Defects of the Carney complex gene (PRKAR1A) in odontogenic tumors

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Abstract

The surgical treatment of some odontogenic tumors often leads to tooth and maxillary bone loss as well as to facial deformity. Therefore, the identification of genes involved in the pathogenesis of odontogenic tumors may result in alternative molecular therapies. PRKAR1A gene displays a loss of protein expression as well as somatic mutations in odontogenic myxomas, an odontogenic ectomesenchymal neoplasm. We used a combination of quantitative RT-PCR (qRT-PCR), immunohistochemistry, loss of heterozygosity (LOH) analysis, and direct sequencing of all PRKAR1A exons to assess if this gene is altered in mixed odontogenic tumors. Thirteen tumors were included in the study: six ameloblastic fibromas, four ameloblastic fibro-odontomas, one ameloblastic fibrodentinoma, and two ameloblastic fibrosarcomas. The epithelial components of the tumors were separated from the mesenchymal by laser microdissection in most of the cases. We also searched for odontogenic pathology in Prkar1a−/− mice. PRKAR1A mRNA/protein expression was decreased in the benign mixed odontogenic tumors in association with LOH at markers around the PRKAR1A gene. We also detected a missense and two synonymous mutations along with two 5′-UTR and four intronic mutations in mixed odontogenic tumors. Prkar1a−/− mice did not show evidence of odontogenic tumor formation, which indicates that additional genes may be involved in the pathogenesis of such tumors, at least in rodents. We conclude that the PRKAR1A gene and its locus are altered in mixed odontogenic tumors. PRKAR1A expression is decreased in a subset of tumors but not in all, and Prkar1a−/− mice do not show abnormalities, which indicates that additional genes play a role in this tumor’s pathogenesis.

Key Words
- mixed odontogenic tumors
- ameloblastic fibroma
- ameloblastic fibro-odontoma
- ameloblastic fibrodentinoma
- ameloblastic fibrosarcoma
- loss of heterozygosity
- benign tumors

Introduction

Odontogenic tumors arise from odontogenic tissues, and they can be aggressive and destructive lesions (Barnes et al. 2005). Surgical treatment may result in high morbidity, because it can lead to tooth and maxillary bone loss as well as facial deformity (Praetorius 2009). Therefore, elucidation of the molecular pathogenesis of these lesions may be useful in designing targeted therapies to be used in large, destructive, aggressive, or recurrent cases.
Mixed odontogenic tumors are a group of rare tumors that have been classified by the World Health Organization (WHO) as odontogenic tumors with odontogenic epithelium and odontogenic ectomesenchyme with or without hard tissue formation (Barnes et al. 2005). This group of tumors comprises the ameloblastic fibroma (AF), ameloblastic fibro-odontoma (AFO), ameloblastic fibrodentinoma (AFD), odontoameloblastoma, denino-genic ghost-cell tumor, calcifying cystic odontogenic tumor, and the odontomas.

The AF is a rare benign tumor characterized by a proliferation of odontogenic ectomesenchyme that resemble the dental papilla, with epithelial strands and nests similar to the dental lamina and enamel organ (Barnes et al. 2005). It is regarded as a true neoplastic lesion with a risk of malignant transformation of the mesenchymal counterpart into ameloblastic fibrosarcoma (AFS) (Phillipsen et al. 1997, Bernardes et al. 2012). In previous studies that included Brazilian as well as Mexican cases, AF represented about 0.7% of the odontogenic tumors and AFS represented only 0.13% (Galvão et al. 2012). In the presence of hard tissues such as dentin or enamel, the lesion may be classified as AFD or AFO respectively (Barnes et al. 2005). AF, AFD, and AFO belong to the group of mixed odontogenic tumors. These lesions histopathologically resemble various stages of tooth formation, although there is still debate about whether they are separate entities or different stages in the maturation of the same lesion (Prætorius 2009).

