

# Identification of a novel heterozygous truncation mutation in exon 1 of ARHGAP29 in an Indian subject with nonsyndromic cleft lip with cleft palate

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## ABSTRACT

**Objective:** Mutations in exon 1 of ARHGAP29, a RhoA specific GTPase have been identified in North American and Filipino subjects with nonsyndromic cleft palate and cleft lip with or without cleft palate. Since the genetic status of ARHGAP29 in Indian subjects with nonsyndromic oral clefts is not known, we designed the present study to investigate the occurrence of the above mutations in them. **Materials and Methods:** Total genomic DNA extracted from peripheral blood of 60 subjects with nonsyndromic cleft palate and cleft lip with or without cleft palate, and equal number of control healthy subjects were amplified with primers flanking exon 1 of ARHGAP29 gene and subjected to direct sequencing. **Results:** Sequencing analysis identified a nonsense mutation in exon 1 of ARHGAP29 that caused substitution of lysine to stop codon at codon position 32 in a subject with nonsyndromic cleft lip with cleft palate. The mutation, however, occurred in heterozygous condition. None of the other subjects carried mutation in this region. **Conclusion:** The study has thus identified a rare but novel truncation mutation in ARHGAP29 gene for the first time in nonsyndromic oral clefts.

**Key words:** ARHGAP29, gene mutation, Indian population, cleft lip, cleft palate

## INTRODUCTION

The development of the maxillary division of oro-facial region is regulated by a cascade of signaling molecules, the expression and/or activation of which is tightly regulated. Disturbances in the signaling cascade due to function impairing defects in developmental genes may cause failure of meeting and fusion of the developing primordium. The extent of manifestation though may vary among the affected children and may include either cleft lip (CL) or cleft palate (CP) (isolated CL or CP) or cleft lip with cleft palate (CLP),<sup>[1]</sup> that may involve one or both halves of the facial region and are classified as unilateral or bilateral clefts.<sup>[2]</sup> Oro-facial cleft may either occur as an isolated event or as a part of other clinical symptoms

and are designated as nonsyndromic or syndromic cases, respectively. Nonsyndromic clefts make about 70% of all reported oro-facial clefts.<sup>[1,2]</sup> Syndrome associated clefts occur in several hundreds of mendelian (autosomal dominant, autosomal recessive, or X-linked) chromosomal conditions,<sup>[3]</sup> that may at times include mental retardation, myopia and cardiac anomalies<sup>[4-8]</sup> as additional clinical manifestation. Of the above two, nonsyndromic clefts of the lip and palate (CL, CP, CLP) occurs in every 1/500-1/2500 of live births<sup>[9,10]</sup> and hence is considered as the most common of all congenital defects.

The cause of development of CL, CP and CLP is believed to be multi-factorial in nature and may include both environmental factors and genetic

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defects.<sup>[11]</sup> Two major environmental factors that the developing embryos get exposed to are byproducts of tobacco smoke and alcohol binging by expectant mothers especially during the early trimester. Both of these agents have been found to be associated with the development of oro-facial clefts in infants.<sup>[12-23]</sup> Besides the above, oro-facial cleft has also been observed in the fetus of mothers undergoing phenytoin drug therapy for epileptic conditions or who were consuming dietary supplement, retinoic acid.<sup>[21,22]</sup> Though the exact the mechanism of development of oro-facial clefts in embryos exposed to these environmental and dietary factors remains yet to be understood, association between functional impairment of molecules responsible for detoxification of environmental agents and drugs and oro-facial clefts have been observed in infants. For example, significant over transmission of G590A variant of NAT2 gene coding N-acetyltransferase 2 enzyme that activates and deactivates arylamine and hydrazine drugs and carcinogens have been observed in subjects with oro-facial clefts relative to controls.<sup>[23,24]</sup> On the other hand, genetic alteration in developmental regulators of palatal shelf such as TGFA, TGF $\beta$ ,<sup>[25,26]</sup> MSX1,<sup>[27]</sup> IRF6,<sup>[28,29]</sup> PVR, PVRL1, PVRL2,<sup>[30,31]</sup> TBX22,<sup>[32]</sup> FGFR1,<sup>[33]</sup> ABCA4,<sup>[34,35]</sup> MAFB1,<sup>[34,35]</sup> and ARHGAP29 have also been observed in several subjects with oro-facial clefts.

Of the above developmental regulators, ARHGAP29 gene encodes for a GTPase-activating protein (GAP) that has a strong affinity to the small GTP-binding protein RhoA than Rac1 or CDC42.<sup>[36]</sup> By binding to the active form of RhoA, the GTPase function of ARHGAP29 converts RhoA-GTP to RhoA-GDP.<sup>[37]</sup> Expression of ARHGAP29 is seen in the mandibular and maxillary processes of developing mouse embryo at E10.5 and the shelves of the secondary palate at E13.5.<sup>[37]</sup> Nonsense mutation with consequent premature truncation of the protein has been identified within the coding region of exon 1 of ARHGAP29 gene in oro-facial cleft subjects from other races.<sup>[37]</sup> Studies from the Indian Genome Variation Consortium have suggested that most of the populations in the Indian subcontinent are distinct from HapMap populations, and that the genetic basis of diseases in the Indian population may be different due to differences in the risk allele frequency and pattern of linkage disequilibrium.<sup>[38]</sup> This prompted us to design the present study, in which, the exon 1 of ARHGAP29 gene was investigated in a small group of Indian subjects with CL, CP or CLP, who belonged to a defined South Indian Dravidian race.

