion–nasal line angle (SN-NL), nasal line–mandibular line angle (ML-NL), sella-nasion–mandibular line angle (SN-ML), sella-nasion–sella-gnathion angle (Y-axis), posterior face height/anterior face height (PFH/AFH), and lower anterior face height/anterior face height (LAFH/AFH). The genetic and environmental components of variance were analyzed with structural equation modeling for multilevel mixed effects.

Results: At 15 years of age, strong dominant genetic control was seen for NL-ML (81%), LAFH/AFH (73%), and Y-axis (57%), whereas strong additive genetic components were found for PFH/AFH (78%), SN-NL (58%), and SN-ML (57%). Unique environmental factors accounted for 18–42% of observed variance, with SN-NL being affected the most (42%). At 18 years of age, only LAFH/AFH (86%) was under strong dominant genetic control, whereas the remainder were under additive genetic influence. The sole exception was SN-NL, which changed from additive to unique environmental influence.

Conclusions: Either additive or dominant genetic components were found at 15 or 18 years of age for most vertical variables. Environmental factors accounted for about 10–40%, with SN-NL being mostly affected. (*Angle Orthod.* 2021;91:384–390.)

KEY WORDS: Craniofacial growth; Twins; Mandibular growth; Cephalometrics; Cohort study; Genetics

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INTRODUCTION

Facial esthetics can affect psychological development, social interactions, and other aspects of life. Socialization and evolutionary theory suggest that attractiveness has an enormous impact on human development and interaction.¹ Therefore, the ability to foresee and improve facial development lies at the heart of orthodontics² but has long remained subjective.³

Craniofacial structures are affected by a combination of genetic and environmental factors,^{4–6} which enables orthopedic intervention. However, the extent to which facial components are heritable remains controversial. Two early studies indicated that vertical characteristics had greater heritability than horizontal ones.^{7,8} These findings were confirmed in a subsequent twin study, which concluded that early intervention would be more effective in the anteroposterior dimension.⁹ This contradicted other studies' conclusions that both the anteroposterior and vertical aspects of the mandible showed strong heritability,¹⁰ leaving limited opportunity

for orthopedic intervention. Another twin study indicated the greater heritability of the structure of the mandible than the size or vertical dimensions.¹¹ Recent data also indicated that the angular aspects of mandibular morphology were more heritable than size.¹²

Simultaneously, many common craniofacial traits are prone to environmental modification.¹³ Because twins share much of their genome, they are a unique resource for evaluating the interaction between genetic and environmental effects, providing a more scientifically based rationale for how orthodontic treatment can influence development.¹⁴ To analyze the degree of genetic contribution to facial growth, several twin studies have been carried out.^{15–17} Classical twin study methods compared the differences within monozygotic (MZ; identical) and dizygotic (DZ; fraternal) pairs, whereas the amount of the difference was interpreted as the relative genetic impact.¹⁸ However, evidence of the specific contribution of genes and the environment on the development of each craniofacial characteristic remains limited.

No previous investigation has examined the heritability of vertical craniofacial growth using a model-fitting statistical analysis of lateral cephalometric variables in twins. This retrospective cohort study aimed to determine the additive genetic and environmental influence using quantitative genetic modeling on vertical skeletal growth during late adolescence in untreated twins.

MATERIALS AND METHODS

Study Sample

Patients were chosen from the Moorrees twin sample that was collected from 1959–1975 at the Forsyth Infirmary for Children. Ethical approval to conduct this study was provided by the Institutional Review Board of Boston University (H-31945). This registry contains nearly 500 twin pairs who came for annual records. Zygosity was determined by serologic testing of 29 factors. All twins were Caucasian with no previous orthodontic treatment. Inclusion factors were (1) no history of craniofacial anomalies or chronic systemic disease and (2) available, good-quality lateral cephalograms. For this study, a sample of DZ twins with currently available high-quality data at 15 years of age was randomly selected to match a previously analyzed sample of MZ twins.¹⁶ This study assessed 64 MZ (44 male, 20 female) and 61 DZ (32 male, 29 female) twins at 15 and 18 years of age.

Cephalometric Measurements

All lateral cephalograms were taken in a standardized position in centric occlusion with the same device

at a constant magnification factor of 6%. The films were scanned (Expression 11000XL; Epson America, Inc, Long Beach, Calif) at 300 dpi, 16-bit gray scale.

After anonymization, the scanned radiographs were traced by two persons (MZ: M.A.H.-Z., DZ: S.N.P.) in Viewbox V4.0 (dhal, Kifissia, Greece). Six vertical measurements were made (Figure 1).

Statistical Analysis

Descriptive statistics included means with standard deviations. Crude differences among MZ and DZ twins with 95% confidence intervals (CIs) were calculated with generalized linear models with standard errors clustered within twin families.

