Sotos Syndrome: A *Genetic* disorder with *Epigenetic* consequences

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The McKusick-Nathans Epigenetics and Chromatin Clinic (ECC)



McKUSICK-NATHANS INSTITUTE



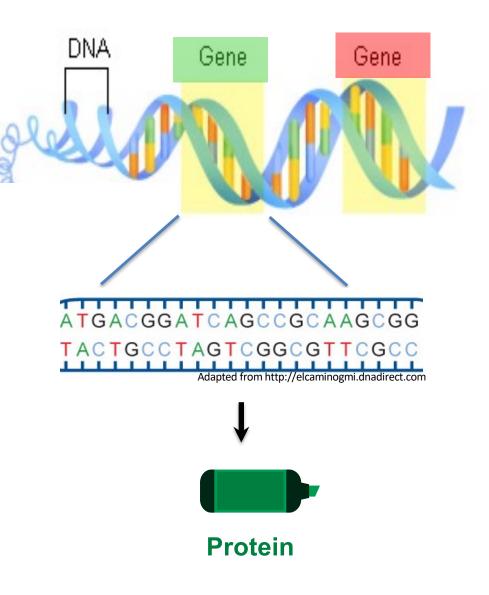
No Disclosures

Objectives

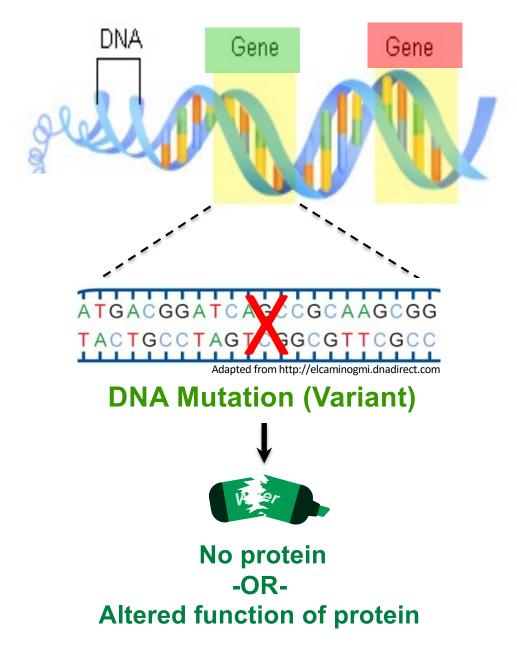
- To introduce concepts of Genetics and Epigenetics
- To understand Sotos syndrome as a genetic disease
- To understand epigenetic consequences of deficiency of *NSD1*
- To provide an update on current knowledge of molecular changes in Sotos syndrome
- To inform you about ongoing research for Sotos syndrome
- To mention our novel & multidisciplinary Epigenetics and Chromatin clinic at Johns Hopkins

DNA, Genes, and the Genetic Code

- Our bodies are made up of billions of cells
- Each cell contains genetic material in the form of DNA
- DNA contains ~22,000 genes
- Genes determine traits
- Each gene is a set of instructions (code) to make a protein with a specific function
- Two copies of each gene
- DNA sequence (code) is made up of 4 bases
- "Genetics" refers to the DNA code



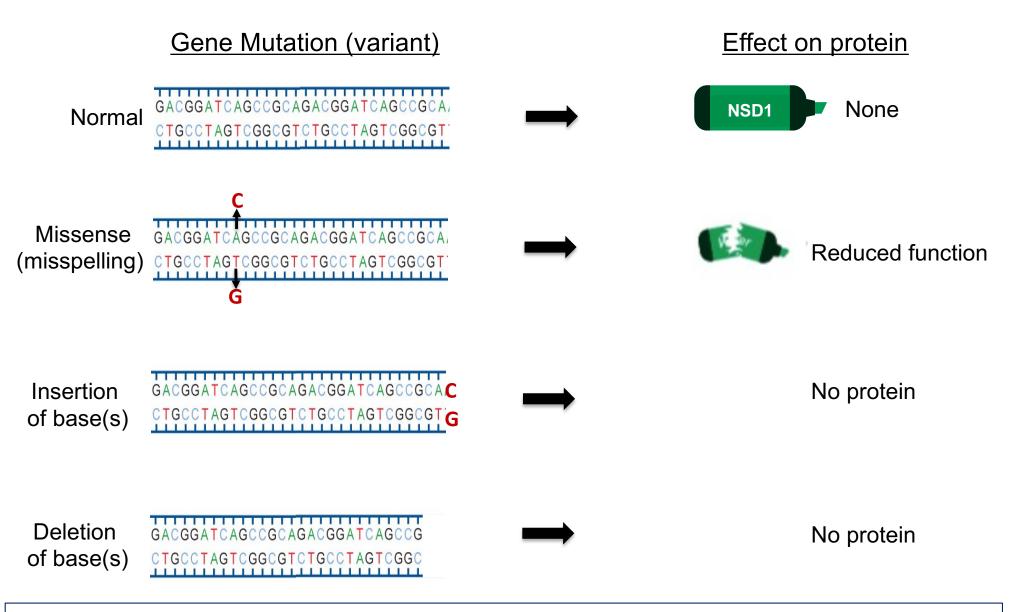
Genetic changes in the DNA code cause disease



Mutation 80% ariants)

- Spelling errors in the DNA code
- Can be:
 - Missing base(s)
 - Extra base(s)
 - Incorrect base(s)
- Result in:
 - production of a
 protein with altered
 function
 - no protein (from that copy)

