

DECRYPTION OF DNA AND ITS ROLE IN TREATING GENETIC DISORDER AT EARLY STAGE

ABSTRACT

Aims: The aim of the study is to perform the task of decryption of deoxyribonucleic acid (DNA) and the role of such decrypted DNA for the treatment of genetic disorders at an early stage. The objective of the study is to analyze the utility of the decryption of DNA.

Study design: Cross sectional study design.

Methodology: The numerous research papers that were utilized for the study were taken from online databases such as European Bioinformatics Institute (EMBL-EBI) and GenBank. Research journals were taken from Google Scholar and ProQuest. Axial coding was performed to evaluate the thematic analysis of the study. Moreover, in this study, a total of 7 sources by Van Der Pol & Moliere, Li et al., El Bairiet al., Raguso et al., Hager & Zienkiewicz, Herzog et al. And North out et al. have been chosen as the relevant selected journals for conducting thematic analysis. PRISMA method was used to reflect upon the several articles presented during the dissertation.

Results: The computation of DNA and its decoding from a particular sector of the body is eminent for studying the concept of the disorder of a particular sort. The abdominal aortic aneurysm is a fatal disorder. Being asymptomatic in nature, it turns deadly until it ruptures. It occurs due to the amplification of the "aorta", which is the principal blood vessel delivering blood at the abdominal level of the body.

Thus, Thus there is strong correlation between genetic disorders and DNA decryption the DNA decryption will unfold the treatment for genetic disorders.

Conclusion: The concepts of genetic disorders and the decoding of DNA are heavily intertwined. The decryption of DNA would lead the researchers to detect disorders early on and analyze their structural integrity to study it further.

Keywords: Decryption, DNA, genetic disorder, early stage, treatment

1. INTRODUCTION

Every organism existing in this domain of the universe possesses the concept of genes and genetic abilities. The concept of heredity and transfer of the genetic composition from parents to their offspring are invariably valuable for the continuation of the generation. Johann Gregor Mendel, who is known as the father of Genetics, worked on the concept of the genetic composition of *Pisum sativum* for the formulation of the various laws of genetics. He coined the terms "recessive traits" and "dominant traits" for indicating the property of genes to express or not to express themselves. The invisible "factors" or the genes are what makes us what we were, what we are and what we will be in future. The importance of the study of genetics has been heightened exponentially in the last few decades. With the world of every

organism evolving around genes and chromosomes, it is essential to solve the puzzle of heredity and untangle the issues of the biological universe.

The aim of the study is to perform the task of decryption of deoxyribonucleic acid (DNA) and the role of such decrypted DNA for the treatment of genetic disorders at an early stage. The objective of the study is to analyse the utility of the decryption of DNA. This is a review paper and previous research papers on the subject have been reviewed to answer the question under investigation. There is also the working towards the identification of the importance of decrypted DNA in human disorders and for the investigation of the role of DNA decryption in treating disorders at an early stage.

As far as research has extended in the department of Biology and the stream of Genetics, the genetic composition of living organisms is known to be of two types - DNA or RNA. DNA or deoxyribonucleic acid is the material of heredity for almost every living organism, including us *Homo sapiens*. RNA or ribonucleic acid is utilized by some viruses and play a role in the processes of coding and decoding. They are also used for the expression and regulation of genes in humans. Thus, it is understandable that the mysteries of life and of the future are present in the double-stranded structure of DNA and the single-stranded structures of RNA. Solving these enigmatic structures may aid the researchers to appreciate and get conscious about the biotic sphere of the world. For working on these microscopic structures, the first step is decoding and decrypting them. Untangling the intertwined bodies will open up the frontier of Genetics.

Genetically engineered and modified organisms can be heavily worked upon for the betterment of humankind (Abbai *et al.* 2019). Both medicinal and industrial usage of such organisms can act as a synergistic body for our day to day utilities (Maria, 2018). Many of the diseases and disorders that are present can be attributed to mutated genetic composition of the bodies. They can either be at the nucleotide level or the chromosomal level. A wrong bonding between the four nucleotides - adenine, guanine, cytosine, thymine (in DNA) and the replacement of thymine with uracil (in RNA) can falter with the genetic makeup of the body too. Thus, by the utilization of DNA cryptography techniques and methods, one can aim to solve the secrets of genetic disorders (Chauhan *et al.* 2021). Cryptography is the brand of science that handles the job of encoding the information from the decrypted data. One of the evolving branches of Genetics, DNA cryptography plays an important role in solving the complexities of the genetic composition of the organisms.

