

Genetics And Dental Disorders – A Clinical Concept.Part;1

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Abstract: In dentistry we encounter numerous differences in the dentofacial characteristics of individuals, even among family members. The three most common problems in dentistry today remain dental caries, periodontal diseases and malocclusion. A multifactorial aetiology for all three conditions has generally been assumed, with both genetic and environmental contributions to observe variability. This article describes the some of the dental disorders and its genetic etiology.

Keywords: Genetics, dental caries, periodontal disease, malocclusion, Oro-facial clefts

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I. Introduction

Genetics is a science of potentials. It deals with the transfer of biological information from cell to cell, from parents to offspring, and thus from generation to generation. Genetics has revealed that any two individuals share 99.9% of their DNA sequences. Thus, the remarkable diversity of humans is encoded in about 0.1% of our DNA.[1] Genetics has revealed that any two individuals share 99.9% of their DNA sequences. According to Stent (1971) the first evidence of inheritance was taught and developed by Hippocrates in fifth century BC in Greece. Hippocrates ideas can be termed as ‘bricks and mortar theory’ which states that hereditary material consists of physical matter.[2]He postulated that elements from all part of the body became concentrated in male semen and then formed into a human in the womb. He also believed in the inheritance of acquired characteristics. A century later Aristotle criticized Hippocrates theory and instead proposed that heredity involved the transmission of information- ‘a blueprint model’. Aristotle discarded Hippocrates theory for several reasons. He pointed out that individuals sometimes resemble remote ancestors rather than their immediate parents.[1,3]

Gregor Mendel (1822-1884) is appropriately called as the —Father of genetics. His precedent- setting experiments with garden peas were published in 1866. Although Mendel devised a precise mathematical pattern for the transmission of hereditary units, he had no concept of biological mechanisms involved.[1] August Weismann (1834– 1914) gave the germ-plasm theory which stated that the germ line is the continuous element, and the successive bodies of higher animals and plants are side branches budded off from it, generation after generation. [2]Galton showed that, on the average, an individual inherits ¼ of his characteristics from each parent, 1/16 from each grandparent, 1/64 from each great-grandparent, and so on. In 1930, G.W. Beadle, B. Ephrussi, E. L. Tatum, J. B. S. Haldane hypothesized that: The gene was at first characterized as an indivisible unit of structure, unit of mutation and unit of function with all three of these attributes considered equivalent. The concept given by them is called one gene-one enzyme concept.[1.3.5]

Concept of the gene has evolved from Mendel’s —unit factor controlling on a phenotypic trait to the unit of genetic material specifying one polypeptide and operationally defined by the complementation test. There has been no change in the concept of the gene as the basic unit of function since its discovery by Mendel in 1866.[2]The discoveries of the mid to late 20th century defined processes that would provide the tools for molecular biology, recombinant DNA technology, and finally the biotechnology industry. Restriction enzymes were discovered and used to construct recombinant DNA molecules. The advent of protein and DNA sequencing launched a new era of phylogenetics. Species could now be compared at the molecular level. The information age is essential to genomics. The electronic analysis, distribution and storage of genomic data are a hallmark of the science.[1.2.3.5] This article describes the some of the dental disorders and its genetic etiology.

Butler’s field theory

Reference is often made to specific teeth seem to show more variation than others. Much of this descriptive information on dental variation can be simplified if Butler’s field theory is understood.[5]In 1939, Butler, an English paleontologist, proposed that the mammalian dentition can be divided into several developmental fields. Within each field, there is a “key” tooth-one that is more stable developmentally –and on either side of this key tooth, the remaining teeth within the field become progressively less stable. The three

fields include those for molars / premolars, incisors, and canines considering each quadrant separately, the molars / premolars field would consist of the first molar as the key tooth, the second the third molars on the distal end of the field, and the first and second premolars on the mesial end.[7] The theory predicts that the third molar and first premolar would be most variable in size and shape. Most clinicians would agree on the third molar but not on the first premolar. Actually the earliest mammals had four premolars and some of the higher primates, including man, have lost the first two, so that the premolars that we refer to as first and second should really be labeled third and fourth. The point is that as Butler's theory predicted, the premolars farthest from the first molar were the first to be lost in an evolutionary sense and therefore can be considered the least stable.