Several studies have focused on the molecular pathogenesis of the odontogenic tumors; however, because mixed odontogenic tumors are rare, studies involving their pathogenesis are scarce. Genes involved in the process of odontogenesis and tumor suppressor genes have been the main targets of molecular studies of odontogenic tumors (Barreto et al. 2004, Perdigão et al. 2004, Gomes & Gomez 2011, Farias et al. 2012). In this context, our group described loss of heterozygosity (LOH) at tumor suppressor gene loci in mixed odontogenic AF and AFO tumors as well as in AFS (Galvão et al. 2012).

**Materials and methods**

**Odontogenic tumors: identification and recruitment**

The present study was approved by the Ethics Committee of the Universidade Federal de Minas Gerais (protocol no. 498/11). Fresh tissue samples were collected from patients who attended at Oral Diagnosis Service at the Dentistry School of UFMG after they provided written informed consent to participate in the present study. Twenty fresh samples were included in the qRT-PCR, consisting of seven ameloblastomas (AM) as a comparison group, one AF (case no. 1), one AFD (case no. 9), five normal oral mucosa (OM), and six pericoronar follicles. Pericoronar follicles were obtained from impacted third molars free of clinical inflammation, and the normal OM included were obtained during surgeries on odontogenic tumors.

Because of the rarity of mixed odontogenic tumors, we included an additional 11 formalin-fixed paraffin-embedded (FFPE) samples: five AF, four AFO and two odontogenic sarcomas (AFS). Table 1 shows the odontogenic tumors investigated and the experiments performed with each tumor.
All of the tumors had hematoxylin and eosin (HE) slides revised by at least two pathologists. Diagnoses were based on previously reported criteria (Barnes et al. 2005).

**Tissue processing**

All of the samples had a provisional diagnosis based on an incisional biopsy, but final diagnosis was based on an excisional biopsy, which entirely represents the tumor. Tumors were collected during the excisional biopsies. A portion of each fresh tissue collected was stored in an RNA holder (Bioagency Biotecnologia, São Paulo, SP, Brazil) and in tissue-tek (Sakura Finetek, Torrance, CA, USA). RNA holder samples were stored at 4°C for 24 h before being frozen in liquid nitrogen, and tissue-tek samples were immediately immersed in nitrogen. A third portion was FFPE for diagnosis confirmation.

**RNA extraction and qRT-PCR**

Total RNA was extracted from the fresh samples of AM (n=7), AF (n=1), AFD (n=1), normal OM (n=5), and pericoronal follicles (n=6) using the TRIZOL reagent method (Invitrogen Life Technologies), and it was evaluated by comparative threshold cycle (Ct) qRT-PCR. After careful evaluation, a pool of six dental follicles were chosen as calibrators because they homogenously expressed the target genes and the endogenous gene, 28S rRNA. The target genes were PRKAR1A (F: 5'-TCTGTGTGCAACTAAGGTCTGTT-3' and R: 5'-GCAGCACCTCCACCGTGTAG-3'; amplicon size 145 bp) and PRKAR2A (F: 5'-GGCCCAACCCGTCTATCC-3' and R: 5'-GACGACCTCCACCGTGTAG-3'; amplicon size 102 bp). The average Ct for three replicates per sample was used to calculate ΔCt. The relative quantification of these gene expressions was calculated using the 2^ΔΔCt formula (Livak & Schmittgen 2001). A melting curve analysis followed each reaction to ensure specificity. qRT-PCR was carried out using 1× SYBR Green PCR Master Mix (Applied Biosystems), as described previously by de Sousa et al. (2014). Expression in odontogenic tumors were compared with that in a normal OM control group.

**Immunohistochemistry**

On the basis of the decreased transcriptional levels of PRKAR1A in the set of odontogenic tumors evaluated, we investigated the immunohistochemical expression of the protein in a larger number of samples, including seven epithelial (AMs) and 11 mixed odontogenic tumors. IHC was not carried out in case nos 2 and 3 because of the small amount of available tissue. Tissue sections of 4 μm thickness were mounted for IHC on StarFrost knittel glass adhesive slides (Waldemar KnittelGlasbearbeitungs GmbH, Braunschweig, Germany). Immunohistochemical reactions

