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Heritability estimates of dental arch parameters in Lithuanian twins

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SUMMARY

Background. The genetic influence on dental arch morphology may be country-specific, thus it is reasonable to check the estimates of genetics across different populations. The purpose of this study was to evaluate the heredity of dental arch morphology in the sample of Lithuanian twins with accurate zygosity determination.

Material and methods. The study sample consisted of digital dental models of 40 monozygotic (MZ) and 32 dizygotic (DZ) twin pairs. The estimates of heritability (h^2) for dental arch breadth and length were calculated.

Results. All dental arch breadths and lengths were statistically significantly larger in men than in women. Arch length differences between genders were less expressed than largest breadth differences. In the upper jaw the largest genetic effect was found on the arch breadth between lateral incisors. The heritability of dental arch length demonstrated similar differences between upper and lower jaw with mandible dental arch length being more genetically determined.

Conclusions. The largest genetic impact was found on the upper dental arch breadth between lateral incisors. Similar, but lower heritability is inherent for canines and first premolars of the upper jaw and first premolars of the lower jaw. It also can be noted, that arch breadths between posterior teeth show lower heritability estimates than between anterior teeth on both jaws. The dental arch in the upper jaw has more expressed genetic component than in the lower jaw.

Key words: twin study, dental arch, heritability, 3D dental cast models.

INTRODUCTION

The research on dental arch breadth and length in humans has provided some estimates of genetic and environmental influences (1). Some authors claim that genetic variation has major effect on arch width and length (2). However, the data on genetic component may be country- or region-specific or have ethnic background, thus it is reasonable to check the estimates of genetics across different populations. But it's worth to mention, that not only the genetic, but also environmental factors play role in the development and shape of dental structures. The environmental influences may be such factors like mouth breathing, loss of deciduous teeth, endocrine changes, injuries, posture and other (3). This is also supposed to be related with the reduction of chewing resistance and growth stimulation due to refined diet.

The studies on genetic influences on dental arch show ambivalent findings. Cassidy and coauthors suggested that arch size and shape are determined more by environmental influences (4), while the study of teenage twins found a high genetic contribution to variation in dental arch dimensions (5). Twin studies have demonstrated that, while genetic variance can be discerned for different occlusal variables, heritability tends to be low, emphasizing the importance

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of environmental influences on occlusal variation (6). Similar results from longitudinal study of siblings concluded that most of the observed variation in occlusion in the permanent dentition was acquired rather than inherited (7).

Therefore, it is not clear how much the dental arch dimensions depend on genetics and how much – on environment, because larger effects of genetics suggest less effective orthodontic treatment outcomes. The stability of such outcomes depends on certain balance between genetic and environmental factors (8).

A basic problem with the previous twin research is the reliability of twin zygosity diagnostics. Zygosity determination for many years was based on assessment of anthropological similarity including tooth anatomy (9). The use of blood group determination, as well as serum and enzyme polymorphism analysis improves the ability to assign zygosity to twins (10). More recently, the use of highly polymorphic regions of DNA derived from blood or buccal cells has proved to be accurate up to 90–95% of cases (11).

The purpose of our study was to evaluate the heredity of dental arch breadth and length in the sample of Lithuanian twins with accurate zygosity determination and using 3D dental cast.

MATERIAL AND METHODS

Study sample. The study subjects were selected from Register of Twin Center (Lithuanian University of Health Sciences) and consisted of 40 monozygotic (MZ) and 32 dizygotic (DZ) twins. The study used following eligibility criteria: (1) permanent occlusion including second molars teeth; (2) no dental extraction, prosthesis, or filling in specific contact or occlusal surfaces; (3) no history of diseases, injuries or surgical intervention in craniofacial region; (4) no previous orthodontic treatment; (5) absence of periodontitis; (6) available zygosity determination; (7) good quality dental arch cast s and their 3D model analogues.

Zygosity determination was conducted at certified laboratory of the enterprise "UAB Synlab Lietuva". The DNA based tests were performed using venous blood. The procedure was started with DNA isolation and purification. Then polymerase chain reaction set AmpFℓSTR®Identifiler® (Applied biosystems, USA) was used to amplify short tandem repeats (STR) and 15 specific DNA markers (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TROX, D18S51, D5S818, FGA), and Amel fragment of amelogenin gene were used for comparison of genetic profiles.