Adapting Butler's theory to the human dentition, Dahlberg suggested the following fields and gradients of stability among teeth – the arrows indicate decreasing stability. With the scheme in mind, it is relatively easy to remember which teeth within a given field will show the greatest variation in size, shape, eruption, and number. It is also possible to predict which teeth are the most likely to be lost in the course of evolution.[6]

Polygenic inheritance

The second principle which will be useful to remember is that most research data suggest that "normal" variation in the dentition is the result of multiple rather than single genes.[5] By normal variation we mean to exclude the genetic defects or syndromes associated with the dentition. Thus unlike disease such as odontogenesis imperfecta and ectodermal dysplasia which result from the segregation of single genes, the size or shape of the teeth is determined by many genes interacting with each other and the environment.[7]

Types of dental variations

The common categories used in anthropologic studies are crown size, the age of eruption, hypodontia (the congenital absence of teeth), and crown morphology. These four forms of dental variation are interrelated and should not be thought of as being biologically independent of each other.

I) Tooth size

Environment plays a major role; high correlations in crown size between siblings or between parents and children. Estimate of heritability: ranges between 0.40 and 0.70, indicating that like most polygenic trait; both the environment and genes are important. The "key" tooth in each morphologic class of teeth has the highest heritability. The more, distal teeth in the same class seem to be more influenced by the environment. Bader (1965) reported a relatively strong genetic contribution to the size of the first and second molars (66 %) and less to the third molar (47 %). He indicated that the intrauterine environment is the single largest source of environmental variation in the dentition.[8,9]

II) Tooth eruption

The heritability of tooth eruption points to multiple genes. The effect of environment on tooth eruption. Low birth weight child seems to be associated with retarded permanent tooth eruption. The weight of a child at birth is determined mainly by the maternal genotype and environment[3,4,10].

III) Tooth morphology

The Cusp of Carabelli and Shovel– shaped incisors are traits of polygenic origin with a discontinuous distribution and can be thought of in much the same way as congenitally absent teeth. That is, they have a quasi-continuous distribution with the complete absence of the trait occurring when a threshold is crossed at the extreme end of the distribution. Studies of mice indicate that changes in maternal environment can influence the morphology of teeth, generally there seems to be a decrease in cusp size and number and an increase in the depth of occlusal pits and fissures. [11]

IV) Congenitally Missing Teeth

Perhaps the best family study of tooth agenesis was done by Grahnén in 1956.[12] He found that if either parent had one or more congenitally missing teeth, there was an increased likelihood that their children also would be affected. This familial relationship suggests that the genes are important. Most dental anthropologists would probably agree that the absence of teeth in the "normal" individual is a polygenic trait. Several investigators have suggested that tooth agenesis is an example of a 'quasi-continuous' trait.[13,14,15,16]

Genetics of common dental disorders

A. Dental caries: A consequence of at least five distinctly separate traits or attributes:

1. The density or structural integrity of the dental enamel
2. Toical and/or communal water fluoridation
3. The composition of the secretions of the salivary glands
4. Nutrition and day-to-day dietary habits
5. Personal and professional oral hygiene.

Salivary glands secretion, density and structural integrity of enamel are directly under genetic control. Klein examined 5,400 individuals who were members of 1,150 different families, and demonstrated that the amount of dental disease (viz., caries) that appeared in the offspring was quantitatively related to that which had been experienced by their parents. **Mansbridge** reported that the resemblance in caries experience between MZ was greater than between DZ twins. **Goodman et al** reported significant heritability for the presence of several oral microorganisms, including Streptococci, and also for salivary flow rate, salivary pH, and salivary amylase activity. **Finn and Caldwell** detected differences between smooth-surface and pit-and-fissure caries lesions, indicating that the smooth surface lesion may be under more strict genetic control.[17-21] Hans Muhlemann presented a philosophical view when considering the scientific evidence about caries (and periodontal diseases) in humans from the genetic point of view. [22] “Dental caries is a polyfactorial entity. Could caries not therefore also have a polygenic heritability? One gene could influence the resistance of enamel by determining its chemistry or its morphology, another gene could control the composition of saliva, which could influence partly the oral flora; a third gene could determine eating habits; a fourth could influence one’s characteristic personal view of or approach to oral hygiene at home. Given this, is a clean genetic analysis possible in man?” study of a large cohort (N = 97) of adult twins (the mean age was 40.6 yr) who had been raised apart since birth, and a control group of dizygous twins also raised apart. [23]This is a powerful method, because the effects of common environment are eliminated; thus, the intraclass correlation coefficient between monozygous twins becomes a direct measure of heritability. Remarkably, of the 17 orofacial parameters studied, were associated with highly significant within-pair resemblance in monozygous twins reared apart. This study has provided new and convincing evidence for a marked genetic component to dentate status and dental caries experience. It also provides strong support for the earlier studies that had implicated hereditary contributions to tooth size, dental malalignment, occlusion, and tooth morphology.[21-23]

