

**Prenatal diagnosis of Tricuspid Atresia in a family with heritability positive for NKx2.5 mutation, atrial septal defect and atrioventricular block**

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Introduction: Mutations in NKx2-5 have been described in families with autosomal dominant heritability for secundum atrial septal defect (II-ASD) and progressive atrioventricular (AV) block. We report a case of prenatal diagnosis of Tricuspid Atresia (TA) in a family with heritability positive for NKx2-5 mutation, II-ASD and AV block.

Case report: A 36-years-old woman was referred to our attention for fetal echocardiography at the time of her first pregnancy with family history positive for II-ASD, AV block (proband and her mother) and sudden cardiac death (two proband's mother sisters). A NKx2-5 mutation (c 458 del T in exon 2) was found both in the female and in her mother while the fetal echocardiography and genetic analysis (array CGH) were found to be normal. This child is currently 5 years old and without cardiac problem. Recently this woman came back to our attention during her second pregnancy at 17 weeks of gestational age, at fetal echocardiography we found a type Ib tricuspid valve atresia (TA). The array-CGH revealed the same NKx2-5 mutation identified in the family. After extensive counseling the couple opted for termination of pregnancy. The fetus's cardiac abnormality was confirmed by autopsy. Discussion: Heterozygous NKx2-5 mutations are increasingly recognized having key role as molecular determinant for nonsyndromic CHD with or without progressive AV block. More than 40 heterozygous NKx2-5 germline mutations have been observed in familial, and more rarely, sporadic CHD cases. The most common phenotypes, are II ASD associated with progressive AV block, but other cardiac anomalies have been reported. However, to our knowledge, a correlation between TA and NKx2-5 mutation in a family with ASD, progressive AV block and NKx2-5 mutation has not been documented in literature.

Conclusion: considerable progress has been made towards the understanding of mechanisms leading to CHD. However, the mechanism by which the same cardiac malformations have been exhibited in different gene mutations or the same mutation produce diverse cardiac malformations remains largely to be determined. Identify a new possible genotype phenotype correlation it will be important to better understanding of NKx2.5 mutation role in cardiac development.