According to Kaur *et al.* (2021), the role of DNA cryptographers is to build up the complexity of the biological world with the usage of DNA nucleotides. Thus, for DNA de-cryptography, the object is to straighten out the double-helical structure of DNA and perform the tasks of understanding the genetic composition. For future work, it is of utmost importance to solve the riddle of the genetic world. There is an acute requirement for the study of Genetics and such DNA decryption methods to understand the configuration of different organisms and their nature. This allows understanding the prevalence of genetics in occurrence of the genetic disorder of varying degree among different species. The DNA decryption and the understanding of genetic disorders will also open the door for understanding the significance of variation and chromosome cross over in case of bringing genetic variability among species.

2. MATERIAL AND METHODS

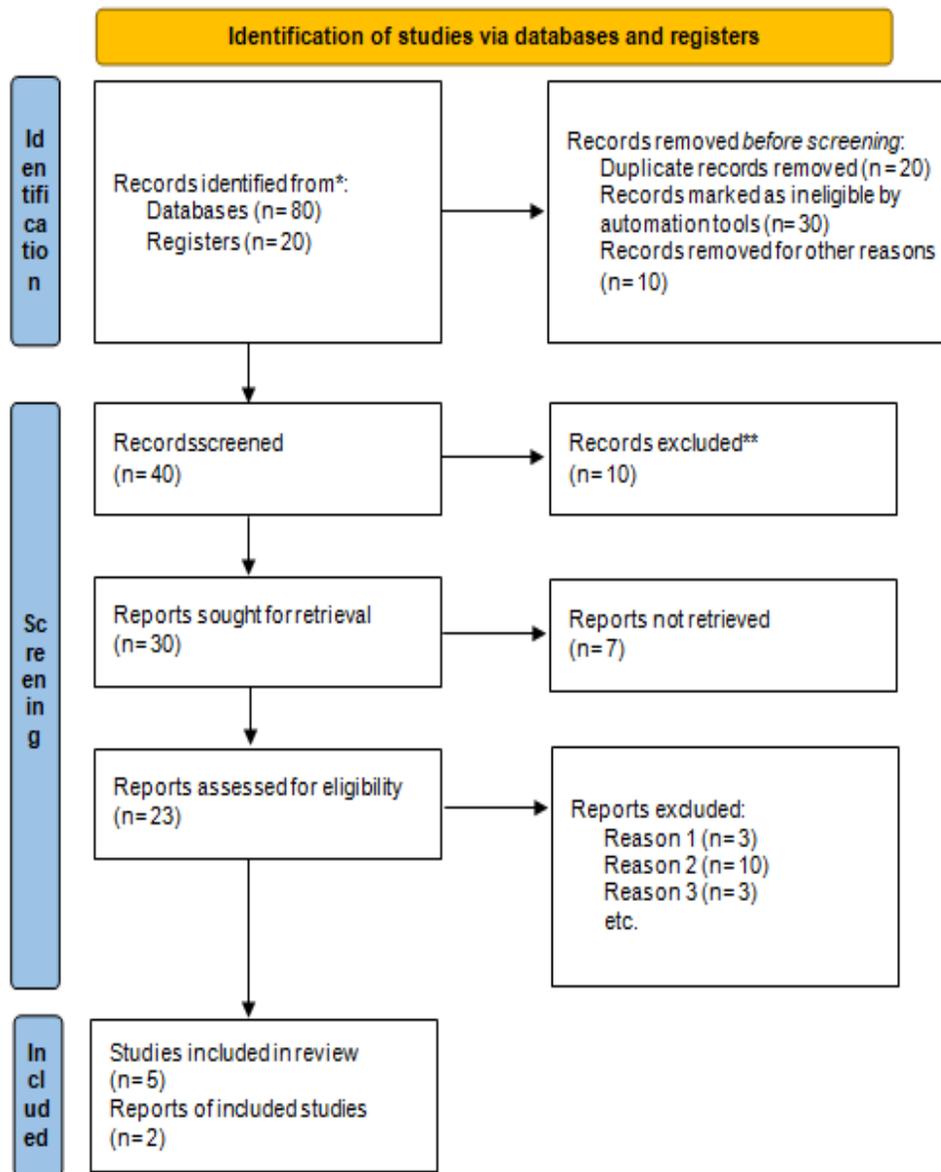


Figure 1: PRISMA Diagram

(Source: Developed by Researcher)

