Molecular Genetics Internship

Identification of Novel Genetic Markers for Complex Diseases like Cancer, Cardiovascular Diseases, and Diabetes
+

This research objective focuses on discovering new genetic markers associated with major complex diseases such as cancer, cardiovascular diseases, and diabetes. These markers can potentially improve diagnostics, treatment personalization, and understanding of disease mechanisms.

Research Methodology

Phase 1: Data Collection

Collect genetic data from diverse populations using high-throughput sequencing technologies to capture a broad spectrum of genetic variation.

Phase 2: Genetic Analysis

Analyze the collected data using bioinformatics tools to identify SNPs, mutations, and structural variants associated with the diseases.

Phase 3: Validation

Validate the identified genetic markers through epidemiological studies and functional assays to confirm their association with disease phenotypes.

Phase 4: Integration into Clinical Practice

Work towards integrating the validated markers into clinical diagnostics and treatment strategies to enhance personalized medicine approaches.

Research Approach

1. Utilize genome-wide association studies (GWAS) to identify potential genetic markers.
2. Apply next-generation sequencing for detailed genomic profiling.
3. Conduct case-control studies to assess the significance of identified genetic markers.
4. Use CRISPR-Cas9 technology for functional validation of candidate genes.

Protocols

1. DNA extraction and quality assessment protocol.
2. Standard operating procedures for sequencing (Illumina or similar platforms).
3. Statistical analysis protocol using software like PLINK and R.
4. Guidelines for ethical considerations, particularly in genetic testing and data privacy.

Elucidation of the Genetic Basis of Rare and Undiagnosed Diseases
+

This research objective aims to uncover the genetic underpinnings of rare and previously undiagnosed diseases, which can lead to targeted therapies and improve diagnostic capabilities.

Research Methodology

Phase 1: Patient Recruitment and Sample Collection

Recruit patients with rare and undiagnosed diseases from diverse backgrounds and collect biological samples (blood, tissue) for genetic analysis.

Phase 2: Genomic Sequencing and Data Generation

Perform whole-exome or whole-genome sequencing to generate comprehensive genetic data from collected samples.

Phase 3: Bioinformatic Analysis

Analyze sequencing data to identify novel mutations and genetic variations that may explain the phenotypes observed in patients.

Phase 4: Functional Studies

Conduct functional genomic studies using techniques like gene editing and in vitro assays to validate the impact of identified mutations on cellular functions.

Phase 5: Clinical Correlation and Reporting

Correlate genetic findings with clinical data to establish a clear genotype-phenotype relationship and disseminate findings through clinical reports and scientific publications.

Research Approach

1. Employ targeted and whole-genome sequencing technologies to uncover genetic abnormalities.
2. Utilize bioinformatics tools to analyze genetic sequences and predict functional impact of variations.

3. Integrate multi-disciplinary approaches involving genetics, molecular biology, and clinical sciences.
4. Collaborate with global rare disease consortia for data sharing and validation.

Protocols

1. Standard protocols for high-throughput genetic sequencing.
2. Bioinformatic analysis protocols, including data cleaning, alignment, and mutation calling.
3. Protocols for in vitro functional assays to study gene expression and mutation effects.
4. Clinical data integration and privacy protocols to ensure ethical handling of sensitive patient information.

Development of Gene Editing Technologies for Therapeutic Applications in Genetic Disorders
+

This objective focuses on advancing gene editing technologies such as CRISPR-Cas systems to treat genetic disorders. The goal is to develop precise, safe, and effective methods to correct defective genes responsible for these conditions.

Research Methodology

Phase 1: Target Identification

Identify and characterize genetic mutations responsible for specific genetic disorders using genomic databases and previous research.

Phase 2: Gene Editing Tool Development

Design and optimize gene editing tools, particularly CRISPR-Cas systems, to target and correct the identified mutations in cellular models.

Phase 3: In Vitro and In Vivo Validation

Test the efficacy and safety of the gene editing tools in vitro (cell lines) and in vivo (animal models) to assess their therapeutic potential.