Additive genetic factors (A), nonadditive (dominant) genetic factors (D, dominance and epistatic interactions between loci), environmental factors shared between twins in pairs (C, the nongenetic sources of variation between individuals experienced by multiple individuals in a population), and environmental factors unique to individuals (E; Appendix 1) were allowed. Structural equation modeling for multilevel mixed-effects ACE (additive-common environmental-unique environmental) variance decomposition were fitted in Stata 14.2 (StataCorp, College Station, Tex). Finally, the classical heritability estimate was calculated for all factors as twice the difference of the MZ and DZ correlations for all variables.¹⁹ The main analysis included 125 participants at 15 years of age, whereas a secondary analysis included 82 participants at 18 years.

Method Error

Intraobserver method error was assessed on 50 cephalograms retraced after 1 month¹⁷ using a coefficient of reliability and the Bland-Altman method.²⁰

RESULTS

The analysis of the repeated measurements showed high reliability and small limits of agreement in all instances, which supported the robustness of the method.¹⁷

In the main analysis, at 15 years of age, 125 participants were studied, including 64 MZ twins ($n = 20$; 31% female) and 61 DZ twins ($n = 29$; 48% female; Table 1). Small differences were found between MZ-DZ twins for all variables, and only the lower anterior face height/face height (LAFH/FH) showed a statistically significant difference of 1.4% (as the 95% CI excluded zero). Crude models were initially selected (Appendix 2) and compared (Table 2). In all instances, an ADE (additive-dominant-unique environmental) model better explained the observed variance, which

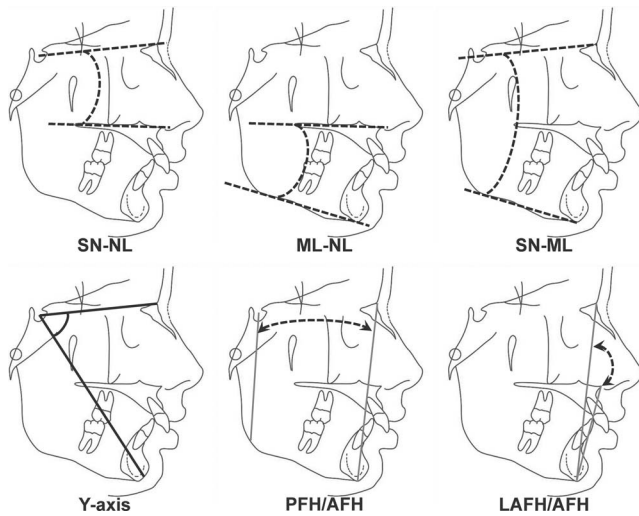


Figure 1. Cephalometric measurements used: A, SN-NL (sella-nasion/nasal line angle); B, ML-NL (nasal line/mandibular line angle); C, SN-ML (sella-nasion/mandibular line angle); D, Y-axis (sella-nasion/sella-gnathion angle); E, PFH/AFH (ratio; posterior face height: anterior face height); and F, LAFH/AFH (ratio; lower anterior face height: anterior face height).

indicated either nonadditive (dominant) or additive genetic influences for all measurements. Models adjusted for sex were chosen for sella-nasion–nasal line angle (SN-NL), nasal line–mandibular line angle (NL-ML), sella-nasion–sella-gnathion angle (Y-axis), posterior face height/anterior face height (PFH/AFH), and LAFH/AFH. Under strong dominant genetic influence were NL-ML (81%), LAFH/AFH (73%), and Y-axis (57%). On the other hand, under the strong additive genetic influence were PFH/AFH (78%), SN-NL (58%),

and SN-ML (57%). Environmental factors accounted for 18–42% of the observed variance, with SN-NL mostly affected (42%). Overall, high classical heritability estimates were seen for all variables except SN-NL, with LAFH/AFH having the highest estimate.

In the secondary analysis at 18 years of age, 82 participants had high-quality films available. These included 46 MZ twins ($n = 14$; 30% female) and 36 DZ twins ($n = 16$; 44% female). Small differences were found between MZ-DZ twins for all variables; only the LAFH/FH variable showed a statistically significant difference of 1.0% (the 95% CI excluded zero). Crude or adjusted-for-sex models were initially selected (Appendix 3) and compared in Table 3. Models adjusted for sex were chosen for SN-NL and PFH/AFH. In almost all cases, an ADE model better explained the observed variance, which indicated either nonadditive (dominant) or additive genetic influences for all vertical measurements. The sole exception was SN-NL, for which an ACE model was better. Only LAFH/AFH was under strong dominant genetic influence at 18 years of age (86%). Conversely, SN-ML (90%), PFH/AFH (89%), Y-axis (85%), and NL-ML (64%) were under strong additive genetic influence. Interestingly, environmental factors common to the twins accounted for 47% of the variance for SN-NL. In contrast, unique environmental factors accounted for 10–39% of the observed variance, with SN-NL being the most affected (39%). In general, high classical heritability estimates were seen for all variables except SN-NL, with highest heritability seen for LAFH/AFH.