The numerous research papers that were utilized for the study were taken from online databases such as European Bioinformatics Institute (EMBL-EBI) and GenBank. Research journals were taken from Google Scholar and ProQuest. Axial coding is performed to evaluate the thematic analysis of the study. Moreover, in this study, a total of 7 resources have been chosen as the relevant selected journals for conducting thematic analysis. "Preferred Reporting Items for Systematic Reviews and Meta-Analyses" or PRISMA will be conducted to reflect upon the several articles presented during the study.

Table 1: Inclusion and exclusion criteria

| Inclusion | Exclusion |
|------------------------------------|-------------------------------------|
| 1. Need to be within last 10 years | 1. Old research papers are excluded |

| | |
|---|---|
| 2. Need to be relevant to the topic | 2. Papers not related to the topic are excluded |
| 3. Need to be primary research article with experiments | 3. Review papers are excluded |
| 4. Need to be peer reviewed | 4. Open access free non peer reviewed papers are excluded |

Table 2: Boolean table for keyword based search

| Keywords | Operator | Keywords | Operator | Keywords |
|---|----------|---------------------------|----------|------------------|
| DNA | OR/AND | Decryption of DNA | OR/AND | Genetic disorder |
| Genetic disorder at an early age | OR/AND | DNA cryptography | OR/AND | DNA mutation |
| Mutation of DNA in the genetic disorder | OR/AND | Treating genetic disorder | OR/AND | DNA sequences |

3. RESULTS AND DISCUSSION

3.1 Themes and code table

Table 3: Themes and code table

| Author | Year of publishing | Aim and objectives | Evaluated theme |
|-----------------------|--------------------|---|--|
| Van Der Pol & Moliere | 2019 | The aim of the research was to find out the methods of “early detection of cancer” by the usage of both “epigenetic and environmental fingerprinting from cell-free DNA.” | DNA decoding by epigenetic and environmental factors “for the early detection of cancer” |
| Li <i>et al.</i> | 2018 | The aim of the study was to utilize the methods of decoding the genomics of the chromosome for the disorder of abdominal aortic aneurysm. | DNA decryption for understanding “the genomics of abdominal aortic aneurysm” and colorectal cancer |

| | | | |
|--------------------------|------|---|--|
| El Bairiet <i>et al.</i> | 2018 | The aim of the research was to understand the study of epigenomics for decoding colorectal cancer. | epigenomics |
| Raguso <i>et al.</i> | 2020 | The aim of the performed research was to produce both chemical and biological probes of "DNA and RNA G-quadruplex structures in the area of genomics." | Chemical and biological approaches for "DNA and RNA G-quadruplex structures in the genome" |
| Hager & Zienkiewicz | 2019 | The aim of the study was to understand the concepts of inflammation, the causative agent for inflammation, the generation of response due to inflammation and the methods to counter such an event. | Usage of DNA approach for the detection of inflammation |
| Herzog <i>et al.</i> | 2019 | The aim of the research was to acknowledge the mechanisms for the decoding of rapid-acting antidepressant treatment strategies and if the modes are related to the gender of the patients. | Decoding the fast-acting strategies for antidepressant treatment by DNA decryption |
| North out <i>et al.</i> | 2018 | The aim of the research was to appreciate the mechanisms for "decoding the chromatin of a proteome in a single genomic locus by the method of DNA sequencing." | Using DNA approaches by DNA sequencing for the decoding the chromatin proteome |

3.1.1 Theme 1: DNA decoding by epigenetic and environmental factors for the early detection of cancer

According to the findings of Van Der Pol & Moliere (2019), DNA decoding is a growing stream in the Department of Genetics. Not only does it help to detect the various genetic disorders, but it also aids in finding a possible approach to rectify the mutated or wrongly-placed nucleotides to recover from the disease. Once a problem is identified, the next approach is to analyze it with the goal of rectifying it. Cancer cells or the oncogenic cells are mutated cells with the presence of wrongly bonded nucleotides, chromosome abnormalities, or point mutations in the nucleotide sequence. They have been known to release a variety of nucleic acids, various proteins, numerous vesicles containing a measured amount of tumor-derived nucleic acids and other components into the bloodstream of the patient. These constituents act as potential biomarkers for the detection of cancer in the early stages. Amongst these circulating tumours DNA (ctDNA) hold a probable mode of approach for the researchers.