Types of mutations (variants) and their effects



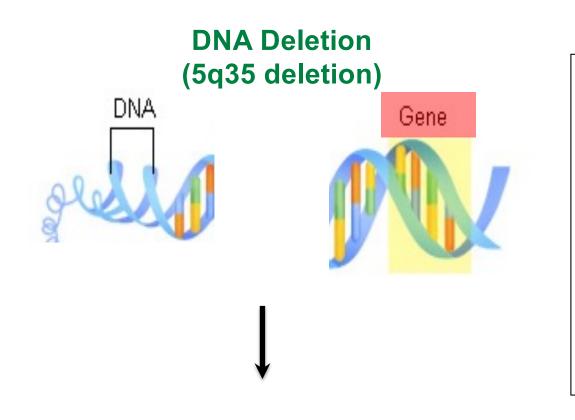
These are what we are referring to when we say Sotos syndrome due to a "mutation."

A different type of genetic change (a larger deletion) in the DNA code can cause Sotos syndrome

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No protein

This is what we are referring to when we say Sotos syndrome due to a "deletion."

Deletions

A single gene

Multiple genes

no protein from that

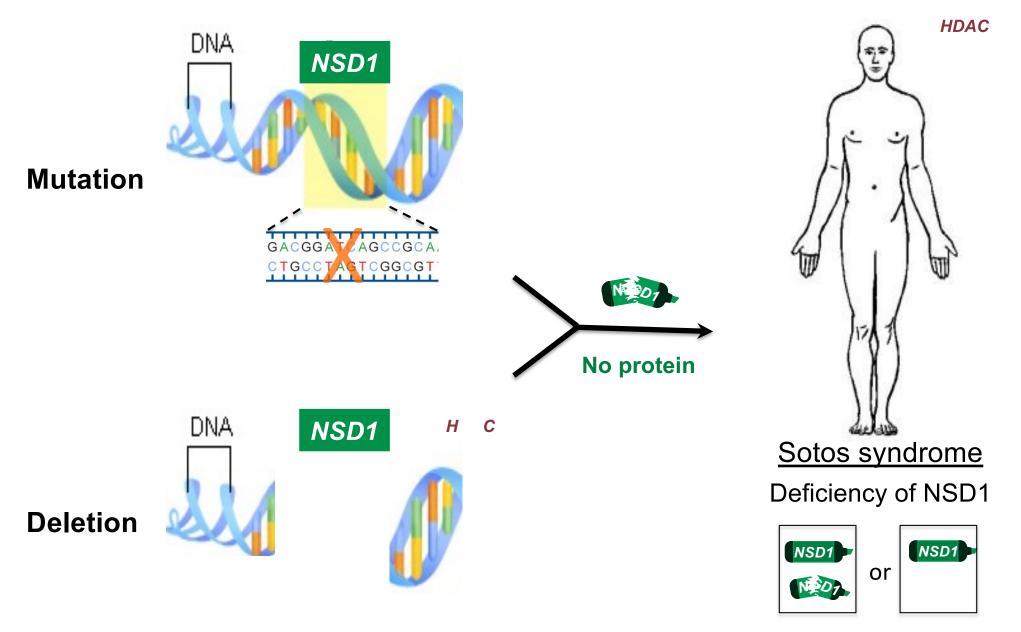
copy of the gene

Can include:

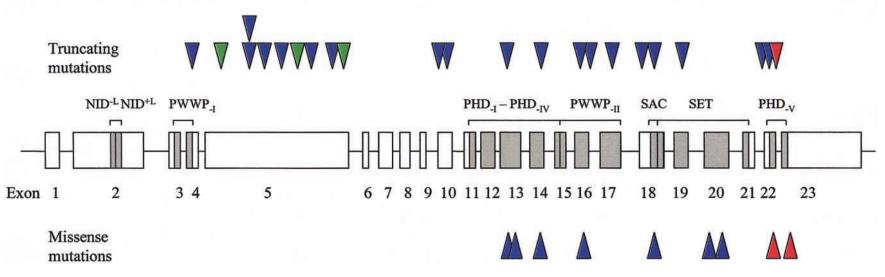
Result in

Missing pieces of DNA

Mutations or Deletions of the NSD1 gene cause Sotos syndrome



Sotos syndrome is caused by heterozygous *de novo* mutations in *NSD1*



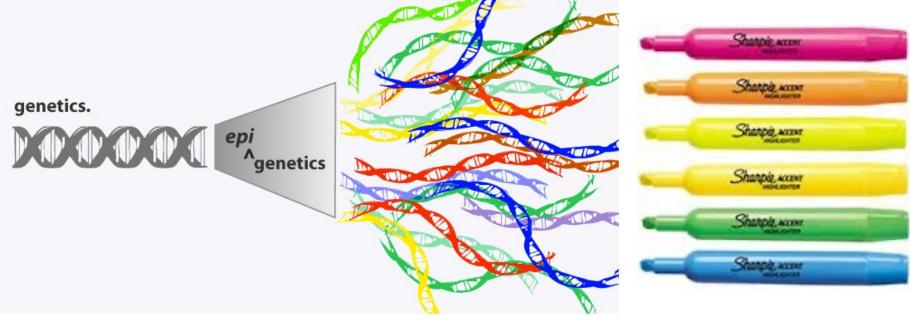
- Inherited in an autosomal dominant manner
- De novo, unique mutations predominate
- Loss of function (truncating) mutations occur throughout (top)
- Missense mutations occur in the functional domains (bottom)
- Mutational mechanism haploinsufficiency
- ~90% of individuals with features of Sotos syndrome have identifiable mutations in NSD1
 - 80% intragenic mutations
 - 10% whole gene deletions +/- additional genes
 - 10% unknown versus misdiagnosis

