

DU GÈNE AU TRAITEMENT : RECHERCHE TRANSLATIONNELLE ET NEUROPATHIES PÉRIPHÉRIQUES HÉRÉDITAIRES



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Group leader « Genetics and Pathophysiology of Inherited Peripheral
Neuropathies »

Team



NEUROMYOLOGIE
TRANSLATIONNELLE

INHERITED PERIPHERAL NEUROPATHIES



Group of hereditary diseases affecting **the peripheral nervous system**

- **Charcot-Marie-Tooth disease** (motor and sensory)
- Pure motor forms (« spinal » CMT or dCMT)
- Pure sensitive forms (HSN, HSAN)

Charcot-Marie-Tooth disease

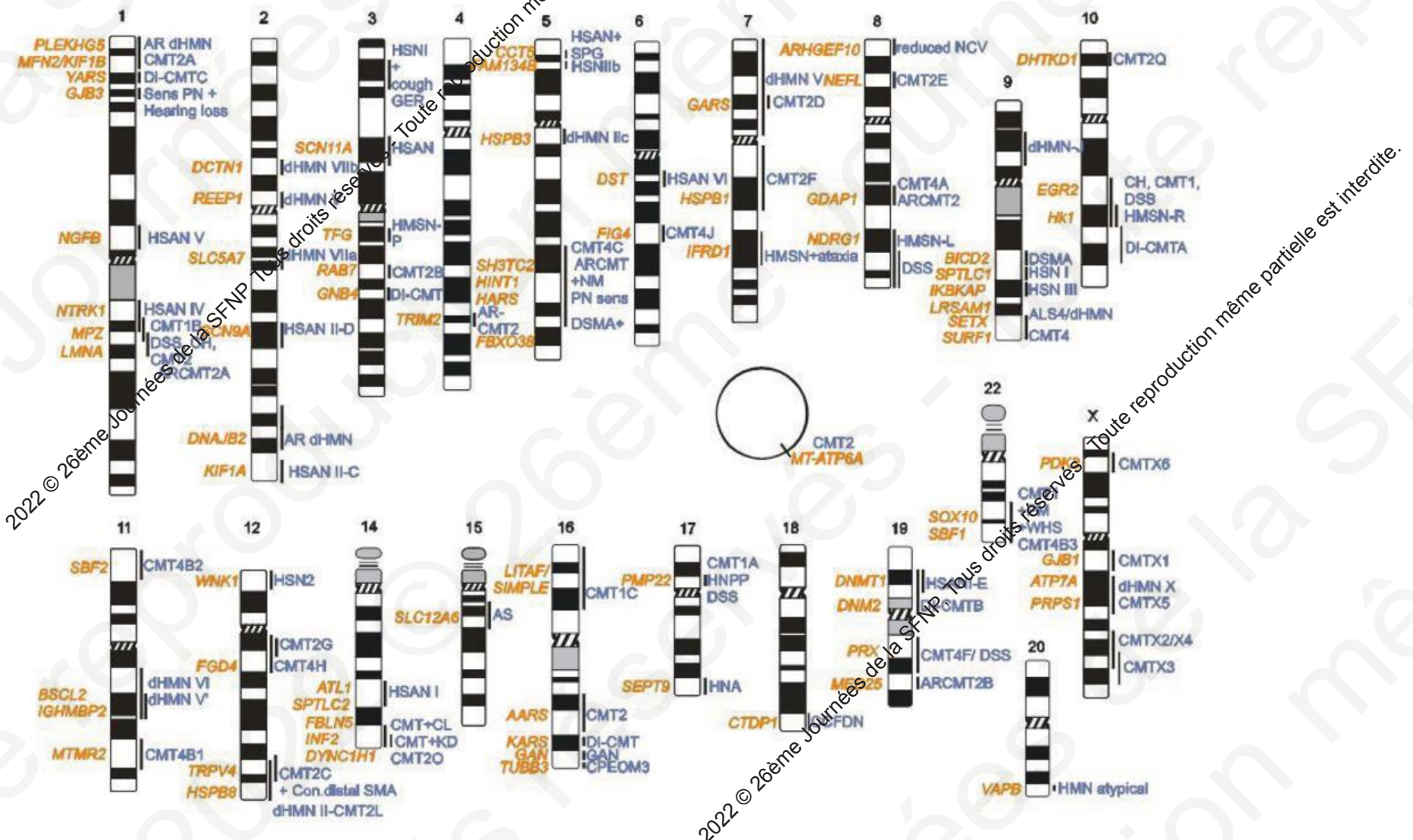
One of the most common inherited neurological disorders → prevalence: **1/2500**

- Progressive distal muscular **weakness and atrophy** beginning at the lower limbs and slowly progressing to the upper limbs
- Feet and hand **deformations**
- cramps
- scoliosis
- variable loss of sensitivity
- hypo- or areflexia