For attempting such an approach, it is invariantly important for scientists to first perform the decryption of DNA from its encrypted form. The double-helical structures needed to be separated before probing at both strands. There needs to be a synergistic approach between both the epigenetic and environmental factors which can assess the occurrence of cancer. Epigenetic approaches are constructed on the test of "cell-free DNA (cfDNA) methylation" design or the investigation of "cfDNA fragmentation". These procedures have the ability to detect the **ovarian or pancreatic cell ctDNA caused due to mutation** present on a large genomic scale without having an antecedent knowledge of "Single-nucleotide variants (SNVs) copy-number aberrations (SCNAs)" (Van Der Pol & Moliere, 2019).

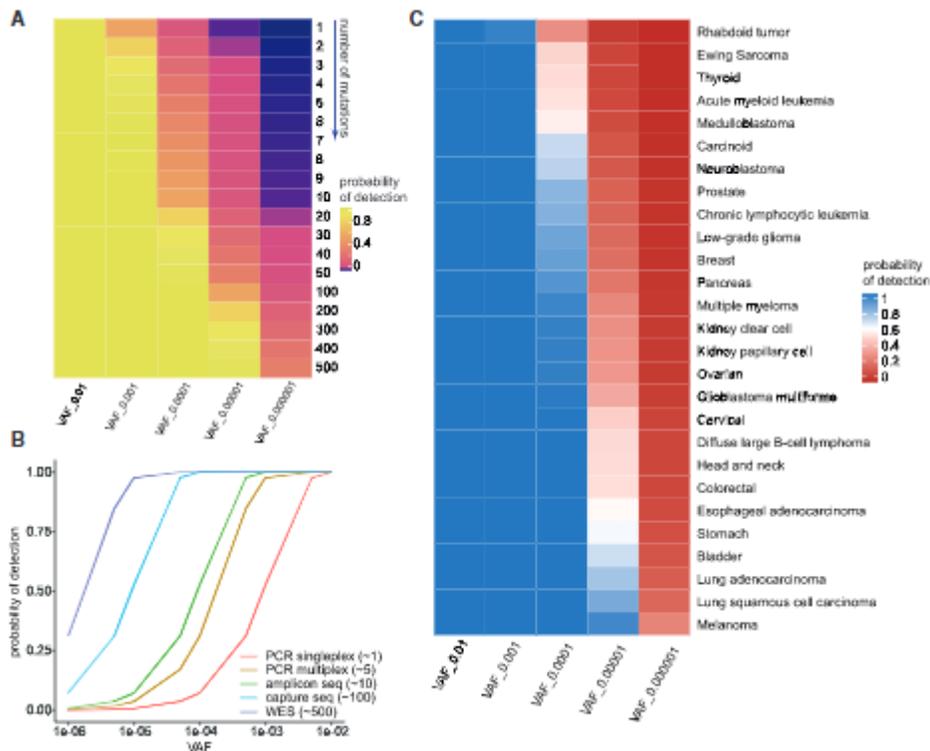


Figure 2: Finding out the probability for the “detection of ctDNA in Mutation-Based Strategies” which depends “upon the Number of Mutations present and Their Clonality”

(Source: Van Der Pol & Mouliere, 2019)

However, the genomic analysis of cancer occurring from the tissue of the DNA is based on the location of the sample and thus, can detect the presence or absence from the localized area. Thus, the localized nature of the genomic approach is usually avoided so as to perform a broad spectrum analysis for the detection of cancer. For an early stage of cancer detection (stage I-II), there is a small amount of cfDNAs which are released into the bloodstream. However, the quantity of cfDNAs is directly proportional to the time the patient goes through the course of the disorder. Thus, during late-stage cancer (stage III-IV), there is a significant release of cfDNA in the blood, compared to healthy individuals (Van Der Pol & Mouliere, 2019).