Dental arch measurements. Every study subject underwent checkup, where anamnesis and clinical diagnosis of teeth and oral cavity were conducted. Then diagnostic alginate impressions were taken using "Kromopan" (Lascod ,Italy) and dental casts produced from stone 'Marmorock N' class IV (by Siladent). The stone casts were set to wax-bite impressions with visual assessment of centric occlusion in the field. The dental casts were scanned using 'Desktop 3D Scanner' by NextEngine and digitized using 'Scan Studio HD 1.3.0'. Every digitized 3D analogue was processed using 'CloudCompare' software. The processed data were then used for measurements of arch breadth and length as defined by: arch breadth is the length between two appropriate points on the dental cast; arch length is the length from midpoints of incisal reference points to the line passing through reference points associated with the second molars.

The visual picture of arch measurements was based on Eguchi (1) and presented in Figures 1 and 2. The arch breadths were measured between teeth 11–21, 12–22, 13–23, 14–24, 15–25, 16–26, 17–27 for upper jaw and between 31–41, 32–42, 33–43, 34–44, 35–45, 36–46, 37–47 for lower jaw. The arch lengths were measured for upper and lower jaw separately.

*Measurement error***.** Intra-observer method error was assessed by measuring 50 randomly selected dental casts twice with a 1-month time interval. The method suggested by Bland & Altman (12) was used to calculate error between the measurements. We found, that mean error of the breadth measurements was 0.27 mm for upper jaw and 0.28 mm for lower jaw, while that of the length measurements – 0.36 mm and 0.42 mm, respectively.

Statistical analysis. The data were analyzed using 'IBM SPSS Statistics 20.0' software. The descriptive statistics were reported using mean ± standard deviation (SD) or median with range (minimum–maximum). For inferential statistics, the statistical significance was set at $P<0.05$. Comparison of study groups by zygosity was conducted using Student's t-test with regard for Levene's test for equal variances (for continuous variables), chi-squared test (for categorical variables). In order to estimate the intraclass correlation within monozygotic and dizygotic twins, the Pearson's intrapair correlation coefficients were calculated. The heritability estimate (coefficient h^2) was calculated using formula (9): $h^2 = 2(r_{mz} - r_{dz})$, where h^2 – heritability coefficient, r_{mz} – paired correlation within monozygotic twins, r_{dz} – paired correlation within dizygotic twins.

*Ethical clearance***.** The research was conducted using Register of Twin Center, Lithuanian University of Health Sciences with permissions to study by Kaunas Regional Bioethics Committee (2005-04-11 Nr. BE-2-21 and 2010-12-10 Nr. P1-52/2005). All

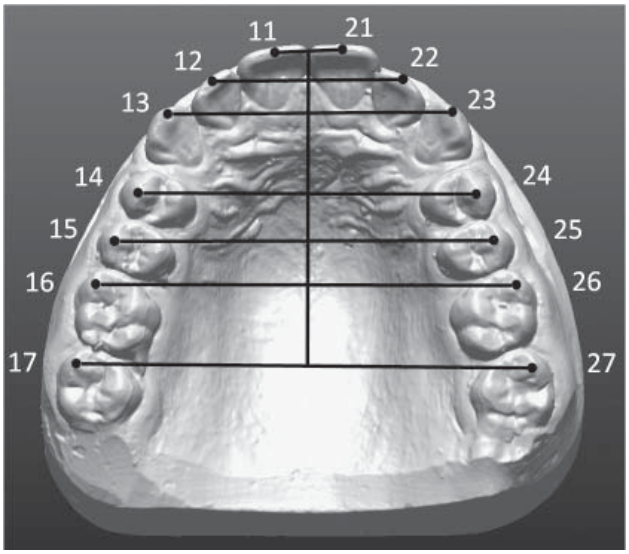

Fig. 1. The upper dental arch parameters

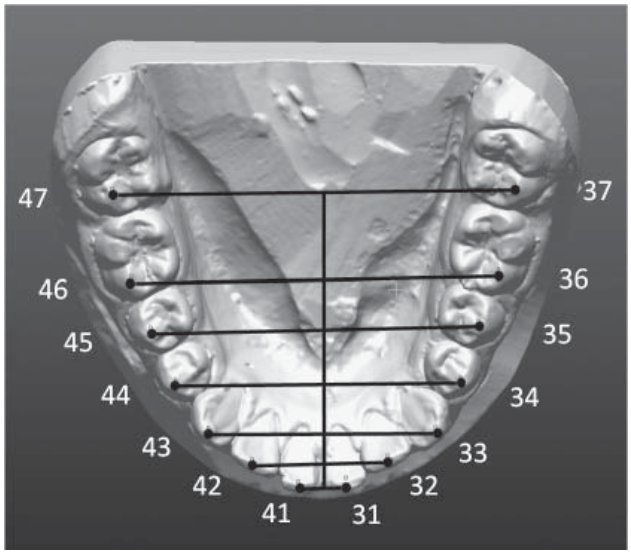

Fig. 2. The lower dental arch parameters

twins or their parents gave informed consent to use the register data for biomedical research

