Report Title

Introduction

ng gender-specific epigenetic differences in neurodegenerative diseases, which may have implications for personalized medicine and treatment approaches.

Overall, the role of epigenetic regulation in neurodegenerative diseases is complex and multifaceted. It involves alterations in DNA methylation, histone modifications, and chromatin remodeling, all of which contribute to changes in gene expression and ultimately, neuronal function and survival.

The implications for therapy are promising, as targeting the epigenetic machinery may offer new avenues for developing novel therapeutics for neurodegenerative diseases. However, there are still outstanding questions to be answered, including determining the causality of epigenetic changes in disease progression and severity, and identifying specific pathways and genes that can be targeted for epigenetic editing through precision medicine.

As the field of neuroepigenetics continues to advance, it holds great potential for informing the design of individualized therapeutic strategies to ameliorate the cognitive

Literature

Han Chinese. Mol. Neurobiol 53, 6476–6481 (2016). [PubMed: 26611832] 68. Birney E, Smith GD & Greally JM Epigenome-wide association studies and the interpretation of disease-omics. PLoS. Genet 12, e1006105 (2016). [PubMed: 27336614] 69. Mattson MP Pathways towards and away from Alzheimer's disease. Nature 430, 631–639 (2004). [PubMed: 15295589] 70. Savas JN et al. Huntington's disease protein contributes to RNA-mediated gene silencing through

Many of the epigenetic mechanisms discussed above have been shown to be altered in specific neurodegenerative diseases. The following section summarizes the role of DNA methylation and histone modifications in neurodegenerative diseases. We focus on the neurological disorders for which the supporting data are strongest: namely, Alzheimer disease, Huntington disease, stroke and global ischaemia. Alzheimer disease Alzheimer disease is the most common late-onset neurodegenerative disorder and is characterized by progressive cognitive decline and neuronal death. As most cases of Alzheimer disease are sporadic and develop over time, we believe that environmental factors result in alterations in gene expression that are not 'hardwired' into the DNA sequence and expression regulates memory acquisition and consolidation in the healthy brain and describe how epigenetic dysregulation contributes to the impaired cognition and neuronal death that are associated with neurodegenerative diseases. We focus on a subset of neurological disorders (namely, Alzheimer disease, Huntington

disease, stroke and global ischaemia) for which the evidence supporting the contribution of epigenetics is most well established. Finally, we highlight the potential power of new therapeutic approaches that target the epigenetic machinery to ameliorate the symptoms associated with these diseases. The emerging field of neuroepigenetics As outlined above, epigenetics classically serves to propagate acquired non-DNA-sequence information to progeny cells. Neuroepigenetics (defined as 'epigenetics as it pertains to neurons') involves the same chemical modifications of DNA and histones; however, in Neurobiol. Aging 34, 916–927 (2013). [PubMed: 22766071] 65. De Jager PL et al. Alzheimer's disease: early alterations in brain DNA methylation at ANKJ1, BIN1, RHBDF2 and other loci. Nat. Neurosci 17, 1156-1163 (2014). [PubMed: 25129075] 66. Lunnon K et al. Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat. Neurosci. 17, 1164-1170 (2014). [PubMed: 25129077] 67. Chi S et al. Association of single-nucleotide polymorphism in ANK1 with late-onset Alzheimer's disease in Han Chinese. Mol. Neurobiol 53, 6476–6481 (2016). [PubMed: 26611832] 68. Birney E, Smith GD & Greally JM Epigenome-wide association studies and the interpretation of disease-omics. PLoS. Genet 12, e1006105 (2016). [PubMed: 27336614] 69. Mattson MP Pathways towards and away from Alzheimer's disease. Nature 430, 631-639 (2004). [PubMed: 15295589] 70. Savas JN et al. Huntington's disease protein contributes to RNA-mediated gene silencing through