Therefore, the decryption of DNA that can analyze the presence or absence of cfDNAs in the bloodstream for the premature observation of cancer is of utmost significance.

3.1.2 Theme 2: DNA decryption for understanding the genomics of abdominal aortic aneurysm and colorectal cancer epigenomics

According to the findings of Li *et al.* (2018), DNA decryption plays a major role in understanding the genomics of the human body. Consisting of trillions of cells, it is impossible to perform the feat of decoding each and every one of them. Therefore, the computation of DNA and its decoding from a particular sector of the body is eminent for studying the concept of the disorder of a particular sort.

The abdominal aortic aneurysm is a fatal disorder. Being asymptomatic in nature, it turns deadly until it ruptures. It occurs due to the amplification of the “aorta”, which is the principal blood vessel delivering blood at the abdominal level of the body. This disorder is associated with the degeneration of the elastic stratum of the “atheromatous aorta”. The underlying procedure for this disorder is still unknown.

Therefore, it is one of the utmost topics of concern for the researchers to understand the fundamental mechanism of this disorder to understand its possibility of happening; if it has occurred, its prognosis and preventive measures for it to happen in the future generations. This can be achieved by understanding the genetic composition of the cells in the

abdomen. Via DNA decryption, if a fault can be seen in the genes, it can be a source where rectification can occur. This would serve as a starting point to cure the disease.

The usage of DNA decryption has been applied to the findings of colorectal cancer (CRC), too. Cancer genomics, a tremendously studied department in the stream of Genetics. Colorectal cancer is a disorder with no cure. Most of the time, the beginning of the disorder can not be known until it is too late. As opined by El Bairi *et al.* (2018), the main cause of this disorder is the progressive accumulation of the sequence of both "genetic and epigenetic" modifications in the typical colonic epithelium cells, which leads to the maturation of "colorectal adenomas" and "invasive adenocarcinomas". Thus, by utilizing the methods of DNA decryption, CRC becomes approachable. Understanding the genetic nature at the cellular level would act as the pioneering source of information. There are various epigenetic markers that act as important hallmarks of the molecular nature of cancer because the presence of these biomarkers occur during the very early stages in the pathogenesis of the disease. These are also involved in all the key pathways which are associated with cancer, and, above all, these biomarkers have the capability of being exploited "as clinically relevant disease biomarkers" for the concepts of disease diagnosis, prognostication and for prediction of treatment response.

3.1.3 Theme 3: Chemical and biological approaches for "DNA and RNA G-quadruplex structures in the genome"

DNA and RNA do not only exist as double helical or single-stranded structures, respectively. These structures have the capability of intertwining amongst themselves and with other molecules to form aggregated compounds. DNA and RNA G-quadruplex are "non-canonical", "four-stranded structures" which are made due to the high content of "guanine-rich DNA and RNA sequences" that are formed under certain physiological conditions. These secondary structures, which are globular and folded in nature, were found in the telomeric DNA (Raguso *et al.* 2020).

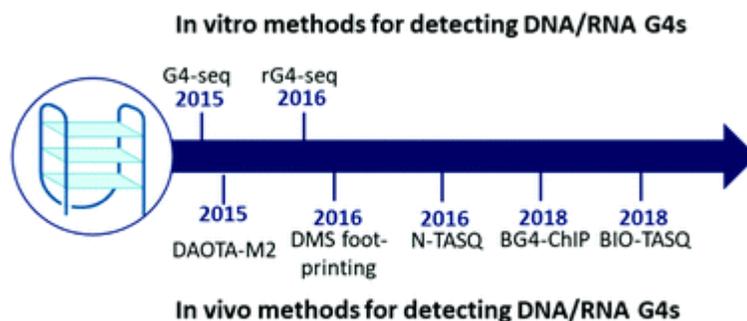


Figure 3: There different in vivo methods for the detection of DNA and RNA G4 complexes

(Source: Raguso *et al.* 2020)

DNA and RNA G-quadruplex (G4) structures can act as therapeutic targets as they are formed directly due to the information stored in the telomeric DNA strands. In vivo methods that are utilized for the detection of these structures use a variety of biomarkers such as the biotin associated version of a known and previously sequenced "G4-specific ligand" or probe. This "template-assembled synthetic G-quartet (TASQ)" has the ability to self-assemble to form a synthetic G-quartet structure, which associates with a G4 target by the mechanism of "end-quartet stacking".

