ERN-ITHACA Webinar 2025





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Helping patients with rare or low-prevalence complex diseases

Rho-GTPase in intellectual disability and neurodevelopmental disorders

In-Depth Webinar - January 21, 2025

Chaired by Valeria Capra, MD - Genomic and Clinical Genetics, IRCCS G.Gaslini, Genoa, Italy.

Contact PM: anne.hugon@aphp.fr



Welcome – Technical points

- Thank you for joining us today
- We are please to be numerous + 103 registration / 75 participants
- Please follow these guidelines during the session:
 - Please mute your microphone and disable your camera.
 - Raise your hand or use the Chat during Q&A sessions
 - A satisfaction survey will be provided afterward
- Webinar is being recorded and available on ITHACA's Website
 - <u>https://ern-ithaca.eu/documentation/educational-resources/</u>
- Contact
 - Anne Hugon Project Manager anne.hugon@aphp.fr



Agenda

- Welcome and Introduction
 - Speaker : Valeria Capra, MD Genomic and Clinical Genetics, IRCCS G.Gaslini, Genoa, Italy.
- 1. Rho family GTPases: key players in neuronal development and synaptic function
 - Speaker : Antonio Falace, PhD Pediatric Neurology and Muscular Diseases Unit, IRCCS Istituto Giannina Gaslini", Genoa, Italy.
- 2. RAC3-related disorders of cortical development in human neurodevelopmental phenotypes
 - Speaker : Marcello Scala, MD PhD "NeuroRacopathies Department of Neurosciences (DINOGMI), University of Genoa, Genoa, Italy; Medical Genetics Unit, IRCCS Istituto Giannina Gaslini, Genoa, Italy.
- 3. Mechanistic analysis of RAC1-related neurodevelopmental disorders
 - Speaker : Tom H. Millard, PhD Division of Developmental Biology and Medicine, Faculty of Biology, Medicine and Health, University of Manchester M13 9PL, UK.
- Discussion & Conclusion with speakers and moderator

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Welcome and Introduction

Valeria Capra, MD - Genomic and Clinical Genetics, IRCCS G.Gaslini, Genoa, Italy



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Rho GTPases



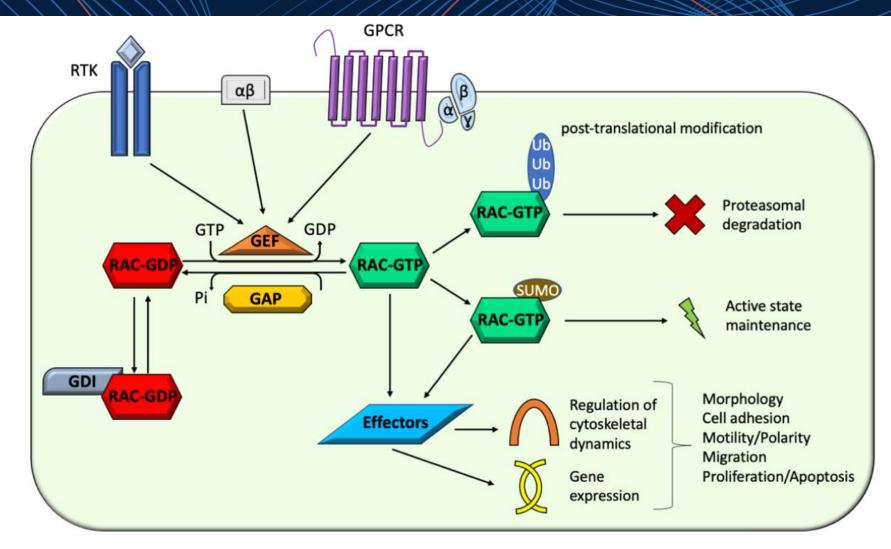
- Rho GTPases belong to the Ras small GTPase superfamily of GTP-binding proteins (that also include Ras, Ran, Rab and Arf GTPases)
- The Rho GTPase family encompasses eight subfamilies, amongst them the RhoA, Rac1, and Cdc42 ones are the best known and more recently Rac3.
- Together with their upstream and downstream regulators, they act as efficient molecular relays to transduce extracellular signals to downstream effectors.
- Like other small classical GTPases, they can be switched between active and inactive conformational states by specific guanine nucleotide exchange factors (GEFs) and GTPase-activating proteins (GAPs), respectively.