<table>
<thead>
<tr>
<th>Sample Description</th>
<th>Assay 1</th>
<th>Assay 2</th>
<th>Assay 3</th>
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<tbody>
<tr>
<td>Ameloblastic fibroma</td>
<td>IHC</td>
<td>MD</td>
<td>LOH</td>
</tr>
<tr>
<td>Case 1</td>
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<td>Case 2</td>
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<td>Case 6</td>
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<tr>
<td>Ameloblastic fibrosarcoma</td>
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<td>Case 7</td>
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<td>Case 8</td>
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<tr>
<td>Ameloblastic fibrodentinoma</td>
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<td>Case 9</td>
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<tr>
<td>Ameloblastic fibro-odontoma</td>
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<td>Case 10</td>
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<td>Case 13</td>
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</table>

F, female; M, male; NA, not available; MD, microdissection; LCM, laser capture microdissection; MM, manual microdissection; LOH, loss of heterozygosity; IHC, immunohistochemistry; SEQ, sequencing; √, performed; –, could not be performed.

*Cases 1 and 9 were fresh tumors. Case 6 did not have a capsule for the evaluation of normal tissue.
were performed using a mouse MAB against the PRKAR1A protein (clone 6C7) (OriGene, Rockville, MD, USA). The processes of deparaffinization, hydration, and antigen retrieval were performed by immersing the slides in Trilogy solution (Cell Marque, Rocklin, CA, USA) and heating them to 98 °C in a steamer for 20 min. The primary antibody was diluted at 1:80 and incubated for 30 min at room temperature. The reactions were revealed by applying 3,3'-diaminobenzidine in chromogen solution (DAB; Dako), and Mayer’s hematoxylin was used for counterstaining. The slides were mounted in Permount (Fisher Scientific, Fair Lawn, NJ, USA). IHC was performed manually, and normal OM was used as positive control. Negative controls were carried out by omission of the primary antibody.

The IHC results were analyzed by three investigators (R S G, S F S, and V F B), who considered the distribution of antibody staining in the entire lesion section, regardless of staining intensity, and categorized the staining as: strong, in the presence of evident staining in the majority of tumor cells (> 50%); moderate, when a significant proportion of the neoplastic cells were positive (10–50%); and weak/negative, in the absence of marked cells or the presence of only occasional stained cells (< 10%).

**Microdissection**

Manual microdissection (MM) and laser capture microdissection (LCM) were performed on all 11 FFPE samples of the mixed odontogenic tumors that harbored normal and tumor areas (Table 1). For MM, an H&E slide was superimposed against a paraffin block for delimitation of the tumor from the capsule. Ten sections were cut at 10 μm thickness for posterior DNA extraction. For LCM, sections were cut at 12 μm thickness onto a MMI membrane (Olympus), and air-dried. Staining procedures were executed as described previously (Strokes et al. 2011). Stained sections were microdissected using an Olympus IX81 microscope and MMI CellCut Plus (Olympus) laser microdissection system. Tumor epithelial cells, tumor mesenchymal cells, and normal cells (capsule or blood vessel endothelium) were collected into separate sterile cap plastic tubes.

**DNA isolation**

Microdissected tissue fragments were digested with proteinase K. Genomic DNA from fresh and FFPE samples were extracted using a DNeasy Blood and Tissue Kit (Qiagen) and a QiaAmp DNA FFPE tissue kit (Qiagen) respectively.

**LOH analysis**

LOH was assessed by using a panel of four polymorphic DNA markers located around PRKAR1A (Fig. 1A). The primers used were selected on the basis of data from the online database (www.ncbi.nlm.nih.gov/probe), and they have been previously used by others (Bertherat et al. 2003). PCR for the four markers was performed as follows: 45 cycles at 96 °C for 10 s, 55 °C for 30 s, and 70 °C for 1 min. The PCR products were resolved on 6.5% non-denaturing polyacrylamide gels with silver staining. All of the PCRs were performed for tumor (epithelium and mesenchyme) and normal (capsule) tissue under the same conditions. Amplification products were detected by capillary electrophoresis on an ABI PRISM 310 (Applied Biosystems). LOH was calculated as previously described by Farias et al. (2012).