Table 1. Average Cephalometric Measurements for the 125 MZ/DZ Twins at 15 and 18 Years of Age

| Variable | 15 y | | | 18 y | | |
|----------|------|------------|---------------------|------|------------|---------------------|
| | n | Mean (SD) | Difference (95% CI) | n | Mean (SD) | Difference (95% CI) |
| SN-NL | | | | | | |
| MZ | 64 | 7.3 (3.2) | 0.5 (−0.9, 1.9) | 46 | 7.5 (3.1) | 0.7 (−0.9, 2.2) |
| DZ | 61 | 6.8 (3.3) | | 36 | 6.8 (2.7) | |
| NL-ML | | | | | | |
| MZ | 64 | 26.0 (4.1) | 1.6 (−0.4, 3.7) | 46 | 24.6 (4.5) | 1.4 (−1.4, 4.3) |
| DZ | 61 | 24.4 (5.8) | | 36 | 23.2 (5.7) | |
| SN-ML | | | | | | |
| MZ | 64 | 33.3 (4.0) | 0.5 (−1.6, 2.7) | 46 | 32.1 (4.3) | 0.2 (−2.8, 3.2) |
| DZ | 61 | 32.8 (5.4) | | 36 | 31.9 (6.1) | |
| Y-axis | | | | | | |
| MZ | 64 | 67.8 (3.2) | 0.7 (−0.9, 2.3) | 46 | 67.7 (3.1) | 1.2 (−1.0, 3.3) |
| DZ | 61 | 67.1 (4.2) | | 36 | 66.5 (4.3) | |
| PFH/AFH | | | | | | |
| MZ | 64 | 65.6 (3.5) | −0.7 (−2.5, 1.1) | 46 | 67.1 (3.8) | 0.3 (−2.4, 2.9) |
| DZ | 61 | 66.2 (4.3) | | 36 | 66.8 (5.3) | |
| LAFH/AFH | | | | | | |
| MZ | 64 | 56.3 (2.2) | 1.4 (0.5, 2.3) | 46 | 56.3 (1.9) | 1.0 (0.1, 2.0) |
| DZ | 61 | 54.9 (2.2) | | 36 | 55.3 (2.1) | |

^a CI indicates confidence interval; DZ, dizygotic twins; MZ, monozygotic twins; SD, standard deviation.

Table 2. Parameter Estimates of Genetic and Environmental Effects on Cephalometric Measurements at 15 Years^a

| Variable | Adjusted | Model | A | | C [D] | | E | | AIC | rMZ | rDZ | h ² |
|----------|----------|------------|-------------|-----|---------------|-------|-----------|-----|--------|------|------|----------------|
| | | | b (SE) | % | b (SE) | % | b (SE) | % | | | | |
| SN-NL | — | <i>ADE</i> | 6.4 (<0.1) | 61% | [<0.1] (<0.1) | [<1%] | 4.1 (0.9) | 39% | 634.62 | 0.61 | 0.43 | 0.36 |
| | Sex | <i>ADE</i> | 5.4 (<0.1) | 58% | [<0.1] (<0.1) | [<1%] | 3.9 (0.9) | 42% | 624.28 | 0.56 | 0.45 | 0.22 |
| NL-ML | — | <i>ADE</i> | <0.1 (<0.1) | <1% | [22.8] (<0.1) | [82%] | 5.1 (1.4) | 18% | 740.14 | 0.73 | 0.11 | 1.24 |
| | Sex | <i>ADE</i> | <0.1 (<0.1) | <1% | [22.1] (<0.1) | [81%] | 5.1 (1.4) | 19% | 737.68 | 0.72 | 0.12 | 1.20 |
| SN-ML | — | <i>AE</i> | 19.3 (3.8) | 81% | — | — | 4.5 (1.2) | 19% | 716.59 | 0.79 | 0.42 | 0.74 |
| | — | <i>ADE</i> | 13.5 (<0.1) | 57% | [5.7] (2.3) | [24%] | 4.4 (1.1) | 19% | 716.36 | 0.79 | 0.42 | 0.74 |
| | Sex | <i>AE</i> | 19.0 (3.8) | 81% | — | — | 4.5 (1.2) | 19% | 717.35 | 0.78 | 0.42 | 0.72 |
| | Sex | <i>ADE</i> | 13.5 (<0.1) | 58% | [5.3] (<0.1) | [23%] | 4.4 (1.1) | 19% | 717.15 | 0.78 | 0.42 | 0.72 |
| Y-axis | — | <i>ADE</i> | 2.6 (<0.1) | 18% | [9.3] (1.4) | [65%] | 2.5 (0.8) | 17% | 654.64 | 0.78 | 0.37 | 0.82 |
| | Sex | <i>ADE</i> | 3.4 (<0.1) | 25% | [8.0] (1.4) | [57%] | 2.5 (0.8) | 18% | 653.84 | 0.76 | 0.37 | 0.78 |
| PFH/AFH | — | <i>AE</i> | 12.2 (2.6) | 78% | — | — | 3.5 (0.7) | 22% | 669.18 | 0.79 | 0.42 | 0.74 |
| | — | <i>ADE</i> | 11.6 (<0.1) | 74% | [0.6] (0.8) | [4%] | 3.4 (0.7) | 22% | 669.17 | 0.79 | 0.42 | 0.74 |
| | Sex | <i>ADE</i> | 12.0 (<0.1) | 78% | [<0.1] (<0.1) | [<1%] | 3.4 (0.7) | 22% | 667.73 | 0.78 | 0.43 | 0.70 |
| LAFH/AFH | — | <i>ADE</i> | <0.1 (<0.1) | <1% | [3.9] (<0.1) | [74%] | 1.4 (0.2) | 26% | 542.65 | 0.72 | 0.03 | 1.38 |
| | Sex | <i>ADE</i> | <0.1 (<0.1) | <1% | [3.7] (<0.1) | [73%] | 1.4 (0.2) | 27% | 538.35 | 0.71 | 0.07 | 1.28 |