Phase 4: Clinical Trials

Progress to clinical trials to evaluate the effectiveness and safety of the gene editing treatment in human subjects.

Research Approach

1. Use of advanced CRISPR technology for precise gene correction.
2. Application of next-generation sequencing to verify the accuracy of gene editing.
3. Engagement with regulatory bodies to ensure compliance with ethical and safety standards.

4. Collaboration with pharmaceutical companies for clinical development and deployment.

Protocols

1. Guidelines for the design and synthesis of guide RNAs.
2. Protocols for the delivery of CRISPR components into cells and tissues.
3. Standard procedures for assessing off-target effects and genomic integrity post-editing.
4. Clinical trial protocols, including patient selection, dosing, and monitoring.

Investigation of the Genetic Factors Contributing to Aging and Longevity
+

This research objective aims to explore the genetic factors that influence aging processes and contribute to longevity, aiming to identify potential targets for anti-aging therapies.

Research Methodology

Phase 1: Genome-Wide Association Studies

Conduct genome-wide association studies (GWAS) on populations with noted longevity to identify genetic variants associated with extended lifespan.

Phase 2: Genomic Sequencing

Sequence the genomes of individuals exhibiting exceptional longevity to uncover rare genetic variants that may contribute to aging and healthspan.

Phase 3: Bioinformatics Analysis

Utilize bioinformatics tools to analyze sequencing data, focusing on identifying and categorizing genetic variants linked to longevity and reduced aging-associated diseases.

Phase 4: Functional Validation

Validate the functional significance of identified genetic markers through in vitro and in vivo experiments, including the use of animal models to study the impact of specific genes on aging processes.

Research Approach

1. Integration of epidemiological data with genetic data to refine candidate longevity genes.
2. Employing advanced sequencing technologies and computational methods for data analysis.
3. Collaborative research with gerontology experts to interpret genetic findings in the context of aging biology.
4. Development of intervention studies to test the effects of manipulating longevity-

associated genes.

Protocols

1. Protocols for collecting and handling biological samples from aged populations.
2. Standard operating procedures for genomic and epigenomic sequencing.
3. Bioinformatic pipelines for analyzing large-scale genetic data.
4. Guidelines for conducting aging-related experiments in animal models.

Exploration of the Genetic Diversity and Evolution of Human Populations Using Advanced Sequencing Technologies
+

This research objective focuses on understanding the genetic diversity and evolutionary patterns among human populations worldwide using state-of-the-art sequencing technologies.

Research Methodology

Phase 1: Sample Collection

Collect DNA samples from diverse ethnic groups across different geographical locations to ensure a wide representation of genetic diversity.

Phase 2: Whole-Genome Sequencing

Perform whole-genome sequencing on the collected samples to obtain detailed genetic information from each population.

Phase 3: Genetic Analysis

Analyze the genetic data to identify unique genetic variations, trace migration patterns, and study evolutionary relationships among populations.

Phase 4: Data Sharing and Collaboration

Share the genetic data with international databases to foster global collaboration and enhance the understanding of human genetic evolution.

Research Approach

1. Utilization of next-generation sequencing and bioinformatics tools for detailed genetic mapping.
2. Interdisciplinary collaboration involving genetics, anthropology, and history to interpret the findings.
3. Engagement with local communities and stakeholders for ethical sample collection and data utilization.

4. Application of machine learning techniques to predict evolutionary trends and population health impacts.

Protocols

1. Ethical guidelines for genetic research and sample collection from diverse populations.
2. Protocols for DNA extraction, storage, and sequencing.
3. Data analysis protocols, including phylogenetic analysis and statistical testing.
4. Standard procedures for data sharing and publication in accordance with global data protection regulations.

Integration of Multi-omics Data to Understand the Gene-Environment Interactions in Human Health
+

This research aims to integrate genomic, transcriptomic, proteomic, and metabolomic data to dissect the complex interactions between genetic factors and environmental influences on human health.

Research Methodology

Phase 1: Data Collection

Collect comprehensive omics data (genomic, transcriptomic, proteomic, metabolomic) from individuals exposed to different environmental conditions.