Summary 1

- DNA is the genetic material and contains genes
- Genes encode proteins that have particular functions in the body
- Genetic mutations are spelling errors in the DNA code that cause disease
- Deletions of genes cause disease because the gene is missing
- Mutations or deletions of NSD1 → Deficiency of NSD1
 → Sotos syndrome

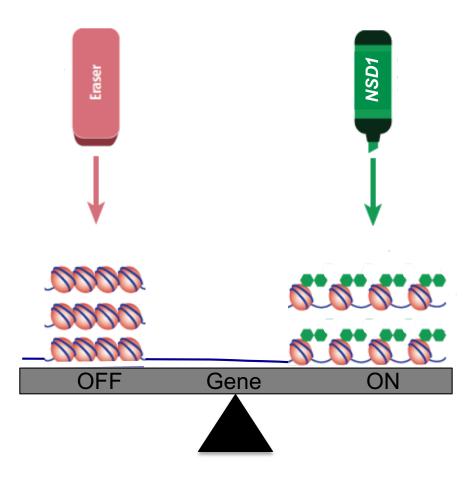
Sotos syndrome is a *Genetic* disorder with *Epigenetic* consequences

Epigenetic Machinery: The Genome's "Highlighter"



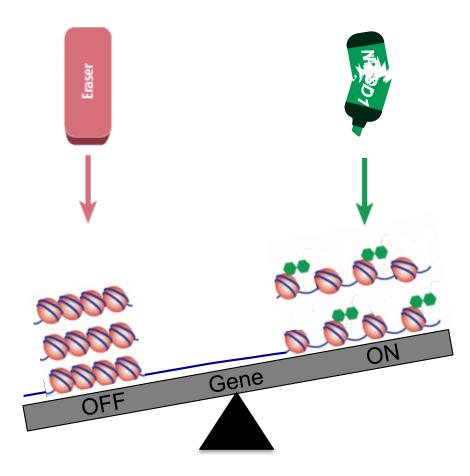
knowingneurons.files.wordpress.com

Epigenetics allows cells with the same genetic information to turn genes on and off differently Deficiency of NSD1 may cause Sotos syndrome by disrupting epigenetic marks and expression of other genes



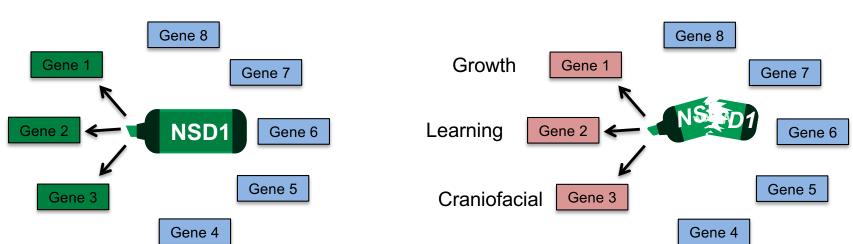
Adapted from Fahrner and Bjornsson, Ann Rev Gen & Hum Gen 2014

Deficiency of NSD1 may cause Sotos syndrome by disrupting epigenetic marks and expression of other genes



Adapted from Fahrner and Bjornsson, Ann Rev Gen & Hum Gen 2014

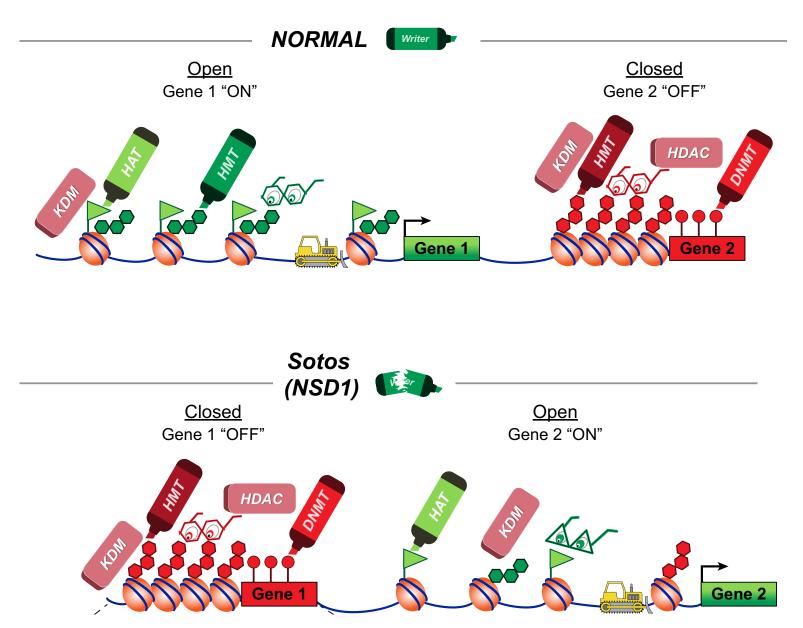
Deficiency of NSD1 may cause Sotos syndrome by disrupting epigenetic marks and expression of other genes