RESULTS

The majority of DZ twins were male (59.4%), while among MZ – female (55.0%; p=0.086). Comparison of study sample by age and zygosity revealed that MZ twins were significantly elder than DZ twins (mean age 17.82±2.755 and 20.20±6.021 years, respectively; p=0.002).

The comparison of twins by zygosity and arch measurements without regard to their intraclass correlations demonstrated that DZ and MZ twins differed only concerning the arch breadth at the level of second molars in upper and lower jaw (p<0.05). All other differences of breadth and length were non-significant (Table 1).

Table 1. Arch parameters by zygosity, mean ± SD

Parameter	DZ	MZ	p
Arch breadth, 11-21	8.337±0.682	8.419±0.824	0.522
Arch breadth, 12-22	22.959±1.471	23.140±1.661	0.497
Arch breadth, 13-23	34.145±2.206	34.327±2.374	0.637
Arch breadth, 14-24	41.260±2.469	40.910±2.750	0.429
Arch breadth, 15-25	46.976±3.000	46.502±3.262	0.371
Arch breadth, 16-26	51.727±3.362	51.858±3.440	0.819
Arch breadth, 17-27	57.395±3.236	58.571±3.440	0.038
Arch breadth, 31-41	5.280±4.702	5.360±0.485	0.319
Arch breadth, 32-42	16.074±1.208	16.312±1.307	0.265
Arch breadth, 33-43	25.523±1.945	25.922±1.683	0.189
Arch breadth, 34-44	33.715±2.102	34.092±2.120	0.289
Arch breadth, 35-45	39.510±2.828	39.532±2.367	0.959
Arch breadth, 36-46	44.934±2.824	45.532±2.727	0.201
Arch breadth, 37-47	49.948±3.135	51.260±2.919	0.011
Arch length, upper	38.907±2.204	28.355±2.884	0.209
Arch length, lower	35.125±1.999	34.980±2.660	0.718

The data were also analyzed comparing the arch indicators by gender (Table 2). It was found that all arch breadths and lengths are statistically significantly larger in men than in women (p<0.05). Evaluation of male-female difference by arch measurements showed that in absolute terms the largest differences were observed in breadth between upper second premolar and between upper first molars teeth (more than 2 mm difference). However, the relative (percentage) estimates of gender differences revealed slightly different pattern: though the largest relative differences were observed in breadth between upper second premolars (5.1%) and between upper first molars (4.9%), but breadth between lower second premolars (4.8%) and between upper first premolars (4.5%) had also quite similar gender differences. Of note, the dental arch length differences between genders were less expressed than largest breadth differences. Additionally, lower jaw length was more similar between men and women than upper jaw length (both in absolute and relative differences).

The heritability estimates in our study were evaluated using heritability coefficient h^2 (Table 3). We found that among breadths of upper jaw the largest genetic effect was between lateral incisors. Similar, but lower estimates were found for canines and first premolars of upper jaw as well as for first premolars of lower jaw. In general it can be seen that upper dental arch breadths were more genetically determined than their lower counterparts. It can also be noted that both in upper and lower arch, the arch breadths between teeth starting from second premolars (fifth teeth onwards) had lower heritability than breadths between more anterior teeth.

The heritability of dental arch length found similar differences between upper and lower jaw with mandible dental arch length being more genetically determined than maxillary (Table 3).

DISCUSSION

Even though there is sufficient research on dental arch parameters and their genetic determination, however, the validity of zygosity measurements (accuracy) in previous research was limited. In addition, 3D measurements of dental arch are have not been widely used this far. Therefore, our study approached the genetic determination of dental arch using modern scientific technologies which enabled us to draw potentially more valid conclusions.

We found that genetic factors of dental arch among Lithuanian twins were more expressed in upper than lower jaw parameters. The mostly expressed genetic component was observed in breadth between upper lateral incisive teeth. All dental arch parameters were higher among men than women, especially in breadth between upper second premolar and first molar teeth.