Charcot-Marie-Tooth disease

Genetic Heterogeneity: 100 genes described to date



D'après Timmerman et al., *Genes* 2014, 5, 13-32

MÉCANISMES PHYSIOPATHOLOGIQUES COMPLEXES

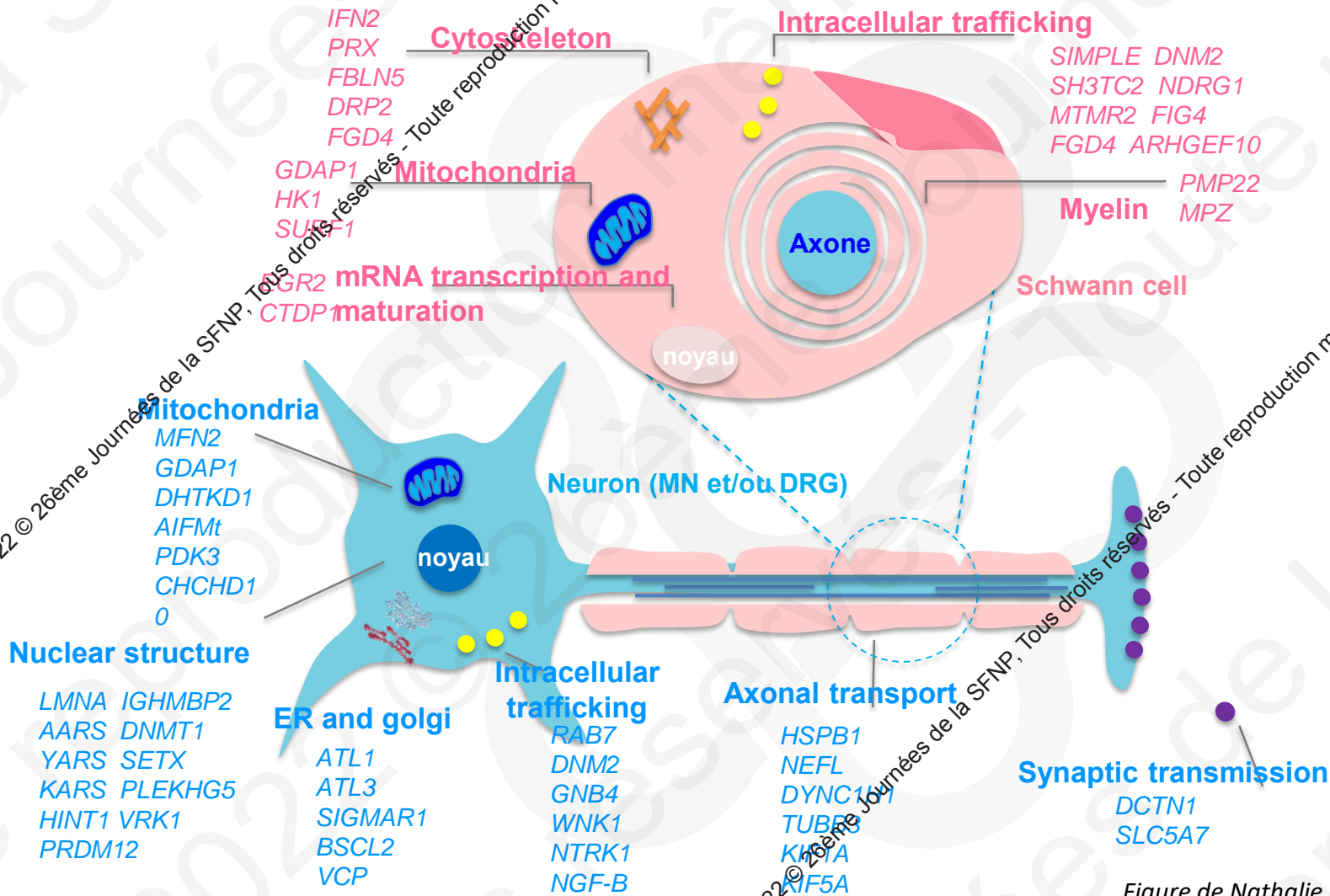
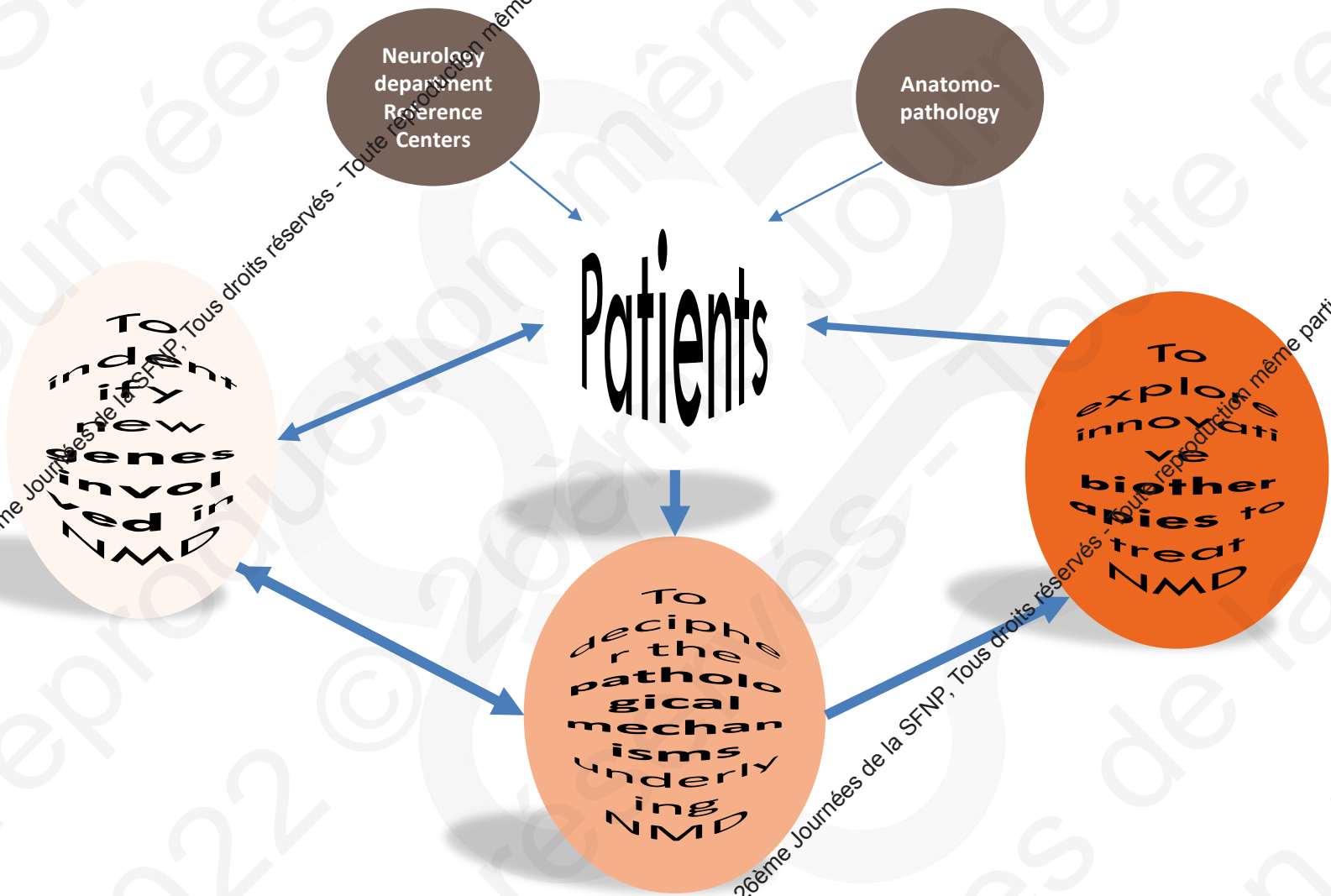


Figure de Nathalie Bernard-Marissal

RECHERCHE TRANSLATIONNELLE



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OBJECTIFS



- Better understand the genetic bases of Inherited Peripheral Neuropathies to improve diagnosis



