Genetical Basis of Cleft Lip & Palate: A Review

MUDASER HUSSAIN ABBASI¹, HAROON HABIB², YASIR ALI BHATTI³

SUMMARY

Orofacial clefts, nonsyndromic cleft lip with or without cleft palate (CL/P) in particular are the mostly occurring craniofacial deformities, affecting one newborn in every 700 to 1000 newborns worldwide. The advancements in the recent past in the fields of genetics and molecular biology have revealed the basis of craniofacial development. Often contradicted and indecisive results have been obtained by various genetic approaches and techniques such as genome-wide and candidate gene association studies as well as linkage analysis. These results reveal the heterogeneity of etiological factors among population and involvement of multiple genes in causative factors of CL/P. In the presence of all the problems, there have been several genes which are associated with the occurrence of CL/P.

Keywords: Cleft lip, cleft palate, craniofacial deformity

INTRODUCTION

Orofacial clefts, nonsyndromic cleft lip with or without cleft palate (CL/P) in particular are the mostly occurring craniofacial deformities, affecting one newborn in every 700 to 1000 newborns worldwide. It has been tempered as a major public health problem all over the world due to its facial growth, function, and social integration. Ethically, there is great diversity in the incidence of CL/P. The highest rates of incidences are seen in Asian and North American populations, intermediate rates are seen in Caucasian populations, whereas lowest rates are seen in African American populations²,³. Even though environmental influences on facial development have been described, a strong genetic component has been demonstrated in these processes⁴. The nature of genetic contribution to the etiology of CLP is still under studied. Although earlier investigations suggested a multifactorial threshold model⁵. More recently complex segregation analysis of several populations have supported mixed models with major gene influences⁶,⁷,⁸. Researchers worldwide are currently studying the genes mutations associated with CL/P. Recently, advances in genetics and molecular biology have revealed the means to identify a number of genes associated with CL/P. Therefore, the purpose of this review is to present current concepts on the etiology of non-syndromic CL/P, in particular the genetic and environmental factors that have been identified in the scientific literature.

EMBRYOLOGY

Formation of the primary palate: The first, second, and third branchial arches play a critical role in the development of the face, mouth, and tongue. The development of the face is well described in terms of its formation and merging of various processes or prominences⁹. At around embryonic day 24 (E24) the fronto-nasal process can be clearly identified, bounded on each side by maxillary processes that are derived from the first branchial arch. By the end of fourth week, bilateral oval-shaped thickenings of the surface ectoderm (nasal placodes) develop on each side of the lower part of fronto-nasal prominence followed by the migration of neural crest cells into that region, and the region from which the maxillary prominences will develop. This migration subsequently causes the mesenchyme to proliferate at the margins of the nasal placodes, producing horseshoe-shaped medial and lateral nasal processes. The maxillary processes at this time grow medially and soon approach both the medial and lateral nasal processes. The frontonasal and maxillary processes grow downward and forward but the mechanism of this interaction and its coordination is unclear.⁹ The medial growth of the maxillary prominences push the medial nasal processes toward the midline, where they merge, eliminating the frontonasal process. This merging mechanism occurs between E40 and E48 (around sixth week of human development). At the same time, the medial nasal prominences merge with each other to form the intermaxillary segment. This segment gives rise to the middle portion or philtrum of the upper lip and the primary palate, an area of the palate bounded by two lines from the incisive foramen along the alveolar bone between the lateral incisor and canine on each side.

¹Associate Prof. Forensic Medicine & Toxicology, Avicenna Medical college, Lahore ²Lecturer in Biochemistry, Avicenna Medical College, Lahore ³Lecturer in Biochemistry, Avicenna Medical College

Correspond to Dr. Mudas Gariin Abbasi, Associate Professor Email: forensico Doctor786@yahoo.com
Previously it was highlighted the importance of the positioning of the olfactory (nasal) placode. Abnormal midline positioning of the placodes could possibly cause facial clefting. In another article it was mentioned that failure in the growth of the median and lateral nasal processes prevents the subsequent merging of these structures. As a consequence, clefts develop between their derivatives.

