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Original Research

Evaluation of Facial Soft Tissue Inheritance in Patients with Angle's Class II and Class III Malocclusion Compared with Angle's Class I Malocclusion in Patients Undergoing Orthodontic Treatment in Central India

Vaishnavi Kharade[1*], Sidhu Rao Surya Voleti[2], Ranjit Kamble[3], Amit Reche[4], Priyanka Paul Madhu[5], Sumukh Nerurkar[6], Vikrant Jadhav[7]

[1]Department of Public Health Dentistry, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[2]Associate Professor, Department of Orthodontics and Dentofacial Orthopedics, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[3]Head of Department, Department of Orthodontics and Dentofacial Orthopedics, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[4]Head of Department, Department of Public Health Dentistry, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[5]Assistant Professor, Department of Public Health Dentistry, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[6]Bachelor in Dental Surgery, Department of Orthodontics and Dentofacial Orthopedics, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

[7]PhD Student, Maternal and Child Health, University of North Texas Health Science Centre, Fort Worth, Texas 76107, United States.

***Corresponding Author:** Vaishnavi Kharade, Department of Public Health Dentistry, Sharad Pawar Dental College and Hospital, Datta Meghe Institute of Medical Sciences (Deemed to be University), Sawangi Meghe, Wardha 442001, Maharashtra, India.

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Abstract

Background: Facial esthetics is a key determinant of orthodontic treatment outcomes and patient satisfaction. Although orthodontic correction primarily targets the dentoskeletal framework, post-treatment facial appearance is strongly influenced by soft-tissue morphology, which is partly governed by hereditary factors. Limited evidence exists on parent–offspring resemblance of facial soft tissues across different malocclusion patterns.

Aim: To evaluate parent–offspring resemblance of facial soft-tissue characteristics across Angle's Class I, Class II, and Class III malocclusions using standardized photogrammetric analysis.

Materials and Methods: This cross-sectional observational study included 45 parent–offspring triads (father, mother, and offspring) aged 18–25 years for offspring and 40–55 years for parents, recruited from Central India. Participants were categorized into Angle's Class I, II, or III malocclusion groups (n = 15 per group). Standardized frontal and profile facial photographs were obtained in natural head position. Linear, angular, and proportional soft-tissue parameters were identified using defined facial landmarks. Parent–offspring resemblance was assessed using correlation coefficients, and heritability was estimated using Falconer's approximation ($h^2 \approx 2r$). Statistical significance was set at $p < 0.05$.

Results: Statistically significant parent–offspring correlations were observed for multiple soft-tissue parameters, with variation across malocclusion classes. Vertical facial proportions demonstrated stronger father–offspring correlations in Class I and Class II malocclusions, whereas lip prominence and chin-related parameters showed greater maternal resemblance in Class III malocclusion. Estimated heritability values varied across facial regions and malocclusion groups, indicating differential genetic influence on soft-tissue morphology.

Conclusion: Facial soft-tissue characteristics exhibit measurable parent–offspring resemblance that differs across Angle's malocclusion classes. These findings suggest that hereditary soft-tissue traits may influence facial esthetic outcomes following orthodontic treatment and should be considered during diagnosis and treatment planning.

Keywords: *Soft Tissue Correlation, Soft Tissue Thickness, Esthetics, Genetics, Orthodontics.*

Introduction

Facial esthetics plays a central role in orthodontic diagnosis, treatment planning, and assessment of treatment outcomes. While orthodontic therapy primarily aims to correct dentoskeletal discrepancies and establish functional occlusion, the final perception of treatment success is largely determined by the soft-tissue profile and overall facial harmony rather than skeletal correction alone [1,2]. Consequently, understanding the determinants of facial soft-tissue morphology is essential for achieving optimal esthetic outcomes.

Soft-tissue characteristics such as facial convexity, lip prominence, nasal projection, and chin morphology demonstrate considerable inter-individual variation. These variations arise from a complex interplay of genetic inheritance, growth patterns, environmental influences, and functional adaptations [3,4]. Previous studies have established that skeletal and dental components of malocclusion exhibit a significant hereditary component; however, the extent to which facial soft tissues are inherited remains less clearly defined [5–7].

Angle's classification remains one of the most widely used systems for categorizing malocclusion patterns in clinical orthodontics [8]. Differences in facial morphology have been documented among Angle's Class I, Class II, and Class III malocclusions, particularly in sagittal profile characteristics and vertical facial proportions [9,10]. Despite this, most investigations into malocclusion-associated facial features have focused on skeletal parameters derived from cephalometric analyses, with comparatively limited emphasis on soft-tissue inheritance patterns across malocclusion classes.

