

ASSOCIATION OF VITAMIN D RECEPTOR GENE POLYMORPHISM WITH EXTERNAL APICAL ROOT RESORPTION IN ORTHODONTICALLY TREATED PATIENTS

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ABSTRACT

The vitamin D receptor influences host immune responses and aspects of bone development, growth, and homeostasis. The aim of this study was to investigate the association of the polymorphism of the vitamin D receptor gene Tagl with external apical root resorption during orthodontic treatment. Methods: Our sample consisted of 50 patients aged between 12 and 40 years, who received fixed total orthodontic treatment during the years 1999 and 2000. External apical root resorption (RAAR) of the maxillary incisors was evaluated on periapical radiographs taken before and after 6 months of treatment. After DNA collection and purification, the analysis of the Taql polymorphism of the vitamin D receptor was performed by polymerase chain reaction followed by restriction fragment length polymorphism. Univariate and multivariate analyses were performed to verify the association of clinical and genetic variables with external apical root resorption (P<0.05). There was a correlation between the VDR and RRAE variables (r= 0.306 and p= 0.030). The genotype resulting from Taq1 cleavage and allele frequencies differed between the groups with and without RAAR. Individuals containing the T allele were more likely to develop RAAR when compared to individuals carrying the tt genotype (OR= 7.5; 95% CI= 1.8 – 31.4; p= 0.0094). The Tagl polymorphism of the vitamin D receptor gene was associated with external apical root resorption in orthodontically treated patients.

Keywords: External Apical Root Resorption. Genetic polymorphism. VDR. Orthodontics.

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INTRODUCTION

Orthodontics is the specialty of dentistry that is characterized by the movement of the teeth to a correct position in the dental arches. By applying force to the tooth, a narrowing of the periodontal ligament is created on the pressure side and an identical compressive action on its limits, that is, the root and bone surface. As cementum is more resistant to resorption when compared to more vulnerable bone, the forces applied usually induce bone resorption, the tooth moves and the periodontal membrane returns to its original dimension. However, resorption of cementum and dentin can also occur (BREZNIAK and WASSERSTEIN, 1993; CAPELOZZA FILHO and SILVA FILHO, 1998). RAAR (external periapical root resorption) mainly affects the maxillary central incisors, and can occur in 2 to 5% of the population (TAITHONGCHAI et al., 1996; KILLIANY, 1999; HARTSFIELD JR et al., 2004).

RAAR is a condition associated with both physiological and pathological processes, resulting in a loss of dentin, cementum, or bone (NE et al., 1999). It is considered a normal, essential and physiological process when it occurs in the deciduous teeth to allow their exfoliation and facilitate the eruption of the permanent successor (BREZNIAK and WASSERSTEIN, 1993).

Genetic, physiological and anatomical factors may be involved in the etiopathogenesis of RRAE (CAPELOZZA FILHO & SILVA FILHO, 1998). According to GRABER & VANARSDALL (1996), the etiology of root resorption during orthodontic treatment is complex and some factors alone or in association can contribute to the development, such as the patient's age, type of orthodontic appliance, duration of force, direction of tooth movement and tooth vulnerability.

There are three types of external root resorption: surface resorption, inflammatory resorption, and replacement resorption. Root resorption associated with corrective orthodontic treatment, due to the application of orthodontic forces, can be of the superficial type or of the transient or progressive inflammatory type, however, resorption by replacement is rarely observed after orthodontic treatment (LINGE and LINGE, 1991, BREZNIAK and WASSERSTEIN, 1993; SHAFER et al., 1987).

Consolaro (2005) established criteria for the classification of pathological tooth resorptions as: affected tooth surface (internal, external and internal-external), phase of process evolution (active, paralyzed and repaired), affected dental region (coronary, cervical, lateral and apical root) and extent of root involvement (single and multiple),



dimension of the cause of the process (local, systemic and idiopathic) and mechanism of occurrence of the process (inflammatory and by substitution). MALMGREN et al. (1982) classified apical root resorptions associated with orthodontic tooth movement into four grades.

While some degrees of root resorption occur in almost all patients (DESHIELDS, 1969), 93% of treated adolescents demonstrated some form of root resorption (KUROL, OWMAN-MOLL, LUDGREN, 1996). Approximately 15% (12-17% of orthodontically treated patients) showed moderate to severe apical root resorption (LINGE and LINGE, 1991) and 10-20% of cases reported severe resorption of >3 mm (LEVANDER and MALMGREN, 1988; LEVANDER et al., 1994). However, in most patients, root resorption is minor and insignificant (LEVANDER and MALMGREN, 1988).

