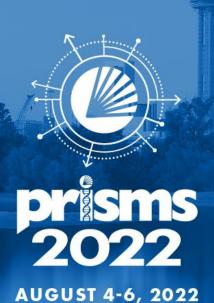


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Envisioning the Possibilities

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Cutting-Edge DNA Sequencing Technologies and Smith-Magenis Syndrome

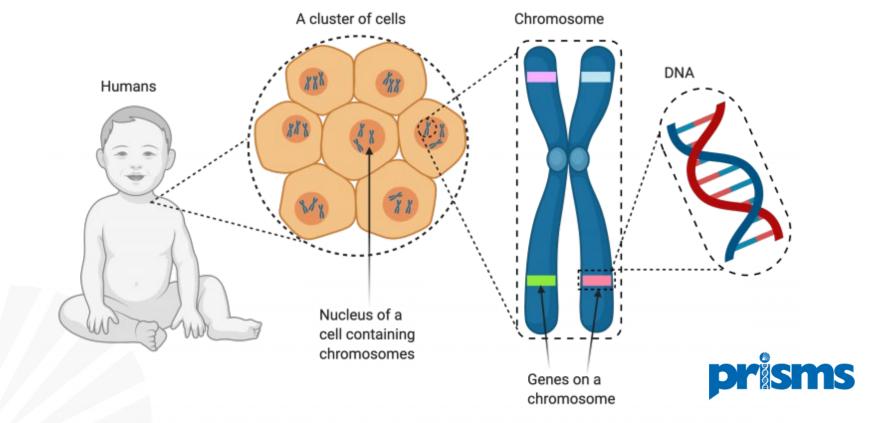
Zain Dardas Ph.D. Candidate Dr. James R. Lupski Laboratory Baylor College of Medicine Genetics and Genomics Graduate Program

August 6th, 2022

Baylor College of Medicine



What makes us up?

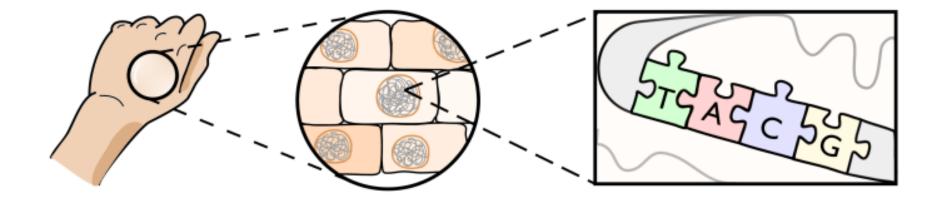


Fun Fact: DNA in a single cell is 2 meters long. DNA in all the cells of your body is enough to reach the moon 6000 times!