B.Genetics And Periodontal Diseases

Periodontal diseases are a heterogenous group of diseases characterized by varying degrees of pathological changes in periodontium. It results in the destruction of the supporting structures and most of the destructive processes involved are host derived. Periodontal diseases may be broadly grouped into two types, Gingivitis and Periodontitis.[24] Gingivitis is the inflammation of gingiva in the absence of clinical attachment loss. Periodontitis is an inflammatory disease of the supporting tissues of the teeth caused by specific microorganisms or groups of specific microorganisms, resulting in progressive destruction of periodontal ligament and alveolar bone with pocket formation, recession or both. While microbial and other environmental factors are believed to initiate and modulate periodontal disease progression, there now exist strong supporting data that genetic polymorphisms play a role in the predisposition to and progression of periodontal diseases.[25] Clinically distinct periodontal infections that can affect young individuals include: 1) dental plaqueinduced gingival diseases; 2) chronic periodontitis; 3) aggressive periodontitis; 4) periodontitis as a manifestation of systemic diseases; and 5) necrotizing periodontal diseases.[26]

Aggressive periodontitis

Evidence for a genetic contribution to individual differences in risk of periodontal disease is clearest for early onset periodontitis. Some of the pioneering initial studies of the mode of inheritance of susceptibility to early onset periodontitis concluded that the increased prevalence in women as well as the lack of father-to-son transmission in families indicated that susceptibility is inherited as an X-linked dominant trait. [24] More extensive analysis of these data has shown that these two indications of X-linked inheritance are due to the differential ascertainment of women or girls with periodontal disease in families. When the original pedigrees were analyzed redressing for ascertainment bias, they were found to be supportive of autosomal inheritance of EOP. [25]Both autosomal-recessive inheritance and autosomal-dominant inheritance of early-onset periodontitis are supported by existing data In the largest study to date (100 families), Marazitta and colleagues (1994) found the strongest evidence for an autosomal-dominant susceptibility gene, with 70% penetrance [27]

Genetic linkage studies have been routinely used to locate disease susceptibility genes in the genome; such studies typically involve detailed genetic and phenotypic studies in families that appear to manifest a

genetically inherited disease predisposition. In a large, five-generation family, an autosomal dominant form of localized juvenile periodontitis was ascertained to be linked to Gc (group-specific component, a vitamin-D-binding protein locus) on the long arm of chromosome 4 (4q).[28]

Gingival Enlargement

It is the overgrowth of gingiva characterized by an expansion and accumulation of the connective tissue with occasional presence of increased number of cells. Gingival enlargement may result from chronic gingival inflammation. It may occur as a drug-related side effect in some individuals. Calcium channel blockers, phenytoin, cyclosporin have been associated with this adverse effect.[28] Hereditary gingival enlargement is characterized by a slowly progressive benign enlargement of the gingival tissues. Hereditary gingival fibromatosis is a rare disease of infancy characterized by progressive gingival enlargement of normal color and firm consistency that is non-hemorrhagic and asymptomatic. It results in diastemas, malpositioning of teeth, prominent lips and open lip posture. Three different loci have been associated with hereditary gingival fibromatosis: two mapping to chromosome 2 (GINGF on 2p1-22 and GINGF3 on 2p22.3-p23.3) which do not overlap, and one mapping to chromosome 5 (GINGF2 on 5q13-q22). [28,29]