Properly functioning NSD1 writer

Sotos syndrome

Direct and indirect effects on target genes in Sotos syndrome



Fahrner and Bjornsson, Hum Molec Genet 2019

Summary 2

- Epigenetic marks "highlight" certain genes to be turned ON or OFF so that cells can function properly
- NSD1 is a writer of an epigenetic mark (histone methylation on H3K36)
- Deficiency of NSD1→ alters histone methylation → genes not turned on and off correctly
- NSD1 target genes determine the clinical features of Sotos syndrome

Common features in individuals with Sotos Syndrome

Modified, Tatton-Brown *et al. AJHG* 2005







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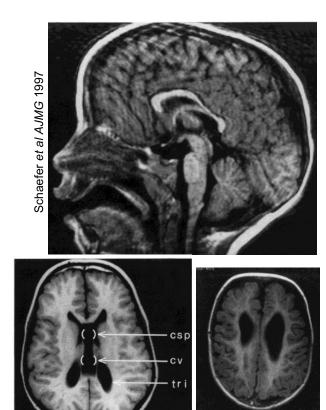
5q35 microdeletion

deletion exons 1-2

Overgrowth

Intellectual disability/developmental delay Characteristic facial features Characteristic behaviors Other findings

- Advanced bone age
- Hypotonia
- Joint laxity
- Scoliosis
- Seizures
- Eye findings
- Cardiac anomalies
- Renal anomalies

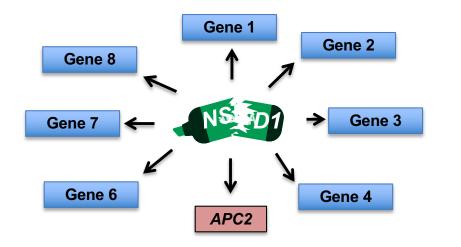


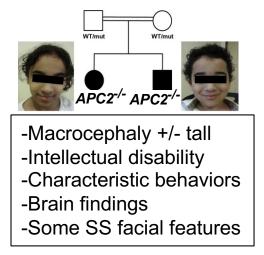
Characteristic brain MRI findings

- Thinning of corpus callosum
- Enlarged lateral ventricles
- Prominent subarachnoid spaces

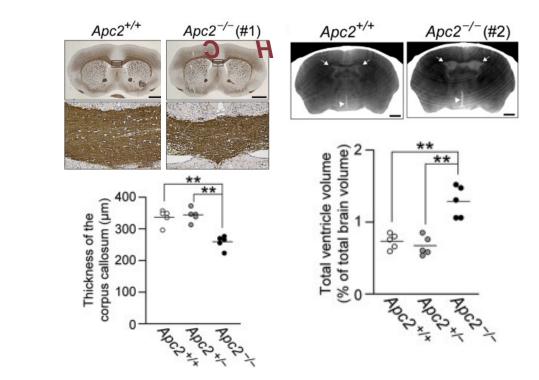
Recent, ongoing, and upcoming research on Sotos syndrome and related disorders

Deficiency of NSD1 may cause Sotos Syndrome by Disrupting Epigenetic Marks and Target Gene Expression

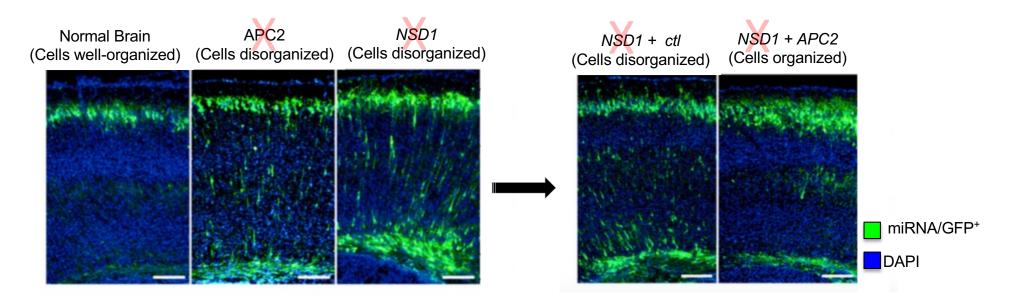




<u>APC2-/- mice</u> -Relative macrocephaly -Abnormal head shape -Impaired learning/ memory/behavior



APC2 is a target of NSD1 and is responsible for some features of Sotos syndrome



Conclusions

APC2 is target of NSD1 APC2 responsible for -Impaired learning -Abnormal behaviors -Macrocephaly -Brain malformations APC2 not responsible for other features of SS