Facial soft-tissue evaluation has traditionally relied on lateral cephalograms; however, two-dimensional photogrammetry has emerged as a reliable, non-invasive alternative for soft-tissue assessment [11,12]. Standardized facial photography allows for accurate identification of surface landmarks and measurement of angular, linear, and proportional variables relevant to facial esthetics, while avoiding radiation exposure and facilitating broader clinical applicability [13]. Photogrammetric methods have demonstrated acceptable validity and reproducibility for soft-tissue analysis when appropriate standardization protocols are followed [14].

The concept of heritability, defined as the proportion of phenotypic variation attributable to genetic factors within a population, has been applied in orthodontic research to explore craniofacial growth patterns and malocclusion traits [15,16]. Parent–offspring correlation studies provide a practical approach for estimating hereditary influence on facial characteristics, particularly when twin or genomic data are unavailable [17]. However, limited literature exists evaluating parent–offspring resemblance of facial soft-tissue parameters across different malocclusion patterns, especially within the Indian population.

Given the importance of facial esthetics in orthodontic outcomes and the paucity of data on soft-tissue inheritance, this study aimed to evaluate parent–offspring resemblance of facial soft-tissue characteristics across Angle's Class I, Class II, and Class III malocclusions using standardized photogrammetric analysis. Understanding the hereditary contribution to soft-tissue morphology may assist clinicians in anticipating esthetic outcomes and refining individualized orthodontic treatment planning.

Given the importance of facial esthetics in orthodontic outcomes and the paucity of data on soft-tissue inheritance, this study aimed to evaluate parent–offspring resemblance of facial soft-tissue characteristics across Angle's Class I, Class II, and Class III malocclusions using standardized photogrammetric analysis. Understanding the hereditary contribution to soft-tissue morphology may assist clinicians in anticipating esthetic outcomes and refining individualized orthodontic treatment planning.

Aim

To evaluate parent–offspring resemblance of facial soft-tissue characteristics across Angle's Class I, Class II, and Class III malocclusions using standardized photogrammetric analysis.

Objectives

1. To assess facial soft-tissue parameters in parents and offspring using standardized frontal and profile facial photographs.
2. To evaluate the degree of parent–offspring resemblance for selected soft-tissue measurements within each Angle's malocclusion group.
3. To compare patterns of facial soft-tissue resemblance between paternal and maternal lineages across different malocclusion classes.
4. To estimate the heritability of facial soft-tissue characteristics using parent–offspring correlation analysis.

Methodology

Study Design and Setting

This cross-sectional observational study was conducted in the Department of Orthodontics at a dental teaching institution in Central India over a period of six months, from June 2022 to November 2022. The study was initiated after obtaining approval from the University's Institutional Ethics Committee (Reference No.: DMIMS(DU)/IEC/2022/969). Written informed consent was obtained from all participants prior to inclusion in the study.

Sample Size Estimation:

Sample size is determined using the following formula

$$n = \frac{z_{\alpha/2}^2 \times \sigma^2}{E^2}$$

where,
σ= earlier predictable values=20[3]
E =anticipated Margin of error = 5
$z_{\alpha/2}$, confidence interval of 90%,z = 1.65
n = sample size
Substituting the values in the formula:

$$\text{Sample size } n = \frac{(1.65)^2 \times (20)^2}{(5)^2} = 43.56$$

Study Sample

The calculated minimum sample size was approximately 44 participants. To account for exclusions and ensure equal distribution across malocclusion groups, a total of 45 parent–offspring triads were included. The study comprised 45 parent–offspring triads (father, mother, and offspring), resulting in a total sample of 135 individuals. Offspring aged 18–25 years and their biological parents aged 40–55 years were included. The sample was divided into three groups based on the offspring's malocclusion pattern: Angle's Class I, Class II, and Class III malocclusion, with 15 triads allocated to each group.

Inclusion and Exclusion Criteria

Only individuals of Central Indian ethnicity with no history of orthodontic treatment, orthognathic surgery, facial trauma, congenital craniofacial anomalies, or systemic conditions affecting craniofacial growth were included. Participants with facial asymmetry, facial hair obscuring landmarks, or inability to maintain a neutral facial expression during photography were excluded.