C.Malocclusion

Genetic and environmental factors play important role in etiology of malocclusion. While phenotype is inevitable the result of both genetic and environmental factors, there is irrefutable evidence for significant genetic influence in many dental and occlusal variable. Genetic however varies according to the trait under consideration. The bulk of the evidence for the heritability of various type of malocclusion arises from family and twin studies .[4,7,15] Genetic factors playing a predominant role in the etiology of malocclusion is backed up by population studies, especially family and twin studies. A literature review carried out by Lauweryns in 1993 concluded that 40% of the dental and skeletal variations that lead to malocclusion could be attributed to genetic factors.[30] Hughes and Townsend in 2001 quantified the extent of variation in different occlusal features such as interdental spacing, overbite, overjet and arch dimensions of Australian twins and indicated a moderate to relatively high genetic contribution to the observed variation.[31] Ting Wong et al in 2011 suggested an association for the genes EDA and XEDAR in dental crowding present in Class I patients by identifying 5 SNPs that were significantly different in a genotype or allele frequency distribution in the Hong Kong Chinese case-control population.[32] While these studies provide evidence for the heritability of dental occlusal characteristics that contribute to malocclusion, other studies have come to the opposite conclusion. For instance, Corruccini, Sharma et al could not demonstrate significant heritability for occlusal traits among Indian twins suggesting that dental patterns are environmentally based.[33] Harris and Johnson also noted almost all of the occlusal variability within their sample of untreated subjects was acquired rather than inherited.[34] These conflicting data suggest that dental variation is more dependent upon environmental factors. In a study of the association of the Pro561Thr (P56IT) variant in the growth hormone receptor (GHR) gene with craniofacial measurements on lateral cephalometric radiographs by Yamaguchi et al, those who did not have the GHR P56IT allele had a significantly greater mandibular ramus length (condylion-gonion) than did those with the GHR P56IT allele in a normal Japanese sample of 50 men and 50 women. The average mandibular ramus height in those with the GHR P56IT allele was 4.65 mm shorter than the average for those without the GHR P56IT allele. This significant correlation between the GHR P56IT allele and shorter mandibular ramus height was confirmed in an additional 80 women.[35]

Theoretically, there are two general ways in which predisposing or causative factors for malocclusion could be due to heritable characteristics. One would be inheritance of a disproportion between the size of the teeth and the jaws resulting in crowding or spacing, whereas the other would be inheritance of a disproportion in the position, size, or shape of the mandible and maxilla. However genetic influences on each of these traits are rarely due to a single gene, which would be necessary for malocclusion to be due to the simple inheritance of discrete skeletal and dental characteristics. Instead they are often polygenic with the potential for environmental influence. Twin studies by Lundstrom showed that heredity played a significant role in determining the following characteristics: tooth size, width and length of the dental arch, height of the palate, crowding and spacing of teeth and degree of overbite.[36] Kraus, Wise and Frei's cephalometric study of triplets showed that the morphology of an individual bone is under strong genetic control but that the environment plays a major role in determining how various bony elements are combined to achieve a harmonious or disharmonious craniofacial skeleton.[37]

Class I:

Mesiobuccal cusp of the maxillary first permanent molar occludes in the buccal groove of the mandibular first permanent molar. Most cases fall into one of three categories:

(1) Local abnormalities:

- a) Crowding of the upper and/or lower incisors,
 - b) Labial inclination of the upper anterior teeth,
 - c) Anterior crossbite
 - d) Posterior crossbite
 - e) Local abnormalities due to premature loss of deciduous molars
- (2) Vertical malrelationships: Excessive overbite (deep bite) or deficient overbite (open bite)[38]

Class II division 1

Extensive cephalometric studies have been carried out to determine the heritability of certain craniofacial parameters in class II division 1 malocclusions. These studies have shown that in class II the mandible is significantly more retruded than in class I patients, with the body of mandible smaller and overall mandibular length reduced. These studies also show a higher correlation between the patients and his immediate family and data from random pairings of unrelated siblings, thus supporting the concept of polygenic inheritance for class II division 1 malocclusion[38-40]

Class II division 2

Class II division 2 comprises the unique combination of deep overbite, retroclined incisors , class II skeletal discrepancy , high lip line with strap like activity of the lower lip and active mentalis muscle .Class II division 2 syndrome is a tendency to a forwardly rotating mandibular movement , which contribute to the deep bite, chin prominence , and reduced lower face height. Familial occurrence of class II division 2 has been documented in several published reports including twin and triplet studies conducted by Kloepfel and Markovic; and in family pedigrees from Trauner and Peck S. [38-40] They carried out a clinical and cephalometric study of 114 class II division 2 cases 48 twin pairs and six sets of triplets. Of the monozygotic twin pairs, 100 percent demonstrated concordance for class II division 2 malocclusion, while almost 90 percent of the dizygotic twin pairs were discordant. This is strong evidence as main etiological factor. [38-40]