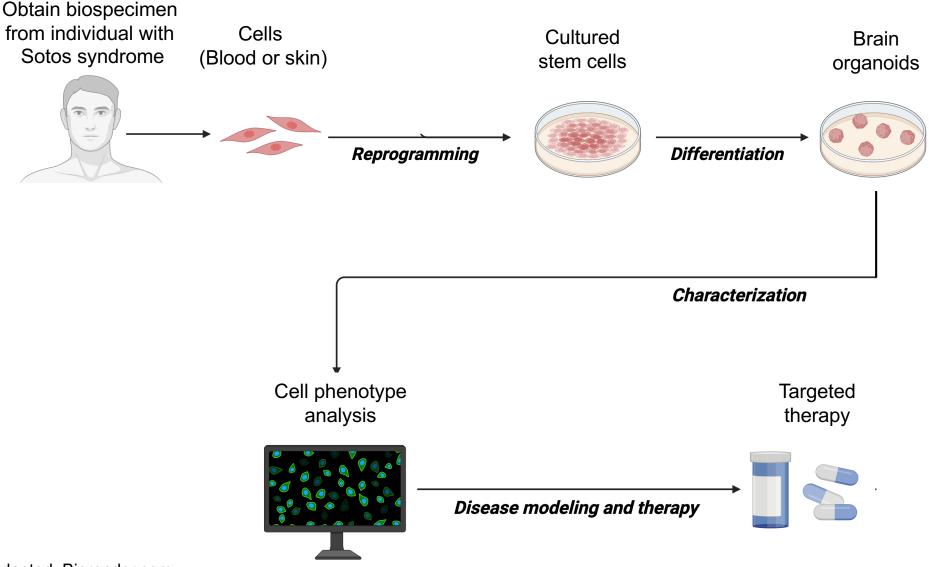
Elegant work but this is not a mouse model of Sotos syndrome because it does not target NSD1 (but rather APC2).

A newer mouse model of Sotos syndrome

- NSD1 expressed mostly in neurons (brain cells) in key brain regions
 - Cerebral cortex/hippocampus/subventricular zone
- Behavioral tests
 - Sotos syndrome mice showed altered social interactions with other mice
 - No difference in learning/memory
- Growth
 - No difference in body weight or brain size
 - Did not assess other growth parameters (body length, head size, bone size)
 (Oishi et al., Genes, Brain, & Behavior 2020)

Further studies of this mouse are needed. I am currently applying for funding to do this and to make a new mouse model of Sotos syndrome.

Human cell models of Sotos syndrome will be used to study disease mechanisms and test therapies

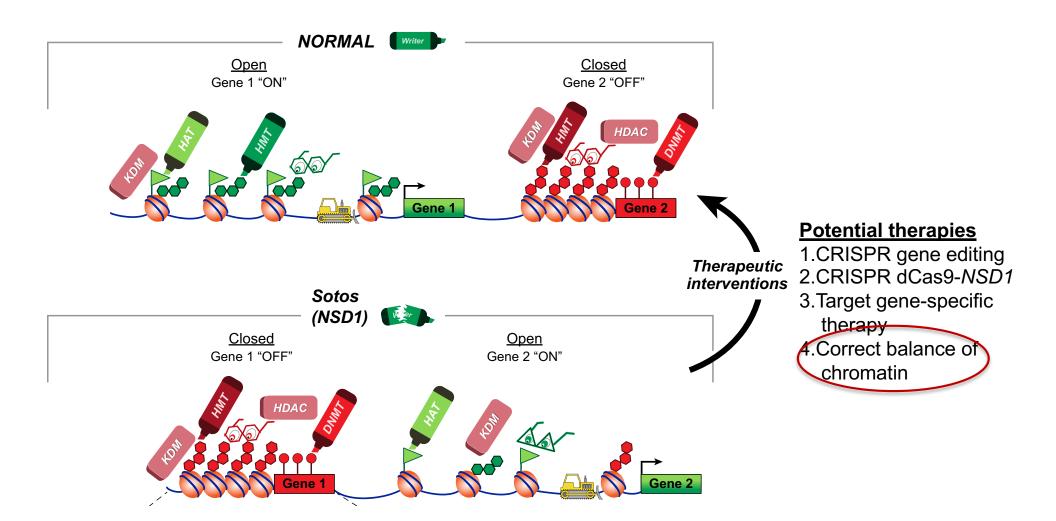


Adapted, Biorender.com

Why is this important?

- Understanding disorders at the molecular level is the first step in thinking about designing therapies
- Medications have to be tested in animal models (*and/or human cell models*) before being given to patients

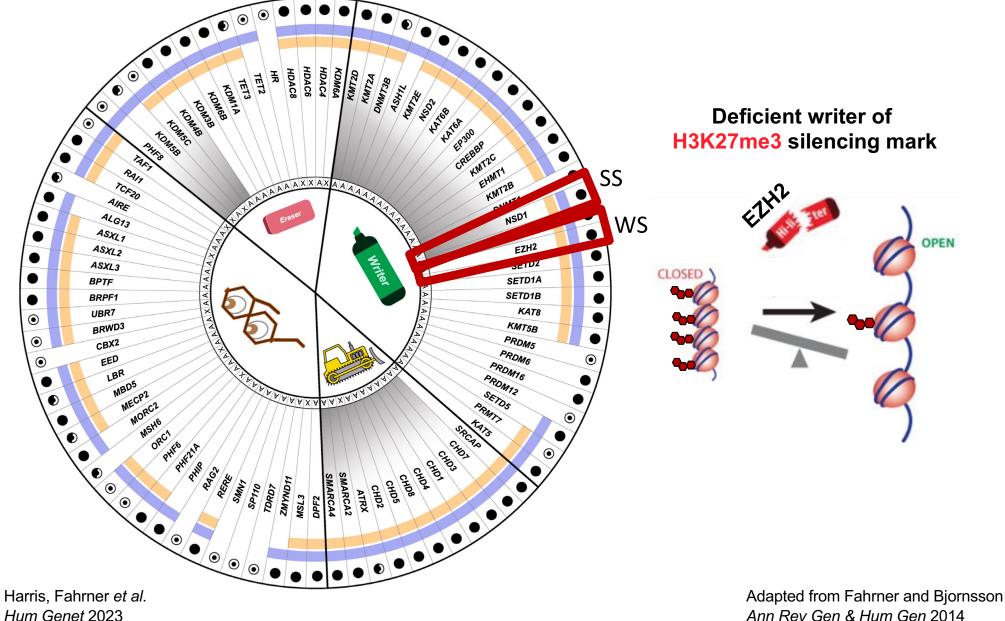
Potential future treatments for Sotos Syndrome