DNA is made up of four different molecules: A, T, C, G





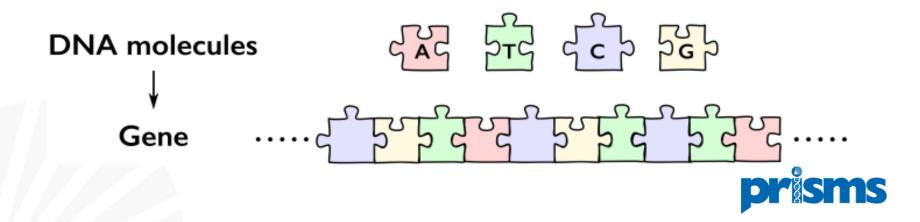
A,T,C,G- Our Body's Alphabets

Alphabet ↓ Word

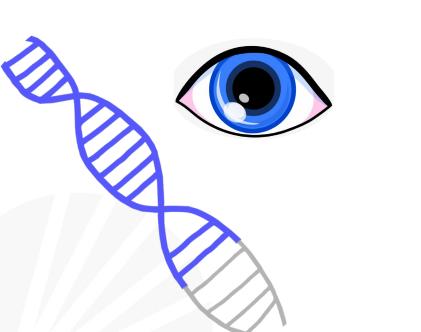


"silent" "listen" *These words use the same selection of

letters, but have different meanings



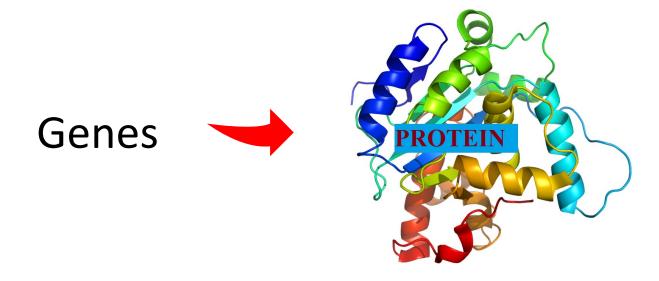
Genes are the instructions for life





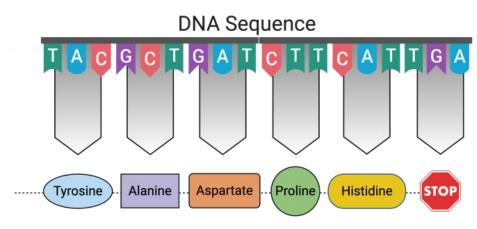






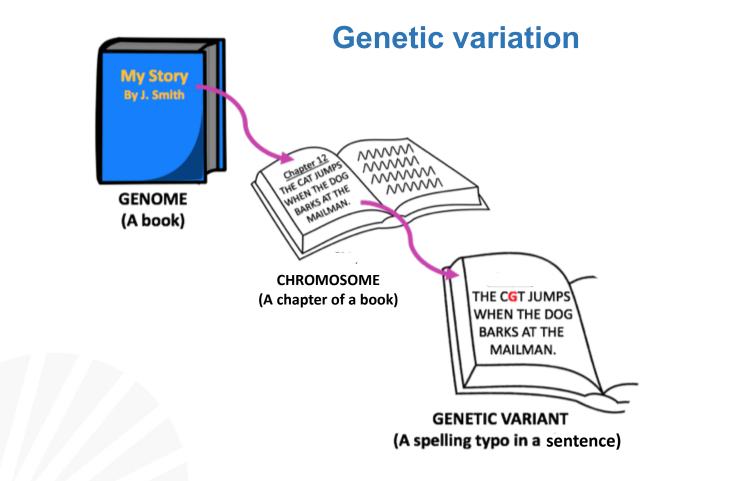


How do genes make proteins?



Protein Amino Acid sequence







NORMAL: "I LIKE TO SWIM IN THE OCEAN BUT / DO NOT LIKE TO SWIM IN THE POOL."

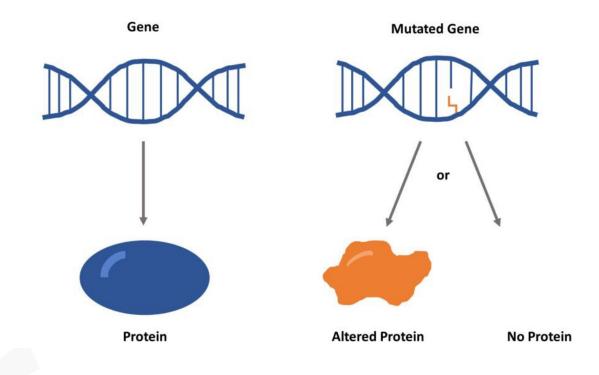
DELETION: "I LIKE TO SWIM IN THE POOL."

DUPLICATION: "I LIKE TO SWIM IN THE OCEAN BUT I DO NOT LIKE TO SWIM IN THE OCEAN BUT I DO NOT LIKE TO SWIM IN THE POOL."

Adapted from L. Potocki & J. R. Lupski



Genetic variation





Smith-Magenis Syndrome (SMS)



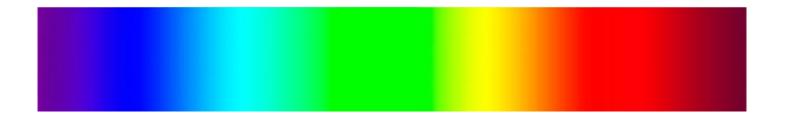
Ann Smith



Ellen Magenis



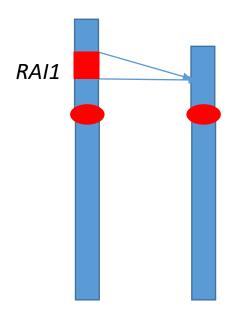
SMS has a wide clinical spectrum





The Genetics of SMS

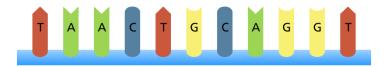
Chr.17 Microdeletion



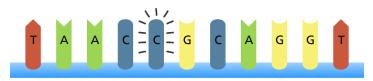


RAI1 Pathogenic Variants

Original sequence

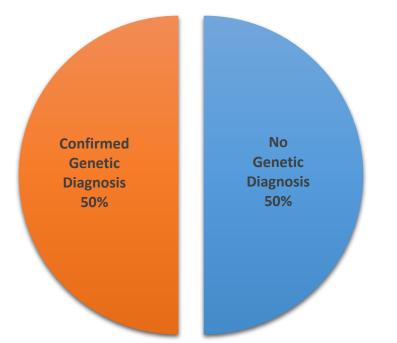


Base substitution





The genetic cause for 50% of individuals with suspected SMS is unknown!