For CONSOLARO (2005), the predisposition to RAAR associated with orthodontic treatment is related to root morphology (shape, length and angle between crown and root) and bone morphology (height, thickness and shape of the alveolar crest).

NEWMAN (1975) was the first researcher to relate heredity traits with root resorption. The following factors were investigated: genetic influences on family members, systemic causes, type of malocclusion, previous medical and dental history, and were related to root resorption. This author considered genetic potential as the cause of greater resorption of teeth with short roots after orthodontic treatment, although the pattern of inheritance was not clear.

AL-QAWASMI et al. (2003a) evaluated the association between polymorphisms in the IL-1 β genes and RAAR resulting from orthodontic treatment. These genes were investigated because they encode cytokines known to be involved in bone resorption accompanied by orthodontic tooth movement. Thirty-five American families were examined. Oral mucosal cells were collected to isolate and analyze the DNA. The RAAR in the maxillary central incisors, mandibular central incisors, and in the mesial and distal roots of the mandibular first molars were analyzed separately and together. There was high (statistically significant) evidence of association between the IL-1 polymorphism β and the RRAE manifestation. In addition, according to these authors, these findings are consistent with the interpretation of RAAR as a complex condition influenced by many factors, with the IL-1 gene *contributing* β an important predisposition to this problem.

The vitamin D receptor is a protein belonging to the superfamily of transcriptional regulatory factors of trans action, composed of steroid and thyroid hormone receptors



(BAKER et al., 1988; HANNAH & NORMAN., 1994). To exert its effects, vitamin D is converted into its active form, to 1,25 dihydroxyvitamin D3 [1,25(OH)2D3] or calcitriol. The action of calcitriol, in turn, occurs through a specific nuclear receptor, the VDR (HAUSSLER et al., 1998; ERBEN, 2001), which regulates gene transcription by binding to the responsive elements of vitamin D in the promoter region of the target genes (HANNAH & NORMAN., 1994; HAUSSLER et al., 1998; JONES et al., 1998; OZISIK et al., 2001; ERBEN, 2001).

METHODOLOGY

The sample was submitted to the UNOPAR Ethics Committee, and a favorable opinion was obtained. A cross-sectional study was carried out with 50 study participants between 12 and 40 years of age, who received fixed total orthodontic treatment during the years 1999 and 2000.

DNA was obtained from epithelial cells of the oral mucosa by mouthwash with 3% glucose for one minute. This solution was centrifuged for 2 min. At 2000 rpm, the discarded supernatant and cells were resuspended in 500 μ L of the TNE extraction solution (AIDAR and LINE, 2007).

DNA extraction was performed using the DNA extraction kit following the manufacturers' instructions. The extracted DNAs were stored properly for later analysis of the polymorphism.

For polymerase chain reaction (PCR) amplification of the VDR gene, the following primers described by HENNING et al. (1999) were used:

- a) Foward 5'- CAG AGC ATG GAC AGG GAG CAA G-3'
- b) Reverse 5'- GGA TGT ACG TCT GCA GTG TG-3'

The PCR mixture consisted of a total volume of 50µl, containing approximately 500ng of genomic DNA, 1µM of each primer, 200µM of dNTPs and two units of Taq DNA polymerase. The solutions were incubated in a Multi-Gene Thermocycler. The amplification conditions were one cycle at 95°C for two minutes of initial denaturation, 35 cycles of amplification consisting of each cycle for 45s at 95°C (denaturation), one minute at 63°C (primer pairing) and one minute at 72°C (polymerization), and one cycle at 72°C for seven minutes for the final extension. The amplified fragment is 340bp.

After amplification, 5 µl of the PCR product was analyzed by agarose gel electrophoresis (1.0%). Subsequently, the gel was stained with ethidium bromide and the newly synthesized fragments were visualized under ultraviolet light. The size of the product



amplified by PCR was estimated from the electrophoretic migration of the product relative to the 100 bp marker DNA Ladder (Invitrogen).

For the RFLP (Restriction Fragment Length Polymorphism) technique, 12μ l of the product amplified by PCR were added to 13μ l of solution, containing 2.5 μ l of NE 10x buffer, 0.4 μ l of Taql (10,000U/ml) and 10.1 μ l of sterile deionized water. The solution was incubated at 65°C overnight.

