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Dental Anomalies in Consanguineous Marriage: A Clinical-Radiological Study

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ABSTRACT

Objective: This study aimed to evaluate nonsyndromic developmental dental anomalies (DDAs) in individuals born from consanguineous and nonconsanguineous marriages and the possible effects of these marriages on self-reported systemic diseases.

Methods: The study comprised a total of 880 patients aged 16 years or older who applied to our clinic for various dental problems. Based on detailed anamnesis, the patients were divided into 2 groups: individuals born from consanguineous (study group, $n = 445$) and nonconsanguineous (control group, $n = 435$) marriages. The parents' consanguinity type was also recorded, as well as the presence of any self-reported systemic diseases. The number, size, erupted, and morphological DDA types were investigated with both clinical and radiological examinations. All data from the 2 groups were recorded, and a statistical analysis was performed.

Results: There was a statistically significant relationship between the consanguineous marriage and the size (microdontia), and morphological (dilaceration and taurodontism) DDA types. Additionally, a significant relationship was found between consanguineous marriage and self-reported systemic disease but not between the parents' consanguinity type and systemic disease.

Conclusion: The results of this study suggest that consanguineous marriage affects DDAs.

Introduction

The word 'consanguinity' is a combination of two Latin words: 'con,' meaning together or with, and 'sanguineous,' referring to blood. In a clinical genetic context, consanguineous marriage is described as a marriage between 2 individuals who are related as second cousins or closer.[1] In other disciplines, close relationships other than those of second cousins are also included within the scope of consanguineous marriage.[2] It is estimated that 1 billion of the current global population prefer consanguineous marriage due to various socioeconomic reasons, with North Africa, Northern India, and the Middle East representing the regions where consanguineous marriage is most common.[3] It is further known that where consanguineous marriage is a common phenomenon, genetic anomalies are observed more frequently.[4,5]

Consanguineous marriage may have many adverse health effects for children born from these marriages.[6,7] Generally, unless both parents have the same gene mutation, it is rare for a recessive disorder to occur in their offspring.[3] Thus, we can infer that consanguineous marriage facilitates the passage of certain autosomal recessive genes inherited from a common ancestor to subsequent generations, leaving them at higher risk for recessive disorders and congenital malformations.[8] This is borne out in the higher incidence of many genetic and systemic issues among individuals born from consanguineous compared with nonconsanguineous marriages.[3,8-14] Reported issues include birth defects, genetic diseases, heart and blood diseases, mental disability, hearing problems, asthma, congenital head and neck malformation, and cleft lip or palate.[3,8-14] Though accepted to have a great impact on general health, the effect of consanguineous marriage on dental development is not fully understood.

Dental anomalies arise from interaction of genetic, epigenetic, and environmental factors in the process of dental formation and can affect quality of life from both a functional and aesthetic perspective.[15] These anomalies are classified

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as either developmental or acquired.[16] Developmental dental anomalies (DDAs) can occur in several different contexts (eg, as isolated findings, as part of a syndrome), be related to different underlying conditions (eg, familial, idiopathic, consanguineous marriage), and be affected by several different factors (eg, genetic factors, environmental conditions, etc.).[17-20] DDAs can be divided into 4 types, with a given anomaly being classified as 1 of these: number, size, erupted, or altered dental morphology.[16] Various DDA types are quite common in clinical practice and can be diagnosed with the aid of clinical and radiological examination. Correctly diagnosing a DDA is especially important for managing the treatment process. Additionally, identifying observed DDAs contributes valuable information, such as population structure, to genetic studies.[21] Therefore, clinicians should thoroughly investigate all possible factors that can play a role in DDA aetiology.

Although the relationship between consanguineous marriage and systemic diseases has been highlighted in many studies,[8-11,13] there are relatively few of these studies in the field of dentistry.[4,17,18,22-24] Previous research has investigated the relationship between consanguineous marriage and specific conditions such as hyperdontia, hypodontia, and aggressive periodontitis.[4,17,23] However, the effect of consanguineous marriage on the DDAs has not been extensively studied. To the authors' knowledge, this is the first study to address the relationship between consanguineous marriage and DDAs, both clinically and radiologically.