Rinaldi et. al. Genes 2022, 13, 335.

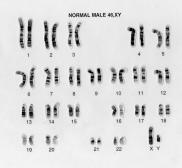
Our Goal

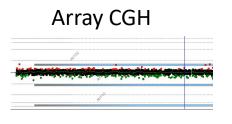
Further investigation of additional SMS associated variants and genes and their underlying mechanisms.

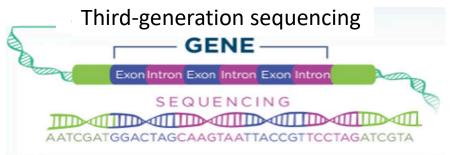




Karyotyping

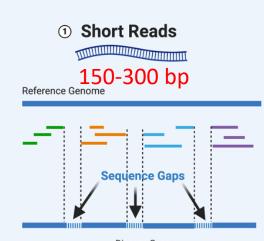








2nd generation VS. 3rd generation DNA sequencing

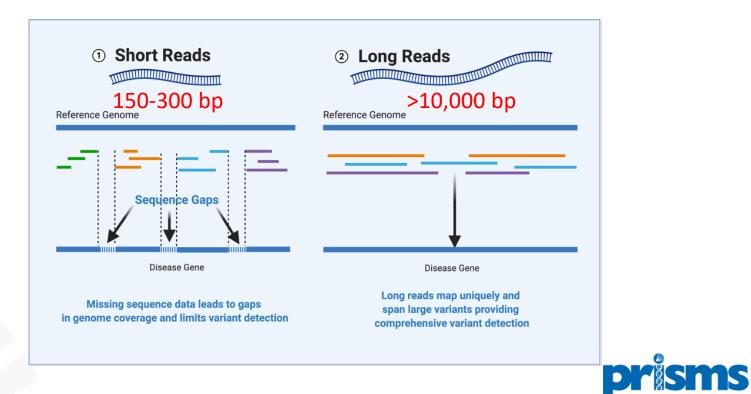


Disease Gene

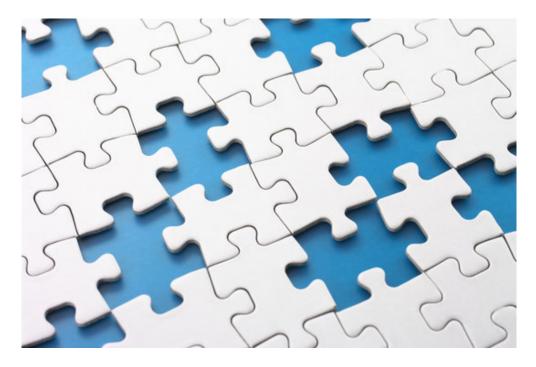
Missing sequence data leads to gaps in genome coverage and limits variant detection



2nd generation VS. 3rd generation DNA sequencing

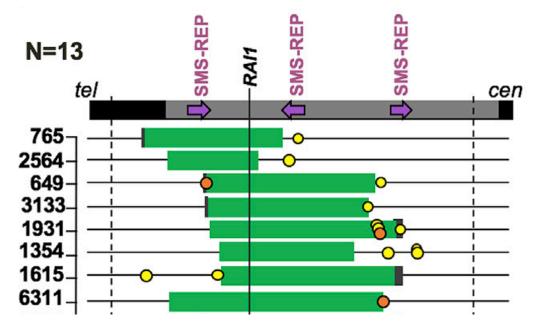


Third-generation sequencing can reveal additional genetic variants in SMS individuals





De novo variants accompany Chr17. microdeletion







Beck et al. Cell (2019) 176 (1310-1324).