Correct the balance of chromatin as a therapeutic approach

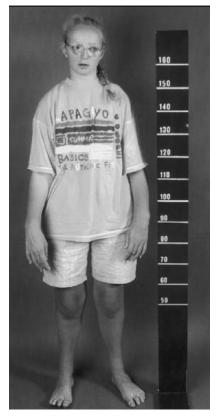
- Epigenetic (or chromatin) marks are more malleable than genetic (DNA sequence) changes
- Specific drugs targeting chromatin are already available and can be repurposed
- This type of approach has worked to improve learning/memory in another related disorder (KS1)

Weaver syndrome is closely related to Sotos syndrome and both disorders are in a larger group of Mendelian disorders of the epigenetic machinery



Ann Rev Gen & Hum Gen 2014

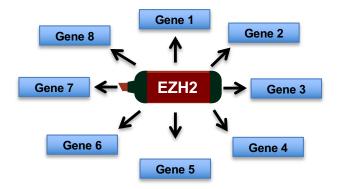
Weaver syndrome has features similar to Sotos syndrome



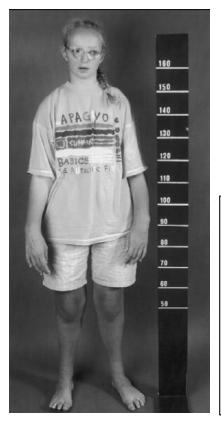
12.5 years



- Overgrowth
- Intellectual disability
- Characteristic facial features (distinct from Sotos)
- Other findings



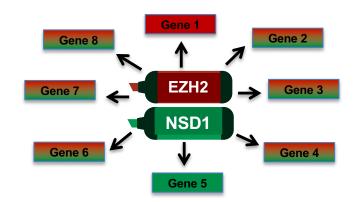
Research links Sotos and Weaver syndromes further at the molecular level: similar types of target genes



12.5 years



- Overgrowth
- Intellectual disability
- Characteristic facial features (distinct from Sotos)
- Other findings

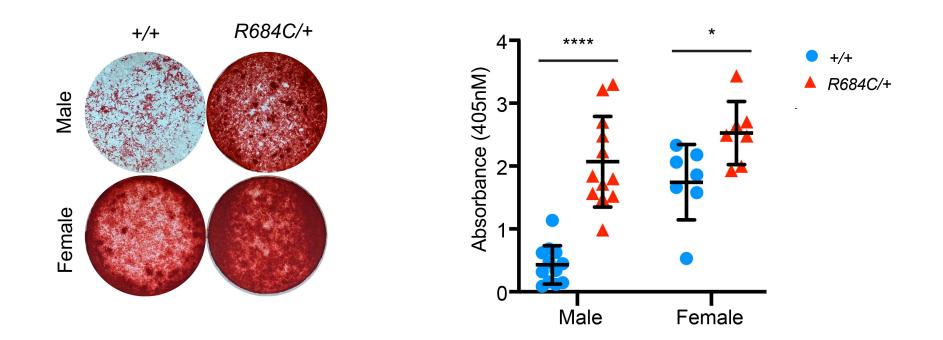


Weaver syndrome mice have skeletal overgrowth

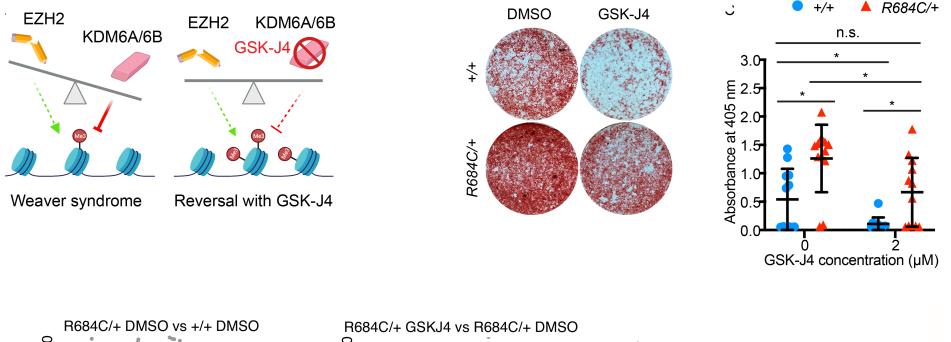
Female

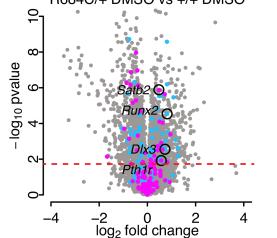
Female WS mice larger than controls WS mouse bones larger than controls 26-R684C/+ +/+ n.s. R684C/+ +/+3.0 24 Lissue area (mm²) 2.0 1.5 -0.1 Body weight (g) *** Male 22 20-18-Female 16 0.5 0.0 0. Male Male Female Sex Sex

