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Polymorphisms in sequence of permanent tooth emergence: a cross-sectional study on Jordanian children and adolescents

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Abstract

Objective. This study aimed at providing the norms of polymorphic gender- variation in the sequence of permanent tooth emergence in Jordanian children and adolescents. ***Materials and methods.*** A total of 2650 Jordanian children and adolescents (1232 males and 1418 females) aged 4–16 years were examined for permanent tooth emergence. By counting the cases of present–absent and absent–present across all possible intra-arch tooth pairs, the frequencies of sequence polymorphisms were calculated and expressed as percentages in and arch-specific matrices. ***Results.*** Sequence polymorphisms were more common in tooth pairs in phase II than in phase I of permanent tooth emergence and only rarely did teeth in phase I reverse sequence with teeth in phase II. In addition, maxillary and mandibular polymorphisms were most common in the sequences of canine–second premolar and first premolar–canine, respectively. Furthermore, central incisor–first molar and second molar–second premolar sequences were much more common in the mandible than in the maxilla. It was noticed that males and females had more similar frequencies of polymorphic sequences in the maxillary than in the mandibular tooth pairs. ***Conclusions.*** This study presented the norms of pairwise sequence polymorphisms in permanent tooth emergence in the Jordanians. Such norms are adequately useful for the evaluation and prediction of tooth emergence sequence in individual children and valuable in the assessment of emergence sequence problems in pediatric dentistry and in planning and following-up orthodontic treatment.

Key Words: *polymorphisms, tooth emergence sequence, permanent dentition, Jordanian children and adolescents*

Introduction

In clinical practice, available chronological standards of tooth emergence are necessary resources that help dental clinicians to identify relevant developmental abnormalities, estimate dental age for forensic purposes, plan and follow-up orthodontic treatment and make the decision upon whether to treat or extract badly carious deciduous teeth and whether to provide space maintenance following their extraction. The variation in the time of permanent tooth emergence from one population or ethnic group to another [1-3] requires that standards of tooth emergence be derived from the population to which they are to be applied. This has prompted investigators all over the world to enrich the literature with published standards of tooth emergence specific to various populations or ethnic groups [4-8].

Such population-specific standards basically provide the median/mean age of emergence per tooth along with its normal percentile range and standard deviation. From median/mean emergence times, an intra-arch sequence can be set up to act as a model in that population. However, population means alone are insufficient for the evaluation and prediction of tooth emergence sequence in a single child because they provide no information on the frequency of sequence variation (normal vs reverse sequence) within pairs of consecutive teeth. Instead, providing norms of polymorphic variation in the sequence of tooth emergence can be more useful in this respect. When such norms are made available, a clinician can assess the ‘normality’ of a given sequence of tooth emergence in a single child. For example, for a child whose maxillary first premolar emerged before the maxillary lateral incisor, learning that such a sequence

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is rare (e.g., less than 5% [9]) in the population to which that child belongs enables a pediatrician to judge how much 'normal' that sequence was.

Not only do norms of sequence variation in tooth emergence find applications in pediatric dentistry, but also in orthodontics where a clinician can predict and assess tooth emergence sequences in treating their individual patients. Likewise, available norms help disregarding rare or improbable sequences when planning a treatment.

Unfortunately, the topic of sequence polymorphisms in tooth emergence has not received worthy interest in the literature and the available published data have been limited to western/developed populations [6,9]. The present study aimed at providing the norms of sequence polymorphisms in permanent tooth emergence in the developing Jordanian population. Such norms, which are intended to be applied on the Jordanians and the ethnically similar populations in the surrounding Arab or Middle Eastern countries, will be valid resources for clinicians treating individual patients in the fields of pediatric dentistry and orthodontics.

Materials and methods

A total of 2650 Jordanian school children and adolescents (1232 males and 1418 females) aged 4–16 years were selected. The study was approved by the Jordan University of Science and Technology (JUST) ethics committee through the Deanship of Research. The children and adolescents were among the participants in a cross-sectional observational study [10] on the timing and sequence of tooth emergence in the Jordanian population.

Jordan is divided into three regions. The Governorates of Irbid, Amman and Karak are the most populous per region and were selected to represent their Northern, Middle and Southern regions, respectively. Each of the selected governorates contained urban and rural districts that were all included in the sampling process. In the urban districts, there were kindergartens and three types of primary schools; governmental, private and UNRWA (United Nations Relief and Works Agency of Palestinian Refugees in the Near East). On the other hand, all rural districts contained governmental schools, some contained kindergartens and none contained UNRWAs or private schools.