**Direct sequencing**

DNA targets were PCR-amplified using primer pairs flanking exons 1–10, as previously described (Kirschner et al. 2000b). Amplified products were confirmed by electrophoresis on 6.5% polyacrylamide gels with silver
staining. PCR products were purified with GFX PCR DNA and a Gel Band Purification Kit (GE Healthcare, Buckinghamshire, UK) and sequenced using a BigDye Terminator (Applied Biosystems) on an ABI PRISM 3130 Genetic Analyzer (Applied Biosystems). Electropherograms were manually analyzed with Sequence Scanner 2 software (Applied Biosystems). The reference sequence adopted was NM_002734.4. All mutation and sequence variances that were found were checked against the Catalogue of Somatic Mutations in Cancer (COSMIC), Ensembl Genome Browser, and NCBI dbSNP databases.

Prkar1a<sup>+/−</sup> mice

Prkar1a<sup>+/−</sup> mice (C57BL/6 background) carrying a deletion of exon 2 (Kirschner et al. 2005) were studied. All animal work in the present study was carried out in accordance with the guidelines of the Institutional Laboratory Animal Care and Use Committee at the National Institute of Child Health and Human Development (NICHD), National Institutes of Health (NIH), Bethesda, MD, USA. A total of five 1-month-old mice and four 6-month-old mice were dissected; their orofacial structures were studied after all of the skin had been removed and they had been fixed in 4% paraformaldehyde (PFA). Bony structures were slowly decalcified with EDTA 0.9 M at pH 7.5 over a period of 20 days, rinsed with distilled water, sectioned, paraffin embedded, and H&E stained. The sections were analyzed under a light microscope.

**Statistical analysis**

Analyses were performed using SPSS version 17.0 (SPSS, Inc.). Normal distribution was assessed by the Shapiro–Wilk test. A Mann–Whitney U test was used to compare the relative quantification of PRKAR1A and PRKAR2A in odontogenic tumors and normal OM. Probability values of <0.05 were considered to be statistically significant.

**Results**

The results of the molecular analysis (mRNA transcription, IHC, LOH, and sequencing) are presented in Figs 1, 2, 3, 4 and 5. A brief outline of the results is given in the following sections.

**Quantitative RT-PCR**

We assessed the mRNA expression levels of PRKAR1A and PRKAR2A in an epithelial odontogenic tumor (AMs, n=7) and in two samples of fresh mixed odontogenic tumors (one AF and one AFD) and compared these expressions with a control group of five normal OM samples by using
a pool of normal dental follicles as reaction calibrators. Both genes were expressed in all of the odontogenic tumors that were evaluated, but the relative quantification of \textit{PRKAR1A} in odontogenic tumors showed decreased expression as compared with normal OM ($P<0.05$) (Fig. 2), whereas \textit{PRKAR2A} mRNA expression was similar between the tumors and normal mucosa (not shown).

### Immunohistochemistry

Although all of the AMs showed positive expression of the protein in the epithelial islands, four AFs showed weak/negative staining in the ectomesenchymal component (Fig. 3A and B), and one case exhibited negative staining not only in the ectomesenchyme but also in the epithelium (Fig. 3B). The AFD sample showed strong expression in both components (Fig. 3C). Two samples of AFO showed a loss of protein expression in the ectomesenchymal component (Fig. 3D). Blood vessels showed positive staining, which was considered a positive internal control (Fig. 3A, B, C and D). The results are shown in Fig 4.

### LOH analysis

Because the mixed odontogenic tumors exhibited a significant loss of \textit{PRKAR1A} expression, we investigated if LOH at the \textit{PRKAR1A} locus could be one of the underlying mechanisms of decreased expression. We assessed LOH with a panel of four polymorphic microsatellite markers (Fig. 1A) in a set of five AF, two AFS, one AFD, and two AFO. For cases 6, 12, and 13, LOH analysis was not carried out either because those cases did not harbor normal control tissue or because the amount of available tissue was small. Four out of five AF exhibited LOH for at least two of the markers evaluated and presented LOH in the ectomesenchyme and/or epithelium (Fig. 1B). One of the two AFO showed LOH. One AFS exhibited LOH in the epithelium for the same markers that showed LOH in the AF. Only four of the cases investigated (cases 2, 8, 9, and 11) did not have LOH (Fig 4).