^a The most parsimonious model that best describes each cephalometric variable is shown in italics. A indicates additive genetic variance; AIC, Akaike information criterion; b, regression coefficient; C, shared environment variance; D, dominant genetic variance; E, unique environment variance; h², classic heritability; rDZ, correlation of dizygotic twins; rMZ, correlation of monozygotic twins; SE, standard error.

DISCUSSION

For this study, 6 vertical measurements were analyzed in 125 participants at 15 years of age, and 82 participants were analyzed at 18 years. Other than LAFH/FH, all variables showed high between-twins concordance, which agreed with previous data.¹⁷ This is understandable because twins brought up together experience a similar environment and have an identical or similar genome.²¹ Nevertheless, classical heritability estimates revealed that not all variables presented similar heritability, while maxillary inclination showed the least heritability (0.22 at 15 years and 0.28 at 18 years).

According to the results, the so-called ADE model better explained the observed variance for most of the variables. This means either that deviations from the mean phenotype were due to inheritance of a particular allele and this allele's relative effect on the phenotype or that dominant genetic variance involved deviation because of interactions between alternative alleles at a specific locus. Regarding this classification, the findings disagreed with a previous study,¹² which found an ACE model was more suitable to explain the observed variance for SN-ML and ML-NL. This might be because the models were not adjusted for sex. Because heritability of craniofacial components can be influenced by sex,¹⁷ models adjusted for sex were chosen

Table 3. Parameter Estimates of Genetic and Environmental Effects on Cephalometric Measurements at 18 Years^a