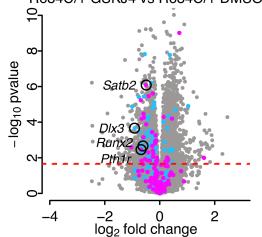
Skeletal overgrowth is due to overactive osteoblasts (cells that make bone)

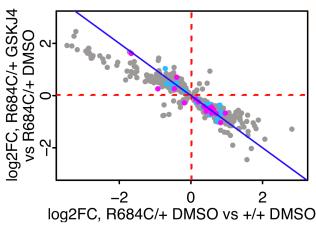


Inhibiting the opposing eraser corrects excess bone formation and gene expression









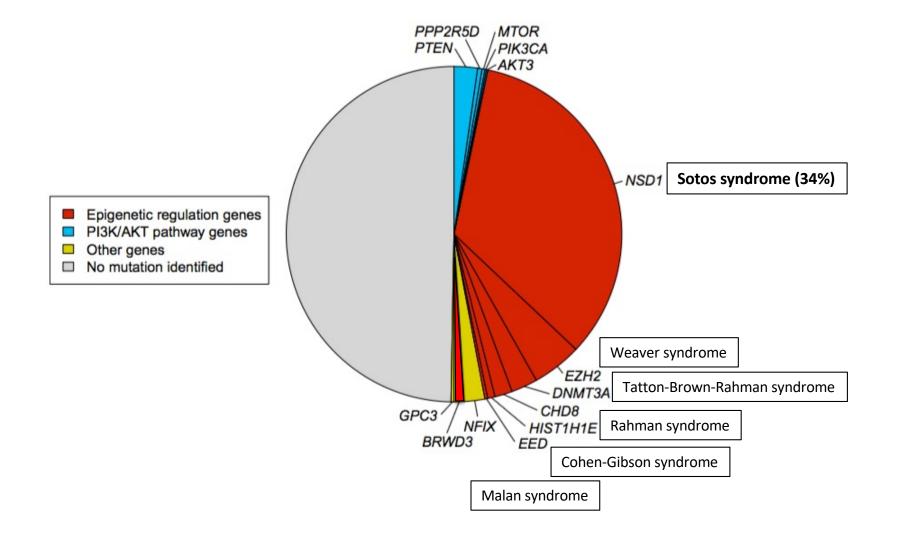
1,045 / 1,075 (97%) of shared genes reverse directionality!

Future research

- Test the ability of the epigenetic therapy GSKJ4 to treat overgrowth and neurobehavioral features in living Weaver (and Sotos) mice
- Generate human cellular models of Sotos (and Weaver) syndrome
 - Make stem cells (iPSCs) from blood samples taken from individuals with Sotos syndrome
 - Use stem cells to make neurons (brain cells) and bone cells to study disease mechanisms
 - Use human brain organoids ("mini brains" in a dish) to study disease mechanisms and potential treatments

What about individuals with features similar to Sotos syndrome but without *classic* Sotos or without *NSD1* mutations?

Many disorders overlap with Sotos syndrome and 45% are due to Mutations in Epigenetic Machinery Genes



Through our prior study, we have identified a cause for some individuals with Sotos-like findings

Malan syndrome (NFIX)



 Received: 28 March 2018
 Revised: 5 June 2018
 Accepted: 7 June 2018

 DOI: 10.1002/humu.23563
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RESEARCH ARTICLE

WILEY HUMAN GENOME

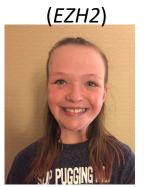
Further delineation of Malan syndrome

Manuela Priolo ^{1*} Denny Schanze ^{2*} Katrin Tatton-Brown ³ Paul A. Mulder ⁴
Jair Tenorio $^5 \mid Kreepa Kooblall^6 \mid Inés Hernández Acero^7 \mid Fowzan S. Alkuraya^8 \mid$
Pedro Arias ⁵ Laura Bernardini ⁹ Emilia K. Bijlsma ¹⁰ Trevor Cole ¹¹
Christine Coubes 12 \mid Irene Dapia 5 \mid Sally Davies 13 \mid Nataliya Di Donato 14 \mid
Nursel H. Elcioglu ¹⁵ Jill A. Fahrner ¹⁶ Alison Foster ¹⁷ Noelia García González ¹⁸
Ilka Huber 19 Maria Iascone 20 Ann-Sophie Kaiser 21 Arveen Kamath 22
Jan Liebelt 23 Sally Ann Lynch 24 Saskia M. Maas 25 Corrado Mammì 1
Inge B. Mathijssen ²⁵ Shane McKee ²⁶ Leonie A. Menke ²⁷ Ghayda M. Mirzaa ²⁸
Tara Montgomery ²⁹ Dorothee Neubauer ² Thomas E. Neumann ³⁰
Letizia Pintomalli 1 Maria Antonietta Pisanti 31 Astrid S. Plomp 25 Sue Price 32
Claire Salter 33 Fernando Santos-Simarro 5 Pierre Sarda 12 Mabel Segovia 34
Charles Shaw-Smith ³⁵ Sarah Smithson ³⁶ Mohnish Suri ³⁷ Rita Maria Valdez ³⁸
Arie Van Haeringen ¹⁰ Johanna M. Van Hagen ³⁹ Marcela Zollino ⁴⁰
Pablo Lapunzina ⁵ 🕴 Rajesh V. Thakker ⁶ 🕴 Martin Zenker ² 🗏 Raoul C. Hennekam ²⁷ 🝺

