

4-2024

The analysis of variants R43W and S133C in the GATA4 gene in (CHD) congenital heart disease

Elaine Vanterpool
Oakwood University, evanterpool@oakwood.edu

Akalya King
Oakwood University

Follow this and additional works at: <https://ouscholars.oakwood.edu/student-posters>

Recommended Citation

Vanterpool, Elaine and King, Akalya, "The analysis of variants R43W and S133C in the GATA4 gene in (CHD) congenital heart disease" (2024). *Student Posters*. 20.
<https://ouscholars.oakwood.edu/student-posters/20>

This Poster is brought to you for free and open access by the Student Creative Works at OUScholars. It has been accepted for inclusion in Student Posters by an authorized administrator of OUScholars.



The analysis of variants R43W and S133C in the GATA4 gene in (CHD) congenital heart disease

Akayla King, Dr.Elaine Vanterpool

Oakwood University,
Department of Biological Sciences
Huntsville AL, 35896



ABSTRACT

Congenital cardiac defects are the source of the symptoms of heart disease. One of the most prevalent diseases in neonates is congenital heart disease. This study aims to shed light on genetic determinants which are the underlying cause of congenital heart disease and their symptoms, particularly to congenital heart disease. Human disorders have been connected to missense mutation genes and cardiac abnormalities in GATA4. In both mice and humans, proper heart development and homeostasis depend on the zinc transcription factor GATA4. Simple ClinVar was used to identify GATA4 gene that was linked to the congenital heart disease. Consequently, this gene has a significant detrimental impact on the development of the heart. Computational tools like SIFT and Polyphen-2 were used to evaluate the pathogenicity of mutations on the protein. The protein's structure was determined through the application of SWISS modeling. GATA4 is a part of the GATA-N superfamily which is the conserved domain. The N-terminal is one of the domain hits of GATA and it's where transcription starts. GATAN is the transcription activator family which is represented by this family. The missense mutations under study was Ser133Cys and Arg43Trp. Ser133Cys is 0.1 and Arg43Trp is 1.0, meaning that it may be harmful. Ser133Cys has a score of 0.09, replacement at pos 133 from S-C is where it's expected to be tolerated, whereas a value 0.00 for Ser133Cys indicates that substitution at position 43 from R to W will have an impact on protein function. The expression of this gene is predominantly seen in the heart and PolyPhen2 predicts R43W to be damaging.

RESULTS

SIFT

| Predictions | Predictions |
|---|---|
| Substitution at pos 133 from S to C is predicted to be TOLERATED with a score of 0.09. Median sequence conservation: 3.10 Sequences represented at this position:13 | Substitution at pos 43 from R to W is predicted to AFFECT PROTEIN FUNCTION with a score of 0.00. Median sequence conservation: 3.00 Sequences represented at this position:14 |
| Figure (1a) Ser133Cys variant affecting GATA4 with a score of 0.09. | Figure (1b) Arg43Trp variant affecting GATA4 with a score of 0.00 |

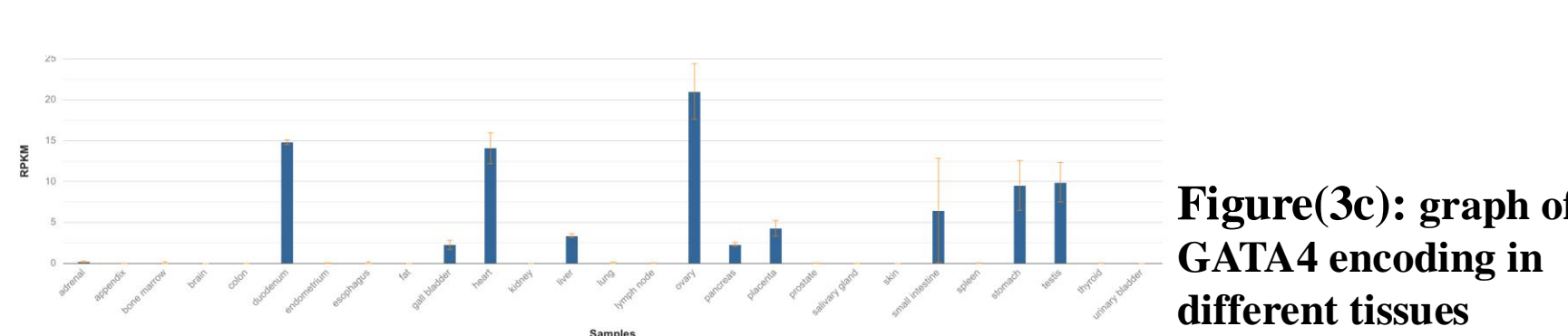
Poly-Phen

| | |
|---|---|
| This mutation is predicted to be POSSIBLY DAMAGING with a score of 0.588 (sensitivity: 0.87; specificity: 0.91) | This mutation is predicted to be PROBABLY DAMAGING with a score of 1.000 (sensitivity: 0.00; specificity: 1.00) |
| | |
| Figure (2a) Ser133Cys variant which is damaging with a score of 0.6. | Figure (2b) Arg43Trp variant which is damaging with a score of 1.000. |