The sampling was based on multi-stage clustering. Within each urban district, two schools per school type (one for boys and one for girls) and one kindergarten were randomly selected. Most of the selected private schools were mixed-gender schools. In such situations, only one private school was selected per urban district. In the rural districts, two governmental primary schools (one for boys and one for girls) and a kindergarten (if present) were selected.

Most of the selected schools comprised grades from 1–10. In each primary school, five students were randomly selected per grade. In kindergartens, five boys and five girls were selected randomly per each of the two levels: KG 1 and 2. The totals of selected primary schools and kindergartens were 40 and 12, respectively.

Through the school administrations, information statements and consent forms were sent to the parents of those selected. When the consent forms were signed and collected by the school administrations, one visit per school was arranged during which each subject was examined for the emergence of permanent teeth by one of four examiners; the author and three research assistants (registered qualified dentists). For the accuracy, reliability and reproducibility of data, prior to sampling, the research assistants were trained by the author on the examination for permanent tooth emergence. However, no intra- or inter-examiner reliability tests were done.

In the dental examination, the examiners collected data on the permanent teeth (except third molars) that were emerged at the time of examination. A tooth was considered emerged should any part of it penetrated the oral mucosa. In this respect, the outcomes were dichotomous (present/absent). Permanent teeth that were believed to have been extracted before examination were considered present. On the other hand, subjects with teeth thought to have been missing (due to agenesis) or impacted were excluded since the inclusion of such subjects would give misleading results, given the type of analysis followed in this study.

Analysis of data

In his study on the Jordanians, Shaweesh [10] found insignificant differences in the timing of permanent tooth emergence across sides, which made him report data for the right side only. In a similar approach, the analysis in the present study involved the teeth on the right side. Across all possible intra-quadrant tooth pairs, cases of present–present, present–absent, absent–present and absent–absent were computed and counted. The counts related to present–present or absent–absent were excluded because they would give no useful information on emergence sequence in this cross-sectional study. For example, when both of the first molars and central incisors were absent at the time of examination, it could not be known which would emerge first. Similarly, when both teeth were already present, one could not know which had emerged first. From pairwise counts related to present–absent and absent–present, the frequencies of sequence polymorphisms were calculated and expressed as fractions or percentages. The numerator was either the present–absent or absent–present count and the denominator the sum of present–absent and absent–present counts for a given intra-quadrant pair of teeth.

Males-Maxilla							
FDI	16	11	12	14	15	13	17
16		(126) 95	(283) 100	(564) 100	(684) 100	(706) 100	(826) 100
11	5		(167) 100	(450) 100	(570) 100	(592) 100	(712) 100
12	0	0		(293) 98	(403) 100	(425) 100	(545) 100
14	0	0	2		(144) 92	(162) 94	(264) 100
15	0	0	0	8		(118) 59	(170) 91
13	0	0	0	6	41		(160) 87
17	0	0	0	0	8	13	

Females-Maxilla							
FDI	16	11	12	14	15	13	17
16		(116) 97	(236) 100	(511) 100	(651) 100	(658) 100	(833) 100
11	3		(126) 100	(401) 100	(541) 100	(548) 100	(723) 100
12	0	0		(285) 98	(415) 100	(422) 100	(597) 100
14	0	0	2		(158) 94	(169) 93	(332) 98
15	0	0	0	6		(139) 53	(210) 93
13	0	0	0	7	47		(211) 91
17	0	0	0	2	7	9	

Males-Mandible							
FDI	46	41	42	43	44	45	47
46		(59) 71	(160) 100	(604) 100	(592) 100	(740) 100	(799) 100
41	29		(135) 100	(579) 100	(567) 100	(715) 100	(774) 100
42	0	0		(444) 100	(432) 100	(580) 100	(639) 100
43	0	0	0		(128) 45	(166) 91	(211) 96
44	0	0	0	55		(172) 93	(223) 96
45	0	0	0	9	7		(123) 74
47	0	0	0	4	4	26	