CHD8



Weaver syndrome



Other study updates -Many still undergoing analysis

We identified a new disorder: *TET3* deficiency (or Beck-Fahrner Syndrome)

REPORT

Delineation of a Human Mendelian Disorder of the DNA Demethylation Machinery: *TET3* Deficiency

David B. Beck,¹ Ana Petracovici,^{2,3,4} Chongsheng He,^{3,4,5} Hannah W. Moore,⁶ Raymond J. Louie,⁶ Muhammad Ansar,⁷ Sofia Douzgou,^{8,9} Sivagamy Sithambaram,⁹ Trudie Cottrell,⁹ Regie Lyn P. Santos-Cortez,¹⁰ Eloise J. Prijoles,⁶ Renee Bend,⁶ Boris Keren,¹¹ Cyril Mignot,^{11,12} Marie-Christine Nougues,¹³ Katrin Õunap,^{14,15} Tiia Reimand,^{14,15,16} Sander Pajusalu,^{14,15,17} Muhammad Zahid,⁷ Muhammad Arif Nadeem Saqib,¹⁸ Julien Buratti,¹¹ Eleanor G. Seaby,^{19,20} Kirsty McWalter,²¹ Aida Telegrafi,²¹ Dustin Baldridge,²² Marwan Shinawi,²² Suzanne M. Leal,²³ G. Bradley Schaefer,²⁴ Decore E. Storencop 6 Siddbarth Paples ^{8,9} Deborto Popacio ^{3,4}

and Jill A. Fahrner²

ARTICLE OPEN

Check for updates

Deficiency of *TET3* leads to a genome-wide DNA hypermethylation episignature in human whole blood

Michael A. Levy^{1,25}, David B. Beck ^{2,25}, Kay Metcalfe^{3,4}, Sofia Douzgou ^{3,4}, Sivagamy Sithambaram⁴, Trudie Cottrell⁴, Muhammad Ansar⁵, Jennifer Kerkhof ¹, Cyril Mignot⁶, Marie-Christine Nougues⁷, Boris Keren⁸, Hannah W. Moore⁹, Renske Oegema ¹⁰, Jacques C. Giltay¹⁰, Marleen Simon¹⁰, Richard H. van Jaarsveld ¹⁰, Jessica Bos¹¹, Mieke van Haelst¹¹, M. Mahdi Motazacker¹², Elles M. J. Boon¹³, Gijs W. E. Santen¹⁴, Claudia A. L. Ruivenkamp¹⁴, Marielle Alders¹⁵, Teresa Romeo Luperchio¹⁶, Leandros Boukas^{16,17}, Keri Ramsey¹⁸, Vinodh Narayanan ¹⁸, G. Bradley Schaefer¹⁹, Roberto Bonasio ^{20,21}, Kimberly F. Doheny^{16,22}, Roger E. Stevenson ¹⁹, Siddharth Banka^{3,4}, Bekim Sadikovic ^{1,23,25 ×} and Jill A. Fahrner ^{16,24 ×}

We initially identified 11 individuals from 8 families with Beck-Fahrner syndrome, and we now know of \sim 60 affected individuals.



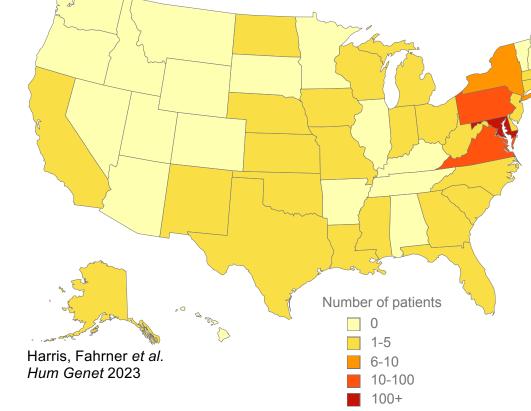


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SSSA

****Study participants and families**** **Baylor Hopkins Center for Mendelian Genomics** My lab/collaborators: Funding sources: NIH/NICHD Christine Gao WanYing Lin Maryland Stem Cell Research Leandros Boukas Fund The Hartwell Foundation Priyanka Kishwaha Ryan Riddle Johns Hopkins Catalyst Award Hans Bjornsson Kasper Hansen

The *multi-disciplinary* Epigenetics and Chromatin Clinic (ECC) at Johns Hopkins



History

- 2012: Founded by Dr. Hans Bjornsson (geneticist)
 & Ms. Carolyn Applegate (genetic counselor)
- * 2013: Dr. Jill Fahrner (geneticist) joined
- * 2014: Ms. Jacquelyn Britton (GC) joined
- 2018: Dr. Jacqueline Harris joined as neurologist/ NDD specialist, making it multidisciplinary
- 2020: Dr. Jill Fahrner became director
- * 2021: Dr. Rowena Ng joined (neuropsychologist)

For more information (research or clinic visit), please email: jfahrne1@jhmi.edu



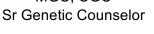
Jill Fahrner, MD, PhD Director



Jacqueline Harris, MD, MS Neurodevelopmental Neurologist



Jacquelyn Britton, MGC, CGC





Rowena Ng, PhD Neuropsychologist



Hans Bjornsson, MD, PhD Associate Director





Carolyn Applegate, Felicia Bartee MGC, CGC Sr Medical Sr Genetic Counselor Office Coordinator

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