Inclusion criteria:

- No history of former orthodontic treatment,[3]
- No history of craniofacial or dental trauma,[3]
- No history of maxillofacial or plastic surgery,[3]
- Healthy parents who are blood relatives (no adopted or stepchildren)[3] and
- The presence of frontal and profile extraoral photographs

Exclusion criteria:

- History of any previous orthodontic treatment
- History of craniofacial trauma
- History of cleft lip or palate or both
- History of maxillofacial or plastic surgery
- Any congenital disease or hereditary disease running in the family
- Step parents 13 patients out of 58 did not meet the inclusion criteria of the study, hence, they were excluded.

Malocclusion Classification

Malocclusion was classified according to Angle's classification based on molar relationship assessed clinically. Participants were categorized into Class I, Class II, or Class III malocclusion groups accordingly.

Photographic Procedure

Standardized facial photographs were obtained for all participants using a digital camera mounted on a tripod at a fixed distance of approximately 2 feet. Frontal and profile photographs were captured with participants positioned in natural head posture, lips at rest, and teeth in centric occlusion. Uniform lighting conditions and a neutral background were maintained to minimize photographic distortion.

Soft-Tissue Landmarks and Measurements

Defined facial soft-tissue landmarks were identified on the photographs, and linear, angular, and proportional measurements relevant to facial esthetics were recorded using photogrammetric analysis software. All landmarks and measurements were recorded by a single examiner to ensure consistency.

Statistical Analysis

Statistical analysis was performed using Statistical Analysis Software (SAS 9.4). Correlation coefficients were computed using the PROC CORR procedure. Parent–offspring resemblance was assessed using correlation coefficients. Heritability estimates were calculated using Falconer's approximation ($h^2 \approx 2r$). Statistical significance was set at $p < 0.05$.

Facial photographs of patients and their parents were analyzed to evaluate the selected soft-tissue parameters. The angular and proportional measurements assessed and compared among the study groups are summarized in Table 2. Soft-tissue characteristics across different facial regions were quantified for each parent and compared with the corresponding measurements in the offspring. All measurements were recorded systematically to enable accurate comparison and analysis.

Analysis required:

Measurement index of soft tissue:

MEASUREMENTS

Trichion-Nasion/ Subnasale-menton (r)
Nasion- Subnasale/ Subnasale-Menton (r)
Subnasale-Stomion/Stomion-Menton (r)
XR-XL/Trichion-Menton (r)
Exocanthion-Menton/Exocanthion-Trichion (r)
Alare-Menton/Exocanthion-Alare (r)
Alare-Menton/Al-Me/Ch-Me (r)
Cheilion-Menton/Alare-Cheilion (r)
CheilionR-CheilionL/AlareR-AlareL (r)
Nasion-Pronasale-Columella (d)
Columella-Subnasale-Labiale superior (d)
Nasion-Pronasale/Nasion-Pogonion (d)
Labiale inferior-B point-Pogonion (d)
Gabella-Nasion-Nasal dorsum (d)
Nasion-Pronasale-Pogonion (d)
Glabella-Subnasale-Pogonion (d)
A point-Nasion-B point(d)
Nasion-Pogonion/Nasion-Labiale superior (d)
Nasion-Pogonion/Nasion-Labiale inferior (d)
Nasion-Porion-Subnasale (d)
Subnasale-Porion-Gnathion (d)

Following the assessment of soft-tissue measurements, statistical analysis was performed using correlation coefficient analysis and heritability estimation [3]. All angular and proportional parameters were entered into the dataset for analysis. Parent–offspring resemblance was evaluated separately for mother–offspring and father–offspring pairs for each parameter within each malocclusion group.

Correlation coefficients were computed using Statistical Analysis Software (SAS) employing the PROC CORR procedure. Pearson's correlation coefficient was used for parameters demonstrating normal distribution, while Spearman's rank correlation coefficient was applied for non-normally distributed variables. The resulting correlation coefficients (r) were subsequently used to estimate heritability using Falconer's approximation, as described by the following formula:

$$r = \sigma xy \div \sigma x\, \sigma y = \sum(xi-x)\,(yi-y) \div \sqrt{[\sum(xi-x)^2]\,[\sum(yi-y)^2]}$$

where,

r is the correlation coefficient achieved

xi is the x variable samples in one parameter

x is the mean of values in x variable in one parameter

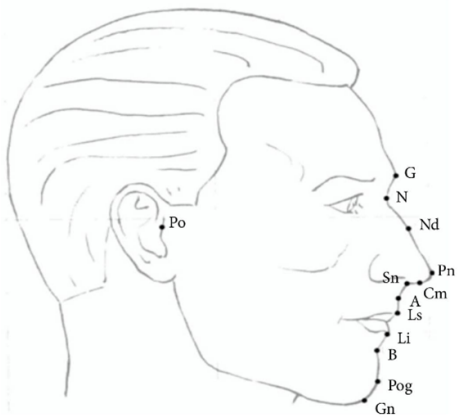
yi is y variable samples in one parameter