The primary aim of this study was to evaluate the DDA status of individuals born from consanguineous and nonconsanguineous marriages, while the secondary aim was to investigate the possible relationship between consanguineous marriage and self-reported systemic diseases.

Methods

This study was approved by the Gazi University Ethics Committee (Document Date and Number: 11/01/2019-E.4699), which complies with the Declaration of Helsinki. Written consent was obtained from either the volunteer participants or, in the case of participants who were minors, from their parents.

A total of 880 patients who visited Oral Diagnosis Clinic, Faculty of Dentistry, Gazi University due to various dental problems between February 2019 and April 2019 were included in this study. Inclusion criteria for selecting study participants encompassed patients who were 16 years or older, not pregnant, and who required panoramic radiography for dental diagnosis and treatment. Patients with a history of any type of syndrome were excluded from the study.[17-19] Patients were classified into 2 groups according to their parents' consanguineous marriage status. The individuals born from consanguineous marriage constituted the study group, and the individuals born from nonconsanguineous marriage constituted the control group.

Evaluation of patients consisted of 3 separate examinations: clinical, intraoral, and radiological. During the clinical examination, patients were questioned about their personal characteristics (age and gender), systemic diseases, and the marriage details of their parents. In the study group, the parents' consanguinity type was also recorded. First cousin (Type 1), second cousin (Type 2), and more distantly related and complex-multiple mattings (Type 3) were all accepted consanguineous marriage types.[2] The types of consanguineous marriage are shown in Figure.

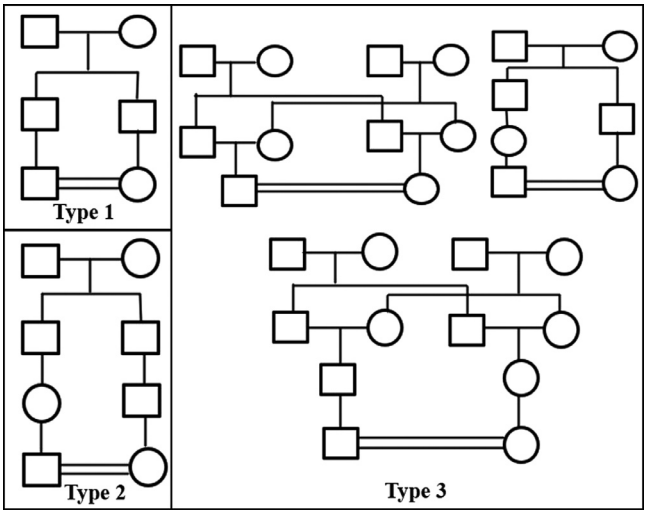

Fig. – Types of consanguineous marriage. Type 1; first cousin, Type 2; second cousin, Type 3; more distantly related and complex-multiple mattings.

The detailed intraoral examination was performed in the clinical setting with a sterile mouth mirror (No. 5) and probe under sufficient light. Panoramic radiographs for the radiological examination were taken on a Sirona-Orthophos XG machine (Sirona-Orthophos XG; Sirona; 60-90 kVp; 8 mA; 14 second). Following the radiological examination, all of a patient's teeth were evaluated in terms of possible DDAs. The presence or absence of DDAs was determined based on clinical and radiological examinations and recorded according to the classification of White and Pharoah.[16] With this classification, DDAs are divided into the following 4 anomaly types and 23 subtypes:[16]

- number anomaly (supernumerary tooth, hypodontia)
- size anomaly (macrodontia, microdontia)
- erupted anomaly (transposition)
- altered dental morphology anomaly (fusion, concrescence, gemination, taurodontism, dilaceration, dens invaginated, dens in dente, dilate odontoma, dens evaginated, amelogenesis imperfecta, dentinogenesis imperfecta, osteogenesis imperfecta, dentin dysplasia, regional odontodysplasia, enamel pearl, talon cusp, turner hypoplasia, congenital syphilis)