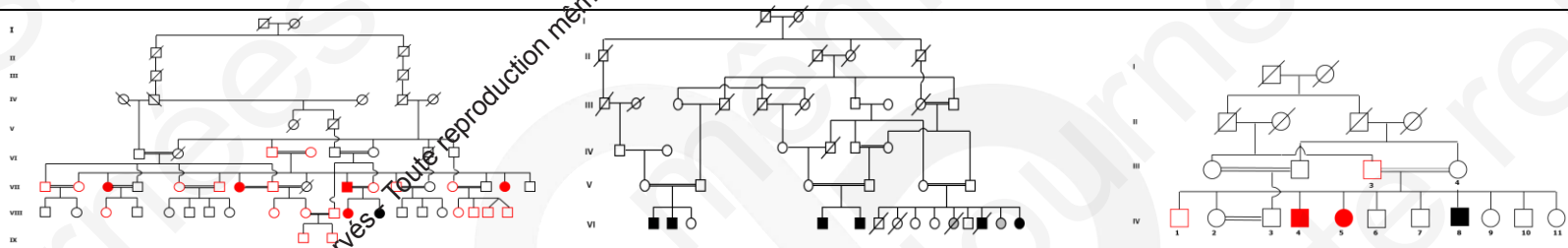
- Understand the pathomechanisms underlying those diseases by studying the role of the defective proteins in the Peripheral Nervous System and discover new actors of the PNS



- Propose and develop biotherapies to improve the treatments of these diseases



Identification de nouveaux gènes mutés dans les IPNs/CMT



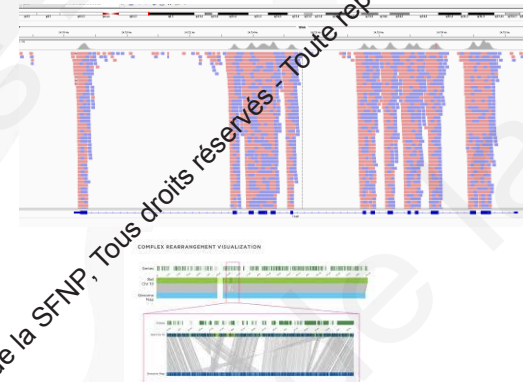
- Large consanguineous families with peripheral nerve diseases
- Autosomal recessive transmission
- Collaboration network with geneticists from the Mediterranean area and the Middle East

Methodology

- Targeted sequencing
- WES, WGS sequencing of trios, quattors..
- Identity by Descent analysis of WES and WGS for SNV
- WGS-based linkage analysis combined with variant analysis of WGS data
- CNV detection on WES, WGS data or by using BioNano Genomics
- Study of the genetic “burden”

Objectives

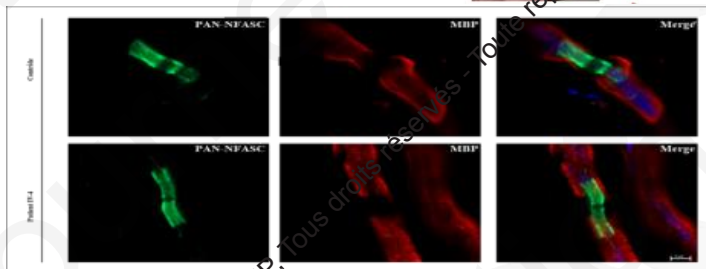
- **Contribute to improve diagnosis strategies**
- Identify new players in muscle and peripheral nerves
- Study the underlying pathomechanisms





Quels modèles?

Tissus de patients



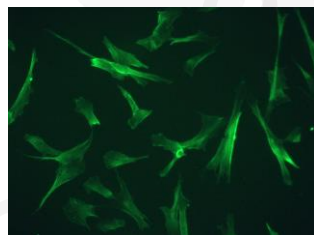
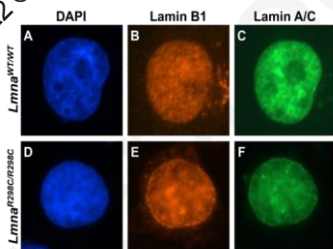
Fibres myélinisées de peau glabre

Modèles animaux



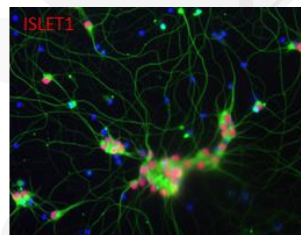
Modèles *in vitro*

Cellules de patients



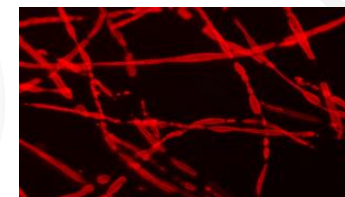
Lignées lymphoblastoïdes

Fibroblastes



Neurones moteurs ou sensitifs dérivés d'hiPSC +/- coculture avec des myoblasts

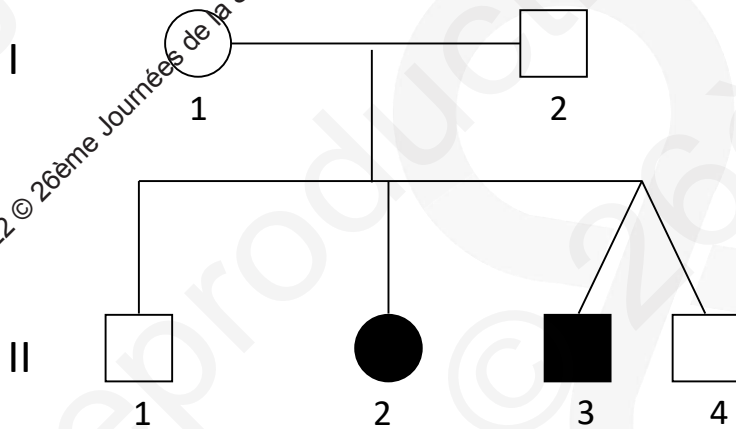
Modèles cellulaires dérivés de modèles animaux



SC/DRG cocultures



- Non consanguineous Lebanese family
- Two affected sibs
- Referred to me as affected with **dHMN+ Upper motor Neuron disease signs**
- Onset: second decade
- Slowly progressive



Clinical examination

- Motor deficit of the four limbs with distal predominance
- Muscle atrophy of hands and legs
- Proprioception and vibration sensation deficit distally bilaterally
- **Hyperreflexia throughout**
- **Babinski signs bilaterally**
- Normal cranial nerves

Electrophysiology

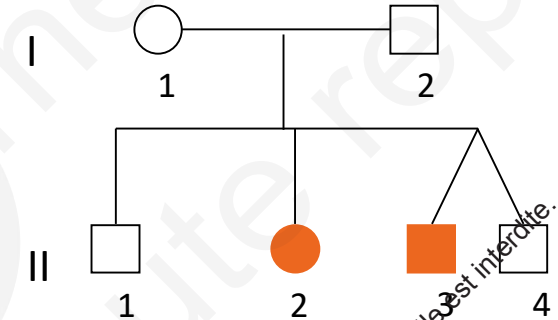
EMG: axonal peripheral neuropathy, motor predominant

GENETIC ANALYSES

Variant segregation and filtering



After alignment to the human genome (hg19), we found:
20911 SNPs in patient II.2
21438 SNPs in her brother II.3