| Variable | Adjusted | Model | A | | C [D] | | E | | AIC | rMZ | rDZ | H ² |
|----------|----------|------------|--------------|-----|---------------|-------|------------|-----|--------|------|------|----------------|
| | | | b (SE) | % | b (SE) | % | b (SE) | % | | | | |
| SN-NL | — | <i>ACE</i> | 1.1 (<0.1) | 14% | 4.0 (1.4) | 49% | 3.1 (0.8) | 38% | 394.08 | 0.65 | 0.54 | 0.22 |
| | Sex | <i>ACE</i> | 1.1 (<0.1) | 14% | 3.8 (1.5) | 47% | 3.1 (0.8) | 39% | 393.99 | 0.64 | 0.50 | 0.28 |
| NL-ML | — | <i>AE</i> | 23.9 (5.7) | 87% | — | — | 3.6 (1.0) | 13% | 474.61 | 0.83 | 0.47 | 0.72 |
| | — | <i>ADE</i> | 17.3 (<0.1) | 64% | [6.3] (4.0) | [23%] | 3.6 (1.0) | 13% | 474.48 | 0.83 | 0.47 | 0.72 |
| | Sex | <i>ADE</i> | 17.3 (<0.1) | 64% | [6.0] (3.9) | [22%] | 3.6 (1.0) | 13% | 475.93 | 0.83 | 0.48 | 0.70 |
| SN-ML | — | <i>ADE</i> | 24.3 (<0.1) | 90% | [<0.1] (<0.1) | [<1%] | 2.6 (0.8) | 10% | 464.04 | 0.85 | 0.59 | 0.52 |
| | Sex | <i>AE</i> | 23.0 (5.5) | 90% | — | — | 2.6 (0.9) | 10% | 465.14 | 0.85 | 0.58 | 0.54 |
| | Sex | <i>ADE</i> | 23.0 (<0.01) | 90% | [<0.1] (<0.1) | [<1%] | 2.6 (0.9) | 10% | 465.14 | 0.85 | 0.58 | 0.54 |
| Y-axis | — | <i>AE</i> | 13.2 (2.4) | 90% | v | — | 1.5 (0.5) | 10% | 417.45 | 0.85 | 0.51 | 0.68 |
| | — | <i>ADE</i> | 12.5 (<0.1) | 85% | [0.7] (0.8) | [5%] | 10.3 (3.3) | 10% | 417.44 | 0.85 | 0.51 | 0.68 |
| | Sex | <i>AE</i> | 12.7 (2.5) | 89% | — | — | 1.5 (0.5) | 11% | 417.60 | 0.84 | 0.52 | 0.64 |
| | Sex | <i>ADE</i> | 12.3 (<0.1) | 86% | [0.4] (0.6) | [3%] | 1.5 (0.5) | 11% | 417.60 | 0.84 | 0.52 | 0.64 |
| PFH/AFH | — | <i>ADE</i> | 18.4 (<0.1) | 90% | [<0.1] (<0.1) | [<1%] | 2.1 (0.6) | 10% | 442.81 | 0.85 | 0.61 | 0.48 |
| | Sex | <i>ADE</i> | 17.3 (<0.1) | 89% | [<0.1] (<0.1) | [<1%] | 2.1 (0.6) | 11% | 441.67 | 0.85 | 0.60 | 0.50 |
| LAFH/AFH | — | <i>ADE</i> | <0.1 (<0.1) | <1% | [3.6] (<0.1) | [86%] | 0.6 (0.1) | 14% | 323.33 | 0.83 | 0.16 | 1.34 |
| | Sex | <i>ADE</i> | <0.1 (<0.1) | <1% | [3.5] (<0.1) | [86%] | 0.6 (0.1) | 14% | 324.24 | 0.82 | 0.19 | 1.26 |

^a The most parsimonious model that best describes each cephalometric variable is shown in italics. A indicates additive genetic variance; AIC, Akaike information criterion; b, regression coefficient; C, shared environment variance; D, dominant genetic variance; E, unique environment variance; h², classic heritability; rDZ, correlation of dizygotic twins; rMZ, correlation of monozygotic twins; SE, standard error.

for most of the variables as they fitted the data better. At 15 years, models modified for sex were chosen for the variables SN-NL, NL-ML, Y-axis, PFH/AFH, and LAFH/AFH. At 18 years of age, models adjusted for sex were chosen for SN-NL and PFH/AFH.

However, in this investigation, the ACE model was deemed appropriate for SN-NL at 18 years only. This indicated that either additive genetic factors or shared respective specific environmental factors played a more important role in the expression of this variable than nonadditive genetic factors did. It was interesting that the main contributions of factors A, C, D, and E changed for most variables between 15 and 18 years. For NL-ML and Y-axis, most changed from D to A, which indicated, at 15 years, a mainly dominant (81% and 57%, respectively) and, at 18 years, a mostly additive genetic (64% and 85%, respectively) influence. In addition, SN-ML and PFH/AFH were mainly under additive genetic control at both time points. It therefore seems that there were considerable differences between 15 and 18 years of age in terms of the type of the genetic component (additive or dominant). This might be explained by the fact that most of the vertical components of growth were complete by 15–17 years of age.²² There might be minor sources of further vertical development that contributed in an additive manner up to 18 years of age, while the contribution of dominant factors had diminished considerably. However, LAFH/AFH was the only variable that was still under nonadditive (dominant) genetic influence at 18 years. It is known from the literature whether the lower third of the face is under strong genetic control^{15,23} or whether anterior vertical parameters are more heritable than posterior ones.^{11,12} Nonadditive genetic variation results from interactions between genes, and although they were ignored in many previous genetic evaluations, there are indications for their contribution.²⁴

In summary, other than the SN-NL angle, all other variables were either under additive or, for LAFH/AFH, under nonadditive (dominant) genetic influence at 18 years of age. Interestingly, SN-NL was mainly under additive genetic control (58%) or environmental control (42%) at 15 years. However, at 18 years, environmental influence (unique and shared) dominated (C: 47%, E: 39%). It might be assumed that certain traits were determined more by genetic and less by environmental influences. This might imply that room for individual development exists in MZ twins. This broadly agrees with previous reports that heritability estimates for skeletal characteristics were greater than for dentoalveolar variables.^{12,25,26} Previous studies also indicated that the function and dysfunction of the tongue, cheeks, and lips, such as impaired oral breathing or certain disorders of mastication and body posture, might influence growth development.^{6,27,28} This might

explain why SN-NL is under environmental control at least at 18 years because all of the above-mentioned factors could cause a change in maxillary inclination.