In this study, it was necessary to define reference values to make the definitive diagnosis of some subtypes.[25-27] For example, when noting the presence or absence of taurodontism, the length (C) of the distance between the bifurcation and the deepest pit of occlusal surface and the length (R) between the bifurcation and the root apex was measured radiographically. A C/R ratio was determined. If

this rate was more than 1.10, it was diagnosed as taurodontism.[25] Dilaceration was accepted as a deviation from the normal crown-root axis of the tooth of 20° or more in the apical part of the tooth root, in the mesiodistal direction, in the panoramic radiography.[26] A morphologically well-defined additional cusp on the palatinal or facial surface of the anterior tooth extending at least half the distance from the cementoenamel junction to the incisal edge was considered a talon cusp.[27]

All evaluations were performed jointly by 2 dentomaxillofacial radiologists, each with at least 3 years of experience. Any interexaminer differences that arose were resolved by discussion and the repetition of each examination until a consensus was reached.[28] A single record documenting the presence or absence of DDAs and self-reported systemic disease was created for each patient. The data were recorded on novel forms generated for this study, as shown in Table 1.

Statistical analysis

Statistical analysis of the data was conducted using SPSS (Statistical Package for the Social Sciences) for Windows, Version 22.0. Descriptive statistics for categorical variables consisted of number of observations and resulting percentages. Pearson χ^2 or Fisher exact test were applied for the significance check of the differences between the ratios. Statistical significance level was accepted as $P < .05$.

Results

This study included a total of 880 participants ranging from16 to 64 years of age. Table 1 shows the distribution of all patients in terms of parameters investigated in this study.

Although DDAs were observed in 48.9% of the patients in the study group, this rate was only 37.7% in the control group,

Table 1 – The form prepared for this study and the distribution of the patients according to personal characteristics, parents' marriage details and birth order, systemic diseases, and DDAs.

Variables	Study group $n = 445$, n (%)	Control group $n = 435$, n (%)	Total $n = 880$, n (%)
Personal characteristics			
Age	28.3 ± 7.8*	33.1 ± 1.9*	30 ± 10.8*
Gender			
Female	317 (55.2%)	257 (44.7%)	574 (65.2%)
Male	128 (41.8%)	178 (58.1%)	306 (34.8%)
Parents' marriage details and birth order of the patient			
Parents' consanguinity type			
Type 1	233 (52.3%)	-	233 (26.4%)
Type 2	75 (16.8%)	-	75 (8.5%)
Type 3	137 (30.7%)	-	137 (15.5%)
Birth order			
First	159 (35.7%)	-	159 (18%)
Second	134 (30.1%)	-	134 (15.2%)
Third	73 (16.4%)	-	73 (8.2%)
Fourth	33 (7.4%)	-	33 (3.7%)
Fifth and above	46 (10.3%)	-	46 (5.2%)
Self-reported systemic disease			
Heart	10 (2.3%)	7 (1.6%)	17 (1.9%)
Blood pressure	14 (3.2%)	6 (1.4%)	20 (2.3%)
Asthma	6 (1.4%)	3 (0.7%)	9 (1%)
Kidney	3 (0.7%)	1 (0.2%)	4 (0.5%)
Blood	5 (1.1%)	10 (2.3%)	15 (1.7%)
Gastrointestinal system	4 (0.9%)	0 (0%)	4 (0.5%)
Eye	2 (0.5%)	0 (0%)	2 (0.2%)
Ear	1 (0.2%)	0 (0%)	1 (0.1%)
Extremity	0 (0%)	0 (0%)	0 (0%)
Developmental dental anomaly types and subtypes			
Number anomaly: Supernumerary tooth, hypodontia,	30 (6.7%)	20 (4.6%)	50 (5.7%)
Size anomaly: Macrodontia, microdontia	38 (8.5%)	22 (5.1%)	60 (6.8%)
Erupted anomaly: Transposition	3 (0.7%)	1 (0.2%)	4 (0.5%)
Altered dental morphology anomaly: Fusion, concrescence, gemination, taurodontism, dilaceration, dens invaginated, dens in dente, dilate odontoma, dens evaginated, amelogenesis imperfecta, dentinogenesis imperfecta, osteogenesis imperfecta, dentin dysplasia, regional odontodysplasia, enamel pearl, talon cusp, turner hypoplasia, congenital syphilis	182 (40.9%)	146 (33.6%)	328 (37.3%)

DDA = developmental dental anomalies.