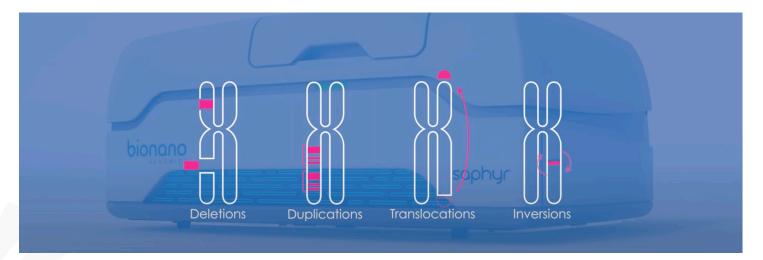
2/3 of the genome is highly repetitive





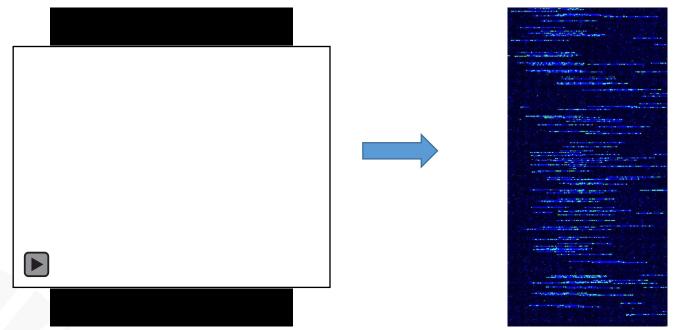
Optical Genome Mapping

• Identify structural variants ranging from 500 bp to whole chromosome lengths, with sensitivity as high as 99%.





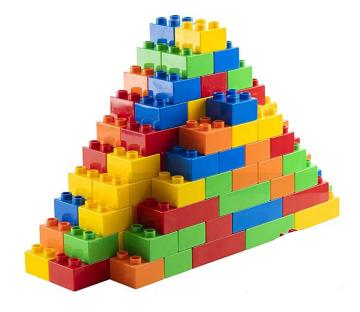
Optical Genome Mapping





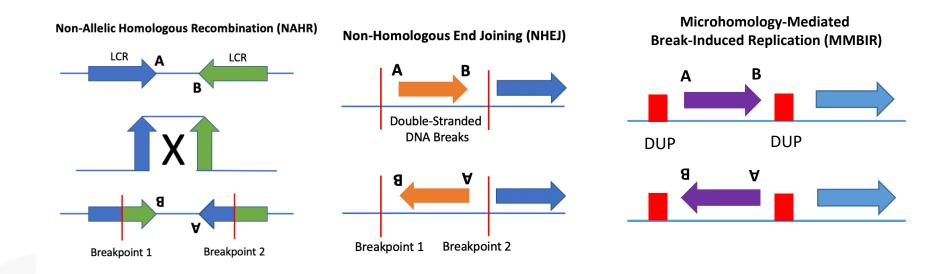
Third-generation sequencing can refine the final genomic architecture



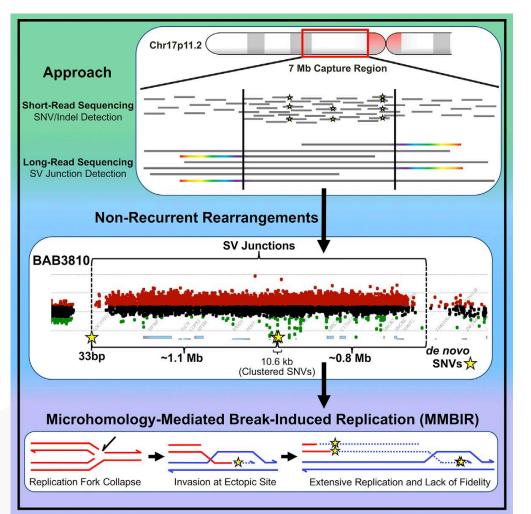




Third-generation sequencing can delineate the underlying mutational mechanism







Combining Technologies to Resolve genomic Structures and underlying mechanisms

Adapted from Beck *et al. Cell* (2019) *176* (1310-1324).



Key Takeaways

- Severity of the SMS phenotypes might be attributed to genetic variability.
- The exact way DNA molecules (A, T, C, G) are ordered is important.
- Advanced DNA sequencing allows scientists and doctors to work out the order of A, T, C, G so to understand the biological meaning for SMS diagnosis and potential treatment.



Thank you!

James R. Lupski

Christopher M. Grochowski Claudia Carvalho Jennifer Posey Haowei Du Dana Marafi Angad Jolly Chaofan Zhang Jawid M. Fatih Ruizhi Duan Shalini Jhangiani Fritz Sedlazeck **Betty Fernandini Marjorie Withers**





National Institute of General Medical Sciences



R35 NS105078 to JRL UM1 HG006542 to JRL Baylor College of Medicine