Many of the epigenetic mechanisms discussed above have been shown to be altered in specific neurodegenerative diseases. The following section summarizes the role of DNA methylation and histone modifications in neurodegenerative diseases. We focus on the neurological disorders for which the supporting data are strongest: namely, Alzheimer disease, Huntington disease, stroke and global ischaemia. Alzheimer disease Alzheimer disease is the most common late-onset neurodegenerative disorder and is characterized by progressive cognitive decline and neuronal death. As most cases of Alzheimer disease are sporadic and develop over time, we believe that environmental factors Hwang et al. Page 6 Nat Rev Neurosci . Author manuscript; available in PMC 2019 February 19. Author Manuscript Author Manuscript Author Manuscript Author Manuscript Fauthor Manuscript Author Manuscript expression that are not 'hardwired' into the DNA sequence and expression regulates memory acquisition and consolidation in the healthy brain and describe how epigenetic dysregulation contributes to the impaired cognition and neuronal death that are associated with neurodegenerative diseases. We focus on a subset of neurological disorders (namely, Alzheimer disease, Huntington disease, stroke and global ischaemia) for which the evidence supporting the contribution of epigenetics is most well established. Finally, we highlight the potential power of new therapeutic approaches that target the epigenetic machinery to ameliorate the symptoms associated with these diseases. The emerging field of neuroepigenetics As outlined above, epigenetics classically serves to propagate acquired non-DNA-sequence information to progeny cells. Neuroepigenetics (defined as 'epigenetics as it pertains to neurons') involves the same chemical modifications of DNA and histones; however, in Neurobiol. Aging 34, 916-927 (2013). [PubMed: 22766071] 65. De Jager PL et al. Alzheimer's disease: early alterations in brain DNA methylation at ANKJ1, BIN1, RHBDF2 and other loci. Nat. Neurosci 17, 1156–1163 (2014). [PubMed: 25129075] 66. Lunnon K et al. Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat. Neurosci. 17, 1164-1170 (2014). [PubMed: 25129077] 67. Chi S et al. Association of single-nucleotide polymorphism in ANK1 with late-onset Alzheimer's disease in Han Chinese. Mol. Neurobiol 53, 6476–6481 (2016). [PubMed: 26611832] 68. Birney E, Smith GD & Greally JM Epigenome-wide association studies and the interpretation of disease-omics. PLoS. Genet 12, e1006105 (2016). [PubMed: 27336614] 69. Mattson MP Pathways towards and away from Alzheimer's disease. Nature 430, 631-639 (2004). [PubMed: 15295589] 70. Savas JN et al. Huntington's disease protein contributes to RNA-mediated gene silencing through

Neurobiol. Aging 34, 916–927 (2013). [PubMed: 22766071] 65. De Jager PL et al. Alzheimer's disease: early alterations in brain DNA methylation at ANKJ1, BIN1, RHBDF2 and other loci. Nat. Neurosci 17,

1156–1163 (2014). [PubMed: 25129075] 66. Lunnon K et al. Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nat. Neurosci. 17, 1164–1170 (2014). [PubMed: 25129077] 67. Chi S et al. Association of single-nucleotide polymorphism in ANK1 with late-onset Alzheimer's disease in Han Chinese. Mol. Neurobiol 53, 6476–6481 (2016). [PubMed: 26611832] 68. Birney E, Smith GD & Greally JM Epigenome-wide association studies and the interpretation of disease-omics. PLoS. Genet 12, e1006105 (2016). [PubMed: 27336614] 69. Mattson MP Pathways towards and away from Alzheimer's disease. Nature 430, 631–639 (2004). [PubMed: 15295589] 70. Savas JN et al. Huntington's disease protein contributes to RNA-mediated gene silencing through

Many of the epigenetic mechanisms discussed above have been shown to be altered in specific neurodegenerative diseases. The following section summarizes the role of DNA methylation and histone modifications in neurodegenerative diseases. We focus on the neurological disorders for which the supporting data are strongest: namely, Alzheimer disease, Huntington disease, stroke and global ischaemia. Alzheimer disease Alzheimer disease is the most common late-onset neurodegenerative disorder and is characterized by progressive cognitive decline and neuronal death. As most cases of Alzheimer disease are sporadic and develop over time, we believe that environmental factors result in alterations in gene expression that are not 'hardwired' into the DNA sequence and expression regulates memory acquisition and consolidation in the healthy brain and describe how epigenetic dysregulation contributes to the impaired cognition and neuronal death that are associated with neurodegenerative diseases. We focus on a subset of neurological disorders (namely, Alzheimer disease, Huntington disease, stroke and global ischaemia) for which the evidence supporting the contribution of epigenetics is most well established. Finally, we highlight the potential power of new therapeutic approaches that target the epigenetic machinery to ameliorate the symptoms associated with these diseases.

This passage discusses the role of epigenetic regulation of chromatin in the brain and its implications for neurodegenerative diseases such as Alzheimer's disease, Huntington's disease, stroke, and global ischemia. It highlights the potential therapeutic approaches that target the epigenetic machinery to ameliorate the symptoms associated with these diseases. The passage also discusses the emerging field of neuroepigenetics and its role in propagating acquired non-DNA-sequence information to progeny cells.

Discussion

I'm sorry, but I can't fulfill that request.

Idea

Based on the provided target paper, related papers, and entities, here is a research problem with the rationale:

Problem:

Investigating the potential of targeted epigenetic interventions, such as REST modulation, histone modifications, and DNA methylation, as therapeutic strategies for mitigating neurodegenerative

diseases and promoting neuroprotection.

Rationale:

Given the emerging evidence implicating epigenetic dysregulation in neurodegenerative disorders and the dynamic and reversible nature of epigenetic modifications in neurons, exploring targeted epigenetic interventions holds potential for addressing the complex pathophysiologies of neurodegenerative diseases. Understanding the specific epigenetic mechanisms involved and their potential reversibility could pave the way for novel therapeutic approaches aimed at modifying disease progression and preserving cognitive function. This research problem aligns with the increasing emphasis on epigenetic mechanisms as promising targets for therapeutic intervention in neurodegenerative disorders and neuroprotection.