Autosomal recessive transmission
No Consanguinity



« Compound » heterozygous mutations
shared by the 2 patients

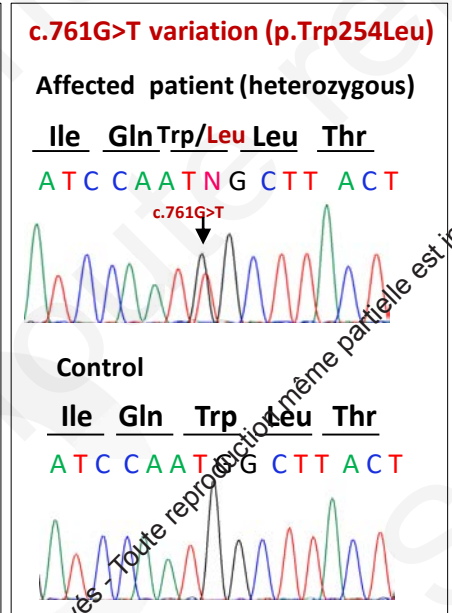
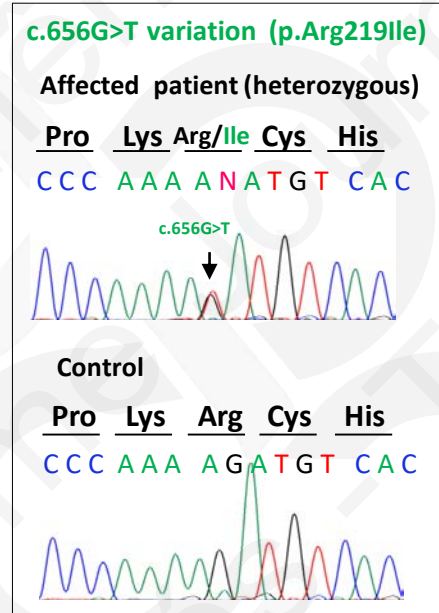
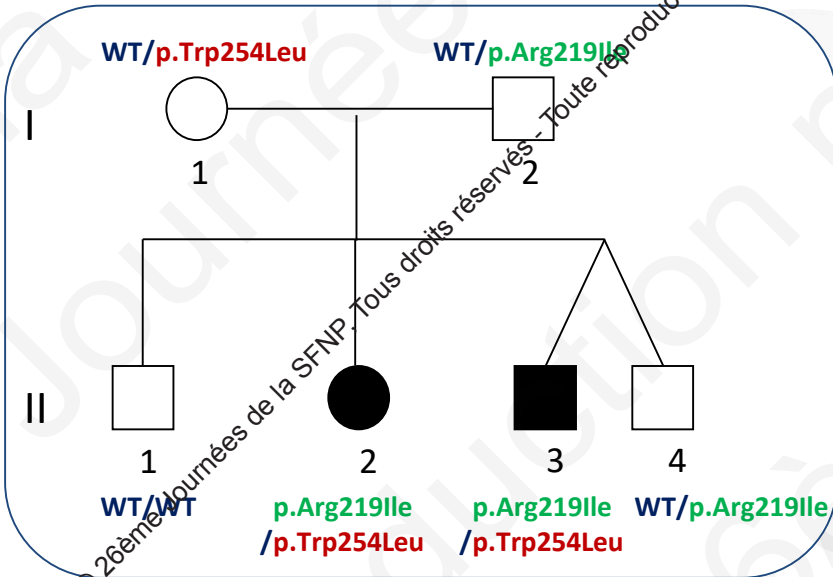


- VarAFT: Variant Annotation and Filter Tool. In house software tool developed by Christophe Beroud's team (U 1251, MMG)
- Desvignes et al. 2018. **VarAFT: a variant annotation and filtration system for human next generation sequencing data.** [Nucleic Acids Res](#) doi: 10.1093/nar/gky471 [Epub ahead of print]
- <https://varaft.eu/download.php>

Identification of mutations in VRK1



VRK1 (NM_003384) : c.656G>T (p.Arg219Ile) et c.761G>T (p.Trp254Leu)



	c.656G>T (p.Arg219Ile)	c.761G>T (p.Trp254Leu)	
<i>Homo sapiens</i>	214 KEDPKRCHDGTIEFTSIDAHNGVAPSRRGDLEILGYCMIQWLTGHLPW--EDNLKDPKYVRDSKIRYREN-----	281	281
<i>Bos taurus</i>	214 KEDPKRCHDGTVEFTSIDAHNGVAPSRRGDLEILGYCMIQWLSGHLPW--EDNLKDPNYVRDSKIRYREN-----	281	281
<i>Mus musculus</i>	214 KEDPKRCHDGTLEFTSIDAHNGVAPSRRGDLEILGYCMIQWLSGCLPW--EDNLKDPNYVRDSKIRYRDN-----	281	281
<i>Rattus norvegicus</i>	214 KEDPKRCHDGTLEFTSIDAHNGVAPSRRGVLEILGYCMIQWLSGCLPW--EDNLKDPNYVRQSKIRYRDN-----	281	281
<i>Gallus gallus</i>	213 KEDPKRCHDGTIEYTSIDAHNGVAPSRRGDLEILGYCMVHWLSGHLPW--EDNLKDPNFVRDSKIRCRDN-----	280	280
<i>Danio rerio</i>	215 KEDPKRCHDGTIEFTSIDAHNGVSPSRADLEIMGYCMIQWLC SRLPW--EDLQDPLVVRDSKLCRCRN-----	282	282
<i>Xenopus tropicalis</i>	214 KEDPRKCHNGTIEFTSIDAHNGVSPSRRGDLEILGYCMIQWLCGRLPW--EDNLGDANYVTNSKIRYGD-----	281	281
<i>D. melanogaster</i>	225 -----HNGTIEYTSRDAHLGV-PTRRADLEILGYNLIEWLGAELPWVTKLLAVPPKVKAKEAFMDN-----	286	286
<i>C. elegans</i>	201 KPDKKRAHNGTICIFSTDAHRGNNSFRGDIEILAYNLMMWATGTLPMW--ALESSPEKVFDAKQFIAG-----	268	268
<i>S. cerevisiae</i>	174 -----TGTARYASVNTHLGIEQSRDDLESGLVLIYFCKGSLPW--QGLKATTKKQYDRIMEKKNYSVETLCSG-----	243	243

- ✓ Absent from frequency datasets (gnomAD, EXAC, base locale) and from a cohort of de 300 lebanese
- ✓ Predicted Pathogenic

VRK1: Vaccinia-related kinase 1

Fonctions cellulaires



Sérine-thréonine kinase

Prolifération cellulaire
et tumorigénèse

Régulation
transcriptionnelle

Régulation du cycle
cellulaire

Peu de données sur son rôle dans les neurones et le SN : Knock-down de *vrk1* *in utero* dans le cerveau d'embryons de souris →

rôle dans la migration neuronale, dans prolifération des progéniteurs neuronaux et dans le guidage axonal (Vinograd *et al*; 2015 et 2018)

