We report on a Saudi infant with Holt-Oram syndrome caused by a de novo missense mutation of the TBX5 gene. The mutation (Thr72Lys) is novel and has not been previously reported. The cardiac and limb defects in our patient were both severe, and the infant also had micrognathia and cleft palate. Previously reported cases of the Holt-Oram syndrome caused by missense mutations were reviewed and their phenotypes were compared with the phenotype of our patient.

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**Case Report.** A 4-month-old female infant presented to us for the treatment of bilateral radial ray deficiency. The infant had a history of complex cardiac anomaly (multiple ventricular septal defects, failure of incorporation of the pulmonary veins, and tricuspid valve insufficiency), which required cardiac surgery soon after birth. Clinical examination and electrocardiogram showed no evidence of any conduction abnormalities. The bilateral radial ray deficiencies were also severe and were manifested as bilateral short radii with radial deviation of the wrists as well as complete absence of both thumbs (Figures 1A & 1B). The infant also had micrognathia and clefting of the soft palate. Ultrasound of the abdomen did not reveal any renal abnormalities. The parents were normal and unrelated. There was no family history of congenital anomalies of the heart or limbs.

After informed consent, genomic DNA from the parents and infant was isolated and amplified for analysis of the complete coding region of the *TBX5* gene and their flanking splice sites. The infant was found to have a novel missense mutation of the *TBX5* gene: c.215C>A, p.Thr72Lys (heterozygous). Both biological parents tested negative indicating that the mutation has arisen de novo.

**Discussion.** The *TBX5* mutation of our patient (Thr72Lys) is novel and has not been previously reported. Although we did not perform functional analysis of the interactions of the mutant protein, this new mutation is believed to be pathogenic for several reasons. Firstly, the Thr72Lys mutation was not observed in over 6000 samples from normal subjects (NHLBI GO Exome Sequencing Project, Seattle, WA; http://evs.gs.washington.edu/EVS/). Secondly, the Thr72Lys change occurs at a highly conserved position within the DNA-binding domain of the *TBX5* protein. Thirdly, all missense mutations at nearby positions (Met74Ile and Gly80Arg) have been reported in association with Holt-Oram syndrome. 2,5,6 Lastly, multiple in-silico analysis models predict that Thr72Lys is damaging to the *TBX5* protein (as per Gene Dx, Gaithersburg, MD 20877, USA). The cardiac and limbs phenotypes were both severe. The literature defines the mild cardiac phenotype in Holt-Oram syndrome as an isolated septal defect, an isolated conduction defect, or an isolated valve defect. Combined defects and more complex anomalies are considered severe as seen in our patient. Similarly, the literature also defines completely absent thumbs (seen in our patient) as severe limb defects. The phenotype in our patient included micrognathia and clefting of the soft palate and these are not known to be among the classic features of Holt-Oram syndrome. We reviewed the literature for all reported missense mutations of the *TBX5* gene, and we found 23 mutations. Two mutations (Gly125Arg and Ser372Leu) were gain-of-function mutations.6 The phenotype of the Gly125Arg mutation was unique and almost all affected family members had radial head dislocation and paroxysmal atrial fibrillation. This indicated that this gain-of-function of *TBX5* activity may lead to specific cardiac and limb phenotypes.10 The second gain-of-function mutation (Ser372Leu) was maternally inherited and both mother and child had cardiac defects with normal upper limbs.14 The remaining 21 mutations were loss-of-function mutations and these are shown in Table 1. Table 1 shows that the cardiac/limb phenotypes in our patient as well as the phenotypes of several other missense mutations do not support the hypothesis of Basson et al. In fact, several mutations have resulted in phenotypes of variable severity in different members of the same family. Another observation from Table 1 is the absence of cardiac or limb defects in several missense mutations. This is important to note because it means that screening for *TBX5* mutations may be indicated in families with isolated cardiac defects or isolated radial ray deficiency. Finally, our literature review revealed that the Ser261Cys mutation reported by Brassington et al was the only mutation that was associated with micrognathia and cleft palate. The phenotype in our case also included micrognathia and cleft palate indicating that these defects may be considered as part of the spectrum of Holt-Oram syndrome.

![Figure 1](https://www.smj.org.sa/SaudiMedJ/2015/36(8)/981/Figure1.png)
the clinical features of Holt-Oram syndrome. However, our case and the case of Brassington et al9 were not subjected to other tests (such as array comparative genomic hybridization analysis and screening of known genes causing isolated cleft palate). Hence, it remains a possibility that a separate second hit is responsible for the micrognathia/cleft palate phenotype.

In conclusion, missense mutations of the TBX5 gene are uncommon and we add a novel mutation (c.215C>A, p. Thr72Lys) to the literature. After reviewing the phenotype in our patient and other cases in the literature, we also conclude that micrognathia and cleft palate may be features of the Holt-Oram phenotype.

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