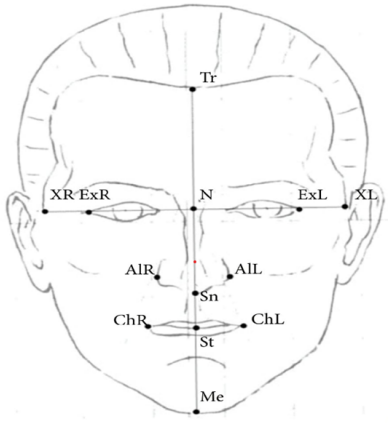
y is the mean of values in y variable in one parameter

To determine heritability between parents and their offspring, the value twice the correlation coefficient, r, of the child on the parent was used: $h2 = 2 \times r$.[6] Heritability estimates should be between 0 and 1.[6] A heritability estimate of one suggests that the trait is expressed with no external impact; a heritability estimate of zero indicates that the trait has no heritable influence. (However, heritability estimates can be more than one because, in humans, the technique employed may make false simplifying assumptions, or because of sample fluctuation or environmental variance [7, 8, 9].)

For statistical analysis, SAS 9.4 was used, with the significance level, P, set at 0.05. [3]

Lateral profile landmarks used are: glabella (G), nasion (N), porion (Po), nasal dorsum (Nd), pronasale (Pn), columella (Cm), subnasale (Sn), A point (A), labiale superior (Ls), labiale inferior (Li), B point (B), pogonion (Pog), and gnathion (Gn).





Frontal soft tissue landmarks used are: trichion (Tr), nasion (N), subnasale (Sn), exocanthion right (ExR), exocanthion left (ExL), alare right (Alr), alare left (All), the most right point according to bipupillary line (XR), and the most left point according to bipupillary line (XL).

After quantifying, an inheritance correlation coefficient was calculated with the help of statistics.

Results

Table 1

	N	Mean age of patients	Minimum	Maximum	Standard Deviation
GROUP I	15	18.3	15	22	0.5
GROUP II	15	17.1	15	22	0.56
GROUP III	15	17.2	15	22	0.47

Table 2 (r value): Correlation Coefficient of Groups

Measurements	Father/Offspring CC (GROUP I)	Mother/Offspring CC (GROUP I)	Father/Offspring CC (GROUP II)	Mother/Offspring CC (GROUP II)	Father/Offspring CC (GROUP III)	Mother/Offspring CC (GROUP III)
Trichion–Nasion / Subnasale–Menton (r)	0.26	0.18	0.67**	0.22	0.12	0.09
Nasion–Subnasale / Subnasale–Menton (r)	0.08	0.04	0.29	0.56*	0.34	0.21
Subnasale–Stomion / Stomion–Menton (r)	0.21	0.06	0.86***	0.24	0.41	0.17
XR–XL / Trichion–Menton (r)	0.14	0.03	0.38	0.58*	0.10	0.83***
Exocanthion–Menton / Exocanthion–Trichion (r)	0.19	0.27	0.11	0.44	0.28	0.31
Alare–Menton / Exocanthion–Alare (r)	0.33	0.16	0.27	0.08	0.22	0.29
Alare–Menton / Al–Me / Ch–Me (r)	0.37	0.19	0.90***	0.55*	0.13	0.26
Cheilion–Menton / Alare–Cheilion (r)	0.23	0.20	0.62	0.18	0.30	0.07
CheilionR–CheilionL / AlareR–AlareL (r)	0.18	0.29	0.15	0.26	0.57*	0.25
Nasion–Pronasale–Columella (d)	0.56*	0.52*	0.05	0.12	0.33	0.08