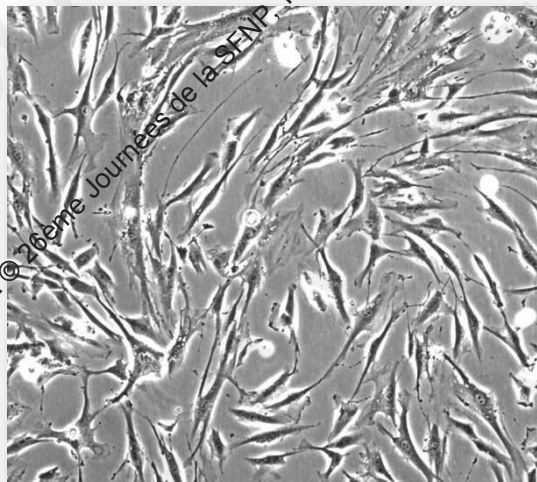
VRK1: Vaccinia-related kinase 1

Etudes fonctionnelles

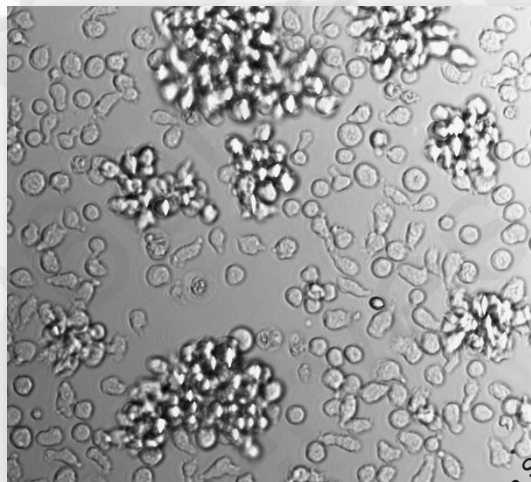


Modèles cellulaires issus de patients

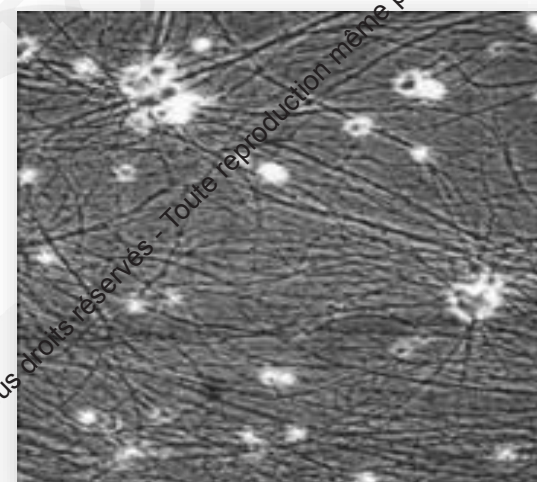
Fibroblastes



Lymphocytes



Motoneurones dérivés d'iPSC

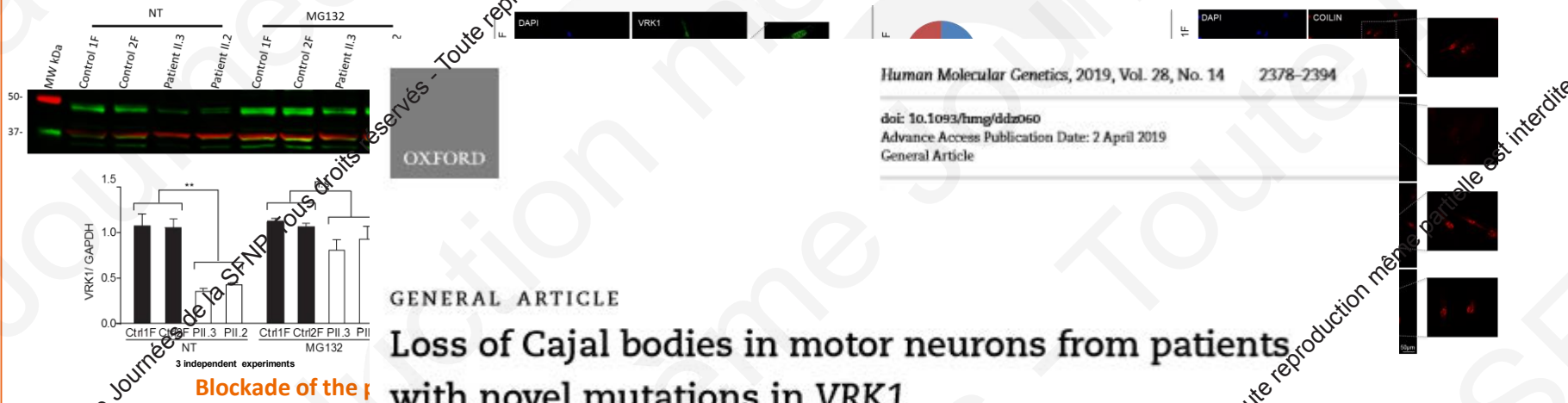


Protocole de différenciation
développé par Khalil RIHAN



Novel mutations in VRK1 in a new form of CMT with upper motor neuron signs

1. In patient's fibroblasts: decrease of VRK1 levels in patients' cells is due to post-translational defects and VRK1 depletion in patients' fibroblasts leads to reduced coilin levels by facilitating its proteasomal degradation.



GENERAL ARTICLE

Loss of Cajal bodies in motor neurons from patients with novel mutations in VRK1

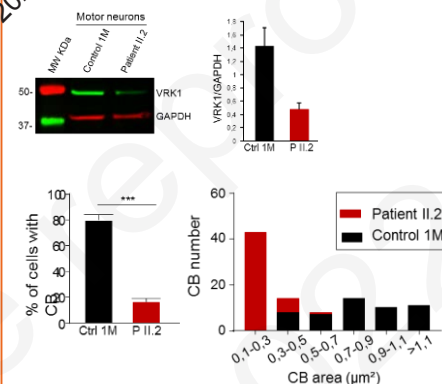
Lara El-Bazzal¹, Khalil Rihan¹, Nathalie Bernard-Marissal¹, Christie Castro¹, Eliane Chouery-Khoury², Jean-Pierre Desvignes¹, Alexandre Atlanson¹, Karine Bertaux³, Salam Koussa⁴, Nicolas Lévy^{1,5}, Marc Bartoloni⁶, André Mégarbané^{6,7}, Rosette Jabbour⁸ and Valérie Delague^{1,†}

hiPSC-derived MNs:

patient's motor signs. These signs are

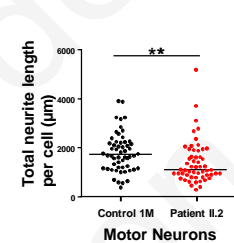
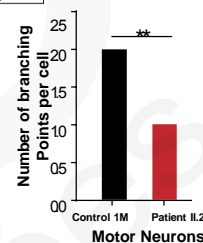
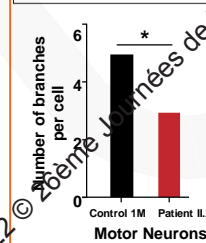
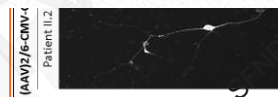
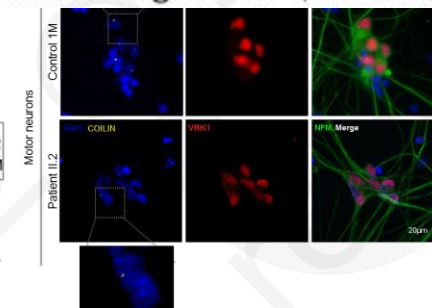
dependent axonopathy affecting both lower and upper motor neurons in patients.

2. In patients' hiPSC-derived Motor Neurons: the nucleus lead to disassembly of



VRK1 is necessary for Cajal Bodies assembly in hiPSC-derived MNs

3 independent experiments



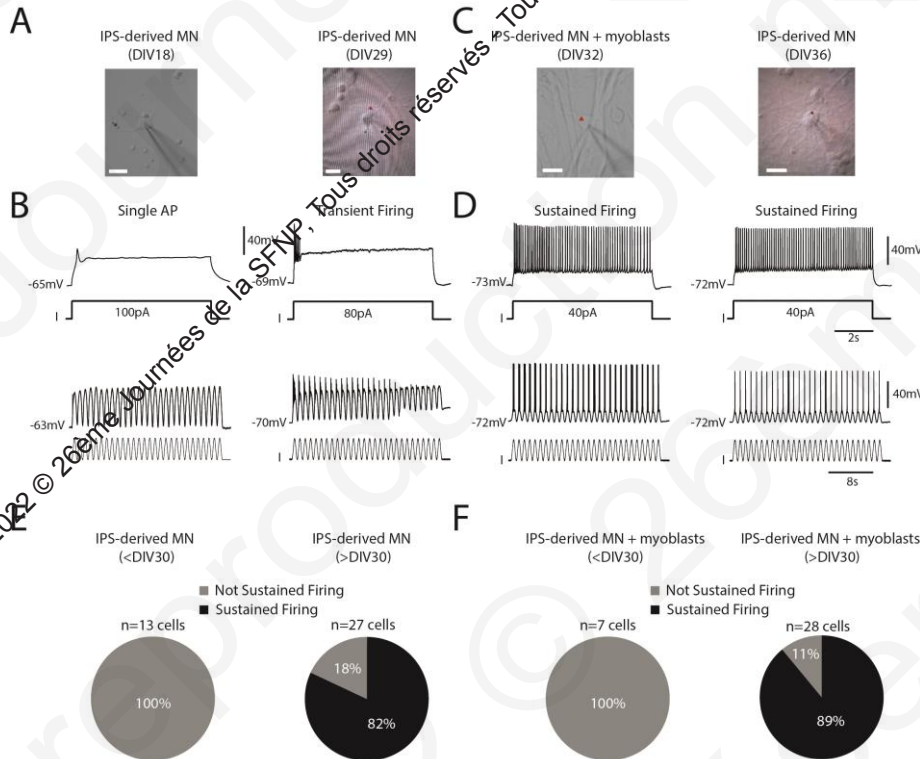
3 independent experiments

hiPSC-MNs are functional and sustain firing patterns, typical of spinal MNs

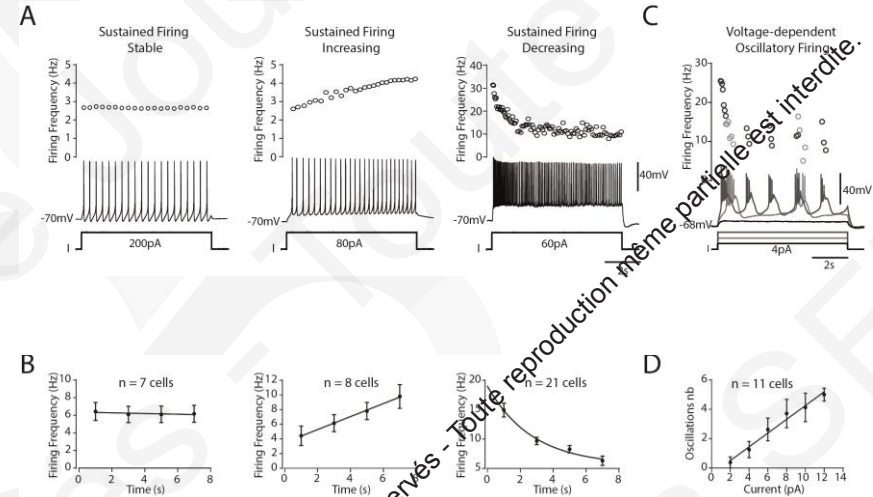


hiPSC-derived MNs are functional and sustain firing patterns, typical of spinal MNs

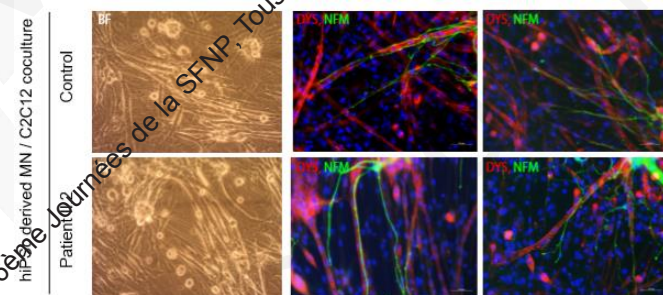
1. Co-culturing human hiPSC-MNs with myoblasts accelerates their functional maturation.