* Mean ± standard deviation.

Table 2 – Distribution of all patients according to DDA types and subtypes for groups, *n* (%), and the statistical analysis.

Variables		Groups				χ^2	*P* value
		Study group (*n* = 445)		Control group (*n* = 435)			
		Present *n* (%)	Absent *n* (%)	Present *n* (%)	Absent *n* (%)		
DDA types and subtypes	**Number anomaly**	**30 (6.7%)**	**415 (93.3%)**	**20 (4.6%)**	**415 (95.4%)**	**1.887**	**.170**
	Supernumerery teeth	10 (2.3%)	435 (97.7%)	4 (0.9%)	431 (99.1%)	2.490	.115
	Hypodontia	20 (4.4%)	425 (93.6%)	16 (3.6%)	419 (96.4%)	0.819	.366
	Size anomaly	**38 (8.5%)**	**407 (91.5%)**	**22 (5.1%)**	**413 (94.9%)**	**4.197**	**.040***
	Macrodontia	4 (0.9%)	441 (99.1%)	4 (0.9%)	431 (99.1%)	—	.626†
	Microdontia	34 (7.7%)	411 (92.3%)	19 (4.4%)	416 (95.6%)	4.162	.041*
	Erupted anomaly	**3 (0.7%)**	**442 (99.3%)**	**1 (0.2%)**	**434 (99.8%)**	—	**.320†**
	Transposition	3 (0.7%)	442 (99.3%)	1 (0.2%)	434 (99.8%)	—	.320†
	Altered dental morphology anomaly	**182 (40.9%)**	**263 (59.1%)**	**146 (33.6%)**	**289 (66.4%)**	**5.063**	**.024***
	Fusion	1 (0.2%)	444 (99.6%)	0 (0%)	435 (100%)	—	.505†
	Taurodontism	8 (1.8%)	437 (98.2%)	1 (0.2%)	434 (99.8%)	—	.021*,†
	Dilaceration	127 (28.6%)	318 (71.4%)	95 (21.8%)	340 (78.2%)	—	.013*,†
	Dens invaginated	52 (11.7%)	393 (88.3%)	54 (12.4%)	381 (87.6%)	0.102	.749
	Dens evaginated	1 (0.2%)	444 (99.8%)	1 (0.2%)	434 (99.8%)	—	.745†
	Enamel pearl	0 (0%)	445 (100%)	1 (0.2%)	434 (99.8%)	—	.495†
	Talon cusp	16 (3.6%)	427 (96.4%)	8 (1.8%)	427 (98.2%)	2.576	.108
	Total	**218 (48.9%)**	**227 (51.1%)**	**164 (37.7%)**	**271 (62.3%)**	**11.169**	**.001***

χ^2 = Pearson chi-square test; DDA = developmental dental anomalies.

* $P < .05$, statistically significant.
† Fisher exact test.

a statistically significant difference (Table 2). Regarding DDA types, the frequency of patients with size and altered dental morphology anomalies was significantly higher in the study group. When we focused on subtypes, the frequency of patients with microdontia, taurodontism, and dilaceration were found to be significantly higher in the study group (Table 2). Some DDAs included for consideration in this study were not observed in any of the patients and are thus not included in our results (Table 2); these unobserved DDAs included concrescence, gemination, dens in dent, dilate odontoma, amelogenesis imperfecta, dentinogenesis imperfecta, osteogenesis imperfecta, dentin dysplasia, regional odontodysplasia, turner hypoplasia, and congenital syphilis.