Table 2 (r value): Correlation Coefficient of Groups

Measurements	Father/Offspring CC (GROUP I)	Mother/Offspring CC (GROUP I)	Father/Offspring CC (GROUP II)	Mother/Offspring CC (GROUP II)	Father/Offspring CC (GROUP III)	Mother/Offspring CC (GROUP III)
Trichion–Nasion / Subnasale–Menton (r)	0.26	0.18	0.67**	0.22	0.12	0.09
Nasion–Subnasale / Subnasale–Menton (r)	0.08	0.04	0.29	0.56*	0.34	0.21
Subnasale–Stomion / Stomion–Menton (r)	0.21	0.06	0.86***	0.24	0.41	0.17
XR–XL / Trichion–Menton (r)	0.14	0.03	0.38	0.58*	0.10	0.83***
Exocanthion–Menton / Exocanthion–Trichion (r)	0.19	0.27	0.11	0.44	0.28	0.31
Alare–Menton / Exocanthion–Alare (r)	0.33	0.16	0.27	0.08	0.22	0.29
Alare–Menton / Al–Me / Ch–Me (r)	0.37	0.19	0.90***	0.55*	0.13	0.26
Cheilion–Menton / Alare–Cheilion (r)	0.23	0.20	0.62	0.18	0.30	0.07
CheilionR–CheilionL / AlareR–AlareL (r)	0.18	0.29	0.15	0.26	0.57*	0.25
Nasion–Pronasale–Columella (d)	0.56*	0.52*	0.05	0.12	0.33	0.08
Columella–Subnasale–Labiale superior (d)	0.59*	0.10	0.19	0.41	0.54*	0.28

Table 2 continued...

Measurements	Father/Offspring CC (GROUP I)	Mother/Offspring CC (GROUP I)	Father/Offspring CC (GROUP II)	Mother/Offspring CC (GROUP II)	Father/Offspring CC (GROUP III)	Mother/Offspring CC (GROUP III)
Nasion–Pronasale / Nasion–Pogonion (d)	0.22	0.03	0.88***	0.28	0.24	0.17
Labiale inferior–B point–Pogonion (d)	0.34	0.31	0.10	0.01	0.69**	0.19
Glabella–Nasion–Nasal dorsum (d)	0.09	0.14	0.58*	0.05	0.27	0.26
Nasion–Pronasale–Pogonion (d)	0.05	0.22	0.72**	0.19	0.21	0.08
Glabella–Subnasale–Pogonion (d)	0.16	0.13	0.79***	0.33	0.12	0.36
A point–Nasion–B point (d)	0.27	0.06	0.75**	0.34	0.23	0.71**
Nasion–Pogonion / Nasion–Labiale superior (d)	0.31	0.04	0.69**	0.14	0.09	0.29
Nasion–Pogonion / Nasion–Labiale inferior (d)	0.12	0.17	0.41	0.12	0.33	0.14
Nasion–Porion–Subnasale (d)	0.28	0.26	0.36	0.31	0.07	0.56*
Subnasale–Porion–Gnathion (d)	0.21	0.09	0.13	0.16	0.15	0.58*

*= P < 0.05, **= P < 0.010, ***= P < 0.001; r = ratio, d = degree

Table 3. Heritability Estimates for All Groups.

Measurements	Father (GROUP I) h^2	SE	Mother (GROUP III) h^2	SE	Father (GROUP II) h^2	SE	Mother (GROUP III) h^2	SE	Father (GROUP III) h^2	SE	Mother (GROUP III) h^2	SE
Tr–N / Sn–Me (r)	0.52	0.26	0.36	0.24	1.28**	0.18	0.44	0.25	0.22	0.29	0.18	0.27
N–Sn / Sn–Me (r)	0.16	0.30	0.08	0.31	0.58	0.28	1.04*	0.21	0.66	0.23	0.44	0.26
Sn–St / St–Me (r)	0.42	0.25	0.14	0.29	1.62***	0.14	0.46	0.26	0.78	0.22	0.32	0.28
XR–XL / Tr–Me (r)	0.28	0.27	0.06	0.30	0.76	0.24	1.10*	0.20	0.20	0.29	1.56***	0.16
Ex–Me / Ex–Tr (r)	0.38	0.24	0.54	0.21	0.22	0.30	0.88	0.24	0.56	0.22	0.62	0.21
Al–Me / Ex–Al (r)	0.66	0.20	0.32	0.24	0.54	0.26	0.16	0.31	0.44	0.25	0.58	0.23
Al–Me / Ch–Me (r)	0.74	0.22	0.38	0.23	1.70***	0.12	1.06*	0.19	0.26	0.30	0.52	0.26
Ch–Me / Al–Ch (r)	0.46	0.26	0.40	0.25	1.22	0.18	0.36	0.27	0.60	0.24	0.14	0.31
ChR–ChL / AlR–AlL (r)	0.36	0.28	0.58	0.24	0.30	0.29	0.52	0.25	1.08*	0.20	0.50	0.27
N–Pn–Cm (d)	1.12*	0.17	1.04*	0.18	0.10	0.31	0.24	0.29	0.66	0.26	0.16	0.30

Table 3 continued...