Conserved Domains

Figure (3a) GATA4 being apart of the GATA-N superfamily. GATA-N is one of the domain sites at intervals 1-205, ZnF_GATA at intervals 217-267. GATA-N is where transcription activates at N-terminal.

Figure (3b) The zinc finger DNA binding domain binds specially to DNA consensus sequence [AT] GATA[AG]



Swiss Modeling

Figure (4): 3D structures of GATA4

DISCUSSION AND CONCLUSION

- GATA4 binding protein 4 gene is on chromosome 8 and encodes for various genes known has zinc transcriptional factor that has a critical role in cardiac hypertrophy, heart failure.
- GATA4 binding protein 4 is present in the GATA-N region. This protein is to regulate genes involved in embryogenesis and myocardial differentiation.
- The mutation Arg43Trp and Ser133Cys is a missense mutation in GATA4 which is causing pathogenesis in transcription for DNA to properly bind to GATA4 protein.
- Congenital heart disease (CHD) is very rarely seen in 1% of live births.
- Arg43Trp and Ser133Cys variants of the GATA4 is expressed highly in the ovaries.
- Defects in alternative splicing are associated with many cardiac septal defects yet relatively little is known about the cell type or alternative splicing is achieved in the heart.
- The activation of GATA4 occurs various cell signaling events. The discovery of interactions of GATA4 with nuclear factor for activated T cells (NFAT) revealed the importance of calcium signaling in the activation of GATA4. GATA4 can also be phosphorylated by mitogen activated protein kinases and protein kinase A. Lysine modifications also occur on the GATA4 molecule including acetylation and sumoylation. Both reactive oxygen-dependent and -independent antioxidant-sensitive pathways for GATA4 activation. The GATA4 activity is also regulated by modulating the level of GATA4 expression transcriptional as well as translational mechanisms.
- Mutations in this gene have been associated with ventricular septal defects (VSD) which is a common form of congenital heart disease.
- These findings will impact the medical community by increasing an understanding of the connection between the relationship of GATA4 being produced in the reproductive system which would cause the abnormality of the gene determinants among possibly infants that expressed the GATA4 gene.

REFERENCES

B.; Z. Y. F. J. (n.d.). *Associations of GATA4 genetic mutations with the risk of congenital heart disease: A meta-analysis*. *Medicine*. <https://pubmed.ncbi.nlm.nih.gov/28471988/>

Gonzalez-Teran B;Pittman M;Felix F;Thomas R;Richmond-Buccola D;Hüttenhain R;Choudhary K;Moroni E;Costa MW;Huang Y;Padmanabhan A;Alexanian M;Lee CY;Maven BEJ;Samse-Knapp K;Morton SU;McGregor M;Gifford CA;Seidman JG;Seidman CE;Gelb BD;Colombo G;Conklin BR:B. (n.d.). *Transcription factor protein interactomes reveal genetic determinants in heart disease*. *Cell*. <https://pubmed.ncbi.nlm.nih.gov/35182466/>

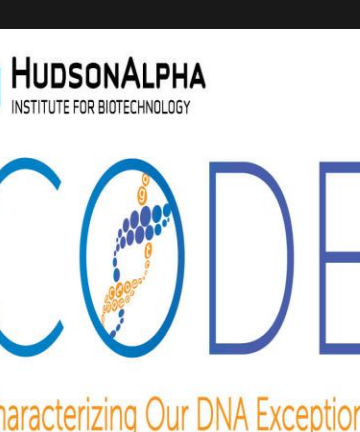
Mayo Foundation for Medical Education and Research. (2023, April 21). *Congenital heart disease in adults*. Mayo Clinic. <https://www.mayoclinic.org/diseases-conditions/adult-congenital-heart-disease/symptoms-causes/syc-20355456>

CDD conserved protein domain family: Znf_gata (no date) National Center for Biotechnology Information. Available at: <https://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=238123> (Accessed: 01 April 2024).

GATA4 gata binding protein 4 [homo sapiens (human)] - gene - NCBI (no date) National Center for Biotechnology Information. Available at: https://www.ncbi.nlm.nih.gov/gene?cmd=retrieve&list_uids=2626 (Accessed: 03 April 2024).