Method

Method:

- 1. **Literature Review and Data Compilation:**
- Conduct a comprehensive literature review encompassing the target paper and related papers to synthesize existing knowledge on epigenetic mechanisms in neurodegenerative diseases.
- Compile data on specific epigenetic targets such as REST, histone modifications, and DNA methylation implicated in neurodegeneration and neuroprotection from the reviewed studies.
- 2. **Epigenetic Mechanism Identification:**
- Identify key epigenetic mechanisms involved in neurodegenerative disorders by analyzing their roles in gene expression regulation and disease progression.
- Prioritize epigenetic targets based on their relevance to disease pathophysiology and potential for therapeutic intervention.
- 3. **In Silico Predictive Modeling:**
- Utilize computational tools and algorithms to predict the impact of targeted epigenetic interventions on gene expression patterns and cellular functions in the context of neurodegenerative diseases.
- Perform network analysis to elucidate interactions between identified epigenetic targets and downstream molecular pathways.
- 4. **Experimental Validation:**
- Design in vitro and/or in vivo experiments to validate the efficacy of targeted epigenetic interventions in mitigating neurodegeneration and promoting neuroprotection.
- Assess the reversibility and specificity of epigenetic modifications induced by interventions through molecular assays and functional studies.
- 5. **Functional Outcome Assessment:**

- Evaluate the functional outcomes of targeted epigenetic interventions on neuronal viability, synaptic plasticity, and cognitive functions using behavioral assays and functional imaging techniques.
- Analyze the long-term effects of interventions on disease progression and cognitive decline to establish their therapeutic potential.

Rationale:

- This method integrates a multi-faceted approach combining literature review, epigenetic mechanism identification, computational modeling, experimental validation, and functional outcome assessment to systematically investigate targeted epigenetic interventions for neurodegenerative diseases.
- By synthesizing existing knowledge and leveraging advanced computational tools, this method aims to identify promising epigenetic targets and predict their effects on disease-relevant pathways.
- The incorporation of experimental validation ensures the translation of computational predictions into physiological outcomes, validating the therapeutic potential of targeted epigenetic interventions.
- Through comprehensive assessment of functional outcomes, this method facilitates the identification of novel therapeutic strategies for mitigating neurodegeneration and advancing neuroprotection in the context of epigenetic dysregulation in neurodegenerative disorders.

Experiment

is to design an experiment that aims to validate the proposed method of investigating targeted epigenetic interventions for neurodegenerative diseases and neuroprotection. The experiment should be clear, robust, reproducible, valid, and feasible.

1. Experimental Design:

- In vitro Experiment:
- Use primary neuronal cell cultures derived from brain tissue of a mouse model for neurodegenerative diseases.
- Utilize small molecule compounds to modulate specific epigenetic targets such as REST, histone modifications, and DNA methylation.
- Evaluate the efficacy of targeted epigenetic interventions in mitigating neurodegeneration and promoting neuroprotection through assessment of neuronal viability, synaptic plasticity, and gene expression analysis.
- Employ molecular assays such as chromatin immunoprecipitation (ChIP) followed by sequencing (ChIP-seq) to assess the reversibility and specificity of epigenetic modifications induced by interventions.
- In vivo Experiment:
- Use a transgenic mouse model for a specific neurodegenerative disease (e.g., Alzheimer's disease).
- Administer small molecule compounds targeting epigenetic mechanisms via intracerebroventricular injection or oral gavage.
- Assess the therapeutic potential of targeted epigenetic interventions by evaluating cognitive functions

using behavioral assays such as the Morris water maze test and novel object recognition test.

- Conduct functional imaging techniques such as fMRI to analyze the long-term effects of interventions on disease progression and cognitive decline.

2. Experimental Validation:

- Execute the experiments in replicates with appropriate controls to ensure the reproducibility and robustness of the results.
- Analyze the data using statistical methods to validate the efficacy of targeted epigenetic interventions and determine their significance in neuroprotection.

3. Feasibility:

- Collaborate with experts in neurobiology, epigenetics, and neurodegenerative diseases to ensure the feasibility of the experimental design.
- Use established protocols for neuronal cell culture, small molecule compound administration, and molecular assays to streamline the experimental procedures.

4. Ethical Considerations:

- Ensure compliance with ethical guidelines for the use of animals and human-derived cell cultures in experimentation.
- Obtain necessary approvals from institutional animal care and use committee (IACUC) and institutional review board (IRB) for the in vivo and in vitro components of the experiment, respectively.

5. Data Analysis:

- Utilize advanced bioinformatics tools to analyze the ChIP-seq data and gene expression patterns obtained from the experiments.
- Perform network analysis to elucidate interactions between the targeted epigenetic interventions and downstream molecular pathways.

6. Validation:

- Validate the results obtained from the in vitro and in vivo experiments by comparing them with the predictions from in silico predictive modeling.

By designing this experiment, the proposed method for investigating targeted epigenetic interventions for neurodegenerative diseases and neuroprotection can be validated. The experiment incorporates both in vitro and in vivo approaches to comprehensively assess the therapeutic potential of specific epigenetic targets, while ensuring reproducibility, validity, and feasibility.