TYMS gene 5’- and 3’-untranslated region polymorphisms and risk of non-syndromic cleft lip and palate in an Indian population

Dear Editor:

Increased homocysteine levels due to vitamin B6 or B12 deficiency or genetic defects in folate pathway genes are associated with an increased incidence of non-syndromic cleft lip with or without cleft palate (NSCLP)[1]. Thymidylate synthase (TS) is a folate-dependent enzyme that catalyzes methylation of 2’-deoxyuridine-5’-monophosphate (dUMP) to 2’-deoxythymidine-5’-monophosphate (dTMP), a rate-limiting step in DNA synthesis, for which 5,10-methylene-tetrahydrofolate (CH2-THF) is the methyl donor. TS competes with 5,10-methylenetetrahydrofolate reductase (MTHFR) for the availability of CH2-THF. The TYMS gene is located on chromosome 18p11.32 and is about 30 kb in length with 7 exons[2]. Two most extensively studied TYMS variants are located in the promoter enhancer region of the 5’-untranslated region (UTR) and 3’-UTR. The VNTR polymorphism (rs45445694) is located in 5’-UTR, consisting of 2 or 3 tandem repeats of 28 bp (2R or 3R). A 6-bp insertion and deletion polymorphism (indel) has been identified in the 3’-UTR (rs16430) of the TYMS[3]. These 2 polymorphisms have been extensively studied for association with cleft lip and palate[4]. Although the TYMS plays a critical role in fetal development, so far it has not yet been reported to be associated with NSCLP in the Indian population. In this study, we investigated the effects of TYMS functional variants (rs45445694 and rs16430) on the risks of NSCLP in a southern Indian population.

The study was carried out in 283 ethnically matched unrelated subjects, including 142 unrelated NSCLP patients (123 with cleft lip and palate and 19 with cleft palate only) and 141 healthy controls without family history of cleft. Subjects with malformation syndromes and major developmental disorders were excluded. The study was approved by the local institutional ethics committee and written informed consent was obtained from all the participants. Peripheral blood (3 mL) was collected from each subject and DNA was obtained using a standard procedure. TYMS 6-bp indel genotyping was performed using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method[5]. TYMS 5’-UTR VNTR was genotyped according to the PCR method[6]. Allele frequencies were estimated by the gene counting method. Hardy-Weinberg equilibrium (HWE) was performed to assess the cases and control groups using chi-square test. Association between two TS SNPs and different cleft phenotypes (NSCLP, CLP and cleft palate only (CPO)) was analyzed by $\chi^2$-test. Odds ratio and 95% confidence intervals (CI) were calculated using low risk genotypes or alleles as the reference group.

The genotype frequencies of TYMS VNTR and 6 bp indel are shown in Table 1 and Table 2, respectively. The genotype frequencies were in HWE in the control group of TYMS VNTR ($P = 0.704$) and 6 bp indel ($P = 0.830$). TYMS VNTR polymorphism showed significant difference in genotypic frequencies between NSCLP ($P = 0.006$) and CLP (0.003) compared

<table>
<thead>
<tr>
<th>Control</th>
<th>NSCLP</th>
<th>OR (95% CI)</th>
<th>P</th>
<th>CLP</th>
<th>OR (95% CI)</th>
<th>P</th>
<th>CPO</th>
<th>OR (95% CI)</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>3R3R</td>
<td>65</td>
<td>59</td>
<td>Reference</td>
<td>54</td>
<td>Reference</td>
<td>5</td>
<td>Reference</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2R3R</td>
<td>60</td>
<td>79</td>
<td>1.45 (0.89–2.36)</td>
<td>0.006*</td>
<td>67</td>
<td>1.34 (0.81–2.21)</td>
<td>0.003*</td>
<td>12</td>
<td>2.60 (0.86–7.81)</td>
</tr>
<tr>
<td>2R2R</td>
<td>16</td>
<td>4</td>
<td>0.27 (0.08–0.81)</td>
<td>2</td>
<td>0.15 (0.03–0.69)</td>
<td>2</td>
<td>1.62 (0.28–9.15)</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>2R3R+2R2R</td>
<td>76</td>
<td>83</td>
<td>1.20 (0.75–1.92)</td>
<td>0.440</td>
<td>69</td>
<td>1.09 (0.67–1.77)</td>
<td>0.720</td>
<td>14</td>
<td>2.39 (0.81–7.10)</td>
</tr>
<tr>
<td>3R allele</td>
<td>190</td>
<td>197</td>
<td>Reference</td>
<td>173</td>
<td>Reference</td>
<td>20</td>
<td>Reference</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2R allele</td>
<td>92</td>
<td>87</td>
<td>0.91 (0.64–1.30)</td>
<td>0.610</td>
<td>71</td>
<td>0.85 (0.58–1.23)</td>
<td>0.383</td>
<td>16</td>
<td>1.65 (0.82–3.34)</td>
</tr>
</tbody>
</table>

NSCLP: non-syndromic cleft lip; OR: odd risk; CI: confidence interval; CLP: cleft lip; CPO: cleft palate only. *P value by $\chi^2$ test (df = 2).
to the controls (Table 1). The TYMS 6 bp indel genotype and allele frequencies were not significantly different between the NSCLP and control group (Table 2). In subgroup analysis, 6 bp indel showed significant association with the CPO group (Table 2). To estimate relative risk of NSCLP, we calculated OR and 95%CI in co-dominant, dominant and allelic models. None of the models revealed significant association between the TYMS VNTR and NSCLP group (Table 1). For TS 6 bp indel, risk analysis showed increased risk in all 3 models and increased risk reached significant level in the dominant model for the NSCLP group (OR = 1.90; CI = 1.02–1.83 and \( P = 0.041 \)) (Table 2).