Class III malocclusion

The relative contribution of genetic and environmental factors to class III malocclusion resulting from a skeletal imbalance between the maxillary and mandibular bases may result from excessive mandibular growth, deficiency in maxillary growth, or a combination of both. Various studies have also highlighted the influence of a distinctive cranial base morphology with a more acute cranial base angle and shortened posterior cranial base resulting in a more anteriorly placed glenoid fossa, thus contributing to mandibular prognathism. (41) Familial studies of mandibular prognathism are suggestive of heredity in the etiology of this condition. [42] Various models have been suggested, such as autosomal dominant with incomplete penetrance simple recessive, variable both in expressivity and penetrance with differences in different racial populations. [43, 44]

D.Oro-facial clefts

Cleft lip (CL), cleft lip with or without cleft palate (CL/P) and isolated cleft palate (CP), collectively termed oral clefts (OC), are the second most common birth defects among newborn. These defects arise in about 1 in 700 live born babies, with ethnic and geographic variation. Approximately 75% of CL/P and 50% of CP cases are isolated defects and no other deformities are found in those children. Those OCs are therefore called nonsyndromic [45].

Although OC is usually not a life-threatening condition, many functions such as feeding, digestion, speech, middle-ear ventilation, and hearing, respiration, facial and dental development can be disturbed because of the structures involved. These problems can also cause emotional, psychosocial and educational difficulties. Affected children need multidisciplinary care from birth until adulthood [48,49,50]. Orofacial clefts pose a burden to the individual, the family, and society, with substantial expenditure, and rehabilitation is possible with good quality care. Care for children born with these defects generally includes many disciplines-nursing, facial plastic surgery, maxillofacial surgery, otolaryngology, speech therapy, audiology, counseling, psychology, genetics, orthodontics, and dentistry. Fortunately, early and good quality rehabilitation of children with OC usually gives satisfactory outcomes[45,46]

Identification of etiological factors for OC is the first step towards primary prevention. Genetic factors contributing to CL/P formation have been identified for some syndromic cases, but knowledge about genetic factors that contribute to nonsyndromic CL/P is still unclear.[46] The high rates of familial occurrences, risk of recurrence, and elevated concordance rates in monozygotic twins provide evidence for a strong genetic component in nonsyndromic CL/P. However, concordance in monozygotic twins ranges between 40% and 60%, which means that the exact inheritance pattern of OC is more complex. It has been suggested that the development of nonsyndromic OC occurs as a result of the interaction between different genetic and environmental factors [46,47]. The identification of the genes responsible for diseases has been a major focus of

human genetics over the past 40 years. The introduction of modern molecular methods, experimental animal knockout models and advances in the technique of gene mapping have provided new candidate genes for orofacial clefting, both for syndromic and nonsyndromic cases. However, the results of earlier candidate-gene-based association studies, performed in different populations, have been conflicting, with only a few candidate loci being implicated in OC phenotypes. This inconsistency indicates the challenges in searching associations with a relatively rare phenotype such as nonsyndromic clefting. [46]

To date, genetic approaches to nonsyndromic CLP have included: linkage analysis; association studies; identification of chromosomal anomalies or microdeletions in cases; and direct sequencing of DNA samples from affected individuals [7]. These methods can be applied to candidate genes or genome-wide strategies can be used. Each approach has its own advantages and disadvantages, some of which will depend on the underlying genetic architecture of the disease, as well as the realities of economics and technology. Findings of linkage studies have suggested various loci could have a causal role in CL/P, including regions on chromosomes 1, 2, 4, 6, 14, 17, and 19 (MTHFR, TGF- α , D4S175, F13A1, TGF- β 3, D17S250, and APOC2), with putative loci suggested at 2q32–q35 and 9q21–q33 [8]. Inconsistent results could be caused by the small size of the studies or genetic heterogeneity association studies. Some genes function as growth factors (eg, TGF- α , TGF- β 3), transcription factors (MSX1, IRF6, TBX22), or factors that play a part in xenobiotic metabolism (CYP1A1, GSTM1, NAT2), nutrient metabolism (MTHFR, RARA) or immune responses (PVRL1, IRF6) [2]. The most intensively investigated genes have been the TGF- α [9-11] and MTHFR [12,13] genes. Inconsistent data have demonstrated the challenges of researching gene disease associations and related interactions. However, IRF6 has shown consistent evidence of association with CL/P across populations of different ancestry [45,46].