Rho GTPases







Genes	Human locus	Human pathology	References
RHO B	2p24.1	No ID but brain malformations $+$ craniofacial anomalies, strabismus (mosaicism), CP	[73]
RHO GEF			
GEFH1 (ARHGEF2)	1q22	ID, midbrain-hindbrain malformations	
TRIO/ARHGEF23	5p15.2	ID, behavioral defects. Schizophrenia, ASD, Bipolar disorder	
C9orf72	9p21.2	ALS and FTD	
ARHGEF10	8p23.3	Spastic paraplegia, slow eye movements, hypomyelination, schizophrenia	
RHO GAP			
OLIGOPHRENIN1	Xq12	ID, psychomotor retardation, ataxia, hypotonia	[<mark>46–50</mark>]
RAC1	7p22.1	ID	[<mark>42</mark>]
RAC effector			
РАКЗ	Xq23	ID, behavioural symptoms, oro-motor hypotonia, CP, motor delay with inability to walk, hyperreflexia, afinalistic movements	[55–57]
RAC GEF			
DOCK3	3p21.2	ID+muscle hypotonia, ataxia (and DMD)	[<mark>44, 45</mark>]
DOCK4	7q31.1	ASD, schizophrenia, dyslexia	[<mark>80</mark>]
TRIO/ARHGEF23	5p15.2	ID, ASD, schizophrenia, psychomotor defects	[81–91]
ALS2	2q33.1	IAHSP and JPLS	[106–110]
RAC1 other activator			
AUTS2	7q11.22	ID, ASD, Schizophrenia, dyslexia, hypotonia	[<mark>76, 77</mark>]
RAC1GAP			
A2-chimaerin (CHN1)	2q31.1	ASD (paralytic strabismus DRS)	[<mark>69–71</mark>]
RAC1-E3-Ubiquitin ligas	e		
Hace 1	6q16.3	ID with spastic paraplegia & psychomotor retardation	[<mark>64</mark> , 65]
CDC42			
AUTS2	7q11.22	ID, ASD, Schizophrenia	[<mark>76, 77</mark>]

Table 1. NDD in humans associating Rho GTPases pathogenic variants and motor symptoms.

NDD neurodevelopmental disorders, ASD Autism Spectrum Disorder, ID Intellectual deficiency, DRS Duane Retraction Syndrome, ALS Amyotrophic Lateral Sclerosis, Analogous to SMA, FTD Frontotemporal Demency, HSP hereditary spastic paraplegia, IAHSP Familal Infantile-onset ascending hereditary spastic paraplegia, JPLS Juvenile-onset primary lateral sclerosis, CMM Congenital Mirror Movements.



RAC1 and RAC3

- The small GTPase RAC1 belongs to Rac1–3 members of the Rho family of GTPases involved in the regulation of actin dynamics.
- Rac1 is a ubiquitous and highly conserved Rho GTPase across species that modulates numerous cellular functions that are essential for normal development.
- Individuals with distinct de novo missense RAC1 mutations present varying degrees of developmental delay and brain malformations.
- Analogously, variants in RAC3, encoding a small GTPase RAC3 which is critical for the regulation of actin cytoskeleton and intra-cellular signal transduction, are associated with a rare neurodevelopmental disorder with structural brain anomalies and facial dysmorphism.

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Antonio Falace, PhD Pediatric Neurology and Muscular Diseases Unit, IRCCS Istituto Giannina Gaslini", Genoa, Italy.





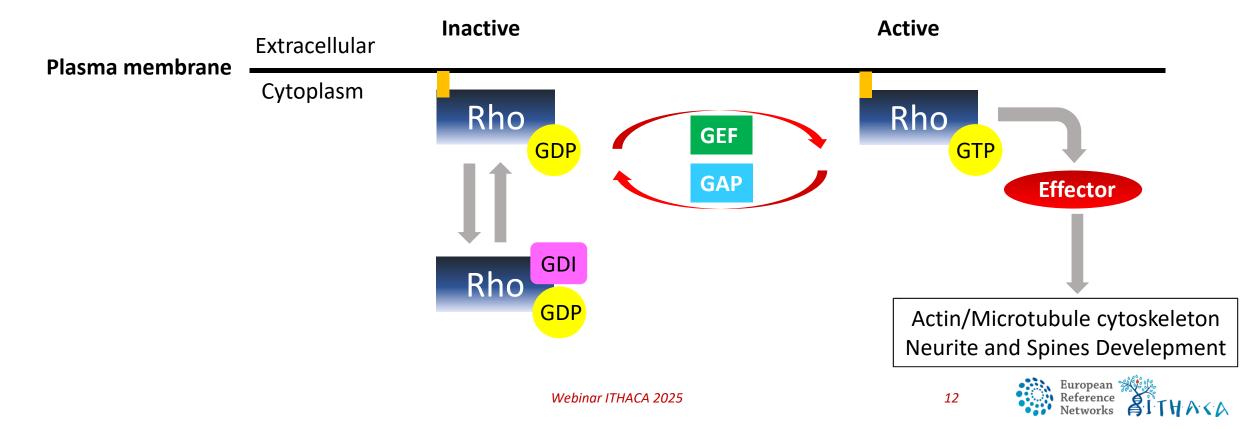
Antonio Falace Pediatric Neurology and Muscular Diseases Unit IRCCS Istituto Giannina Gaslini, Genoa