The usage of BioTASQ for capturing G-quadruplex-RNAs from the cancer cells in human breast cancer, in the "log-phase growth", has been utilized in the medical fields. The biochemical structures of DNA and RNA G-quadruplex (G4) complexes, thus, require the system of DNA decryption to understand the underlying mechanism in the cancer cells. Therefore, a thorough analysis of the DNA sequence is vital for understanding the structural integrity of the G-quadruplex and how it gets associated with the strands.

3.1.4 Theme 4: Decoding the fast-acting strategies for antidepressant treatment by DNA decryption

The pathological and psychological aspect of any human plays an important role in the day to day activities performed. This not only depends upon the environmental factors but also on the genetic composition of the individual. According to the working by Herzog *et al.* (2019), there is a mean value of 2:1 female-male ratio in the developed nations for the disorder of depression which is consistently observed.

Major depressive disorder or MDD is a looming threat to the mental health of people all around the world. There are underlying pathways that are driven by the presence of hormones and other kinds of molecular structures that play a role in the gender-specific approach to MDD research. Any kind of hormonal influence is thus due to the genetic disposition. In addition, there is the approach of gene accessibility by numerous epigenetic modifications that can mitigate the causes of MDD. The transcriptome profile and DNA fingerprinting are ways that the depressive disorder can be approached. DNA decryption of the individual can lead the researchers and doctors to analyze the causes of the depressive episodes, which can therefore be worked upon to reduce their occurrences.

Hence, with the facility of DNA decryption and knowing where the target molecules are, there can be the production of fast-acting strategies during the treatment of the disorder. Many antidepressants are produced in such a manner, such as

Ketamine, Scopolamine, Cannabidiol and major Psychedelics like Lysergic acid diethylamide (LSD), 2,5-Dimethoxy-4-iodoamphetamine (DOI), N, N-Dimethyltryptamine (DMT) and 3,4-Methylenedioxymethamphetamine (MDMA), which is also known colloquially as ecstasy (Herzog *et al.* 2019).

Table 4: **Mode Of Action Of Drugs**

| Drug | Decryption based mode of action |
|---------------------------------|---|
| DNA methyltransferase 3a | Allows development of mal phenotype and DNA decryption allows the role of its disruption in feminization of the human brain |
| serotonin | Make epigenetic changes such as post transcriptional changes to BDNF, CRF, GDNF, and GR genes which causes changes in their expression |
| fluoxetine | Changes expression of genes that code for myelin sheath and its decryption allows understanding the role of myelin sheath development and the impact of antidepressants on it |

3.2 Discussion

Thus, it is invariably visible that there is a strong connection between the phenomena of DNA decryption to the detection of genetic disorders at an early stage (Lokuge&Ganegoda, 2019). The acute responsibility of scientists to understand this entanglement paves the path in the future prospectus of the study of Genomics. The role of DNA computing is growing at an exponential rate. The branch of DNA encryption is employed as a model for hiding data by using DNA sequences. This tremendous level of security can be availed by organizations to stay ahead of the attackers from the loss of intellectual property, data and information (O'Toole & Sedor, 2018).