It remains controversial whether vertical or horizontal components are more genetically determined. Some authors have claimed that vertical measurements had greater heritability,^{7,11,29,30} whereas others have described a more substantial genetic contribution for horizontal characteristics.^{12,31} To estimate how much phenotypic variation is attributable to genetic influence, the assessment of a trait's heritability is generally the first step in such genetic studies.²³ On the other hand, heritability estimates should be interpreted with caution, because there are possibilities for several types of bias.³²

Previous studies in the literature indicated that estimates of craniofacial heritability increased with age,³³ and therefore, genetic evaluation might be better performed when most growth has been completed. This is why two time points (15 and 18 years of age) were examined in the present study. It is known from previous studies that mandibular size and shape have lifelong changes, but Buschang³⁴ showed that the residual skeletal growth of the mandible 2 years after the preadolescent growth spurt completion was, in most instances, clinically insignificant.

The strengths of the present study included the evaluation of both MZ and DZ twins that enabled a more accurate partitioning of the genetic and environmental components of craniofacial variation and the quantitative genetic modeling used to investigate the heritability of vertical craniofacial morphology. However, this was a purely clinical/radiographic study, and genome-wide association studies are needed to identify the exact involvement of any genes in craniofacial growth. A comparison of the results with other twin studies is challenging. Because of the differences in zygosity determination, maturity age, sample size, and statistical analysis, comparisons are difficult. In the past, zygosity determination was based on assessment of anthropological resemblance.³⁵ Even though a comparison of physical appearance can be useful, errors can reach 15–20%.³⁶ The ability to assign zygosity to twins improves with serologic testing.³⁷ However, new testing methods, including the use of highly polymorphic regions of deoxyribonucleic acid, are much more accurate and can measure zygosity in up to 90–95% of cases.³⁸ Since similar studies are still rare, a direct comparison is often impossible. The current study indicates that most of the vertical components of the craniofacial complex are under considerable genetic control. Treatment influences the basic growth pattern within individual biological limits, and the environmental contribution to craniofacial variability should not be ignored.

Although the sample in this study had no systemic diseases or anomalies, factors such as airway disorders or habits could have influenced their growth. Because there was no access to medical records, these conditions could not be factored out. In addition, any variation is a sum of growth, environmental impacts, and random error. In addition, low-quality or missing films led to a subsequent loss of power through sample reduction and might have introduced sampling differences. Lastly, all subjects were Caucasian; therefore, the results might not be generalizable.

CONCLUSIONS

- At 15 and 18 years of age, strong additive or dominant genetic components were identified for most vertical cephalometric variables.
- For SN-ML and Y-axis, strong dominant genetic components were found at 15 years but changed to a mainly additive genetic component at 18 years.
- At both 15 and 18 years, environmental factors accounted for 10–40% of the observed variance, with SN-NL being the most affected.
- High heritability was found for most variables pertaining to the inclination of the mandibular corpus, Y-axis, PFH/AFH, and LAFH/AFH, whereas SN-NL showed considerably lower heritability.