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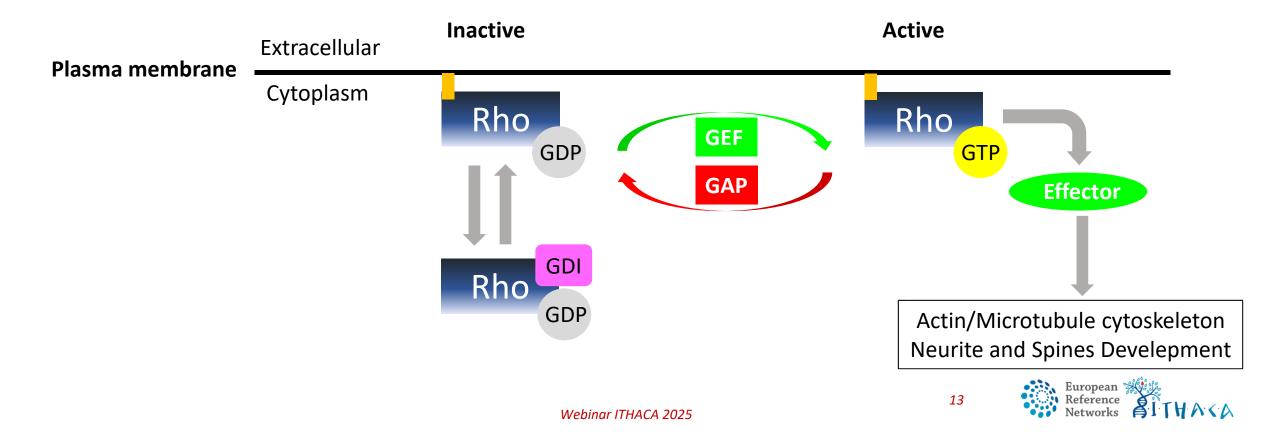
CORE CONCEPTS

- The Rho GTPase family belongs to the Ras superfamily of low molecular weight GTP binding proteins
- These proteins act as molecular switches, cycling between an active GTP-bound state and an inactive GDP-bound state, thereby transducing signals from cell surface receptors to downstream effectors



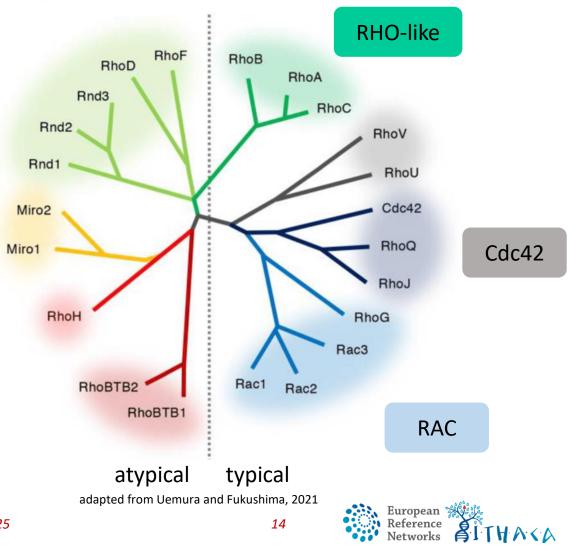
CORE CONCEPTS

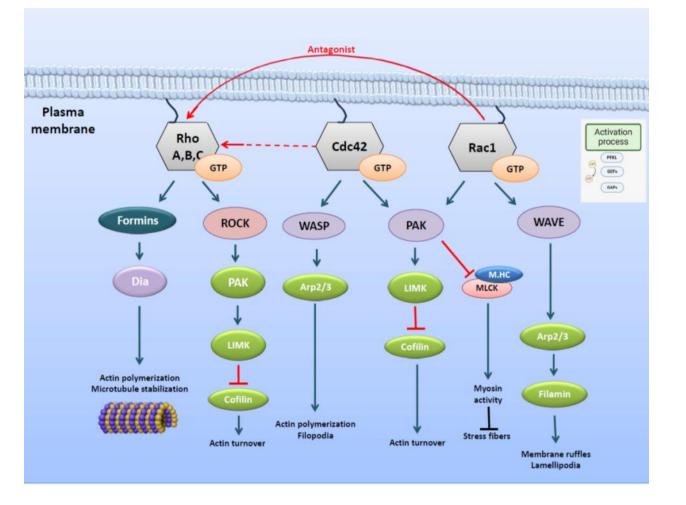
- Rho-GTPases are activated by guanine nucleotide exchange factors (GEFs)
- while are **inactivated by GTPase-activating proteins (GAPs)** that stimulate the GTPases' enzymatic activity