A total of 480 DDAs were detected in 382 of the patients (43.4% of the participants); 276 (57.5%) of these DDAs were in 218 (57.1%) patients in the study group, and 204 (42.5%) of these DDAs were in 164 (42.9%) patients in the control group. A rate of 1.25 DDAs per patient was observed; this value was higher in the study group than in the control group, with rates of 1.26 and 1.24, respectively. In terms of any DDA type, the difference was not statistically significant between the groups (Table 3). Of the total 480 DDAs, 383 (79.8%) were in the maxilla and 97 (20.2%) were in the mandible, a difference that was statistically significant (Table 3). The frequency of DDAs was higher in the maxilla in both the study and control groups (Table 3). Most frequently observed DDAs in the maxilla were, in descending order, dilaceration, dens invaginated,

Table 3 – Distribution of DDA types and jaw involvement for both groups, *n* (%), and the statistical analysis.

Variables	Groups		Total (*n* = 480)	χ^2	*P* value
	Study group (*n* = 276) *n* (%)	Control group (*n* = 204) *n* (%)	*n* (%)		
Number anomaly	30 (10.8%)	20 (9.8%)	50 (10.4%)	0.461	.497
Size anomaly	38 (13.7%)	23 (11.2%)	61 (12.7%)	0.642	.423
Erupted anomaly	3 (1%)	1 (0.4%)	4 (0.8%)	—	.433†
Altered dental morphology anomaly	205 (74.2%)	160 (78.4%)	365 (76%)	1.699	.192
Jaw involvement				28.518	.000*
Maxilla					
	196 (71.1%)	187 (91.6%)	383 (79.7%)		
Mandible					
	80 (28.9%)	17 (8.3%)	97 (20.3%)		
Total	276 (100%)	204 (100%)	480 (100%)		

χ^2 = Pearson chi-square test; DDA = developmental dental anomalies.

* $P < .05$, statistically significant.
† Fisher exact test.

Table 4 – Distribution of all patients in the study group according to parents' consanguineous marriage type and birth order for DDA types, *n* (%), and the statistical analysis.

Variables	Developmental dental anomaly types											
	Number anomaly *n* (%)	χ^2	*P* value	Size anomaly *n* (%)	χ^2	*P* value	Erupted anomaly *n* (%)	χ^2	*P* value	Altered dental morphology anomaly *n* (%)	χ^2	*P* value
Parents' consanguinity types												
Type 1	19 (63.3%)	1.557	.459	22 (57.9%)	0.626	.731	3 (100%)	f	f	96 (52.7%)	3.542	.170
Type 2	4 (13.3%)			5 (13.2%)			0 (0%)			24 (13.2%)		
Type 3	7 (23.3%)			11 (28.9%)			0 (0%)			62 (34.1%)		
Birth order												
First	12 (40%)	f	f	15 (39.5%)	f	f	2 (66.7%)	f	f	70 (38.5%)	1.659	.798
Second	7 (23.3%)			13 (34.2%)			1 (33.3%)			52 (28.6%)		
Third	8 (26.7%)			5 (13.2%)			0 (0%)			28 (15.4%)		
Fourth	2 (6.7%)			3 (7.9%)			0 (0%)			15 (8.2%)		
Fifth and above	1 (3.3%)			2 (5.3%)			0 (0%)			17 (9.3%)		
Total	30 (100%)			38 (100%)			3 (100%)			182 (100%)		

χ^2 = Pearson chi-square test; f = test failed.
*$P < .05$, statistically significant.

and microdontia, respectively. Most frequently observed DDAs in the mandible were, in descending order, dilaceration, taurodontism, and hypodontia.

The parents' consanguinity types of 218 patients that were observed to have DDAs in the study group numbered 119 (51.1%), 31 (41.3%), and 68 (49.6%) for Type 1, Type 2, and Type 3, respectively. There was not a statistically significant relationship between the parents' consanguinity types and the observed DDA types (Table 4). The birth order of patients that were observed to have DDAs in the study group numbered 84 (52.8%), 64 (47.8%), 35 (47.9%), 17 (51.5), and 18 (39.1%), for the birth orders of first, second, third, fourth, and fifth and above, respectively. There was not a statistically significant relationship between birth order and DDA types (Table 4).

The frequency of patients with self-reported systemic disease was higher in the study group, with a statistically significant difference between the study and control groups (Table 5). However, no single specific self-reported systemic disease showed a difference between the groups. Table 5 shows the distribution of patients with self-reported systemic disease according to both groups. In addition, the distribution of self-reported systemic diseases according to parents' consanguinity type was $n = 19$ (8.1%) for Type 1, $n = 9$ (14%) for Type 2, and $n = 8$ (5.8%) for Type 3, with no significant difference ($\chi^2 = 0.778$, $P = 0.679$).