Females-Mandible							
FDI	46	41	42	43	44	45	47
46		(52) 77	(152) 100	(500) 100	(538) 100	(692) 100	(754) 100
41	23		(124) 100	(472) 100	(510) 100	(664) 100	(726) 100
42	0	0		(348) 100	(386) 100	(540) 100	(602) 100
43	0	0	0		(104) 68	(216) 94	(262) 98
44	0	0	0	32		(186) 91	(238) 95
45	0	0	0	6	9		(170) 68
47	0	0	0	2	5	32	

Figure 1. Matrices of pairwise frequencies (%) of emergence sequence separated by gender and arch. Teeth listed vertically are 'present' and teeth listed horizontally are 'absent'. Teeth are annotated according to the FDI system. Total numbers of present–absent and absent–present occurrences are given above the diagonal in parentheses.

In accordance with the method adopted by Smith and Garn [9], frequencies are rounded to the nearest whole percentage since errors in recording present and absent teeth at the time of examination could give rare frequencies when the actual frequency should have been nil. Similar to the approach of Smith and Garn, frequencies less than 5% were considered rare and above 5% polymorphic. The limit 5% was chosen because any frequency equal or above 5% should be significantly different from zero at a *p*-value of 0.05 [9].

Results

Figure 1 presents four matrices that describe the pairwise frequencies of emergence sequence separated by gender and arch. The presentation in matrix form follows the approach used in similar studies on different populations [6,9]. In each matrix, teeth are ordered according to the sequence reported by Shaweesh [10], which was determined by the median tooth emergence ages for the Jordanian children and adolescents. In the matrices, teeth listed vertically are 'present' and teeth listed horizontally are 'absent'. Therefore, below the diagonal are the frequencies of present–absent and above the diagonal are the absent–present frequencies. The total numbers of present–absent and absent–present occurrences (the frequency denominator or the sample size) for each pair are given above the diagonal in parentheses. As teeth were listed according to the sequence of their median emergence age, the frequencies of present–absent designate the less common occurrences (reverse sequence).

In both males and females, maxillary tooth pairs exhibiting sequence polymorphisms were 15–14, 13–14, 13–15, 17–15 and 17–13. In males, the frequency of the pair 11–16 was also polymorphic, although marginal (5%). The highest polymorphic frequency in the maxillary arch was that of the pair 13–15 in both males (41%) and females (47%). Thus, generally sequence polymorphisms were more common in pairs of teeth emerging during the second phase of permanent tooth emergence. Additionally, no sequence polymorphisms were evident in tooth pairs crossing the two phases of permanent tooth emergence.

For the mandibular arch, both males and females had a polymorphic sequence in the pairs of 41–46, 44–43, 45–43, 45–44 and 47–45. Females also had a marginal polymorphic sequence in the pair of 47–44. The highest value among the polymorphic frequencies was that of the mandibular pair 44–43 in males (55%). The same pair in females had a lower but still considerable polymorphic frequency (32%). Also considerably polymorphic were the frequencies of the mandibular pairs 41–46 and 47–45 in both males and females. The equivalent maxillary pairs of

11–16 and 17–15 were much less polymorphic (or rare for 11–16 of females).

Compared with the maxillary teeth, teeth in the mandibular arch showed sequence polymorphisms within both phases of the permanent tooth emergence, although involving more tooth pairs in phase II. On the other hand, similar to the finding of the maxillary teeth, none of the tooth pairs crossing the two phases of permanent tooth emergence showed sequence polymorphisms.

In analysis by gender, generally both males and females had similar polymorphic and non-polymorphic frequencies. The only noticeable difference was for the relatively higher frequency of the mandibular pair 44–43 in males compared to females.

Discussion

In the present study, the Jordanian population was classified into three geographical regions and the most populous governorate per region was considered the representative of the region. The Governorates of Irbid and Amman are similar in terms of the distribution of school types and kindergartens. School children in both governorates are believed to be similar with respect to the urban–rural living standards, socio-economic status, level of nutrition and the access to dental care and dental education. Therefore, it is assumed that there are no significant differences between subjects from the Governorates of Irbid and Amman according to the above-mentioned factors.

On the other hand, school children in the Governorate of Karak have relatively different urban–rural living standards and lower levels of socio-economic class, nutrition and access to dental care and dental education. It is anticipated that these factors may have some impact on the time and sequence of permanent tooth emergence. For example, lower levels of socio-economic class and access to dental care may predispose to premature loss of predecessor teeth, which has been found to affect the time of emergence of the successors [11,12].