CORE CONCEPTS

- 22 Rho-GTPases divided into 8 subfamilies
- The atypical Rho GTPases are predominantly GTP-bound
- Nearly 90 GEFs, 60 GAPs, combining with several Rho-GTPase effectors in the mammalian genome
- RAC, Cdc42 and RHO-like subfamilies are the most studied



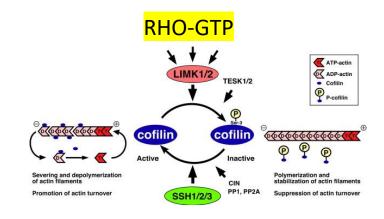


RHO FAMILY GTPases

A hub for many **signalling pathway**

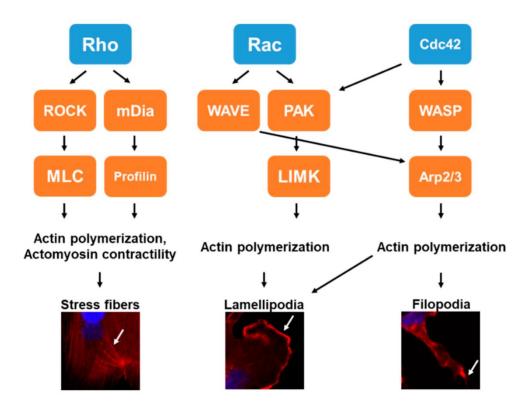
They regulates **cytoskeletal dynamics** by controlling **actin polimerization**.

Rho activation lead to the phosphorylation and inactivation of the actin **severing enzyme cofilin**.