Discussion

In the present clinical and radiological study, the frequency of patients in which we observed DDAs, and particularly size anomaly types (eg, microdontia) and altered dental morphology anomaly types (eg, dilaceration and taurodontism), was significantly higher in the study group. Additionally, the frequency of patients with self-reported systemic disease was significantly higher in the study group. Because this study aimed to evaluate the effect of consanguineous marriage on DDAs, we only included individuals without any history of a

Table 5 – Distribution of patients with self-reported systemic diseases status for both groups, *n* (%), and the statistical analysis.

Self-reported systemic disease	Groups				^{2}	*P* value
	Study group ($n = 445$)		Control group ($n = 435$)			
	Present*n* (%)	Absent*n* (%)	Present*n* (%)	Absent*n* (%)		
Heart	10 (2.3%)	435 (97.7%)	7 (1.6%)	428 (98.4%)	0.479	.489
Blood pressure	14 (3.1%)	431 (96.9%)	6 (1.4%	429 (98.6%)	3.109	.078
Asthma	6 (1.4%)	439 (98.6%)	3 (0.7%)	432 (99.3%)	0.949	.330
Kidney	3 (0.7%)	442 (99.3%)	1 (0.2%)	434 (99.8%)	0.964	.326
Blood	5 (1.1%)	440 (98.9%)	10 (2.3%)	425 (97.7%)	1.802	.180
Gastrointestinal system	4 (0.9%)	441 (99.1%)	0 (0%)	435 (100%)	—	.065†
Eye	2 (0.5%)	443 (99.5%)	0 (0%)	435 (100%)	—	.255†
Ear	1 (0.2%)	444 (99.8%)	0 (0%)	435 (100%)	—	.505†
Extremity	0 (0%)	445 (100%)	0 (0%)	435 (100%)	f	f
Total	36 (8.1%)	409 (91.9%)	19 (4.4%)	416 (95.6%)	5.241	.022*

χ^2 = Pearson chi-square test; f = test failed.
* $P < 0.05$, statistically significant.
† Fisher exact test.

syndrome, thereby eliminating the possibility of observing DDAs that had resulted from a syndrome.[17-19] We noted in the literature review conducted for this study that this distinction was not always made in previous research.[4,22,23]

In line with our results, a limited number of studies on this subject have generally found a strong relationship between consanguineous marriage and DDAs, though there are differences among the DDA types and subtypes reported in these studies.[17,18,22,23] Similar to our results, Khan[18] found that the frequency of DDAs was 24.2% in individuals born from consanguineous marriage, a higher frequency than that of the control group (4.6%). Khan[18] reported that DDAs such as nonsyndromic supernumerary teeth, fusion, and microdontia were observed significantly more frequently in individuals born from consanguineous marriage. Lakshmayya et al[22] observed malocclusion, nonsyndromic oligodontia, and enamel hypoplasia more frequently in individuals born from consanguineous marriage. Shokry and Alenazy[23] documented a strong relationship between supernumerary teeth and consanguineous marriage. Alsoleihat and Khraisat[17] reported an increased frequency of hypodontia in the Druze population, where consanguineous marriage is common. The reason behind this variation of reported DDA types and subtypes may be related to differences in sample size, diagnostic methods (eg, clinical vs radiological examination), inclusion criteria (eg, age), or even ancestral differences between the studied populations.

In epidemiological studies conducted on dental anomalies and spanning many different countries and geographical regions, the frequency of DDAs has been reported at intervals ranging from 0.3% to 45.1%.[21,29-31] In the present study, 48.9% ($n = 218$) of the study group, 37.7% ($n = 164$) of the control group, and 43.3% ($n = 382$) of the total patients had at least 1 DDA. Though we observed DDAs in a total of 382 patients, some patients had more than 1 DDA, making the total number of observed DDAs 480. The rate of observed DDAs per patients was 1.25 in the total sample size, and 1.26 and 1.24 in the study and control groups, respectively. Our findings are consistent with previous studies that focused on the general population in Turkey and the Middle East.[30,31] However, it is the opinion of the authors that failing to note the general marriage habits of the community in which these studies took place represents an important deficiency that the current study aims to avoid.