Although TS is a folate-dependent enzyme, there are very few studies on the association of the TYMS gene with human orofacial clefts. TS is an autoregulatory protein composed of 313-amino acids and binds to its messenger RNA (mRNA) directly and inhibits mRNA translation. A Norway family based association study did not find evidence of an association between several TYMS variants and folate intake on risk of orofacial clefts [6]. A family-based association study of NSCLP with TYMS gene variants showed altered familial transmission of haplotypes in the non-Hispanic group for cleft risk [7]. However, these two studies did not investigate the TYMS variants in our study.

The 5’-UTR VNTR was found to influence the efficiency of TYMS expression. TS genes with the 2R2R repeat sequence showed that the expression activity of the gene was lower than that of the gene with the 3R3R repeat sequence [8]. A recent case-control study showed that the homozygous 2R2R repeat sequence influenced CP risk [9]. Another 6 bp indel suggest that the homozygous insertion (+6 bp/+6 bp) had significantly higher TS mRNA levels compared to individuals with homozygous deletion (-6 bp/-6 bp), which is associated with decreased TYMS mRNA stability [10]. Individuals with the homozygous (-6 bp/-6 bp) genotype have higher red blood cell folate levels and lower plasma homocysteine levels compared to (+6 bp/+6 bp) or (+6 bp/-6 bp) genotypes [10]. A recent case-control study does not indicate that SNP rs16430 genotype contributes to CLP or CP risks either alone or in combination with folate intake [10].

In conclusion, we report that the TYMSs 5’UTR VNTR and 3’UTR 6-bp indel are significantly associated with increased risk of NSCLP in a southern Indian population. To obtain more evidence on the association between TYMS polymorphisms and NSCLP, population studies conducted among other ethnicities are required. Furthermore, the analysis of biochemical mechanisms of the TYMS polymorphisms in the pathogenesis of NSCLP requires investigation.

Yours sincerely,

Dr. Jyotsna Murthy
Department of Plastic Surgery,
Sri Ramachandra University,
Chennai,
India.

Dr. Venkatesh Babu G. and Dr. L. V. K. S. Bhaskar
Department of Biomedical Sciences,
Sri Ramachandra University,
Chennai,
India.

Tel: 8224979600
E-mail: lvksbhaskar@gmail.com

The authors reported no conflict of interests.
Received 15 October 2014, Revised 25 January 2015, Accepted 12 February 2015, Epub 10 April 2015

Acknowledgements

L.V.K.S. Bhaskar acknowledges funding from the Indian Council of Medical Research (ICMR), Government of India (Project Ref. No. 56/15/2007-BMS).

| Table 2 Association of TYMS gene 6 bp indel with NSCLP |
|---------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
|                                | Control OR (95% CI) | P             | CLP OR (95% CI) | P             | CPO OR (95% CI) | P             |
| -6 bp/-6 bp                    | 32 / 19 Reference  | 19 Reference  | 19 Reference  | 15 Reference  | 15 Reference  | 15 Reference  |
| +6 bp/-6 bp                    | 69 / 77 1.89(0.98–3.61) | 0.124*       | 62 / 15.1(0.78–2.94) | 0.284*       | 15 / 0.023*   |
| +6 bp/+6 bp                    | 40 / 46 1.94(0.95–3.95) | 42 Reference | 1.77(0.87–3.61) | 4 Reference   |               |
| (+6 bp/-6 bp)+(-6 bp/-6 bp)    | 109 / 123 1.90(1.02–1.83) | 0.041        | 104 / 1.61(0.86–3.01) | 0.136        | 19 Reference  |
| -6 bp allele                   | 133 / 115 Reference | 100 Reference | 15 Reference | 15 Reference  |               |
| +6 bp allele                   | 149 / 169 1.31(0.94–1.83) | 0.109        | 146 / 1.31(0.92–1.85) | 0.132        | 23 / 1.37(0.69–2.73) | 0.372 |

NSCLP: non-syndromic cleft lip; OR: odd risk; CI: confidence interval; CLP: cleft lip; CPO: cleft palate only. *P value by \( \chi^2 \) test (df = 2).
References


CLINICAL TRIAL REGISTRATION

The Journal requires investigators to register their clinical trials in a public trials registry for publication of reports of clinical trials in the Journal. Information on requirements and acceptable registries is available at www.icmje.org/faq_clinical.html.