## MATERIALS AND METHODS

### Study design and subjects

A cross-sectional study was designed and 60 subjects with either NS-CL or CP or CLP, but otherwise medically able were included in the study after obtaining informed consent. As controls, an equal number of race matched healthy volunteers were included. Subjects with syndromic CL or CP or CLP, and those who were not willing to be a part of the study were excluded.

### DNA extraction and polymerase chain reaction

About 200  $\mu$ l of peripheral blood was processed to extract chromosomal DNA with Gen-Elute Blood DNA Extraction Kit (Sigma-Aldrich, USA) according to the manufacturer's protocol. The exon 1 region of ARHGAP29 was amplified with intronic primers (sequence information available upon request) flanking splice donor and acceptor sites. The gene region was amplified under following conditions: Initial denaturation at 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 45 s, primer annealing at 55°C for 45 s, primer extension at 72°C for 1 min, with a final extension at 72°C for 5 min. The PCR amplicons were confirmed in comparison to DNA size markers and were subsequently eluted with Genelute DNA gel elution kit (Sigma Aldrich, cat# NA1111) and subjected to direct sequencing with same set of primers that were used for PCR amplification.

## RESULTS

In order to determine the occurrence of mutation in exon 1 of ARHGAP29 gene in Indian subjects with either NS-CL or CP or CLP, and thus to understand the risk potential of mutant ARHGAP29 in the development of CL/CP/CLP, we screened the chromosomal DNA from 60 CL/CP/CLP subjects along with equal number of healthy volunteers. DNA from peripheral blood was amplified with exon 1 specific primers, and the PCR amplicons were subjected to direct sequencing after gel purification. Analysis of the sequencing data showed a nonsense mutation, c. 94A>T, in a subject with NS-CLP that resulted in the substitution of lysine amino acid with stop codon at codon position 32 in exon 1 (AAG32TAG). However, the mutation was identified to be heterozygous as both wild type AAG, and mutant TAG codons were present at codon position 32 [Figure 1].