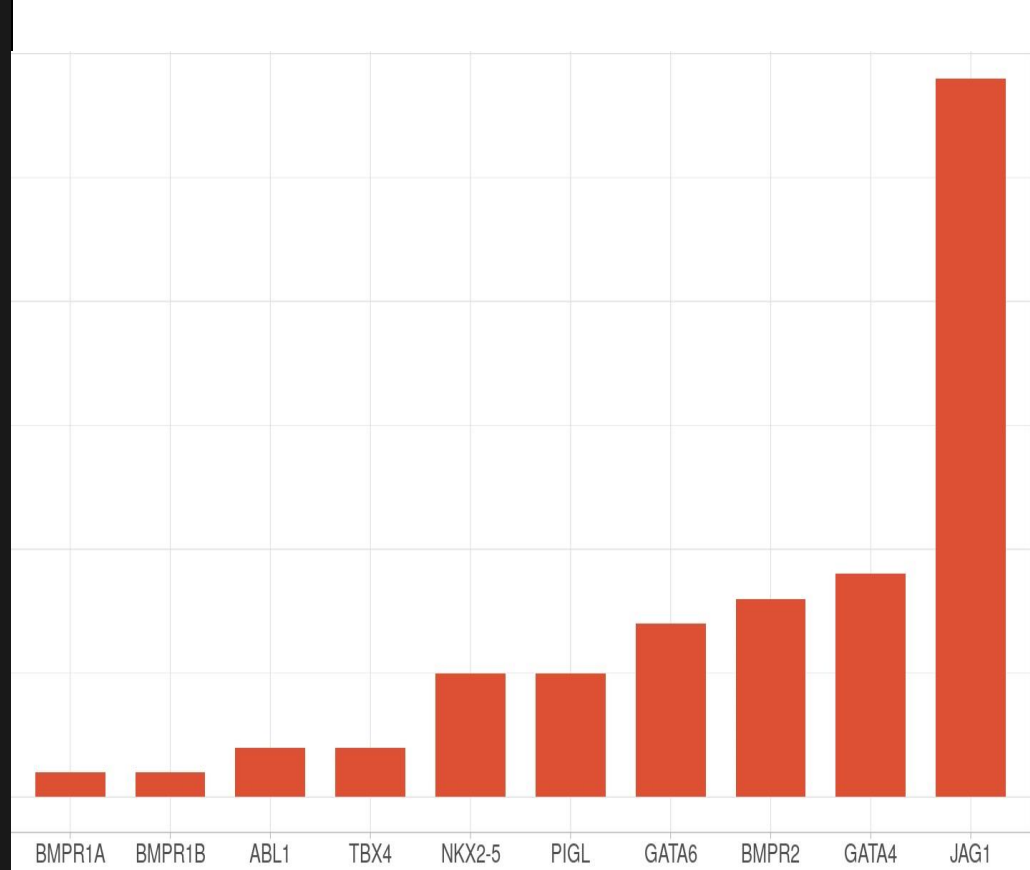
ACKNOWLEDGEMENTS

This program was supported by Hudson and Alpha Institute for Biotechnology, Biological Science Department at Oakwood University and a very special thanks to Elaine Vanterpool, PhD.



INTRODUCTION

Congenital means that you're born with such condition. Congenital heart disease (CHD) is one of the causes of childhood diseases and mortality is mainly triggered by environmental and genetic factors. Congenital heart disease in adults and children can change the way blood flows through the heart. There are different types of congenital heart defects. It's an abnormality in the heart that can develop before birth. Congenital heart defect is one of the most common types of birth defects. The symptoms that may occur is abnormal heart rhythms, shortness of breath, failure to feed or develop normally, and swollen body tissue or organs. In addition to the heart, GATA4 plays important role in the reproductive system. GATA4 is a present in many genes and regulates genes involved in embryogenesis and myocardial differentiation. GATA-4 interacts with many members of the spliceosome complex in human induced pluripotent stem cell-derived progenitors. In this study it results in the embryonic stem cells to become damaging. Congenital disease is passed down through birth 1% of the time. In this study congenital heart disease is causing abnormality in the genetic determinants.



METHODS

- Simple-Clinvar was used in this study to observe GATA4 gene in congenital heart disease.
- Swiss Modeling was used to obtain the 3-D model of GATA.
- PolyPhen-2 was used to predict the serio of the gene variations associated with GATA4.
- SIFT programming which takes the sequence to predict whether an amino acid substitution will affect the protein function.