Phase 2: Data Integration and Analysis

Use advanced bioinformatics tools to integrate and analyze multi-omics data to identify patterns and interactions that correlate with health outcomes.

Phase 3: Experimental Validation

Conduct experimental studies to validate the findings from the data analysis, focusing on specific gene-environment interactions that influence disease risk and health.

Phase 4: Development of Predictive Models

Develop predictive models based on integrated omics data to forecast health outcomes under various environmental scenarios.

Research Approach

1. Collection of multi-layered omics data from both controlled cohort studies and large-scale population data.
2. Application of systems biology approaches to model the complexity of gene-environment

interactions.
3. Utilization of machine learning and statistical methods to analyze and predict outcomes from integrated datasets.
4. Collaboration with environmental health scientists to interpret the results and validate models.

Protocols

1. Standardized protocols for the collection and processing of omics data.
2. Data integration techniques, ensuring data quality and comparability across different omics layers.
3. Protocols for the ethical handling of personal and sensitive health data.
4. Guidelines for the design and execution of validation experiments, including cell culture and animal models.

Advancement of Personalized Medicine through Genome-Wide Association Studies and Pharmacogenomics
+

This research aims to advance personalized medicine by utilizing genome-wide association studies (GWAS) and pharmacogenomics to identify genetic variants that influence drug responses and disease risk.

Research Methodology

Phase 1: Genetic Data Collection

Collect genetic data from diverse populations to identify genetic variants associated with drug efficacy and side effects.

Phase 2: Pharmacogenomic Analysis

Analyze genetic markers to understand how they affect individual responses to drugs, aiming to optimize drug therapy based on genetic profiles.

Phase 3: Clinical Trials

Integrate pharmacogenomic data into clinical trials to validate genetic markers as predictors of treatment outcomes.

Phase 4: Implementation

Develop guidelines for implementing pharmacogenomic findings into clinical practice to personalize patient care.

Research Approach

1. Conducting GWAS to identify relevant genetic variants linked to drug metabolism.
2. Using high-throughput screening methods to test pharmacological responses in genetic variant carriers.
3. Collaborating with clinical and pharmaceutical partners to apply findings in real-world settings.
4. Engaging with regulatory bodies to update treatment protocols based on genetic insights.

Protocols

1. Standard procedures for genetic data collection and handling.
2. Protocols for analyzing pharmacogenomic data and interpreting results.
3. Clinical trial design incorporating pharmacogenetic testing.
4. Guidelines for ethical considerations in genetic testing and patient privacy.

Study of Mitochondrial Genetics in Human Disease and Mitochondrial Replacement Therapies
+

This research focuses on exploring the role of mitochondrial genetics in human diseases and developing mitochondrial replacement therapies to treat mitochondrial disorders.

Research Methodology

Phase 1: Identification of Mitochondrial Mutations

Identify mutations in mitochondrial DNA that are linked to various diseases using next-generation sequencing.

Phase 2: Development of Mitochondrial Replacement Techniques

Develop and refine techniques for replacing mutated mitochondrial DNA in affected cells or embryos.

Phase 3: In Vitro and In Vivo Testing

Test the safety and efficacy of mitochondrial replacement in cell cultures and animal models.

Phase 4: Clinical Applications

Translate successful techniques into clinical trials to assess therapeutic potential in humans.

Research Approach

1. Utilizing molecular biology techniques to isolate and characterize mitochondrial DNA.

2. Applying gene editing tools to correct mitochondrial mutations.
3. Collaborating with reproductive technology specialists for embryo manipulation.
4. Evaluating ethical, legal, and social implications of mitochondrial replacement.

Protocols

1. Protocols for mitochondrial DNA extraction and sequencing.
2. Standard operating procedures for mitochondrial DNA replacement in vitro.
3. Animal model testing guidelines for assessing the impact of mitochondrial replacement.
4. Clinical trial protocols for mitochondrial replacement therapies.