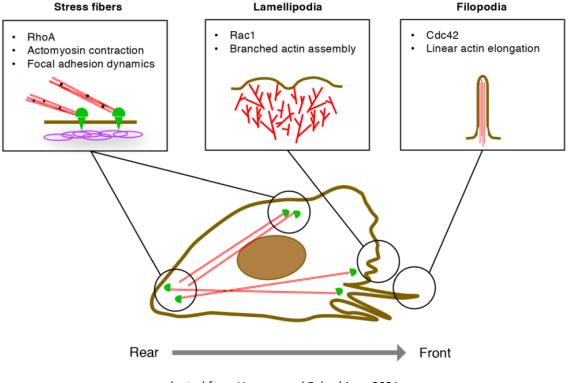


adapted from Mizuno, 2021





adapted from Humphries, 2020

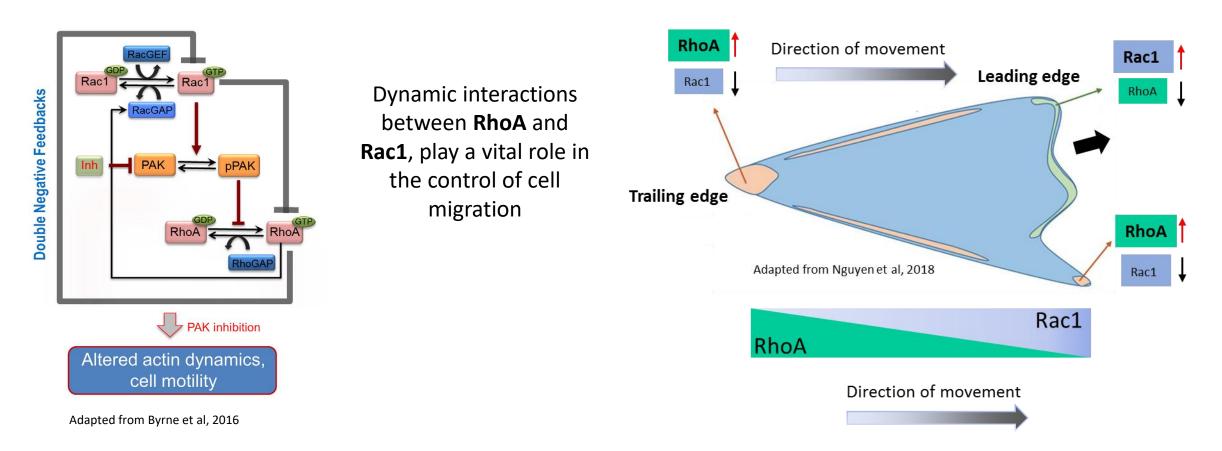


adapted from Uemura and Fukushima, 2021

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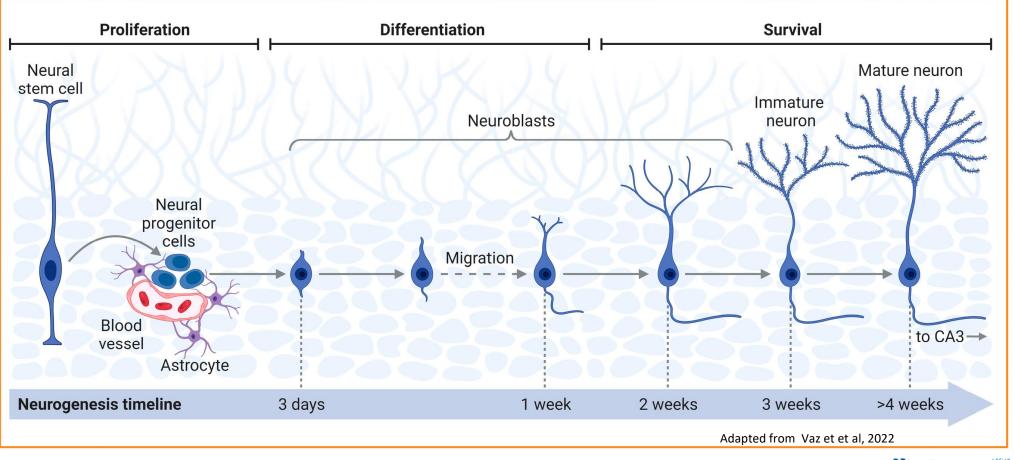


• RhoA and Rac1 are linked by a double-negative feedback loop





• RHO family GTPases in the brain development and function



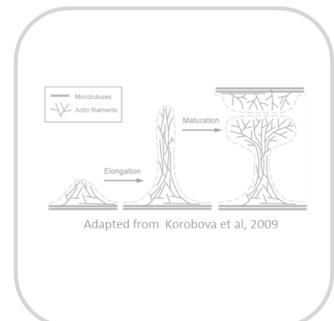




Neuronal migration Image: state state

Stage 1 Construction Construct

Synaptogenesis

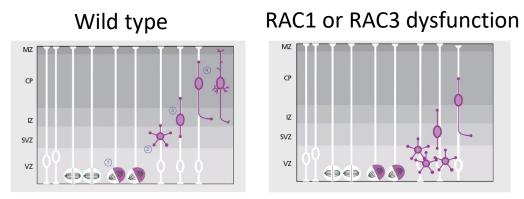




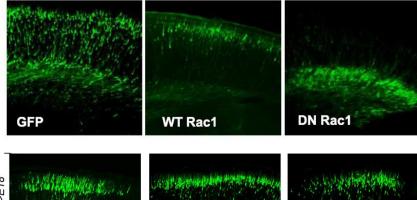
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Adapted from Yoshimura et al, 2006

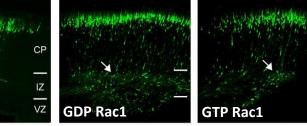
• **RAC1/RAC3** deregulation impairs neuronal migration



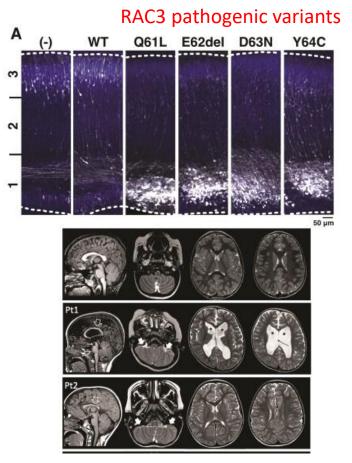
Adapted from Guarnieri et et al, 2018



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Adapted from Yang et al, 2012 and from Falace et al, 2024



Adapted from Scala et al, 2022

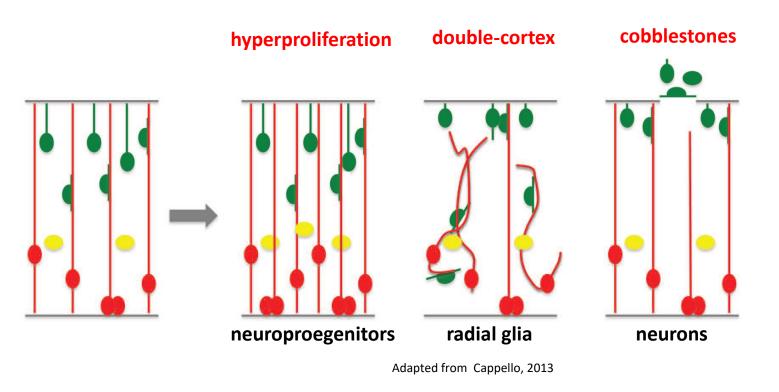
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Cell autonomous role for RAC1 and RAC3 in neuronal migration

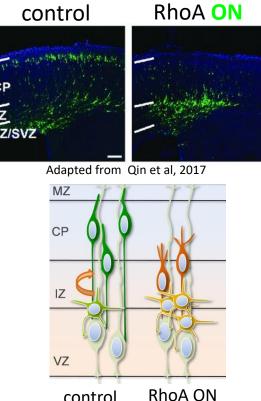


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 genetic deletion of RhoA in the developing mouse cerebral cortex results in three distinct cortical malformations