In the present study, the selection of subjects did not consider the potential influence of the varying school type or socioeconomic class of children on the timing of permanent tooth emergence. The varying school type is believed to be correlated with the socio-economic class of subjects. Private school children are usually expected to belong to a higher socio-economic class than that of governmental or UNRWA school children. Although such influence of the two correlated factors is intended to investigate and present in future works, the postponement of that influence may be a limitation in the current study.

For the present study, four examiners collected the data about tooth emergence with no inter-examiner reliability test done. Considering the cross-sectional nature of this study, getting a considerable number of school children re-examined by the same or another examiner at a second occasion might be expensive, time-consuming, disconcerting to those children and, more importantly, misleading as new teeth might have emerged in the interim. Besides, the binary type of the examination outcomes and the simple way for recoding the findings by any dentist minimizes the possibility of errors given the large size of the sample. Moreover, the potential effects of intra- or inter-examiner errors do not seem to have greatly biased the outcomes because, prior to the examination, the author conducted a clinical training program for the other three examiners to ascertain that reliable and reproducible data were collected.

This study involved clinical examination of subjects without the use of radiographs. In the absence of confirming radiographs, teeth recognized clinically as unerupted (recorded as 'absent') or extracted (recorded as 'present') might have been congenitally missing or impacted. Likewise, teeth recorded as congenitally missing might have been still unerupted or have been extracted. Nevertheless, misidentification of such clinical findings is not thought to have biased the statistical outcomes significantly for two reasons. First, the prevalence of hypodontia among the Jordanians is small [13] and involves some but not all permanent teeth. Secondly, the potential effect of those few misidentification cases (if present) is expected to be diluted by the relatively large sample size.

Other errors could be the result of misrecording at the time of examination or during the entry of data into the computer. For minimizing potential recording/data entry errors, it was ascertained that the data were entered into the computer by one investigator (the author).

To further control any remaining errors, the emergence sequence frequencies were adjusted to the nearest whole percentage. This approach, which was followed previously in similar studies [6,9], was anticipated to reduce the chance of possible unreliable misidentification or misrecording errors to present as rare frequencies [9].

A sequence of permanent tooth emergence can be constructed by more than one approach. The simplest one is based on putting the means/medians of tooth emergence ages in ascending order. However, this presentation, which has been provided as the population model sequence in many previous studies, is insufficient because it provides no information on the frequencies of sequence variability [9,14]. Therefore, such a presentation can be misleading to use for the evaluation and prediction of tooth emergence sequence in individual cases. For instance, if the sequence 46–41 was derived from a given order of means/medians of tooth emergence ages in a population, it should be inferred that the frequency of the reverse sequence 41–46 is zero. This result is misleading for the evaluation of a single child with the sequence of 41–46. However, learning that the frequency of 41–46 was 20%, for example, means that it is not uncommon for this sequence to occur among children in that population. On the other hand, a frequency of 2% for the 41–46 sequence means it is rare.

The alternative approach used in the current study and in two previous studies [6,9] was based on presenting pairwise frequencies of sequence variability in the form of matrices. This overcomes the limitation of providing tooth emergence sequences as orders of means or medians of emergence ages. Therefore, the data provided can be effectively used for the evaluation and prediction of emergence sequences in individual children. Although this approach makes it useful to express variability in tooth emergence sequences, it only provides bi-directional (present–absent or absent–present) variations between two teeth at a time without considering sequence variations among all teeth in a quadrant. However, this can be the most suitable approach, given the cross-sectional nature of this study.

Cross-sectional studies can only provide pairwise frequencies because each subject is examined once. During such a single examination, the subject will have the sequence of tooth emergence cross-sectioned to detect the teeth that have emerged (the present teeth) and the teeth that are to emerge (the absent teeth). For example, for a child with the maxillary emergence of 11–12–13–14–15–16, it is not possible to build an intra-quadrant sequence based on the cross-sectional detection of the given emerged teeth. For such a child, the only clinical manifestation of use will be the present–absent pairs of 11–17, 12–17, 13–17, 14–17, 15–17 and 16–17. Nevertheless, cross-sectional studies remain easier to conduct, less expensive and capable of including significantly larger samples.