### Direct sequencing

Because the \textit{PRKAR1A} gene is mutated in several human tumors, including the odontogenic myxomas (Pereidgão et al. 2005), we sequenced DNA from exons 1–10 in the epithelium and ectomesenchyme of those tumors that had sufficient tissue available (cases 1–2, 4–7, and 9–11). Nucleotide numbering reflects cDNA numbering, with +1 corresponding to the A of the ATG translation initiation codon in the reference sequence (NM_002734.4). All the \textit{PRKAR1A} mutations and the single nucleotide polymorphisms (SNPs) identified are summarized in Table 2.

We found three sequence alterations in the coding region of the \textit{PRKAR1A} gene, including two synonymous and one missense alteration. The missense mutation (c.802G>A) was found in exon 8 and only in the
ectomesenchymal component of case 11. This mutation leads to a nonconservative amino acid substitution (p.A268T). The possible effects of this substitution on the stability and function of the protein were predicted to be damaging by SIFT (http://sift.jcvi.org) (score 0.01) and by PolyPhen-2 (http://genetics.bwh.harvard.edu/pph2/) (score 1.000).

In addition, we identified two sequence alterations in the 5′-UTR and four intronic variants. We also found three previously identified SNPs. All of the alterations found are represented in Fig. 5A, and the screenshots from the sequencing electropherograms of the missense mutation, one synonymous and one 5′-UTR mutation, are shown in Fig. 5B, C and D.

Table 2  Sequence alterations, including known SNPs of the PRKAR1A gene identified in mixed odontogenic tumors

<table>
<thead>
<tr>
<th>Mutation</th>
<th>Location</th>
<th>Effect</th>
<th>Diagnosis</th>
<th>Case number</th>
<th>Component</th>
</tr>
</thead>
<tbody>
<tr>
<td>c.-50C&gt;T</td>
<td>Exon 1B</td>
<td>5′-UTR</td>
<td>AF</td>
<td>1</td>
<td>Epithelial</td>
</tr>
<tr>
<td>c.-27C&gt;T</td>
<td>Exon 1B</td>
<td>5′-UTR</td>
<td>AF</td>
<td>1</td>
<td>Epithelial</td>
</tr>
<tr>
<td>c.159C&gt;T</td>
<td>Exon 2</td>
<td>Synonymous</td>
<td>AFD</td>
<td>9</td>
<td>Epithelial</td>
</tr>
<tr>
<td>c.492G&gt;A</td>
<td>Exon 4B</td>
<td>Synonymous</td>
<td>AF</td>
<td>5</td>
<td>Tumor*a</td>
</tr>
<tr>
<td>c.802G&gt;A</td>
<td>Exon 8</td>
<td>Missense</td>
<td>AFO</td>
<td>11</td>
<td>Mesenchymal</td>
</tr>
<tr>
<td>c.503-10C&gt;T</td>
<td>Intron 4B–5</td>
<td>Intronic</td>
<td>AFO</td>
<td>11</td>
<td>Mesenchymal</td>
</tr>
<tr>
<td>c.550-35G&gt;A</td>
<td>Intron 5–6</td>
<td>Intronic</td>
<td>AFO</td>
<td>11</td>
<td>Mesenchymal</td>
</tr>
<tr>
<td>c.891+13G&gt;A</td>
<td>Intron 8–9</td>
<td>Intronic</td>
<td>AFO</td>
<td>11</td>
<td>Mesenchymal</td>
</tr>
<tr>
<td>c.973+15C&gt;T</td>
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<td>Intronic</td>
<td>AFO</td>
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<tr>
<td>c.-453C&gt;A</td>
<td>Exon 1A</td>
<td>5′-UTR</td>
<td>AF, AFO</td>
<td>1, 11</td>
<td>Both</td>
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<tr>
<td>c.349-5_349insT</td>
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<td>Intronic</td>
<td>AF, AFO</td>
<td>1, 9, 11</td>
<td>Both</td>
</tr>
<tr>
<td>c.770-24G&gt;A</td>
<td>Intron 7–8</td>
<td>Intronic</td>
<td>AF, AFO</td>
<td>1, 4, 9, 11</td>
<td>Both</td>
</tr>
</tbody>
</table>

AF, ameloblastic fibroma; AFD, ameloblastic fibrodentinoma; AFO, ameloblastic fibro-odontoma.