In terms of DDAs and location in the context of the jaw, the present study found that the frequency of DDAs was significantly higher in the maxilla. The relationship between DDAs and location within the jaw has been reported in the literature. Our findings are consistent with some studies that investigated this topic.[32,33] Temilola et al[32] observed dental anomalies to be more common in the maxilla. Udeyo and Jafarzadeh[33] have reported the same results, especially for dilaceration. Just as we found higher frequency of maxillary DDAs in the study group, higher frequency was reported for both supernumerary teeth and hypodontia in the maxilla in previous studies investigating dental anomalies in individuals born from consanguineous marriage.[17,23]

It is known that genetic factors play a role in the aetiology of DDAs.[16] However, the biological or embryological reason for DDAs associated with consanguineous marriage has not yet been definitively explained in the literature. In particular, several case reports have been published regarding gene mutations in individuals born from consanguineous marriages, specifically related to amelogenesis imperfect and tooth agenesis.[34-36] In reports of patients whose parents were consanguine, observed DDAs have included supernumerary teeth, oligodontia, mesiodens, fusion, dentin dysplasia, amelogenesis imperfecta, and talon cusp.[19,37-42] It has further been suggested that the higher variation of dental anomalies among individuals born from consanguineous marriages is due to an increase in homozygosity and a resulting loss of resistance to environmental stress.[43]

The effects of consanguineous marriage on the general health of individuals born from these marriages have been demonstrated in numerous studies. Various chromosomal and congenital abnormalities and genetic diseases such as heart disorders (ventricular and atrial septal defects), blood diseases (hemophilia, α-thalassemia), Down syndrome, various craniofacial abnormalities, hydrocephalus, postaxial polydactyly, congenital head and neck malformation, orofacial pigmentation, and cleft lips or cleft palate have been reported in individuals whose parents are consanguineous.[5,22,44-46] As in previous studies, the results of this study showed a statistically significant relationship between consanguineous marriage and self-reported systemic diseases.

This study is not without limitations, one of which is an absence of genetic analysis. Performing genetic analysis to reveal possible syndromes in individuals who were both born from consanguineous marriage and had DDAs could provide more comprehensive results and aid in understanding the genetic factors behind the observed DDAs. Not all syndromes present with pronounced symptoms that are easily noticed, whether by the individual or by a physician during a clinical examination; genetic analysis could help discover some of the more elusive syndromes that could be present in the study participants. Although we did not include patients with any syndromes in this study to eliminate the possibility of DDA arising from any syndrome, it should not be overlooked that many syndromes are related to consanguineous marriage. In this case, it can be said that, where the cause of a syndrome is consanguineous marriage, DDA related to syndrome also occurs as a result of consanguineous marriage. Another limitation to this study is that other family members, including the parents, were not examined. One final limitation of this study is the possibility that some teeth of the participants may have been extracted or treated, given that individuals aged 16 and older were included. For this reason, the DDA frequency we observed both in individuals born from consanguineous and nonconsanguineous marriages may not reflect the actual frequency in the population.

Conclusion

The results of this study suggest that consanguineous marriage has an effect on DDAs. These DDAs were microdontia as a size anomaly and dilaceration and taurodontism as altered dental morphology anomalies. In addition, we found that DDAs and self-reported systemic diseases were significantly higher in individuals born from consanguineous marriage.

The aetiology of DDAs that aesthetically and functionally affect the quality of life, as seen so frequently in societies, should be examined in more detail.

Author Contributions

NB: the conception and design of the study, acquisition of data, and drafting the article; UP: the conception and design of the study, acquisition of data, revising it critically for important intellectual content, and final approval of the version to be submitted; BA: analysis and interpretation of data; İP: the conception and design of the study, revising it critically for important intellectual content, and final approval of the version to be submitted.

All authors have approved the final article.

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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