RFLP was created by the transition of a single base (T/C) at codon 352 of exon 9 of the VDR gene upon exposure to the restriction enzyme Taq1. The alleles were designated "t" (presence of the site for Taq1, forming a fragment of 260 bp and another with 80 bp) and "T" (absence of site for Taq1, maintaining the fragment of 340 bp).

The digestion products were separated by electrophoresis in 1.0% agarose gel, stained with ethidium bromide and visualized under ultraviolet light. Figure 01.

м	27 TT	28 Tt	29 Tt	30 Tt	31 tt	32 Tt	33 Tt	34 TT	35 TT	36 TT	37 TT
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Figure 01. Agarose gel electrophoresis (2%) of PCR-amplified products

RESULTS

In the present study, 50 individuals between 12 and 40 years of age who were orthodontically treated between 1999 and 2000 were evaluated, in which 60% of the sample corresponded to the female gender and 40% to the male gender. Regarding age, 54% were between 12 and 18 years old, 22% between 19 and 22 years old, and 24% between 23 and 40 years old (Table 01)

Similar proportions (32%) of dominant homozygotes (TT) and recessive homozygotes (TT) were found (Figure 02). The frequency of heterozygous individuals (Tt) was 36% (Table 02)



It is noteworthy that there was a correlation between the VDR and RRAE variables (r= 0.306 and p= 0.030).

The genotype resulting from Taq1 cleavage and allele frequencies differed between the groups with and without RAAR. Individuals containing the T allele were more likely to develop RAAR when compared to individuals carrying the tt genotype (OR= 7.5; 95% CI= 1.8 - 31.4; p= 0.0094).

Table 01. Characteristics of individuals treated orthodontically in terms of gender and age (N=50).

VARIABLES	Ν	%
GENDER Male Female	20 30	40 60
AGE 12-18 19-22 23-40	27 11 12	54 22 24

Table 02. Genotypic frequency of VDR gene polymorphism in orthodontically treated individuals (N=50).

Genotypic Frequency	N	%
TT dominant homozygous Homozygous Recessive tt Heterozigoto Tt	16 16 18	32 32 36

DISCUSSION

The VDR gene is expressed in a large number of tissues, but the highest concentrations are in the intestine, where vitamin D exerts its main function: to increase the absorption of calcium and phosphorus (HAUSSLER et al., 1998; JONES et al., 1998; ERBEN, 2001). Although osteoblasts (NARBAITZ et al., 1983) and osteoclast precursor cells (ROODMAN, 1996) also express the VDR gene, the direct action of vitamin D on bone metabolism cannot yet be confirmed.

The findings of the present study are consistent with the interpretation of RAAR as a complex condition influenced by many factors, and the polymorphism in the VDR gene predisposes the individual to this problem. Thus, the results of this study are consistent with the literature showing that teeth without strength have less resorption than teeth that have undergone orthodontic treatment (Mohandesan et al., 2007).



It has been shown that upper incisor earr, observed during the initial months of treatment, may be a predictor of increased risk of continued resorption during treatment. (Wierzbicki et al., 2009; Levander et al., 1998). Consequently, it has been recommended that periapical radiographs should be obtained after the first 6 months of treatment (Levander et al., 2000).

Other authors have evaluated the association between polymorphisms in the IL-1 β genes and RAAR resulting from orthodontic treatment (AL-QAWASMI et al.; 2003a). These genes were investigated because they encode cytokines known to be involved in bone resorption accompanied by orthodontic tooth movement. Thirty-five American families were examined. Oral mucosal cells were collected to isolate and analyze the DNA. The RAAR in the maxillary central incisors, mandibular central incisors, and in the mesial and distal roots of the mandibular first molars were analyzed separately and together. There was high (statistically significant) evidence of association between the IL-1 polymorphism β and the RRAE manifestation. In addition, according to these authors, these findings are consistent with the interpretation of RAAR as a complex condition influenced by many factors, with the IL-1 gene *contributing* β an important predisposition to this problem.

Our findings of a clinically significant association between LARR and orthodontic treatment suggest that patients susceptible to RASR can be identified early at the beginning of treatment, however few studies investigating the relationship between gene polymorphism and LARR have been described in the literature, evidencing the need for additional studies.

CONCLUSION

It was possible to conclude with the present study that TST individuals are 7.5 times more likely to develop RAAR compared to recessive homozygous (tt) and heterozygous (Tt) individuals.

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To patients treated orthodontically.



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