REFERENCES

- Langlois J, Kalakanis L, Rubenstein A, Larson A, Hallam M, Smoot M. Maxims or myths of beauty? A meta-analytic and theoretical review. *Psychol Bull.* 2000;126:390–423.
- Pace M, Cioffi I, D'antò V, Valletta A, Valletta R, Amato M. Facial attractiveness of skeletal Class I and Class II malocclusion as perceived by laypeople, patients and clinicians. *Minerva Stomatol.* 2018;67:77–85.
- Bishara SE. Facial and dental changes in adolescents and their clinical implications. *Angle Orthod.* 2000;70:471–483.
- Enlow D. *Handbook of Facial Growth.* Philadelphia, Pa: Saunders; 1982.
- McNamara JA Jr. Neuromuscular and skeletal adaptations to altered function in the orofacial region. *Am J Orthod.* 1973;64:578–606.
- Moss ML, Salentijn L. (1969) The primary role of functional matrices in facial growth. *Am J Orthod.* 1969;55:566–577.
- Hunter WS. A study of the inheritance of craniofacial characteristics as seen in lateral cephalograms of 72 like-sexed twins. *Rep Congr Eur Orthod Soc.* 1965;41:59–70.
- Lundström A, McWilliam JS. A comparison of vertical and horizontal cephalometric variables with regard to heritability. *Eur J Orthod.* 1987;9:104–108.
- Peng J, Deng H, Cao C, Ishikawa M. Craniofacial morphology in Chinese female twins: a semi-longitudinal cephalometric study. *Eur J Orthod.* 2005;27:556–561.
- Townsend G, Richards L. Twins and twinning, dentists and dentistry. *Aust Dent J.* 1990;35:317–327.
- Manfredi C, Martina R, Grossi GB, Giuliani M. Heritability of 39 orthodontic cephalometric parameters on MZ, DZ twins and MN-paired singletons. *Am J Orthod Dentofacial Orthop.* 1997;111:44–51.
- Šidlauskas M, Šalomskienė L, Andriuskevičiūtė I, et al. Heritability of mandibular cephalometric variables in twins with completed craniofacial growth. *Eur J Orthod.* 2016;38:493–502.
- van der Linden FP. Genetic and environmental factors in dentofacial morphology. *Am J Orthod.* 1966;52:576–583.
- Lauweryns I, Carels C, Vlietinck R. The use of twins in dentofacial genetic research. *Am J Orthod Dentofacial Orthop.* 1993;103:33–38.
- Dudas M, Sassouni V. The hereditary components of mandibular growth, a longitudinal twin study. *Angle Orthod.* 1973;43:314–322.
- Hersberger-Zurfluh MA, Papageorgiou SN, Motro M, Kantarci A, Will LA, Eliades T. Soft tissue growth in identical twins. *Am J Orthod Dentofacial Orthop.* 2018;154:683–692.
- Hersberger-Zurfluh MA, Papageorgiou SN, Motro M, Kantarci A, Will LA, Eliades T. Vertical growth in mono- and dizygotic twins: a longitudinal cephalometric cohort study. *Orthod Craniofac Res.* 2020;23:192–201.
- Lundström A. Nature versus nurture in dentofacial variation. *Eur J Orthod.* 1984;6:77–91.
- Christian JC, Kang KW, Norton JJ Jr. Choice of an estimate of genetic variance from twin data. *Am J Hum Genet.* 1974;26:154–161.
- Bland JM, Altman DG. Statistical methods for assessing agreement between two methods of clinical measurement. *Lancet.* 1986;1:307–310.
- Pam A, Kemker SS, Ross CA, Golden R. The “equal environments assumption” in MZ-DZ twin comparisons: an untenable premise of psychiatric genetics? *Acta Gen Med Gemellol (Roma).* 1996;45:349–360.
- Snodell SF, Nanda RS, Currier GF. A longitudinal cephalometric study of transverse and vertical craniofacial growth. *Am J Orthod Dentofacial Orthop.* 1993;104:471–483.
- Amini F, Borzabadi-Farahani A. Heritability of dental and skeletal cephalometric variables in monozygous and dizygous Iranian twins. *Orthod Waves.* 2009;68:72–79.
- Gengler N, VanVleck LD, MacNeil MD, Misztal I, Pariacote FA. Influence of dominance relationships on the estimation of dominance variance with sire-dam subclass effects. *J Anim Sci.* 1997;75:2885–2891.
- Nakasima A, Ichinose M, Nakata S, Takahama Y. Hereditary factors in the craniofacial morphology of Angle's Class II and Class III malocclusions. *Am J Orthod Dentofacial Orthop.* 1982;82:150–156.
- Lundström A, McWilliam J. The influence of heredity and environment on six variables describing incisor orientation. *Eur J Orthod.* 1986;8:259–264.
- Sidlauskienė M, Smailienė D, Lopatiene K, Čekanauskas E, Pribušienė R, Šidlauskas M. Relationships between malocclusion, body posture, and nasopharyngeal pathology in pre-orthodontic children. *Med Sci Monit.* 2015;21:1765–1773.
- Kasparaviciene K, Sidlauskas A, Zasciurinskiene E, et al. The prevalence of malocclusion and oral habits among 5-7-year-old children. *Med Sci Monit.* 2014;20:2036–2042.
- Savoye I, Loss R, Carels C, Derom C, Vlietinck R. A genetic study of anteroposterior and vertical facial proportions using model-fitting. *Angle Orthod.* 1998;68:467–470.
- Carels C, Van Cauwenberghe N, Savoye I, et al. A quantitative genetic study of cephalometric variables in twins. *Clin Orthod Res.* 2001;4:130–140.