Nonetheless, there are hurdles that still have not been mitigated by scientists. The process of DNA decryption is complicated and requires advanced technology and high intellect and knowledge in the particular department. There is a need to construct biomarkers and probes, which are both extensive and expensive (Yang *et al.* 2020). This eminently increases the price of the procedure to analyze the genetic disorders at an early stage and cannot be availed by most of the patients. From the review it can be understood that DNA RNA intertwined complexes acts as biomarkers in case of cancers caused due to genetic abnormality. The decryption of the DNA sequence in such DNA RNA complexes allows better understanding of the genetic mechanism causing breast cancer. The G quadruplex complex allows better understanding of the importance of DNA decryption for genetically caused cancer. As per the review it can also be understood that DNA decryption plays the sole role in understanding the underlying genetic defect at DNA level and ways to rectify the defect so as to treat the genetic disorder. The development of cancer can also be attributed to an underlying genetic issue because in case of cancer the genetic codes are mutated and there are alterations of a single code or series of codes leading to translation of wrong proteins or malfunctioning of the gene expression. The decryption of the genetic code plays an essential role in understanding the abdominal aortic aneurysm as it is asymptomatic in nature and the decryption of DNA allows understanding the genetic cause of such disease development. Along with abdominal aortic aneurysm colorectal cancer is also a major disease which needs to be detected in early stage and the decryption of DNA is an effective method to understand the first steps in development of cancer. The identification of the epigenetic markers of the colorectal cancer identified by DNA preventing colorectal cancer in stage one. Decryption is essential in understanding the target of antidepressants in case of MDD. DNA decryption allows better understanding of the genetic causes of the disease which can help in retargeting the antidepressants for long lasting action.

4. CONCLUSION

The concepts of genetic disorders and the decoding of DNA are heavily intertwined. The decryption of DNA would lead the researchers to detect disorders early on and analyze their structural integrity to study it further.

Not only do the methods of DNA decryption allow the researchers to study the underlying mechanisms of the disorders and diseases, but they also help them to rectify the mistakes in the genetic disposition of individuals. This aids for better treatment procedures, less painful ways of treatment, mentally calming practices and the hope for a better future for the upcoming generations. Further studies would enhance the public to utilize such advanced mechanisms. A reduction in the cost would occur when these streams are highly worked upon so that the need for such methodologies will be funded by the government of the countries.

4.1 Limitations

While performing the study, there were some research gaps that were faced. Most of them occurred due to the presence of vague and unrelated data. The pandemic posed a threat to the collection of data directly from the laboratories. Face to face interviews with the researchers or a collaborative panel discussion could not be held. So, there was total dependability on the research journals and acted as a secondary source of data collection. There was the omission of journals and data findings that were older than the last five years. Thus, relevant data were also left out from the discussion.

4.2 Future Scope

The study of Genetics has soared exponentially over the last decade. As a result, there has been an increase in budding researchers and scientists who have devoted their work to broaden the scope of the ancestral and xenogenetic study. According to the findings of Islam (2018), the advancement of technology has fulfilled its goal for the implementation of the various methods of genetic mapping of the human genome. The fundamentals of DNA and their study can help to understand the fundamentals of biological objects. Identification, localizing and treatment of genetic disorders can be achieved even before birth.

REFERENCES

- Abbai, R., Singh, V. K., Nachimuthu, V. V., Sinha, P., Selvaraj, R., Vipparla, A. K., ... & Kumar, A. (2019). Haplotype analysis of key genes governing grain yield and quality traits across 3K RG panel reveals scope for the development of tailor-made rice with enhanced genetic gains. *Plant biotechnology journal*, 17(8), 1612-1622. doi: 10.1111/pbi.13087
- Chauhan, D., Saxena, A., & Sharma, S. (2021). Portable and Error-Free DNA-Based Data Storage. In *2021 4th International Conference on Recent Developments in Control, Automation & Power Engineering (RDCAPE)* (pp. 418-421). IEEE. DOI: [10.1109/RDCAPE52977.2021.9633694](https://doi.org/10.1109/RDCAPE52977.2021.9633694)
- El Bairi, K., Tariq, K., Himri, I., Jaafari, A., Smaili, W., Kandhro, A. H., ... & Ghazi, B. (2018). Decoding colorectal cancer epigenomics. *Cancer genetics*, 220, 49-76. Retrieved from <https://doi.org/10.1016/j.cancergen.2017.11.001>
- Hawiger, J., & Zienkiewicz, J. (2019). Decoding inflammation, its causes, genomic responses, and emerging countermeasures. *Scandinavian journal of immunology*, 90(6), e12812. DOI: 10.1111/sji.12812 DOI: 10.1111/sji.12812
- Herzog, D. P., Wegener, G., Lieb, K., Müller, M. B., & Treccani, G. (2019). Decoding the mechanism of action of rapid-acting antidepressant treatment strategies: does gender matter?. *International journal of molecular sciences*, 20(4), 949. Retrieved from <https://doi.org/10.3390/ijms20040949>
- Islam, K. (2018). The bump-and-hole tactic: expanding the scope of chemical genetics. *Cell chemical biology*, 25(10), 1171-1184. <https://doi.org/10.1016/j.chembiol.2018.07.001>
- Kaur, M., Singh, S., & Kaur, M. (2021). Computational Image Encryption Techniques: A Comprehensive Review. *Mathematical Problems in Engineering*, 2021. Retrieved from <https://doi.org/10.1155/2021/5012496>