Other research found that arch size is more subject to environmental than heredity factors; however, they also found that arch widths had highest heritability estimates (4), at least in adolescents. They suggest that arch length and width growth factors are largely independent. Indirectly we can see this in our findings, where heredity estimates differed between arch breadth and length.

Analysis of twin data from Australia revealed that arch length is more to do with genetics than arch breadth parameters (1). They also found that in upper jaw the breadths have increasing heritability with increasing distality of teeth, while in lower jaw this is less expressed. Our study did not repeat that trend – we found the arch breadth heritability to be independent from distality of teeth.

Dempsey and colleagues (13) analyzed the widths of teeth and revealed that general genetic factor influenced all of the incisors. In contrast, our study showed that the breadths between incisor teeth were more genetically determined in upper than in lower jaw. It should not be excluded the possibility, than teeth widths and dental arch parameters related with those teeth are determined by different he-

Table 2. Arch parameters by gender, mean ± SD

Parameter	Females	Males	p	Difference, mm	Difference, %
Arch breadth, 11-21	8.240±0.652	8.517±0.836	0.027	0.278	3.37%
Arch breadth, 12-22	22.664±1.443	23.434±1.616	0.003	0.770	3.40%
Arch breadth, 13-23	33.580±2.233	34.876±2.185	0.001	1.296	3.86%
Arch breadth, 14-24	40.139±2.342	41.942±2.591	0.001	1.804	4.49%
Arch breadth, 15-25	45.525±2.846	47.837±3.016	0.001	2.312	5.08%
Arch breadth, 16-26	50.540±3.035	52.992±3.301	0.001	2.453	4.85%
Arch breadth, 17-27	57.066±3.004	58.978±3.491	0.001	1.912	3.35%
Arch breadth, 31-41	5.190±0.513	5.451±0.408	0.001	0.261	5.03%
Arch breadth, 32-42	15.966±1.263	16.434±1.234	0.026	0.467	2.93%
Arch breadth, 33-43	25.262±1.687	26.202±1.812	0.002	0.940	3.72%
Arch breadth, 34-44	33.211±1.973	34.600±2.030	0.001	1.388	4.18%
Arch breadth, 35-45	38.564±2.206	40.429±2.579	0.001	1.865	4.84%
Arch breadth, 36-46	44.404±2.553	46.082±2.749	0.001	1.678	3.78%
Arch breadth, 37-47	49.784±2.643	51.520±3.234	0.001	1.736	3.49%
Arch length, upper	37.798±2.099	39.359±2.825	0.001	1.561	4.13%
Arch length, lower	34.438±2.279	35.618±2.351	0.003	1.180	3.43%

Table 3. Twin correlations of dental arch parameters by zygosity and heritability coefficients

Parameter	rDZ (95% CI)	rMZ (95% CI)	h2
Arch breadth, 11-21	0.347 (0.008; 0.616)	0.840 (0.720; 0.912)	0.986
Arch breadth, 12-22	0.196 (-0.155; 0.504)	0.876 (0.778; 0.932)	1.360
Arch breadth, 13-23	0.343 (0.003; 0.613)	0.867 (0.763; 0.927)	1.048
Arch breadth, 14-24	0.286 (-0.061; 0.572)	0.794 (0.645; 0.885)	1.016
Arch breadth, 15-25	0.417 (0.089; 0.664)	0.762 (0.595; 0.866)	0.690
Arch breadth, 16-26	0.575 (0.292; 0.767)	0.834 (0.708; 0.908)	0.518
Arch breadth, 17-27	0.503 (0.196; 0.721)	0.858 (0.748; 0.922)	0.710
Arch breadth, 31-41	0.362 (0.024; 0.626)	0.715 (0.523; 0.838)	0.706
Arch breadth, 32-42	0.497 (0.189; 0.717)	0.836 (0.712; 0.909)	0.678
Arch breadth, 33-43	0.439 (0.116; 0.679)	0.829 (0.701; 0.906)	0.780
Arch breadth, 34-44	0.271 (-0.077; 0.561)	0.784 (0.629; 0.879)	1.026
Arch breadth, 35-45	0.396 (0.064; 0.650)	0.699 (0.500; 0.828)	0.606
Arch breadth, 36-46	0.571 (0.285; 0.764)	0.897 (0.815; 0.944)	0.652
Arch breadth, 37-47	0.632 (0.371; 0.801)	0.818 (0.683; 0.899)	0.372
Arch length, upper	0.333 (-0.009; 0.606)	0.833 (0.708; 0.908)	1.000
Arch length, lower	0.506 (0.199; 0.723)	0.791 (0.641; 0.884)	0.570

redity factors, while their environmental component may also be remarkably different.