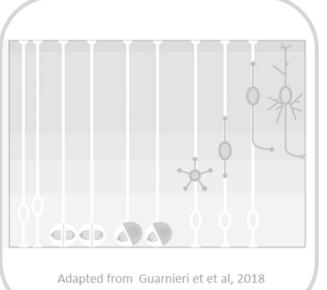
 genetic activation of RhoA impairs neuronal migration



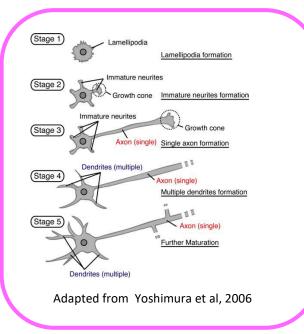
control RhoA ON Adapted from Chen et al, 2018



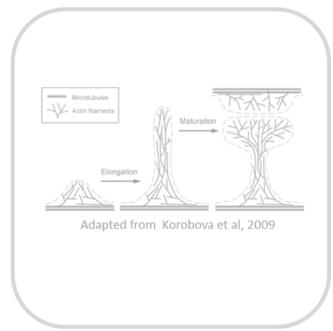
Neuronal migration



Neuronal polarity

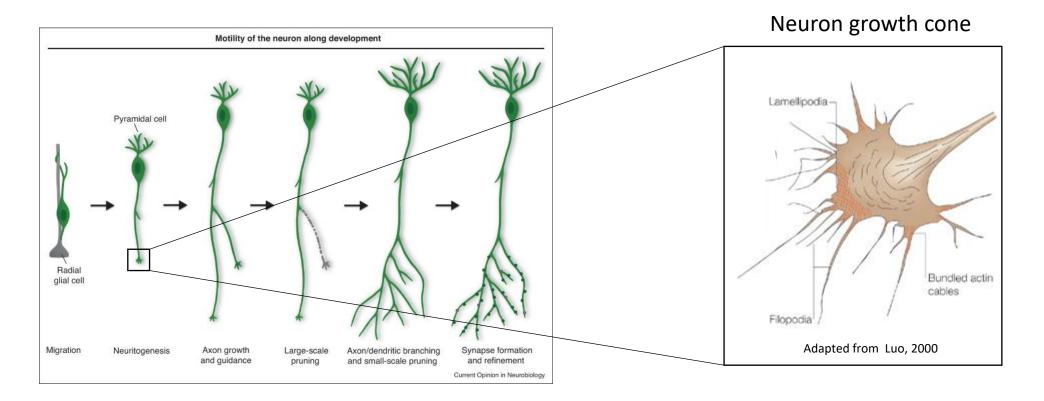


Synaptogenesis



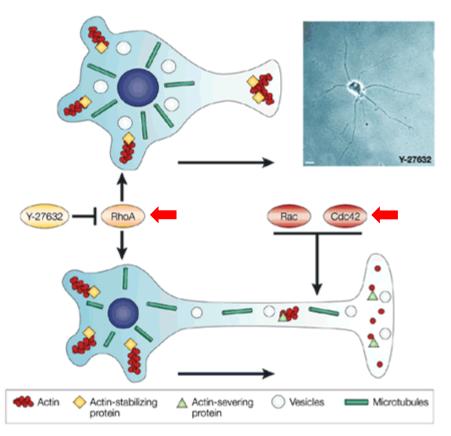


• RHO family GTPases in axonogenesis

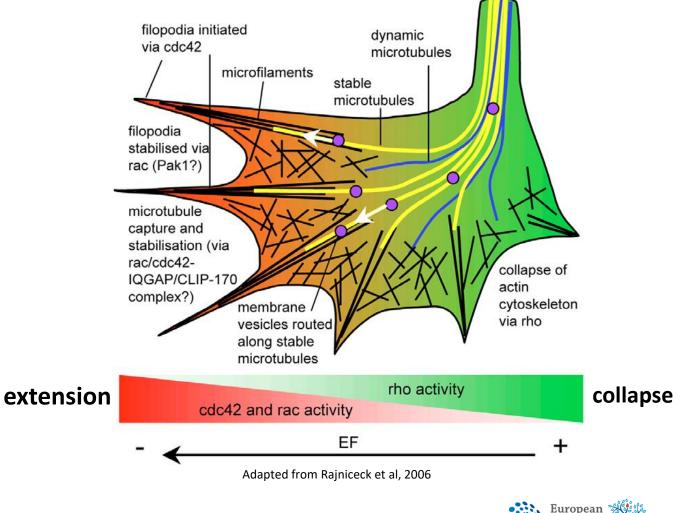




• actin-based motility is regulated by Rho family GTPases interplay at the growth cone