Stanier and Moore [51] provided the first population-based evidence that OC has a strong genetic component. Carcini et al. [52] separated cleft palate only (CPO) and CL/P. There is evidence that families with patients affected by OC have a different genetic background. Conventionally, it has been decided to classify patients with CP only and the remaining patients as CL/P. The high rates of familial occurrences, recurrence risks, and elevated concordance rates in monozygotic twins provide evidence for a strong genetic component in nonsyndromic CL/P. The disorder has a complex inheritance pattern with no clear mode of inheritance and reduced penetrance, with a positive family history for clefting in approximately one third of patients. A sibling risk ratio of approximately 40 has been reported, and there is a 2-5% increased risk for offspring of affected individuals. Concordance in monozygotic twins ranges between 40% and 60%, but it is only 5% in dizygotic twins [1,46]. The lack of total concordance in monozygotic twins suggests that genetic factors alone do not fully account for the pathogenesis of the phenotype; this discordance may be a result of either some degree of nonpenetrance, perhaps as a consequence of random developmental events, or environmental influences in utero. However, the highly increased monozygotic twin concordance does strongly support a major genetic component to orofacial clefting [1,3,53]. The advent of gene targeting technology and basic conventional techniques using animal models has led to the identification of genes associated with known and unknown etiologic factors. Animal models, with clefts arising spontaneously or as a result of mutagenesis experiments, provide another exciting avenue for gene mapping. The mouse is an excellent model for studying human clefting because the development of craniofacial structures in these two species is remarkably similar. Whereas CP is a common phenotype in the mouse, CL is rare [46]. Conservation of genes and linkage relationships between mice and humans is well documented, and the chromosomal location of a gene in humans can often be predicted from its genetic map position in mice. Development of the orofacial complex is very similar between mouse and human embryos, and much of the understanding of developmental mechanisms in humans has been inferred from mice [19]. It has become evident that CL/P is heterogeneous, and different chromosome regions such as 1q, 2p, 4q, 6p, 14q and 19q have been claimed to contain a clefting locus [1-5].

The genetic mechanisms underlying lip and palate development may be due to the disruption of important signaling pathways at various levels that are required for the formation of specific anatomical structures. The challenge is now to perform full-scale genome sequencing in order to identify genetic variants which are more likely to increase the susceptibility to OC. However, estimations of the total genetic contributions to the disease indicate that additional genetic factors involved in OC need to be identified, and both the functional effects of associated variants and the molecular mechanisms behind different pathways must still be ascertained. Further research using large, multicentre, collaborative studies is necessary to identify both genetic and environmental risk factors related to nonsyndromic clefts [45,46,47].

II. Recent Advances

DNA vaccination

A direct injection of the plasmid DNA encoding antigenic proteins enables expression of the protein intracellular. This leads to a strong response involving both humoral and cellular immune system.[54]

Biochips

Biochips are also referred as DNA chips, usually helpful in drug discovery, pharmacogenomics, toxicological research, and toxicogenomics.[54]

Human cloning

It is used for mass production of animals engineered to carry human genes for the production of certain proteins that could be used as drugs and genetically modified organs that could be safely transplanted into humans. The perpetuation of endangered species, reproduction in infertile couples, production of offspring free of a potentially disease causing genetic flaw carried by one member of a couple.[55]

Recombinant DNA technology

This can be used in variable number tandem repeated in forensic medicine, this technology is helpful for gene therapy production of transgenic animals and plants and also recombinant drugs.[56]

Transcriptome analysis

The term used to describe the approach in which mRNA, and consequently gene expression, is analyzed in a biological sample under certain conditions at a given point in time.[57]

Proteomics

It aims to characterize all proteins in a biological sample at the functional level.[58]

Metabolomics

It is used to describe the quantitative analysis of all metabolites in a biological system such as cell, tissue, or biological fluid.[59]

Nutrigenomics

It aims to reveal the relationship between nutrition and the genome and to provide the scientific basis for improved public health through dietary means.[50]

III. Conclusion

Dental and medical care is generally based on an examination and assessment of the patient's status, diagnosis, and prescription of treatment. The treatment is typically based on a positive response in the majority of individuals with the diagnosis. A permanent interaction between genetic and environmental factors, both of a continually altering nature, determine the dentofacial morphology. Genetic information in the molecular form of RNA is transmitted and odontogenesis is initiated. Consideration of genetic factors is an essential element of diagnosis that underlies virtually all dentofacial anomalies. Thus it is important to recognize the genetic aberrations in the early stages before their full establishment. Orthodontists maybe interested in genetics to help understand why a patient has a particular occlusion and consideration of genetic factors is an essential element of diagnosis that underlines virtually all the dentofacial anomalies.

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