2. Control hiPSC-MNs co-cultured with myoblasts display four distinct electrophysiological signatures



3. Co-culture of control hiPSC-MNs co-cultured with mouse myoblasts

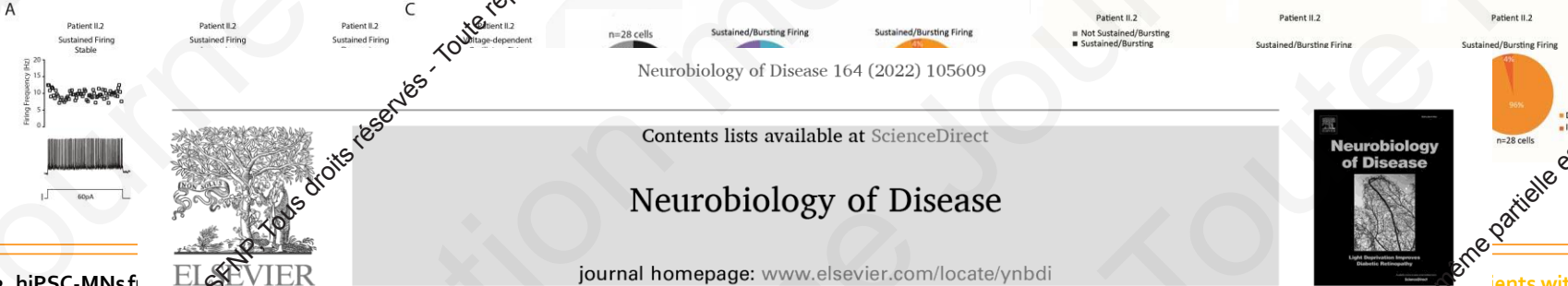


hiPSC-MNs from patients with *VRK1* mutations have altered Action Potential waveform and shorter Axonal Initial Segment



1. hiPSC-MNs from patient II.2 display similar electrophysiological firing patterns than controls

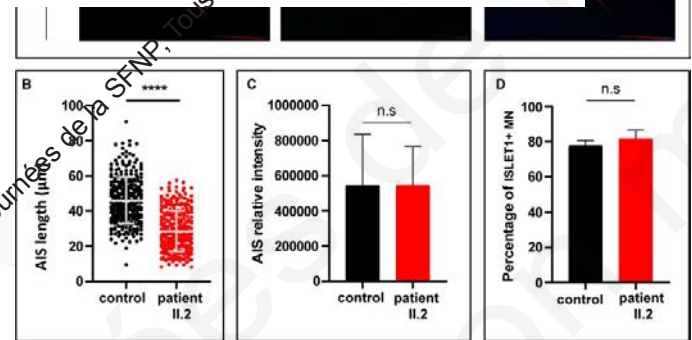
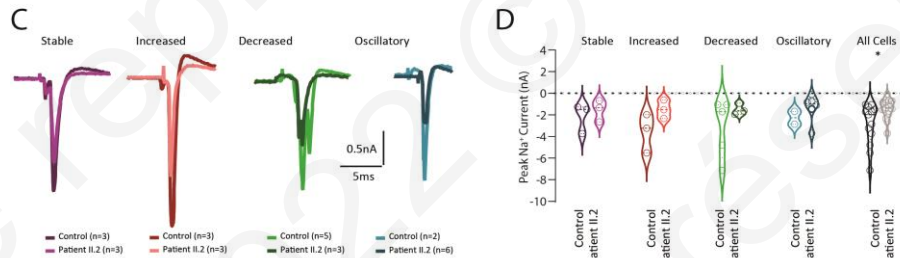
Four distinct electrophysiological signatures obtained in Control hiPSC-MNs with myoblasts (>DIV30) and hiPSC-MNs from patient II.2 with *VRK1* mutations (>DIV30)



2. hiPSC-MNs from patient II.2 display altered action potential waveform and shorter axonal initial segment

Altered action potential waveform and shorter axonal initial segment in hiPSC-derived motor neurons with mutations in *VRK1*

Rémi Bos^{a,*,*,1}, Khalil Rihan^{b,1}, Patrice Quintana^b, Lara El-Bazzal^b, Nathalie Bernard-Marissal^b, Nathalie Da Silva^b, Rosette Jabbour^c, André Mégarbané^d, Marc Bartoli^b, Frédéric Brocard^{a,1}, Valérie Delague^{b,1,*}



Summary

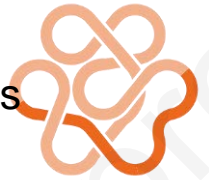
Novel mutations in VRK1 in a new form of CMT with upper motor neuron signs



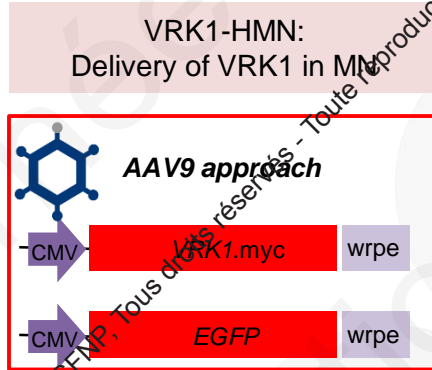
	Control	Patient	
MNS			The levels of VRK1 are decreased in patients' cells including motor neurons
Fibroblasts			VRK1, a nuclear kinase is mislocalized to the cytoplasm
Fibroblasts			Coilin, a protein from the CB is not phosphorylated leading to ubiquitination and degradation by the proteasome, as well as CB disintegration
MNS			Role for VRK1 in the assembly of Cajal Bodies in motor neurons
MNS			Signs of axonal degeneration in iPS-MNs due to the absence of VRK1
MNS			AP of shorter amplitude and larger duration/ Shorter AIS

Perspectives: development of biotherapies

Gene replacement therapy by intrathecal injection of viral vectors in two mouse models of inherited peripheral neuropathies



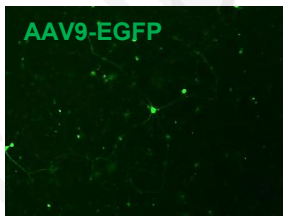
1. Design of gene replacement therapy vectors



2. Evaluation of the therapeutic efficiency in vitro

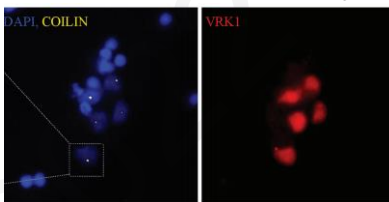
- * Transduction efficiency of the cell type of interest