31. Kim E, Sung J, Song YM, et al. Heritability of facial skeletal and dental characteristics of monozygotic and dizygotic twins using cephalometric analysis and Falconer's method. *J Craniofac Surg.* 2018;29:e274–e279.
32. Allen G. Comments on the analysis of twin samples. *Acta Genet Med Gemellol (Roma).* 1955;4:143–160.
33. Harris EF, Johnson MG. Heritability of craniometric and occlusal variables: a longitudinal sib analysis. *Am J Orthod Dentofacial Orthop.* 1991;99:258–268.
34. Buschang PH. Craniofacial growth and development. In: English J, Akyalcin S, Peltomaki T, Litschel K, eds. *Mosby's Orthodontic Review.* 2nd ed. St Louis, Mo: Mosby; 2014:1–13.
35. Lundström A, McWilliam JS. A comparison of vertical and horizontal cephalometric variables with regard to heritability. *Eur J Orthod.* 1987;9:104–108.
36. Vuollo V, Sidlauskas M, Sidlauskas A, et al. Comparing facial 3D analysis with DNA testing to determine zygosity of twins. *Twin Res Hum Genet.* 2015;18:306–313.
37. Townsend G, Hughes T, Luciano M, Bockmann M, Brook A. Genetic and environmental influences on human dental variation: a critical evaluation of studies involving twins. *Arch Oral Biol.* 2009;54:45–51.
38. Nyholt DR. On the probability of dizygotic twins being concordant for two alleles at multiple polymorphic loci. *Twin Res Hum Genet.* 2006;9:194–197.

APPENDIX 1

Additional Details of the Statistical Model

A pair of MZ twins is genetically identical (ie, genetic correlation of 1). ACE and AE models assume that genetic effects are additive (ie, there is no epistasis); therefore, by Mendelian inheritance rules, the genetic correlation within a pair of DZ twins is 0.5. ADE models assume interactions between genetic influences inducing nonadditive—dominant—genetic effects, with a genetic correlation within a pair of DZ twins of 0.75 (0.5 additive genetic correlation and 0.25 dominant genetic correlation). Further assumptions include the lack of assortative mating of the twins' parents and the equal environments' assumption for MZ/DZ twins (which was supported by the Forsyth Moorrees twin study description), while the AE/ADE models assume no environmental effects shared by both twins of a twin pair (no C).

Appendix 2. Model Selection for Cephalometric Measurements at 15 Years of Age for the Unadjusted Model Based on the Akaike Information Criterion^a

| Variable | Crude | | | | Adjusting for Sex | | | |
|----------|--------|--------|--------|----------|-------------------|--------|--------|---------|
| | ACE | AE | ADE | Choice | ACE | AE | ADE | Choice |
| SN-NL | 638.35 | 636.62 | 634.62 | ADE | 627.20 | 626.28 | 624.28 | ADE |
| NL-ML | 746.89 | 744.89 | 740.14 | ADE | 744.21 | 744.21 | 737.68 | ADE |
| SN-ML | 718.59 | 716.59 | 716.36 | AE / ADE | 719.35 | 717.35 | 717.15 | AE / DE |
| Y-axis | 658.05 | 656.05 | 654.64 | ADE | 657.00 | 655.00 | 653.84 | ADE |
| PFH/AFH | 671.18 | 669.18 | 669.17 | AE / ADE | 671.73 | 669.73 | 667.73 | ADE |
| LAFH/AFH | 547.27 | 545.27 | 542.65 | ADE | 544.68 | 542.68 | 538.35 | ADE |

^a A indicates additive genetic variance; C, shared environment variance; D, dominant genetic variance; E, unique environment variance.

Appendix 3. Model Selection for Cephalometric Measurements at 18 Years of Age for the Model Adjusted for Sex Based on the Akaike Information Criterion^a

| Variable | Crude | | | | Adjusted for Sex | | | |
|----------|--------|--------|--------|--------|------------------|--------|--------|--------|
| | ACE | AE | ADE | Choice | ACE | AE | ADE | Choice |
| SN-NL | 394.08 | 395.51 | 395.51 | ACE | 393.99 | 395.25 | 395.25 | ACE |
| NL-ML | 476.61 | 474.61 | 474.48 | AE/ADE | 478.04 | 476.04 | 475.93 | ADE |
| SN-ML | 467.93 | 466.04 | 464.04 | ADE | 467.08 | 465.14 | 465.14 | AE/ADE |
| Y-axis | 419.45 | 417.45 | 417.44 | AE/ADE | 419.60 | 417.60 | 417.60 | AE/ADE |
| PFH/AFH | 446.59 | 444.81 | 442.81 | ADE | 445.53 | 443.67 | 441.67 | ADE |
| LAFH/AFH | 325.32 | 325.32 | 323.33 | ADE | 328.16 | 326.16 | 324.24 | ADE |

^a A indicates additive genetic variance; C, shared environment variance; D, dominant genetic variance; E, unique environment variance.