Research on the Implications of CRISPR and Other Gene-Editing Technologies on Human Embryos and Germline Cells
+

This research aims to explore the ethical, biological, and technical implications of applying CRISPR and other gene-editing technologies to human embryos and germline cells. The focus is on understanding the potential benefits and risks, with an emphasis on ethical considerations, safety, and regulatory compliance.

Research Methodology

Phase 1: Ethical Review and Protocol Development

Develop a comprehensive ethical framework and obtain necessary approvals to conduct research involving gene editing in human embryos and germline cells.

Phase 2: Gene-Editing Technique Optimization

Optimize CRISPR and other gene-editing techniques for precision, efficiency, and safety in human embryonic and germline cells.

Phase 3: In Vitro Experiments

Conduct in vitro experiments to study the effects of gene editing on gene function, development, and potential off-target effects.

Phase 4: Regulatory and Public Engagement

Engage with regulatory bodies and the public to discuss findings, address concerns, and shape future policies regarding the use of gene-editing technologies in human reproduction.

Research Approach

1. Comprehensive review of existing literature and current ethical guidelines regarding gene editing in humans.

2. Development of new methodologies to improve the specificity and efficiency of CRISPR applications in early-stage human cells.
3. Collaboration with bioethicists and public health experts to ensure balanced and transparent communication of research outcomes and implications.
4. Conducting seminars and workshops to gather public opinion and educate on gene editing advancements and ethical considerations.

Protocols

1. Standardized protocols for gene editing in vitro, including CRISPR-Cas9 system delivery and targeting.
2. Protocols for detecting and analyzing off-target effects and unintended genetic modifications.
3. Guidelines for handling and manipulating human embryonic and germline cells under controlled laboratory conditions.
4. Compliance protocols with international regulations and ethical standards for research involving human genetic material.

Comprehensive Mapping of Epigenetic Modifications Across Different Human Populations and Their Impacts on Health and Disease
+

This research objective focuses on mapping epigenetic modifications such as DNA methylation, histone modification, and non-coding RNA expression across diverse human populations to understand their impacts on health and disease susceptibility.

Research Methodology

Phase 1: Sample Collection

Collect tissue samples from diverse ethnic groups under various environmental conditions to capture a broad spectrum of epigenetic diversity.

Phase 2: Epigenetic Profiling

Perform comprehensive epigenetic profiling using technologies like CHIP-seq, ATAC-seq, or bisulfite sequencing to identify patterns of methylation and histone modifications.

Phase 3: Data Analysis

Analyze epigenetic data to identify common and unique patterns related to specific health conditions or traits.

Phase 4: Functional Studies

Conduct functional studies to validate the biological significance of identified epigenetic markers

and their relation to disease phenotypes.

Phase 5: Integration and Translation

Integrate epigenetic data with genomic and environmental data to develop comprehensive models of disease risk, aiming to translate findings into clinical and public health strategies.

Research Approach

1. Utilization of advanced epigenetic mapping techniques to generate high-resolution data.
2. Interdisciplinary collaboration with geneticists, epidemiologists, and clinicians to analyze and interpret data.
3. Engagement with communities and stakeholders to ensure ethical considerations are met and data is representative.
4. Development of computational tools to integrate and analyze multi-dimensional epigenetic data.

Protocols

1. Protocols for ethical sample collection, storage, and epigenetic analysis.
2. Data processing protocols to handle large datasets from high-throughput epigenetic profiling technologies.
3. Standard operating procedures for validating epigenetic modifications through in vitro and in vivo functional assays.
4. Guidelines for integrating epigenetic findings with clinical data to inform treatment and prevention strategies.

Other Objectives

1. Characterization of non-coding RNAs and their role in gene regulation and disease.
2. Investigation of 3D genome organization and its influence on gene expression and cellular function.
3. Development of synthetic biology approaches to engineer genetic circuits for therapeutic applications.
4. Elucidation of genetic susceptibility to infectious diseases and vaccine responses.
5. Exploration of gene therapy techniques for the treatment of genetic eye disorders.
6. Study of genetic interactions and their implications in multi-genic disorders.
7. Advancement of technologies for in vivo imaging of gene expression and chromatin dynamics.
8. Research on the role of telomeres and telomerase in cancer and aging.
9. Development of gene drive systems to control populations of disease vectors.
10. Elucidation of genetic mechanisms underlying neurodegenerative diseases like Alzheimer’s and Parkinson’s.
11. Investigation of the genetics of behavioral traits and their evolution.
12. Development of machine learning models to predict genetic mutations and their phenotypic

outcomes.