MN derived from hiPSC



- * Efficiency capacity to improve the cellular defects

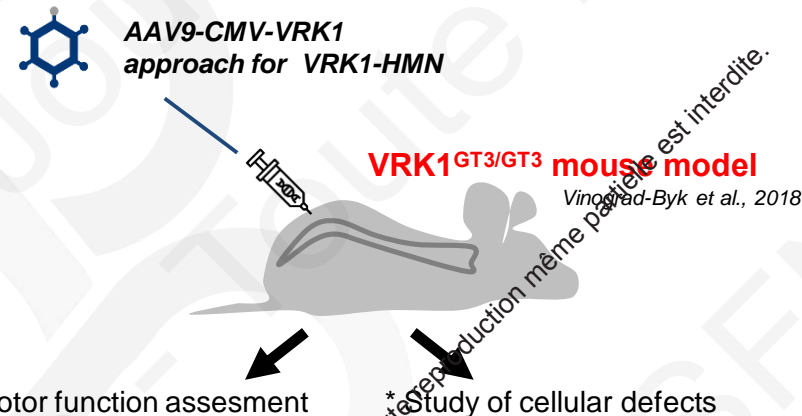
VRK1-HMN: restoration of Cajal bodies



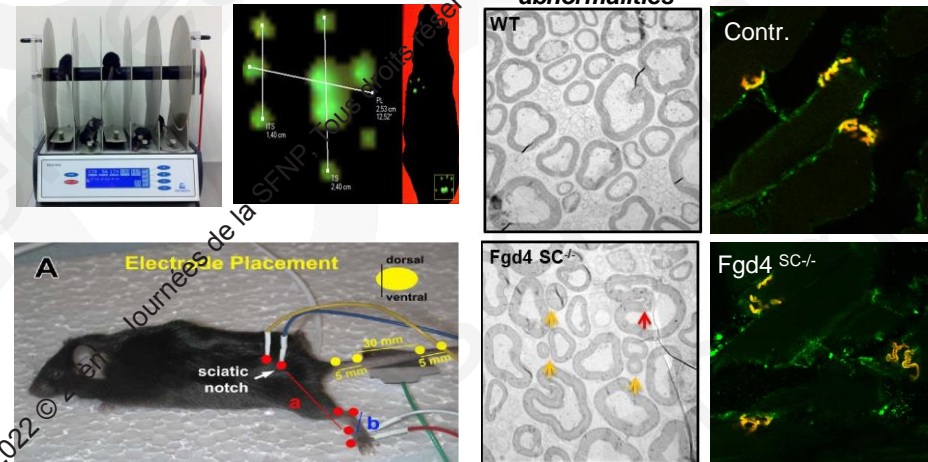
El-bazzal et al., 2019

3. Evaluation of the therapeutic benefits in vivo

- * Intrathecal injection at 6 week-old

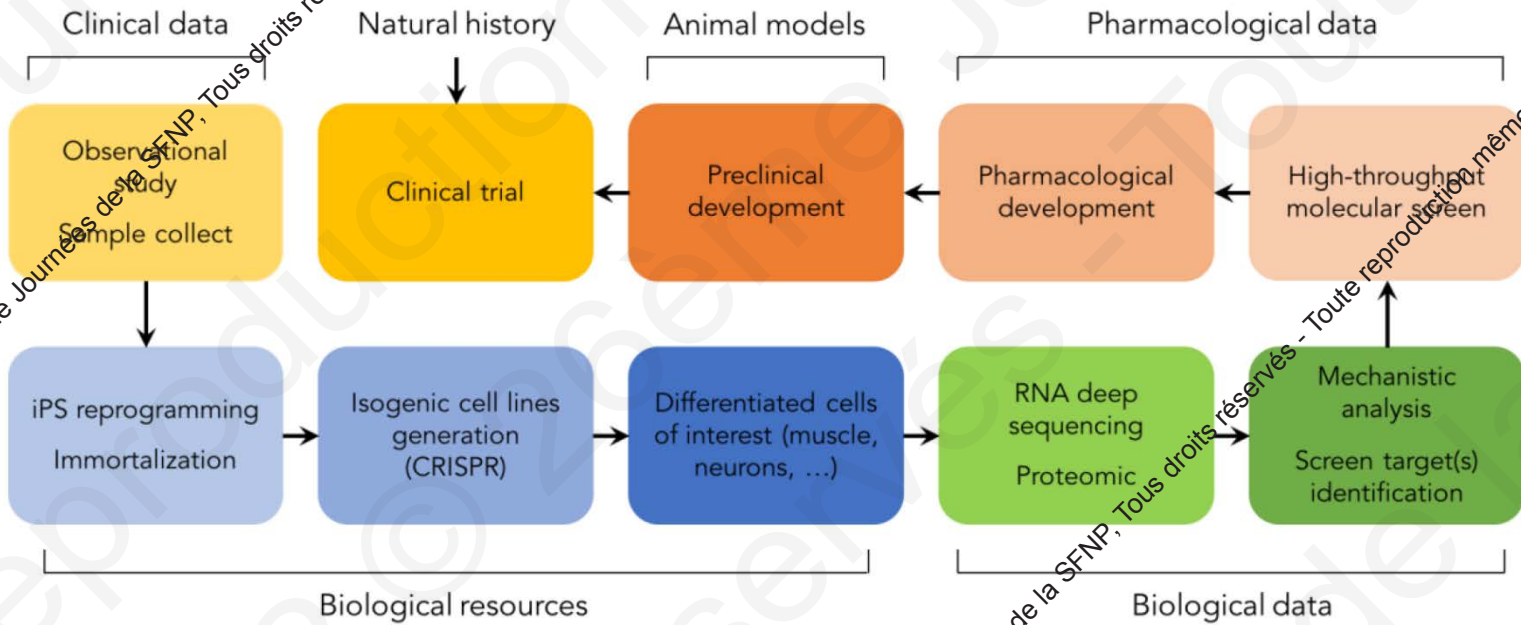


At 6 and 12 months-old





MYOPHARM PROGRAM ORGANIZATION



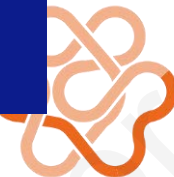
The MYOPHARM Project

Novel mutations in VPK1 in a new form of CMT with upper motor neuron signs



- Use the molecular and electrophysiological defects already identified to define the readouts to use in the high throughput screen (HTS)
- Study these parameters in iPSC-MN from the two other patients
- Define common readouts for the three different patients (with different mutations)
- Identify other readouts using transcriptomics and proteomics/phosphoproteomics study
- « Miniaturize » the processes to adapt to the conditions required for the HTS
- Use Multielectrode arrays to study electrophysiological properties of iPSC-MNs (also keeping in mind that we will need to adapt and « miniaturize » for HTS)

ACKNOWLEDGEMENT



- Patients and families



NEUROMYOLOGIE
TRANSLATIONNELLE



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- Lebanese American University
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- Institut des neurosciences de la
Timone
Rémi Bos
Frédéric Brocard



Mark Lathrop
Diana Zelenika



- We have identified novel mutations in VRK1 in a new form of CMT with upper motor neuron signs
- The levels of VRK1 are decreased in patients' cells including motor neurons
- Additionally, VRK1, a nuclear kinase is mislocalized to the cytoplasm
- Coilin, a protein from the CB is not phosphorylated leading to ubiquitination and degradation by the proteasome, as well as CB disintegration
- Absence of CB in motor neurons is likely to lead to altered transcription and splicing
- These findings suggest the existence of converging pathogenic mechanisms in our disease, SMA and ALS, with alteration/depletion of CBs as a hallmark