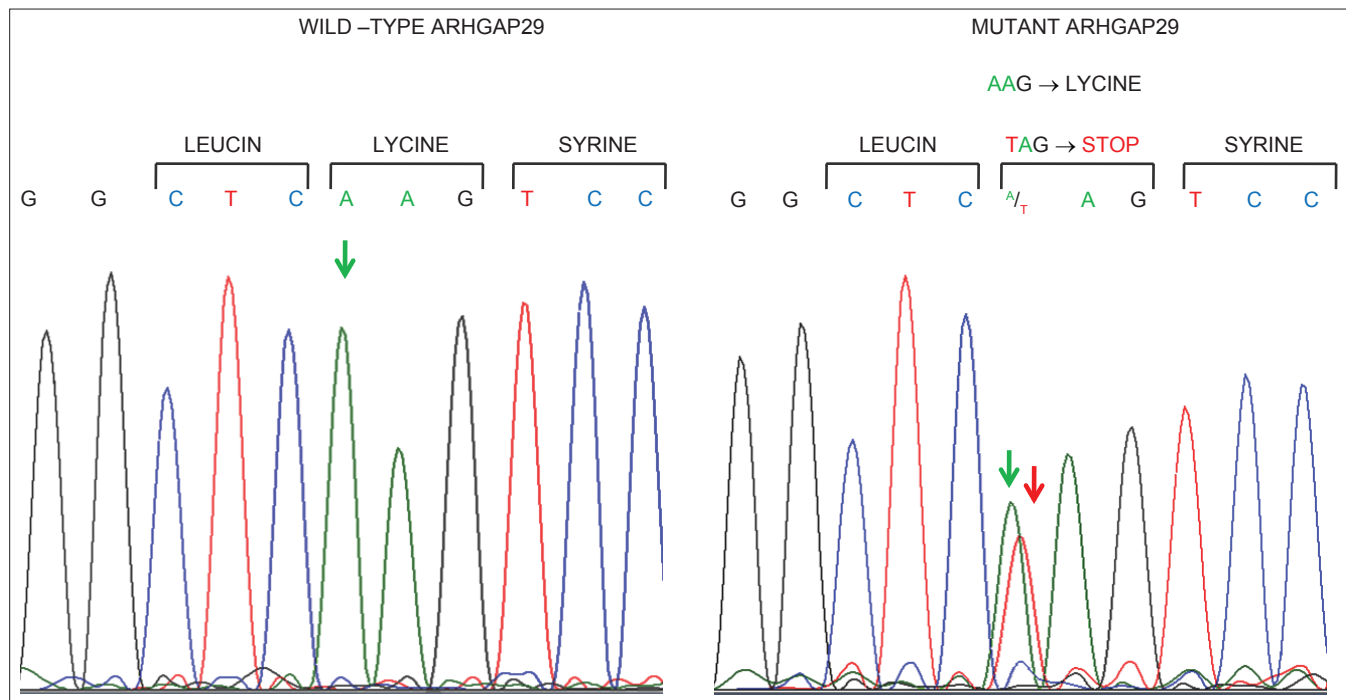
## DISCUSSION

A total of 60 subjects with NS-CL, CP or CLP and 60 normal subjects were analyzed for the presence of the mutation in ARHGAP29 gene. Both groups of subjects were selected from Tamil speaking Dravidians from the Southern region of India, in order to minimize race dependent genetic variations as genetic diversity has been observed in the population from different parts of India.<sup>[38]</sup> Though the development of NS-CP/CL/CLP is believed to be due to gene-environment interaction, the present study was focused only on the genetic aspect as no records of the subject's prenatal period or that of respective mother's were available. Direct sequencing analysis of PCR amplicons of exon 1 coding region of ARHGAP29 identified a single mutation in a subject with NS-CLP. The mutation caused substitution of lysine amino acid at codon 32 with a premature stop codon in one copy of ARHGAP29, as the mutant codon occurred along with wild-type lysine codon (indicated by two arrows in mutant ARHGAP29 panel in Figure 1). The identification of K32STOP mutation in only one of 60 CL, CP or CLP subjects who were investigated in the present study indicates that the mutation may be a rare event in CL, CP or CLP from this region. By analyzing 1440 and 360 subjects with CL, CP or CLP from Philippines and US respectively, Leslie *et al.* identified a nonsense (c. 62\_63delCT) and a missense

mutation (c. 76A>G) in two independent subjects from Philippines, and a missense mutation (c. 137A>G) in a subject from the US.<sup>[37]</sup> Considering the occurrence of c. 94A>T mutation in a single NS-CLP subject from a sample size of 60 analyzed in the present study, it may be inferred that the relative prevalence of this mutation may be higher than those observed by Leslie *et al.* This claim, however, requires to be confirmed by analyzing a higher sample size by including subjects from similar racial background.

Both nonsense mutations, c. 94A>T identified by us, and c. 62\_63delCT causes premature truncation of the ARHGAP29 protein. While c. 94A>T creates an in-frame stop codon, c. 62\_63delCT causes a frame-shift that consequently results in the premature occurrence of stop codon after twenty misread codons. Both mutations, however, are expected to cause loss of function of ARHGAP29 protein. In contrast, the two missense mutations, c. 76A>G and c. 137A>G that causes substitution of threonine with alanine at codon 26 (T26A) and lysine with arginine at codon 46 (K46R) respectively are expected to have a benign effect on the function of ARHGAP29.<sup>[37]</sup>

The identification of c. 94A>T mutant allele of ARHGAP29 in heterozygous condition along with wild-type allele suggests that the mutation event causes haplo-insufficiency. It is important to note that



**Figure 1:** Chromatogram of wild type and mutant sequences within exon 1 of ARHGAP29 gene. Note that the mutant sample carries both wild type nucleotide "A" (indicated by a green arrow) and mutant nucleotide "T" (indicated by a red arrow) at first position of codon 32



the deletion mutation (c. 62\_63delCT) reported by Leslie *et al.* was homozygous in nature.<sup>[37]</sup> Although biallelic inactivation of genes has often been described as a cause for development and progression of diseases, haplo-insufficiency of genes has also been observed in several disease conditions. For example, haplo-insufficiency has been observed in cancerous lesions,<sup>[39-41]</sup> neurodegenerative disorders,<sup>[42]</sup> myopathies,<sup>[43]</sup> inflammatory conditions,<sup>[44]</sup> and developing tissues leading to birth defects including syndromes such as Frias syndrome (haplo-insufficiency of BMP4),<sup>[45]</sup> and CNS malformation syndrome (haplo-insufficiency of NFIA).<sup>[46]</sup> These findings clearly suggest that the heterozygous c. 94A>T mutation identified in the present study may present haplo-insufficiency effect during the development of oro-facial cleft region. As expression of ARHGAP29 transcript is detected strongly in medial and lateral nasal processes and to a lesser extent in the mandibular and maxillary processes at E10.5 and shelves of the secondary palate at E13.5,<sup>[37]</sup> the haplo-insufficiency effect of c. 94A>T mutant ARHGAP29 may have acted as one of the causative factor in the development of NS-CLP as the etiology of NS-CL/CP/CLP is believed to be polygenic. However, a knock-in experiment to recreate the above heterozygous condition along with other reported mutations in transgenic mice is essential to validate the above observation.

## CONCLUSION

The present study has identified for the first time a novel nonsense mutation c. 94A>T in the gene ARHGAP29 in a South Indian Dravidian subject with NS-CLP. The occurrence of a mutation in one of 60 subjects with NS-CL/CP/CLP suggests that the mutation event may be rare.

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