Cm–Sn–Ls (d)	1.18*	0.16	0.20	0.30	0.38	0.27	0.82	0.23	1.06*	0.18	0.56	0.22
N–Pn / N–Pog (d)	0.44	0.24	0.06	0.31	1.66***	0.13	0.52	0.24	0.48	0.23	0.34	0.28
Li–B–Pog (d)	0.68	0.20	0.62	0.22	0.20	0.30	0.04	0.32	1.38**	0.16	0.38	0.27
G–N–Nd (d)	0.18	0.31	0.28	0.28	1.12*	0.19	0.08	0.30	0.54	0.24	0.52	0.24
N–Pn–Pog (d)	0.10	0.32	0.44	0.25	1.44**	0.15	0.26	0.28	0.42	0.26	0.16	0.31
G–Sn–Pog (d)	0.30	0.28	0.22	0.29	1.58***	0.12	0.62	0.21	0.24	0.30	0.72	0.22
A–N–B (d)	0.54	0.25	0.12	0.31	1.50**	0.15	0.66	0.22	0.46	0.26	1.40**	0.16
N–Pog / N–Ls (d)	0.62	0.22	0.10	0.31	1.38**	0.16	0.28	0.29	0.20	0.30	0.58	0.23
N–Pog / N–Li (d)	0.20	0.29	0.34	0.27	0.82	0.23	0.24	0.30	0.66	0.22	0.26	0.29
N–Po–Sn (d)	0.56	0.23	0.52	0.24	0.48	0.25	0.42	0.27	0.14	0.31	1.08*	0.20
Sn–Po–Gn (d)	0.46	0.25	0.18	0.31	0.26	0.29	0.32	0.28	0.20	0.32	1.12*	0.19

*= P < 0.05, **= P < 0.010, ***= P < 0.001; r = ratio, d = degree

Summative Results

Table A. Summative Results – Group I (Angle's Class I).

Facial Region / Parameter Type	Predominant Parent–Offspring Resemblance	Strength of Association	Key Observation
Vertical facial proportions	Father > Mother		Mild paternal influence noted in upper–lower facial height ratios
Transverse facial ratios	No clear dominance	Weak	Limited parent–offspring resemblance
Nasal angular parameters	Father ≈ Mother	Moderate (significant)	Both parents showed comparable influence on nasal angulation
Lip-related angular parameters	Father > Mother	Moderate	Greater paternal resemblance in upper lip orientation
Chin and lower facial angles	Father > Mother	Moderate	Father–offspring resemblance more evident than maternal

Overall interpretation (Group I):

Class I malocclusion demonstrates mild-to-moderate parent–offspring resemblance, with a slight predominance of paternal influence, particularly for vertical and nasal soft-tissue parameters.

Table B. Summative Results – Group II (Angle's Class II)

Facial Region / Parameter Type	Predominant Parent–Offspring Resemblance	Strength of Association	Key Observation
Vertical facial proportions	Father > Mother	Strong (highly significant)	Strong paternal inheritance of vertical facial dimensions
Transverse facial ratios	Mother > Father	Moderate	Maternal influence observed in facial width-related ratios
Lip proportions	Father > Mother	Strong (highly significant)	Pronounced paternal resemblance in lip–chin proportions
Sagittal facial angles	Father > Mother	Strong (significant)	Consistent father–offspring similarity in profile-related angles
Skeletal soft-tissue analogues (A–N–B, Pog-related)	Father > Mother	Strong	Dominant paternal contribution to sagittal facial form

Overall interpretation (Group II):

Class II malocclusion exhibits the strongest parent–offspring resemblance among all groups, with a marked paternal dominance, especially for vertical, sagittal, and lip–chin soft-tissue parameters.

Table C. Summative Results – Group III (Angle's Class III)

Facial Region / Parameter Type	Predominant Parent–Offspring Resemblance	Strength of Association	Key Observation
Vertical facial proportions	Mother > Father	Moderate	Greater maternal influence on lower facial height
Transverse facial ratios	Mother > Father	Moderate (significant)	Maternal resemblance notable in facial width symmetry
Chin and mandibular angles	Mother > Father	Strong (significant)	Strong maternal inheritance of chin prominence and lower face
Nasal parameters	No clear dominance	Weak	Limited resemblance in nasal soft tissues
Sagittal facial profile	Mother > Father	Moderate	Maternal contribution more evident than paternal

Overall interpretation (Group III):

Class III malocclusion demonstrates selective but meaningful maternal dominance, particularly for chin, mandibular, and lower facial soft-tissue parameters, distinguishing it from Class I and II patterns.