13. Study of the impact of genetic variations on drug metabolism and response in psychiatric disorders.
14. Exploration of the potential for gene therapies in autoimmune diseases.
15. Characterization of somatic mutations in cancer and their implications for personalized treatment.
16. Development of gene-editing tools for correcting mutations in hematological disorders.
17. Research on stem cell genetics for regenerative medicine and tissue engineering.
18. Investigation of genetic factors in fertility and reproductive health.
19. Elucidation of the molecular mechanisms of genetic disorders affecting muscle function.
20. Study of the genetic basis of sensory disorders such as hearing and vision impairments.
21. Exploration of genetic predispositions to addiction and substance abuse.
22. Development of next-generation sequencing technologies for faster and more accurate genetic profiling.
23. Investigation of the interplay between genetic factors and environmental toxins in disease manifestation.
24. Elucidation of the role of genetic factors in metabolic syndrome and obesity.
25. Study of genetic influences on the immune system and the development of autoimmune conditions.
26. Exploration of therapeutic targets in genetic disorders using CRISPR-based screens.
27. Characterization of the genetic architecture of skin diseases and dermatological conditions.
28. Development of bioinformatics tools for large-scale genetic data analysis and interpretation.
29. Research on genetic engineering for enhanced human capacities, such as increased cognitive or physical abilities.
30. Investigation of ethical, legal, and social implications of advanced genetic technologies.
31. Elucidation of genetic factors in respiratory diseases and their treatments.
32. Study of genetic modifications to improve human adaptation to extreme environments.
33. Exploration of gene-environment interactions in the development of allergic and asthmatic conditions.
34. Development of diagnostic tests based on genetic biomarkers for early detection of diseases.
35. Research on the modulation of gene expression as a therapeutic strategy in cancer.
36. Investigation of the genetic basis of pain perception and its management.
37. Elucidation of genetic contributions to circadian rhythms and sleep disorders.
38. Study of genetic factors influencing nutritional requirements and disorders.
39. Exploration of genetic engineering to prevent genetic diseases before conception.
40. Characterization of genetic variations contributing to differences in human physical traits.
41. Development of gene therapies for diseases caused by mitochondrial DNA mutations.
42. Investigation of transgenerational genetic effects and their implications for human health.
43. Elucidation of the role of genetic factors in gastrointestinal diseases.
44. Study of the genetic underpinnings of immune response to emerging infectious diseases.
45. Exploration of the use of gene editing for the development of personalized cancer vaccines.
46. Characterization of the genetic determinants of bone density and risk of osteoporosis.
47. Development of CRISPR-based diagnostics for rapid genetic testing in clinical settings.
48. Research on the role of genetics in the effectiveness of physical rehabilitation.

