An Epigenomic ID for a better Diagnosis





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La science pour la santé From science to health

ABSTRACT

Recent breakthroughs in sequencing technology have ushered in a new era of patient diagnosis. However, a significant number of cases continue to evade resolution due to elusive mutations and regulatory sequences. This project is dedicated to expediting diagnostics by constructing Epigenetic Identification (Epigenetic ID) maps for diseases, with a specific focus on growth-related disorders commonly associated with epigenetic regulator mutations.

We will rigorously analyze 41 lymphoblastoid cell lines and patient/control DNA samples using cutting-edge techniques, including ChIP-Seq, and Illumina EPIC arrays for methylome analysis, meticulously profiling five key epigenetic markers. These efforts will culminate in the development of Epigenetic IDs for nine growth-related pathologies across two distinct patient cohorts. This ambitious initiative promises to yield profound insights into the underlying epigenetic mechanisms, fostering the creation of functional hypotheses and innovative diagnostic methodologies.

This project represents a significant advancement in medical diagnostics, offering a comprehensive approach to the understanding, diagnosis, and management of complex pathologies. It will refine our grasp of disease-related epigenetic mechanisms and potentially pave the way for further research. Epigenetic IDs hold the promise of reshaping our approach to diseases, ultimately benefiting patients and the broader healthcare community.

BACKGROUND

METHODOLOGY





Epigenetic modifications and their effects on gene expression



Dominant
Recessive
A Autonomol
A Autonomol
A Autonomol

X X-linked A Autosomal

ORPHAcode	Disease	Clinical signs			Growth	
ORPHA:2554	Meier-Gorlin syndrome	Very short stature, Patella aplasia/hypoplasia, small ears, microcephaly, Cryptorchidism			Glowin	
ORPHA:138	Charge syndrome	Cup-shaped ears, coloboma, delayed puberty, hearing loss, short stature, Choanal atresia, heart defects				
ORPHA:404440	Intellectual disability-facial dysmorphism syndrome due to SETD5 haploinsufficiency	llectual disability-facial ism syndrome due to SETD5 haploinsufficiency			Dwarfism	
To come	Heyn-Sproul-Jackson syndrome	Short stature, Microcephaly, Impaired intellectual development, Short broad phalanges		nt 1		
ORPHA:821	Sotos syndrome	Tall stature, macrocephaly, variable intellectual impairment		Coho		
ORPHA:404443	Tatton-Brown-Rahman syndrome	Tall stature, Large head circumference, Narrow palpebral fissures, Hypermobile joints, Intellectual disability, mild to moderate			Overgrowth	
ORPHA: 599082	Snijders Blok-Campeau syndrome Intellectual impairment, macrocephaly, dysmorphic facies				Not related to gr	
OMIM# 615032	Intellectual developmental disorder with autism and macrocephaly Autism, macrocephaly, tall stature, distinct facial features					
	Alpha-thalassemia-X-linked intellectual	intellectual disability, facial dysmorphism, genital		Cohort 2	Dwarfism	
ORPHA:847	disability syndrome	abnormalities, alpha thalassemia, Ambiguous genitalia, autism			Overgrowth	

	Growth	Disease	Genes	# Patients	#LCL
Cohort 1		Meier-Gorlin syndrome	ORC1, ORC4, ORC6, CDC6, CDC45, CDT1	3	2
	Dwarfism	Charge syndrome	CHD7	3	1
		Intellectual disability-facial dysmorphism syndrome due to SETD5 haploinsufficiency	SETD5	3	
		Heyn-Sproul-Jackson syndrome	DNMT3A	3	
	Overgrowth	Sotos syndrome, Sotos-like syndrome	(NSD1) SETD2	3	2
		Tatton-Brown-Rahman syndrome	DMNT3A	3	
		Snijders Blok-Campeau syndrome	CHD3	3	
		Intellectual developmental disorder with autism and macrocephaly	CHD8	3	
	Not related to growth	Alpha-thalassemia-X-linked intellectual disability syndrome	ATRX	3	2
	Controls	healthy donors		6	4
Cohort 2	Dwarfism	Unknown		4	1
	Overgrowth	Unknown		4	3





Motif for TF B

ATAC seq protocol

Conditions analyzed and epigenetic regulator genes involved



- Is there an epigenomic signature for dwarfism vs overgrowth syndromes ?
- Is epigenome characterisation (Epi ID) a powerful tool to improve diagnostic yield ?

1 3 3				
whole blood analysis aimed at confirming the results already published in literature	establishment of patient derived LCLs and methylome comparison to whole blood	Test of 6 parameters on the first cohort of patients: • H3K4me3 • H3K27me3 • H3K9me3 • H3K36me3 • Chromatin accessibility • DNA methylation	Epi-ID development from data acquired on cohort 1 patients with known mutations in epigenetic machinery	Test of same parameters and validate epigenome ID diagnostic capabilities on cohort 2 patients with no known mutations in the involved genes

CTL, Kabuki, Sotos-like



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