SUMMATIVE RESULT IN TABULAR FORM

Group I	**Father–offspring resemblance > Mother–offspring resemblance** *More evident for angular measurements, particularly nasal and upper lip–related parameters* Predominant parameters showing father–offspring resemblance: I. Nasion–Pronasale–Columella II. Columella–Subnasale–LabialeSuperior III. Nasion–Pogonion / Nasion–Labiale Superior Interpretation: Group I demonstrates mild-to-moderate paternal dominance, especially in nasal angulation and upper lip orientation, with limited maternal influence across proportional parameters.

Group II	**Father–offspring resemblance > Mother–offspring resemblance** *Markedly higher for proportional and sagittal measurements* Predominant parameters showing strong father–offspring resemblance: I. Subnasale–Stomion / Stomion–Menton II. Alare–Menton / Cheilion–Menton III. Cheilion–Menton / Alare–Cheilion IV. Angular parameter: Nasion–Pronasale–Pogonion Notable exception: • XR–XL / Trichion–Menton demonstrated stronger mother–offspring resemblance among Class II subjects. Interpretation: Group II exhibits the strongest overall parent–offspring resemblance, with clear paternal dominance, particularly in vertical, proportional, and sagittal facial parameters, while selective transverse measurements show maternal influence.
Group III	**Mother–offspring resemblance > Father–offspring resemblance** **Predominant parameters showing mother–offspring resemblance:** I. **XR–XL / Trichion–Menton** *(proportional)* II. **A Point–Nasion–B Point** *(angular)* III. **CheilionR–CheilionL / AlareR–AlareL** *(transverse proportional)* IV. **Nasion–Porion–Subnasale** *(angular)* **Interpretation:** Group III demonstrates **selective but consistent maternal dominance**, particularly involving **transverse facial proportions, mandibular/chin-related angles, and lower facial orientation**, distinguishing it from Groups I and II.

Discussion

In this study, we evaluated parent–offspring resemblance in facial soft-tissue morphology across Angle's Class I, Class II, and Class III malocclusions using standardized photogrammetric analysis and correlation-based heritability estimation. Our findings demonstrate that facial soft-tissue characteristics exhibit measurable familial resemblance; however, the pattern and strength of this resemblance vary across malocclusion classes, supporting the multifactorial nature of craniofacial morphology, wherein genetic and environmental influences interact [5,14,19].

Importance of soft-tissue evaluation in orthodontics

Orthodontic treatment outcomes are increasingly judged by facial esthetics rather than occlusal correction alone. Soft-tissue profile, including nasal projection, lip posture, and chin morphology, plays a decisive role in determining facial harmony and patient satisfaction. Classical orthodontic literature emphasizes that hard-tissue correction alone does not necessarily predict favorable esthetic outcomes, underscoring the need for comprehensive soft-tissue evaluation during diagnosis and treatment planning [17]. Therefore, our focus on facial soft-tissue parameters is clinically relevant and aligns with established orthodontic principles.

Interpretation of Group I findings

In Group I malocclusion, we observed predominantly mild to moderate parent–offspring resemblance, with slightly stronger associations noted for select angular parameters, particularly those related to nasal and upper lip morphology. This finding is consistent with previous reports indicating that while several craniofacial traits are heritable, the magnitude of inheritance varies considerably among different facial components [5,9,12]. Class I malocclusion encompasses a broad range of near-normal skeletal relationships, which may explain the relatively weaker and more variable familial resemblance observed in this group. These findings suggest that in Class I individuals, environmental factors and individual growth variation may play a more prominent role in shaping soft-tissue morphology.

Interpretation of Group II findings

Group II malocclusion demonstrated the strongest overall parent–offspring resemblance, with particularly high correlations observed for proportional and sagittal facial parameters. The predominance of father–offspring resemblance across several variables suggests a substantial inherited component influencing vertical facial proportions, lip–chin relationships, and sagittal facial profile in Class II individuals. These results agree with earlier family-based and cephalometric studies reporting moderate to high heritability estimates for craniofacial dimensions and sagittal relationships, especially in Class II malocclusion patterns [7,8,13,15]. Our findings further support the concept that genetic influence on facial morphology may be more pronounced in specific malocclusion categories rather than uniformly distributed across all occlusal patterns.