49. Investigation of the genetics of stress and anxiety disorders.
50. Elucidation of the role of genetics in cardiovascular function and heart diseases.
51. Study of the genetic basis of hormonal disorders and their treatments.
52. Exploration of genetic factors in the aging process and interventions to mitigate age-related diseases.
53. Characterization of genetic determinants of blood pressure and their role in hypertension.
54. Development of gene silencing technologies to treat genetic diseases.
55. Investigation of the role of genetics in the development and treatment of liver diseases.
56. Elucidation of genetic factors in kidney function and disorders.
57. Study of the interplay between human genetics and the gut microbiota in health and disease.
58. Exploration of genetic therapies for the treatment of genetic skin disorders.
59. Characterization of genetic factors influencing the development of psychiatric disorders.
60. Development of genetic tools for the prevention and treatment of viral infections.
61. Research on the potential for genetic enhancement of human sensory capabilities.
62. Investigation of the role of genetic variation in response to climate change and environmental stressors.
63. Elucidation of the molecular genetics of blood coagulation disorders.
64. Study of the genetic influences on child development and pediatric diseases.
65. Exploration of the genetics of human reproductive technologies and their implications.
66. Characterization of genetic factors contributing to autoimmune skin disorders.
67. Development of targeted gene therapies for specific ethnic populations based on genetic variations.
68. Investigation of genetic factors influencing recovery from neurological damage.
69. Elucidation of genetic bases for differences in pain management efficacy among populations.
70. Study of the genetics of inflammatory responses and their role in diseases.
71. Exploration of the role of gene therapy in correcting immune deficiencies.
72. Characterization of genetic factors influencing metabolic pathways in different tissues.
73. Development of gene-based strategies for enhancing human resilience to diseases.
74. Research on genetic predictors of aging and strategies to extend healthspan.
75. Investigation of genetic factors that modulate responses to physical activity and exercise.
76. Elucidation of the genetic foundations of learning disabilities and educational interventions.
77. Study of genetic contributions to the variation in human cognitive abilities.
78. Exploration of the impact of gene-environment interactions on the development of mental health conditions.
79. Characterization of genetic factors in the response to surgical interventions and healing processes.
80. Development of predictive genetic models for complex diseases using artificial intelligence.
81. Investigation of the genetic underpinnings of addiction to digital and virtual environments.
82. Elucidation of genetic influences on the effectiveness of psychological therapies.
83. Study of the role of genetic factors in the human response to global dietary changes.
84. Exploration of the role of genetic engineering in enhancing human adaptability to technological advancements.

85. Characterization of the genetic basis of immune system disorders and their potential treatments.
86. Development of genetic interventions to combat antibiotic-resistant bacterial infections.
87. Research on the implications of genomic research for public health policy and medical ethics.
88. Investigation of the role of genetic factors in the development of chronic pain conditions.
89. Elucidation of the role of genetic variations in the pharmacokinetics and pharmacodynamics of drugs.
90. Study of the application of genetic research in improving global health disparities.
91. Exploration of gene therapy approaches for the treatment of genetic disorders in pediatric populations.
92. Characterization of the genetic aspects of human adaptation to space environments.
93. Development of genomic tools for the management and conservation of human genetic diversity.

Fee Structure

Note 1: Fee mentioned below is per candidate.
Note 2: Fee of any sort is NON REFUNDABLE once paid. Please cross confirm all the details before proceeding to fee payment

2 Days Total Fee: Rs 1983/-
Reg Fee Rs 595/-
5 Days Total Fee: Rs 4957/-
Reg Fee Rs 1487/-
10 Days Total Fee: Rs 7600/-
Reg Fee Rs 2280/-
15 Days Total Fee: Rs 12000/-
Reg Fee Rs 3600/-
20 Days Total Fee: Rs 17733/-
Reg Fee Rs 5320/-
30 Days Total Fee: Rs 28165/-
Reg Fee Rs 5500/-

45 Days Total Fee: Rs 42918/-

Reg Fee Rs 5500/-

2 Months Total Fee: Rs 53200/-

Reg Fee Rs 5500/-

3 Months Total Fee: Rs 81067/-

Reg Fee Rs 5500/-

4 Months Total Fee: Rs 107667/-

Reg Fee Rs 5500/-

5 Months Total Fee: Rs 135533/-

Reg Fee Rs 5500/-

6 Months Total Fee: Rs 162133/-

Reg Fee Rs 5500/-

7 Months Total Fee: Rs 190000/-

Reg Fee Rs 5500/-

8 Months Total Fee: Rs 216600/-

Reg Fee Rs 5500/-

9 Months Total Fee: Rs 243200/-

Reg Fee Rs 5500/-

10 Months Total Fee: Rs 271067/-

Reg Fee Rs 5500/-

11 Months Total Fee: Rs 297667/-

Reg Fee Rs 5500/-

1 Year Total Fee: Rs 325533/-

Reg Fee Rs 5500/-

Please contact +91-9014935156 for fee payments info or EMI options or Payment via Credit Card or Payment using PDC (Post Dated Cheque).