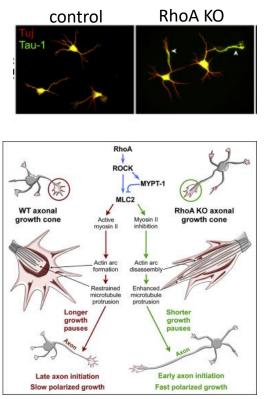


Adapted from Da Silva and Dotti, 2002



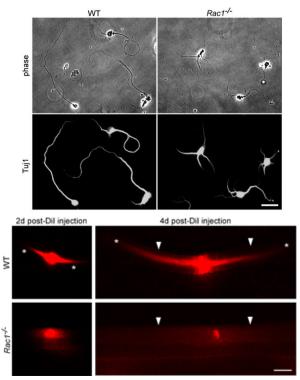
Reference

• RhoA restrains axon initiation and growth independent of specification



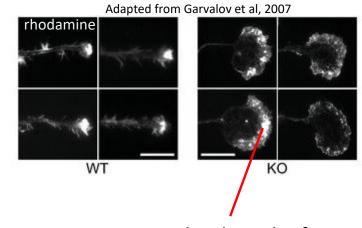
Adapted from Dupraz et al, 2019

• Rac1 loss impairs axonogenesis *in vitro* and *in vivo*



Adapted from Tahirovic et al, 2010

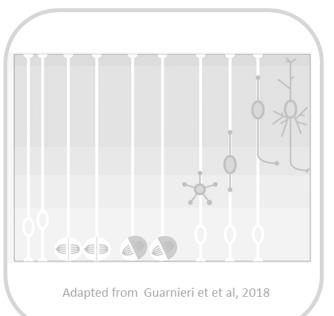
 Cdc42 loss impairs growth cone development



