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Review Article

Morphological variation of the maxillary lateral incisor



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KEYWORDS

Twin model; Genetic factors; Environmental factors; Epigenetics; Compensatory interactions; Inhibitory cascade **Summary** The maxillary lateral incisor is a variable tooth morphologically. This tooth frequently shows reduction in size, and also various alterations in shape, for example, peg-shaped, cone-shaped, barrel-shaped and canine-shaped. The lateral incisor variant can be analyzed by family studies and using twin models, and these approaches have shown that genetic, epige-netic and environmental factors can all contribute to variation in the trait. Discordance of the phenotype in monozygotic twin pairs could be explained by the following two hypotheses: (1) the embryological environment of monochorionic twin pairs who share the same placenta and chorionic membrane during the prenatal period may differ, (2) phenotypic variation may be caused by epigenetic influences. Possible developmental factors are discussed in this review. Recent studies suggest that *Msx1*, *Pax9* and *Axin2* genes predispose to lateral incisor agenesis. Tooth reduction and agenesis seem to represent inter-related complex multifactorial traits, influenced by a combination of gene expression and function, environmental interaction and developing timing. Thus, accumulation of large data banks of morphological data is needed to support and clarify ongoing molecular genetic studies of dental development.

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1. Introduction

The maxillary lateral incisor is a variable tooth morphologically. This tooth frequently shows reduction in size [1,2], but it can occasionally be as large as the central incisor [3,4]. It also frequently shows different crown shapes, for example, peg-shaped, cone-shaped, barrel-shaped and canine-shaped [1,2]. Interruption grooves and deep lingual pits are also found more frequently on the lateral incisor than the central [1,2]. Reduced size or shape of the maxillary lateral incisor reflects the interaction of genetic, epigenetic and environmental factors [5–9]. In this paper we describe some genetic studies of reduced crown form in maxillary lateral incisors, and discuss some developmental aspects.

2. Frequencies of occurrence of crown reduction in the maxillary lateral incisor

Reduced crown form in maxillary lateral incisors has been reported to occur in from 0 to 10 percent of individuals in various populations but the anthropological interrelationships of the different lateral incisor variants remain obscure [10]. It has been thought that lateral incisor variants are intermediate in form between normal and congenitally missing teeth [11]. The third molar is most frequently absent in the permanent teeth, followed by the mandibular second premolar [12]. In a Japanese population, agenesis of the maxillary lateral incisor was ranked third, but its freguency of absence (1.32–1.33%) was about half that of the mandibular second premolar (2.84–3.26%) [13]. This result is consistent with meta-analyses of the prevalence of dental agenesis for many human populations from all over the world [14,15]. Thus, the maxillary lateral incisor shows a relatively common tendency to reduction in crown size, but its frequency of congenital absence is low. In contrast, the mandibular incisors are found to be congenitally absent relatively frequently, but reduced form of these teeth is rarely seen [2]. These facts suggest that crown reduction and congenital absence of a tooth do not necessarily appear at the same pace.

3. Genetic analysis of maxillary lateral incisor variants

The influence of genetic factors on missing maxillary lateral incisors has been analyzed by family studies that have shown a genetic influence on this trait, but have not been able to discover any evidence of a single gene being involved [16,17]. The expression of this trait is best explained by a polygenic, multifactorial model, and non-syndromic simple hypodontia and tooth size can be considered as representative dental quantitative traits [8,18]. It is considered that other maxillary lateral incisor variants are also likely to be best explained by a polygenic model.

Kondo et al. [7] have reported the findings of a genetic analysis that focused on maxillary lateral incisor variants in a sample of Japanese twins (Figs. 1 and 2). The classical twin model, where similarities in monozygotic twin pairs are compared with similarities in dizygotic twin pairs, is very useful to clarify the contribution of genetic and environmental influences to variation in the size and shape of teeth. Monozygotic (MZ) twin pairs are assumed to share all the same genes whereas dizygotic (DZ) twin pairs only share 50% of their genes on average, similar to other sibling pairs. Various twin research study designs, including comparisons of the similarities within MZ and DZ twin pairs, have enabled researchers to further quantify the relative contributions of genetic, epigenetic and environmental factors to variation in maxillary lateral incisors [6].

Among 1005 twin pairs, a reduced form of the maxillary lateral incisor was seen in 121 twin pairs [7]. In this study, a reduction was defined as being present if it was seen in at least one side of either member of a twin pair. The reduction was divided into size and shape elements, so that these features could be assessed separately. Size was classified into three types by calculating the ratio of the crown sizes of the lateral incisor compared with the central incisor as follows: normal (>80%), small (70.0–79.9%) and diminutive (<70%). Shape was classified as normal, canine-shaped, peg-shaped and cone-shaped. Anything other than normal shape was considered to represent an example of the reduced trait. Concordance rates of the reduced form between right and left sides, and between co-twins of a pair were calculated.

The concordance rates between right and left sides ranged from 52.5% to 71.9%, and were not significantly different between MZ and DZ twin pairs (Table 1). The concordance rate between twin pairs was significantly larger within MZ twin pairs than within DZ twin pairs (Table 2), suggesting a genetic basis to variation but environmental and/or epigenetic factors were considered to also be important because the percentage concordance within MZ twin pairs was only 50–60%. Since the concordance rate within MZ twin pairs was larger for the size element than for the shape component, it is possible that hereditary factors influence tooth size more strongly than shape, but more sophisticated

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