**Development of the Secondary Palate:** The secondary palate is a structure that separates the nasal passage from the oral cavity. The palate proper develops from both primary and secondary components. The secondary palate begins its development in the sixth week from medial projections of the paired maxillary processes of the first branchial arches, termed palatal shelves or lateral palatine processes. Initially these shelves grow medially towards each other and lie in a vertical position on each side of the developing tongue, but as development proceeds the shelves become horizontal and fuse with the primary palate. An intrinsic shelf-elevating force, generated by the hydration of hyaluronan, primarily causes elevation of the palatal shelves. This osmotic shelf-elevating force is directed by the collagen fibers, mesenchymal cell orientation, and contraction within the palate.

Fusion begins anteriorly in the palate during the ninth week and is completed posteriorly by the twelfth week of embryonic life. During fusion, the apposed epithelia form an epithelial seam that undergoes apoptosis, migration or transformation and results in mesenchymal continuity. The basal epithelial layer constitutes the medial edge epithelium (MEE) of each shelf. The shelves grow toward the midline, and the MEE of each shelf approximates and forms the midline epithelial seam. This seam is subsequently disrupted, leading to mesenchymal confluence between the two shelves.

Perturbations caused by genetic, mechanical, or teratogenic factors can occur at any of these steps, and may result in a cleft palate. The event most subject to error in human palate development is removal of the tongue from between the palatal shelves. This event appears to involve active movement such as jaw opening and tongue protrusion, as well as differential growth of the lower jaw.

**Candidate genes or loci for non-syndromic cleft lip and palate:** A candidate gene is a gene known to be located in a region of interest in the genome, and whose product(s) has/have biochemical or other properties suggesting that it may be the gene being sought. The following candidate genes have been identified in the etiology of CLP.

**Transforming growth factor-alpha (TGFA):** Transforming growth factors (TGFA) are an extensively studied family of growth factors. The gene is located at chromosome 2p13. TGFA have been shown to be present in the regulation of palate development and are present at high levels in the MEE of palatal shelves. Previous genetic studies have demonstrated a significant association between transforming growth factor-alpha (TGFA) and CL/P. In contrast, with two studies which showed no association between TGFA with CL/P in non-Caucasian population. There is also evidence from some studies that reported that the combined effects of a TGFA mutation and maternal smoking could increase the risk of CL/P. Furthermore, another study showed that infants with TGFA genotype whose mothers did not used multivitamins containing folic acid periconceptionally are at a higher risk of being born with CL/P.

**Transforming growth factor - B2 (TGF B2):** TGFBR2 is a member of the highly conserved TGF superfamily and is located at chromosome 1q41. It is expressed in mesenchymal cells adjacent to medial edge epithelium. TGFBR2 and TGFBR1 regulate mesenchymal cell proliferation and extracellular matrix synthesis of palate, while TGFBR3 orchestrates fusion of the palatal seam. Two previous studies in Asian populations found contrasting findings. In Japanese significant differences in TGFBR2 polymorphism between a patient group with non-syndromic CL/P and control group of Japanese people. In contrast a study in the Philippines conducted showed no association between this particular gene and CL/P formation.

**Transforming growth factor – B3 (TGF B3):** The role of TGFBR3 in clefts has emerged from animal studies which indicate that TGFBR3 play a crucial role in secondary palate development. In humans, TGFBR3 is associated with non-syndromic CL/P in different populations. TGFBR3 is located at chromosome 14q24. There are mixed reports regarding the role of this gene in relation to incidence of CLP. For South American it was suggested that the mutation of MSX1 and TGFBR3 in South American populations may contribute to CL/P. A similar study in Korean populations revealed that the TGFBR3 polymorphism was strongly associated with an increased risk CL/P patients compared to controls.