A third approach for expressing tooth emergence sequences considers sequence variations across all intra-quadrant teeth instead of pairwise variations. For this to be possible, subjects are longitudinally examined and followed up for a period of time. This approach, which was followed by Leroy et al. [14] and involved multi-occasion examination of children, made it possible to follow-up emergence sequences across all intra-quadrant permanent teeth (except third molars) to provide seven-teeth sequence frequencies instead of frequency pairings. However, the more expensive and time-consuming longitudinal approach should be weighed in contrast to the less expensive and time-saving cross-sectional approach.

Since no published data about frequencies of emergence polymorphisms seem to have been reported for Jordanian, Middle-Eastern or Arab populations, comparisons were made with the findings reported for Caucasoid Australians [6] and Caucasoid White Americans [9]. The latter studies followed the approach of expressing sequence variations in the form of pairwise matrices; the one used in the current study.

In reviewing sequence polymorphisms by jaw, the maxillary teeth in both males and females generally showed a polymorphic emergence sequences within phase II of permanent tooth emergence. Phase I teeth reversed sequence with phase II teeth only rarely between the end of phase I (lateral incisor) and beginning of phase II (first premolar). Maxillary polymorphisms were most common in the canine–second premolar sequence. All these maxillary polymorphic findings generally agree with those reported for Australian [6] and White American children [9].

In both genders, the mandibular sequence polymorphisms were more common in tooth pairs in phase II than in phase I of permanent tooth emergence and similar to the maxillary jaw, none of teeth of phase I reversed sequence with teeth of phase II. These findings are consistent with those reported for Australian [6] and White American children [9]. In contrast to the findings of the maxillary jaw, the central incisor–first molar sequence was much more common in the mandibular jaw. This agrees with the findings for Australians and North Americans. However, compared with the data for Australians and North Americans, the latter mandibular sequence was relatively less common. The second molar–second premolar sequence was also more common in the mandible than in the maxilla, which is in agreement with the data reported for the Australians and White Americans. However, the mandibular second molar–second premolar sequence was relatively less common than that for Australians, although similar to that for North Americans. In addition, mandibular polymorphisms were most common in the first premolar–canine sequence. In contrast, the most common mandibular polymorphic sequence for Australians and North Americans was that of central incisor–first molar.

In reviewing the sequence by gender, males and females had more similar frequencies of polymorphic sequences in the maxillary than in the mandibular tooth pairs. The maximum mandibular difference between males and females was in the frequency of first premolar–canine sequence, being higher in males. This is thought to be related to the faster emergence of mandibular premolars in males compared to females. In the absence of studies on prevalence of premature loss of deciduous molars among Jordanian boys and girls, the loss is expected to be more common in boys because, compared to girls, boys seem to spend more time outdoors, putting their eating behavior and the frequency of tooth brushing under less parental supervision. This may shorten the life of deciduous molars because of caries and eventually may lead to their earlier loss. As it has been confirmed in previous studies [11,12] loss of deciduous molars during the late development of their successors accelerates the emergence of their successors. This particular sexual dimorphism was only evident in the mandible because probably the difference in the time of emergence between the mandibular canine and first premolar was smaller than the difference among the first premolar, second premolar and canine of the maxillary jaw.

As the mandibular first premolar–mandibular canine sequence in males was more common than its reverse sequence, it is suggested that the mandibular emergence sequence in Jordanian males be adjusted from the one reported by Shaweesh [10] to become: first molar–central incisor–lateral incisor–first premolar–canine–second premolar–second molar. Other than the above-mentioned polymorphic sequence, none of the maxillary and mandibular sequences in males and females were more common than their reverse sequences. Therefore, the maxillary and mandibular sequences in females and the maxillary sequence in males should remain according to the one reported by Shaweesh [10] in the ascending order of the tooth-specific median ages of tooth emergence (maxillary sequence for males and females: first molar–central incisor–lateral incisor–first premolar–second premolar–canine–second molar; mandibular sequence for females: first molar–central incisor–lateral incisor–canine–first premolar–second premolar–second molar).

In conclusion, this study presented the norms of bidirectional pairwise sequence polymorphisms in permanent tooth emergence that are adequately useful for the evaluation and prediction of tooth emergence sequence in individual children. Therefore, the norms provided will be valuable in the assessment of emergence sequence problems in pediatric dentistry and in planning and following up orthodontic treatment.

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