In our study we established, that upper dental arch length is more likely to be genetically determined than lower length (heritability coefficients 1.00 and 0.57, respectively). However, other researchers found (14) that heritability of lower arch length in Australian twins can be as high as 0.92 and has to do more with genetics than arch breadth (0.82). Such diffuse findings may be explained by general population and or specific sample differences or the methodology that was used for zygosity determination. Less consistent differences between upper and lower arch parameters were also found elsewhere, with more prevailing heritability in upper than in lower jaw (1). More opposite findings were presented by Šidlauskas (15) who found that total mandibular and corpus lengths are more heritable than maxillary. This may suggest that heritability findings on total jaw parameters do not apply to dental arch indicators.

Secondary analysis of our study results demonstrated that dental arch breadth and length are larger in men than women. This is consistent with other studies. This can be explained by evolutionary arguments: men are more preferable for mating with larger jaws than thinner while masculine face profile is also related with better health (16).

One of our study strengths is that we used very accurate test for zygosity of the twins. Another relevant positive aspect of the study was that it applied 3D dental models for determination of necessary parameters of dental arch. Also, our findings are based not on small, but rather on relatively medium sample size which was strictly scrutinized for the absence of dental extraction, prosthesis, specific restorations or injuries that all can have impact on dental arch measurements. Therefore, our findings are robust in that those exclusion criteria enabled us to eliminate the potential effects of such conditions on dental arch parameters and their associations with heritability.

However, we should also discuss some issues of our study related with methodology of analysis. First of all it should be noted that comparison of twins simply based on their mean estimates does not allow estimating how much the twins in fact differ. Moreover, from our calculations it can be seen that such simplistic analysis may be misleading: t-test comparisons of twins by zygosity revealed largest (and significant) differences of breadth between second molar teeth, while the heredity analysis using heritability coefficient demonstrated that breadth between these teeth is one of the least genetically determined from all analyzed teeth breadths. Thus, such simplistic approach countervails the true associations inherent for subgroups and possibly more advanced statistical methods are needed.

Another methodological concern is the heritability coefficient h^2. It is defined as double difference of intraclass correlations between MZ and DZ twins. However, since the difference between correlations theoretically can exceed 0.5, the coefficient can be greater than 1. This can lead to misinterpretation of the whole concept of heritability coefficient which conventionally is regarded as a percentage estimate of genetic component versus environmental. However, as in majority of genetic research, the estimates of heritability show not the percentage of genetic factors within certain phenotype, but rather the variance of parameter that can be explained by genetic factors. So, how our findings of heritability with coefficient greater than one could be interpreted in light of previous research?

The apparent paradox of the heritability greater than one can be resolved by noting that if selection is so intense (i.e., so small) that only one phenotype can survive, the phenotypic variance can be smaller than the genotypic (i.e. many genotypes can produce the same phenotype) (17). This may also have some evolutionary effects that prevented the development of larger variance in dental arch traits of humans. Inbreeding in small populations can also contribute to such bias (18), but this is usually more common for animal than for human populations, were genetic relatedness greater than theoretically expected is more common (19). In contrast, some researchers suggest that the estimates of heritability for some quantitative traits can be greater than one regardless of the relatedness (20).

In general we see, that the heritability above one may indicate that comparison of intraclass correlations may not be the best way for estimating heritability. On the other hand, heritability coefficient still can be regarded as a proper measure to evaluate relative heritability, i.e. the coefficient could be interpreted as reflecting relative heritability of different phenotypes or features. In our study example this would mean, that the dental arch breadths between the first four teeth are more genetically determined than more distal teeth breadth. Similarly, upper jaw dental arch seems to be more heritable than the lower jaw dental arch.

CONCLUSIONS

The largest genetic impact was found on the upper dental breadth between lateral incisors. Similar,

but lower heritability is inherent for canines and first premolars of the upper jaw and first premolars of the lower jaw. It also can be noted, that arch breadths between posterior teeth show lower heritability estimates than between anterior teeth on both jaws. The dental arch in the upper jaw has more expressed genetic component than in the lower jaw.

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