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# Possible Single Nucleotide Polymorphism (SNP) in the Nucleic Sequence of A-kinase-anchoring Protein 9

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## Abstract

**In cardiac physiology, ion channel macromolecular complexes can be formed by the strong correlation of A-kinase anchoring proteins, therefore, AKAP becomes an important antiarrhytmic target. Here, the author performed a bioinformatics analysis to study the possible single nucleotide polymorphism (SNP) in the amino acid sequence of AKAP9. In this work, the author could not identify any SNP with in AKAP9. This confirms that there is no report on SNP on this molecule.**

**Key words**: A-kinase anchoring protein; Arrhythmia; Single nucleotide polymorphism

## Introduction

In normal cardiac physiology, sympathetic nervous system (SNS) regulation of cardiac action potential duration (APD), mediated by beta-adrenergic receptor (betaAR) activation, usually requires assembly of A-kinase anchoring protein (AKAP)9 (Yotiao) with the I(Ks) potassium channel alpha subunit (KCNQ1) (Chen et al., 2007). Ion channel macromolecular complexes can be formed by the strong correlation of AKAPs (Chen and Kass, 2006; Marx and Kurokawa, 2006). Therefore, AKAP becomes an important antiarrhytmic target (Marx and Kurokawa, 2006). Analysis on the AKAP in depth helps better understand the pathogenesis of this protein-relate arrythmic disorder. AKAP disorder can be seen in the recent reports (Lin et al., 1998; Tao et al., 2006), however, the prevalence of mutations in the AKAP is not well known. In addition, single nucleotide polymorphism (SNP) within AKAP has never been mentioned.

Importance of SNP study for AKAP and other AKAP targets for new therapeutic interventions should be mentioned. Burns-Hamuro et al. (2004) said that there had been considerable progress in understanding the structural features of this AKAP and its interaction with protein kinase A (Burns-Hamuro et al., 2004). Burns-Hamuro et al. (2004) reported that comprehensive analysis of the PKA binding motif could lead to the development of novel peptides derived from D-AKAP2 and could be useful tools in probing the function of this AKAP in cellular and animal models (Burns-Hamuro et al., 2004). However, there is limited reported on AKAP9. There was a paper by Rudd et al. (2006) describing the possible correlation of SNP for AKAP9 and lung cancer (Rudd et al., 2006). However, there was no proof from this work (Rudd et al., 2006). Here, the author performed a bioinformatics analysis to study the SNP in the amino acid sequence of AKAP9.

## Materials and Methods

At first, the database Expert Protein Analysis System (ExPASY) (Gasteiger et al., 2003) was used for searching for the amino acid sequence of AKAP9. Then the derived sequences were used for further study for SNP. GEN-SNiP was further used for identification on SNP within the derived sequence. Briefly, GEN-SNiP help finds polymorphisms present in DNA sequences with respect to a standard reference sequence. This tool is selected because it is only one simple online access tool and is confirmed for its validity. The output lists substitutions, insertions and deletions. Since there is no other similar tool to GEN-SNiP, further comparative study to other tool cannot be performed.

## Result

In this work, AKAP9 (NG_007968) was used for further study. There is no identified SNP for this sequence.

## Discussion

Importance of SNP search for target drug discovery/ new therapeutic interventions should be mentioned in the present post-genomics era. The analysis of SNPs permits determining relationships between genotypic and phenotypic information as well as the identification of SNPs related to a disease, which can be useful for further drug development (Shah and Kusiak, 2004). The good examples are on antineoplastic (Mack et al., 2008) and cardiovascular drugs (Borgiani et al., 2007). There are numerous experimental and clinical data supporting the existence or variant AKAP proteins (Chen et al., 2001). However, the exact functions of variant AKAP proteins, either physiological or pathological, are still unclear, although roles for some AKAP variants in cardiac arrythmia progression might be consistent with the accumulated data (Chen et al., 2001; Saucerman et al., 2004). On one hand, AKAP polymorphism might connect with some rare syndromes of arrhythmic disorder and on other side it is the post-receptor modifications that very well explain the molecular pathogenesis of AKAP and arrythmia. Identification of the SNP within AKAP can be useful for further researches to understand the pathogenesis of AKAP disorder. In this work, the author could not identify any SNP with in AKAP9. This confirms that there is no report on SNP on this molecule although there is for other AKAPs (Burns-Hamuro et al., 2004; Frank et al., 2008).

## Conclusions and Future Perspectives

In this work, the author used a novel bioinformatics tool to find possible SNP in the amino acid sequence of AKAP9 and found no SNP. This might imply that the AKAP9 might have no polymorphism. However, due to the limitation of the present tool, the conclusion cannot be reached. Future analysis by future available tool is suggested. In addition, a study on the probable mutated prone position, weak linkage analysis, is another *in silico* methods suitable for this AKAP protein.

## Declaration on Conflict of Interest

The author hereby would like to declare for no conflict of interest in this work.

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