*aCase 5 was manually microdissected into tumor and capsule.

Figure 5  Structure of the PRKAR1A gene and protein, and screenshots of sequencing electropherograms. (A) The locations of all of the sequence alterations and SNPs found in our samples. (B) A heterozygous synonymous sequence change in exon 4B (c.492G>A) (WT codon GTG→new codon GTA). (C) A 5′-UTR mutation in exon 1B (c.-50C>T). (D) A missense mutation found in exon 8 (c.802G>A) (WT codon GCT→mutant codon ACT) and localization of this mutation in the structure of the PRKAR1A protein. NH2, amino-terminal extremity; COOH, carboxy-terminal extremity; D, dimerization domain; H, hinge region; cAMP1 and cAMP2, cAMP-binding domains. A full colour version of this figure is available at http://dx.doi.org/10.1530/ERC-15-0094.
Analysis of H&E staining of orofacial tissues from Prkar1a\textsuperscript{+/−} mice

There were no abnormalities in any of the mice that were studied.

Discussion

There have been few investigations about the molecular pathogenesis of mixed odontogenic tumors because of the rarity of these lesions. The majority of studies have been based on IHC findings for diagnostic and prognostic biomarkers. After the identification of the first PRKAR1A mutations in humans with a variety of tumors, including myxomas (Kirschner \textit{et al.} 2000\textit{a,b}), PRKAR1A was shown to be involved in the pathogenesis of odontogenic myxomas both at the protein level and due to somatic mutations at the genetic level, as reported by Perdigão \textit{et al.} (2005). The odontogenic myxoma is an odontogenic tumor that probably derived from the ectomesenchymal tissue during disruption of odontogenesis (reviewed by Gomes \textit{et al.} (2011)). Mixed odontogenic tumors share this ectomesenchymal origin as well as the participation of the odontogenic epithelium. Therefore, it is possible that these tumors share similarities with the odontogenic myxomas in their molecular pathogenesis. Because we have previously shown PRKAR1A and PRKAR2A expression in tooth germs (de Sousa \textit{et al.} 2014), we initially investigated their expression in mixed odontogenic tumors and AMs, which are the most common epithelial odontogenic tumors. We focused the present study on PRKAR1A, because it showed decreased mRNA levels in odontogenic tumors as compared with normal OM and because of the lack of PRKAR1A protein expression in some mixed odontogenic tumors. In addition, about half of these benign tumors showed a loss in PRKAR1A protein expression, mainly in their mesenchymal portion. AM samples, on the other hand, did not show a loss of PRKAR1A protein expression, so we therefore decided to further investigate PRKAR1A only in mixed odontogenic tumors. Cases with decreased protein expression had also undergone LOH at the PRKAR1A locus in the epithelial and/or mesenchymal component, which indicates that the LOH found in these tumors could be one reason for their loss of protein expression. Conversely, although one AFS exhibited LOH in two of the three informative markers in the epithelial component, the two cases of AFS showed moderate expression of PRKAR1A protein and did not reveal the presence of PRKAR1A mutations. Despite the small number of AFS samples, these findings indicate that PRKAR1A alterations may play an important role in the pathogenesis of benign mixed odontogenic tumors. Another possibility is that, as previously proposed for adrenocortical adenomas (Bertherat \textit{et al.} 2003), PRKAR1A down-regulation may be an early event in tumorigenesis, but it is quickly bypassed by other pathways that are more important for cell survival.