- Korthout, T., Poramba-Liyanage, D. W., van Kruijsbergen, I., Verzijlbergen, K. F., van Gemert, F. P., van Welsem, T., & van Leeuwen, F. (2018). Decoding the chromatin proteome of a single genomic locus by DNA sequencing. *PLoS biology*, 16(7), e2005542. Retrieved from <https://doi.org/10.1371/journal.pbio.2005542>
- Li, J., Pan, C., Zhang, S., Spin, J. M., Deng, A., Leung, L. L., ... & Snyder, M. (2018). Decoding the genomics of abdominal aortic aneurysm. *Cell*, 174(6), 1361-1372. Retrieved from <https://doi.org/10.1016/j.cell.2018.07.021>
- Lokuge, L. D. C. S., & Ganegoda, G. U. Review of Prediction of Human Diseases using DNA Sequencing Technologies. Retrieved from https://www.researchgate.net/publication/344594808_Review_of_Prediction_of_Human_Diseases_using_DNA_Sequencing_Technologies
- Maria, G. (2018). In-silico Design of Genetic Modified Micro-Organisms (GMO) of Industrial Use, by Using Systems Biology and (Bio) Chemical Engineering Tools. Simi Valley. *Juniper Publ.*
- O'Toole, J. F., & Sedor, J. R. (2018). CKD, Genetic Variation, and the Epigenome: Decrypting the Code. *American Journal of Kidney Diseases*, 72(2), 164-167. Retrieved from <https://linkinghub.elsevier.com/retrieve/pii/S027263861830581X>
- Raguseo, F., Chowdhury, S., Minard, A., & Di Antonio, M. (2020). Chemical-biology approaches to probe DNA and RNA G-quadruplex structures in the genome. *Chemical Communications*, 56(9), 1317-1324. Retrieved from <https://pubs.rsc.org/en/content/articlelanding/2020/cc/c9cc09107f/unauth>
- Van Der Pol, Y., & Mouliere, F. (2019). Toward the early detection of cancer by decoding the epigenetic and environmental fingerprints of cell-free DNA. *Cancer cell*, 36(4), 350-368. Retrieved from <https://doi.org/10.1016/j.ccell.2019.09.003>
- Yang, X. Z., Sun, R., Guo, X., Wei, X. R., Gao, J., Xu, Y. J., & Ge, J. F. (2020). The application of bioactive pyrazolopyrimidine unit for the construction of fluorescent biomarkers. *Dyes and Pigments*, 173, 107878.

APPENDIX
Appendix 1: Database screenshot

The screenshot shows the ProQuest database interface. At the top, the ProQuest logo is on the left, and 'Access provided by HOLMES INSTITUTE' is in the center. A search bar contains the text 'DNA encryption'. Below the search bar, it indicates '1,181 results'. On the left side, there are filter options: 'Applied filters' (Clear all filters, Last 5 Years), 'Show results outside my library's subscription', 'Sorted by' (Relevance), and 'Limit to' (Full text, Peer reviewed). The main results area shows two entries:

- 1. A novel image encryption algorithm using PWLCM map-based CML chaotic system and dynamic DNA encryption. Tien Junfeng, Lu, Yi, Zuo Xianyu, Liu, Yang, Qiao Beojun, et al. *Multimedia Tools and Applications*; Dordrecht Vol. 80, Iss. 21-23, (Sep 2021): 32841-32861. Citation/Abstract
- 2. A robust and lossless DNA encryption scheme for color images. Wu, Xiangjun; Kurths, Jürgen; Kan, Hebin. *Multimedia Tools and Applications*; Dordrecht Vol. 77, Iss. 10, (May 2018): 12349-12376. Full Text

(Source: ProQuest, 2021)