**MSX1:** Evidence of linkage between non-syndromic CL/P and markers on the long arm of chromosome 4q25 has suggested that a cleft susceptibility locus may reside within this region. It was found that the significant association of MSX1 and TGFB3 with non-syndromic clefting in humans using a linkage disequilibrium (LD) strategy, suggesting that these genes are involved in pathogenesis of clefting.
further suggested that the combined genetic background of rare variants of TGFβ3 and MSX1 could increase the risk of CL/P, demonstrating the significance of gene-gene interaction in the etiology of non-syndromic CL/P. Subsequently, another study described a family with a common pattern of tooth agenesis associated with CL/P. Recently, direct sequencing of MSX1 (two exons and one intron) was performed on 917 CL/P patients and gene mutation was identified in 16 patients with CL/P. This report demonstrates that the MSX1 mutations appear to contribute about 2% of cases of non-syndromic CL/P.

**MTHFR:** Methylene tetrahydrofolate reductase (MTHFR) maps on chromosome 1q36 is a key enzyme in folate acid metabolism. The size of this gene is about 19kb and contains 5 exons. The C677T mutation of MTHFR is thermally labile and considered a risk factor of neural tube defects as it lowered the plasma level of folate. During investigating Irish cases, found that the homozygosity for the common folate-related polymorphism associated with thermo-labile form of MTHFR is significantly more frequent in CL/P. Previous studies in non-syndromic CL/P, the MTHFR C77T genotype in the mother conferred an increased risk of C/LP in their offspring. Similarly another study demonstrated a significantly higher mutation frequency of MTHFR in mothers of children with CL/P. Thus, the important of peri-conceptional folate intake were emphasized in these studies and its deficiencies could lead to CL/P.

**Proto-oncogene BCL3:** Although the role of B-cell leukemia/lymphoma 3 (BCL3) in the etiology of CL/P is unknown, BCL3 is related to genes involved in cell lineage determination and cell cycle regulation. Epithelial cell disruption at the edges of the developing maxillary process and growth of underlying mesenchyme leading to mesenchymal continuity and seam formation are critical in palate development. A dominant mutation in BCL3, resulting in increased binding to the transcription factor, could lead to inhibition of the expression of genes important to growth in the developing mesenchyme. Growth failure in these cells could result in CLP.

It was demonstrated that the linkage of nonsyndromic CL/P to BCL3, a growth factor in 17 multigenerational CL/P families. Their analyses showed evidence for involvement of chromosome 19 in the etiology of clefting. Another study supported these findings using different methods. In addition the data reported for the chromosome region 19q13.2 provided "suggestive" linkage, i.e., statistical evidence expected to occur one time at random in a genome scan. Although suggestive linkage is only indicative, by definition, so far three different groups have found a suggestive linkage for this locus, a sign that the locus is relevant for different populations. It was believed that BCL 3 or a nearby gene seems to be implicated in some way in this congenital facial malformation.

**Retinoic Acid Receptors (RARA):** Retinoic acid receptor alpha (RARA) showed a significant association with CLP in an Australian population, but no association in a British population. A study on mouse gene they found the chromosomal location of the mouse gene in which mutation occurs that can cause non-syndromic CLP. The region on chromosome 11 associated with CLP in this animal model is homologous to 17q21–q24 in humans. This region, marked by retinoic acid receptor-a (RARA) has shown association with CLP in some populations. This study has strengthened the case for CLP locus linked to RARA in humans.

**CONCLUSION**

In general, the genetic basis of CL/P is still controversial because of genetic complexity of clefting. Results from previous studies support the presence of heterogeneity among populations and the presence of multiple genes involved in the etiology of CL/P. Genetic interaction with environmental factors will become apparent through further studies involving maternal and fetal genotypes along with differing environmental exposures. Furthermore, recent technical advances in gene manipulation promises a stimulating time ahead for CL/P research.

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