New missense and synonymous variants were also found in noncoding regions of PRKAR1A, such as the 5′-UTR region and introns in four benign mixed odontogenic tumors. Similarly to the missense mutation that was previously found in odontogenic myxomas (Perdigão \textit{et al.} 2005), the missense mutation described in the present study occurred in the second cAMP binding domain. This may have effects on the interaction of this protein with its ligand, cAMP, which in turn affect its function. The effect of this substitution was predicted to be damaging \textit{in silico}. The absence of LOH and the strong immunoexpression seen in both components of this sample indicate that either the substitution p.A268T did not cause a decrease in PRKAR1A protein expression that could be detected by IHC or that the mutation occurred only in a group of cells as a result of tumor heterogeneity. The missense mutation occurred in the somatic state in the ectomesenchymal part of an AFO case of one of the youngest patients in our series (6 years). The presence of a missense mutation in only the AFO case is interesting, seeing as there is ongoing debate in the literature about the true neoplastic nature of the AFO versus it being considered a developing odontoma (i.e., a hamartoma) (Buchner \textit{et al.} 2013).

The synonymous sequence alterations that were also found in the somatic state are believed to be silent, because they do not alter the protein sequence. However, it has recently been proposed that such changes could affect mRNA stability and/or the timeliness of translation, the efficiency of splicing, and other factors that affect gene expression (Supek \textit{et al.} 2014, Zheng \textit{et al.} 2014). Moreover, there is increasing evidence that noncoding DNA changes may affect disease susceptibility (Castillo-Davis 2005). Some noncoding regions are recurrently mutated in cancer, especially regulatory regions at the 5′ ends of genes, such as promoters and 5′-UTRs (Weinhold \textit{et al.} 2014). Although the significance of the 5′-UTR changes that we found remains unknown, the results of some studies have indicated that truncations or mutations in the 5′-UTR often lead to impaired protein synthesis, as demonstrated in the analysis of the 5′-UTR BRCA1 mRNA, which revealed that a G→C mutation close to the end of
the 5′-UTR was associated with decreased BRCA1 gene expression (Signori et al. 2001).

Human tumors often display intratumor heterogeneity in histology, gene expression, and genotype (Michor & Polyak 2010). An interesting finding in the present study is the molecular heterogeneity found when we compared the epithelial component and the mesenchymal cells of the tumors, which showed differences in LOH and the presence (or absence) of sequence changes. This could only be achieved by using laser microdissection, and it is the first evidence, to our knowledge, that these tumor parts are different not only histologically but also molecularly.

The Prkar1a+/− orofacial tissues that we examined did not demonstrate any odontogenic tumor formation and had normal odontogenesis without any disruption, even at a young age (1 month). The present results are consistent with the results of Almeida et al. (2010), who provided evidence that Prkar1a haploinsufficiency is a relatively weak tumorigenic signal that acts synergistically most of the time (Almeida et al. 2010). It should be noted that there is no question that PRKAR1A participates in the formation of orofacial structures, as has been demonstrated by knocking out both alleles of the Prkar1a gene in tyrosinase-expressing Cre 1 mice, which resulted in profound craniofacial abnormalities (Jones et al. 2010). To date, no patients with Carney complex have developed any orofacial tumors (other than schwannomas); however, skeletal tumors, albeit rare, are present.

In conclusion, the results of the present study indicated that PRKAR1A expression is decreased in benign mixed odontogenic tumors in association with somatic sequence alterations and LOH of the PRKAR1A gene. Although no abnormalities were found in Prkar1a+/− mice, these results indicate that PRKAR1A and perhaps other molecules of the cyclic AMP-dependent PKA pathway participate in the pathogenesis of these rare tumors.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Funding
This study was supported in part by the intramural research program (IRP) of NICHD, NIH, and by the following Brazilian funding agencies: Coordination for the Improvement of Higher Education Personnel (CAPES), Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG), and the National Council for Scientific and Technological Development (CNPq), Brazil. R S Gomez and C C Gomes are research fellows at CNPq, and M G Diniz is a research fellow at CAPES.

Acknowledgements
The authors acknowledge the Centro de Aquisição e Processamento de Imagens (CAPI-ICB/UFMG) for the LMD technical support and Dr Adriano Loyola for the donation of two tumor samples for the study.

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Received in final form 23 March 2015
Accepted 30 March 2015
Made available online as an Accepted Preprint 13 April 2015