Interpretation of Group III findings

In Group III malocclusion, we identified a selective maternal predominance in parent–offspring resemblance, particularly for transverse facial proportions, chin-related parameters, and certain angular measurements. Class III malocclusion is characterized by distinctive craniofacial morphology, often involving mandibular prognathism and altered sagittal relationships, which have been shown to possess a strong hereditary component in previous studies [4,8]. The observed maternal dominance may reflect the inheritance of mandibular and lower facial traits that manifest more prominently in soft-tissue profile. However, this finding should be interpreted with caution, as familial resemblance may also be influenced by shared environmental factors and household habits, which can contribute to apparent parent–offspring similarity independent of genetic transmission [14].

Methodological considerations and use of photogrammetry

We employed standardized facial photography to assess soft-tissue parameters, an approach supported by previous studies demonstrating acceptable correlation between photogrammetric and cephalometric measurements when appropriate standardization protocols are followed [18]. The use of photography offers advantages such as reduced radiation exposure and ease of clinical application. Nevertheless, two-dimensional photogrammetry cannot fully capture depth and three-dimensional facial contours, and some variability may arise due to head posture, facial expression, and age-related soft-tissue changes [18,19]. These methodological limitations may partly explain the variability in correlation strength observed across different parameters.

Interpretation of heritability estimates

Heritability in this study was estimated using a correlation-based approach derived from quantitative genetic principles [6]. While this method provides a useful approximation of genetic influence, it relies on several assumptions, including additive genetic effects and minimal shared-environment confounding. Previous orthodontic studies have noted that heritability estimates derived from family data may exceed theoretical limits or vary widely due to sampling variability and environmental influences [5,7,13]. Heritability values exceeding unity likely reflect sampling variability, shared environmental effects, and limitations inherent to correlation-based estimation rather than true biological heritability. Therefore, the heritability values reported in this study should be interpreted as relative indicators of genetic contribution, rather than absolute measures.

Clinical implications

Our findings suggest that consideration of familial facial soft-tissue characteristics may aid orthodontists in anticipating esthetic outcomes, particularly in malocclusions with pronounced sagittal or vertical discrepancies. Recognizing familial patterns in facial morphology may help clinicians set realistic treatment expectations and tailor treatment plans to individual patients, especially in adult or late adolescent populations where growth modification is limited [17,19].

Limitations of the Study

This study has several limitations that should be considered when interpreting the findings. First, the sample size within each malocclusion group was relatively small, which may limit the generalizability of the results and reduce statistical power for detecting weaker parent–offspring associations. Second, the study employed a cross-sectional design, which does not allow assessment of longitudinal changes in facial soft-tissue morphology or differentiation between genetic influence and age-related variation.

Third, facial soft-tissue parameters were assessed using two-dimensional photogrammetry. Although standardized photography is a validated and clinically useful method for soft-tissue analysis, it cannot fully capture three-dimensional facial depth and contour, and measurements may be influenced by head posture, facial expression, and photographic distortion. Fourth, differences in age between parents and offspring may have affected the degree of resemblance observed, as soft-tissue characteristics are known to undergo changes throughout adulthood.

Additionally, parent–offspring resemblance may be influenced by shared environmental factors such as lifestyle, nutrition, and habitual facial expressions, which could not be controlled in this study. Heritability estimates derived from correlation-based methods rely on simplifying assumptions and may be affected by sampling variability and environmental confounding; therefore, these values should be interpreted as indicative rather than absolute measures of genetic contribution. Finally, sex-specific effects were not analyzed separately, which may have obscured potential differences in inheritance patterns between male and female offspring.

Conclusion

Within the limitations of this study, we conclude that facial soft-tissue characteristics demonstrate measurable parent–offspring resemblance, and that the pattern and magnitude of this resemblance vary across Angle's Class I, Class II, and Class III malocclusions. Class II malocclusion exhibited the strongest overall familial resemblance, predominantly in proportional and sagittal facial parameters, while Class I malocclusion showed comparatively weaker and more variable associations. In contrast, Class III malocclusion demonstrated selective maternal predominance, particularly in transverse and chin-related soft-tissue parameters.

These findings support the concept that facial soft-tissue morphology is influenced by both genetic and environmental factors and that inherited traits may manifest differently depending on the underlying malocclusion pattern. Consideration of familial facial characteristics may therefore assist clinicians in anticipating esthetic outcomes and refining orthodontic diagnosis and treatment planning. Further research with larger samples, longitudinal designs, and three-dimensional imaging techniques is recommended to better delineate the genetic and environmental determinants of facial soft-tissue morphology.

Conflict of Interest

The authors declare no conflict of interest.

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