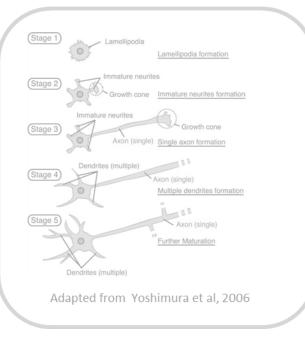
Smooth-Filopodia free growth cone



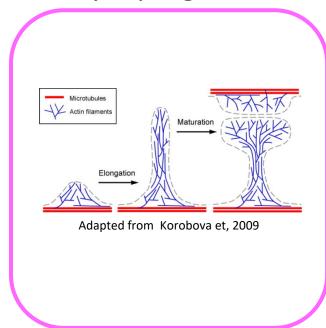
Neuronal migration



Neuronal polarity



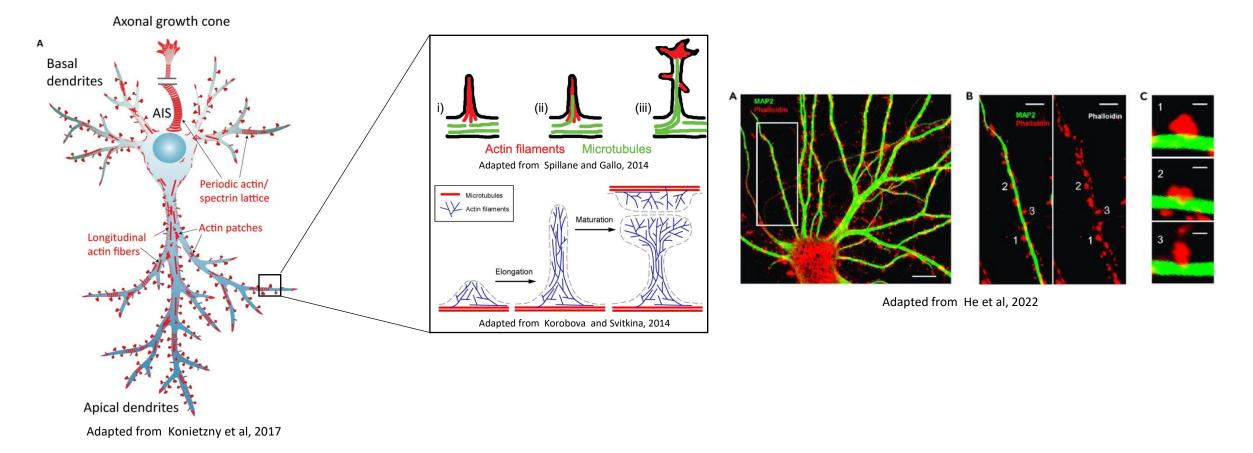
Synaptogenesis



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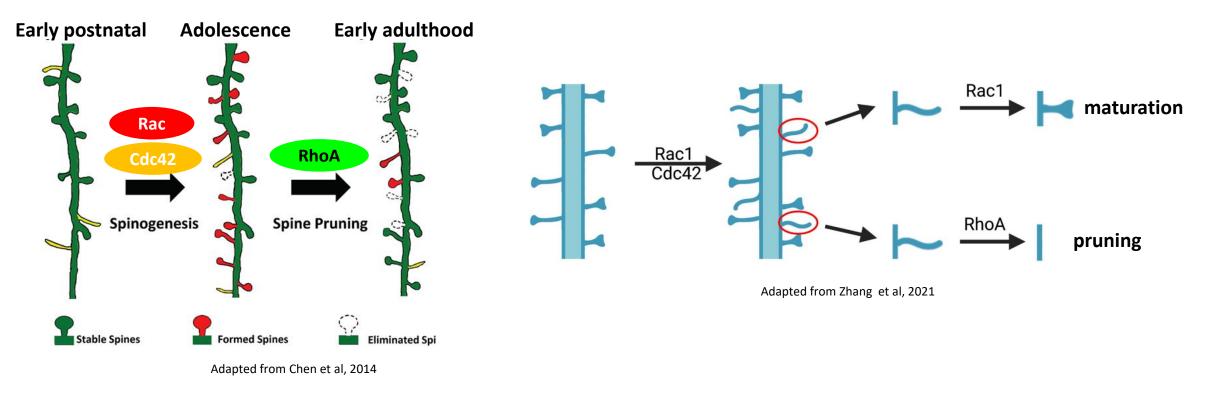


• Dendritic spines formation, maturation, and plasticity heavily depend on the actin cytoskeleton remodeling





• The key role Rho family GTPases interplay in dendritic spines development and function



- The activation of **Rac1** and **Cdc42** leads to increased immature spines
- Mature morphology through **Rac1**-dependent mechanisms
- Pruning by RhoA-dependent processes

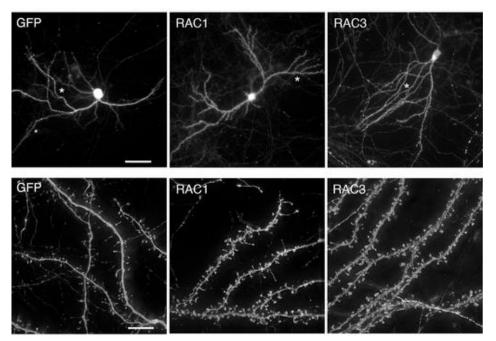


• The key role Rho family GTPases interplay in dendritic spines development and function

control

control

 Overexpression of RAC1 and RAC3 increases the density and size of dendritic spines



Adapted from Pennucci et al, 2019

• Deletion of both RAC1 and RAC3 deeply affects spinogenesis

GFP + PSD-9

GFP + PSD-

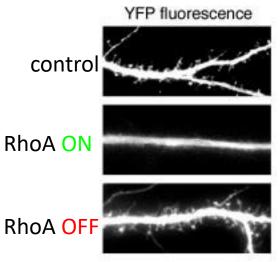
Rac1 KO

Rac3 KO

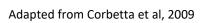
GFP+PSD-

GFP+PSD-

• RhoA activity inhibits spines formation



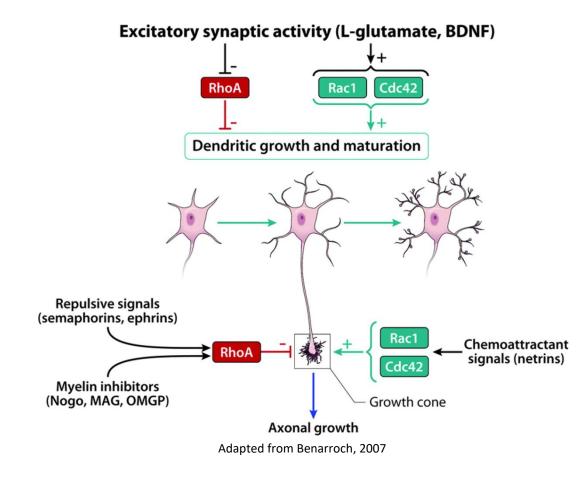
Adapted from Zhang and Macara, 2008

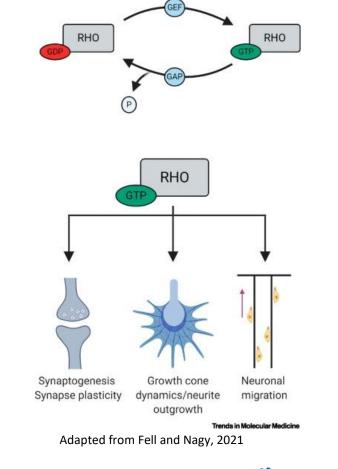




TAKE HOME MESSAGE

Rho family GTPases interplay regulates neuronal development and function







THANKS FOR YOUR ATTENTION

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2.RAC3-related disorders of cortical development in human neurodevelopmental phenotypes

Marcello Scala, MD PhD "NeuroRacopathies – Department of Neurosciences (DINOGMI), University of Genoa, Genoa, Italy; Medical Genetics Unit, IRCCS Istituto Giannina Gaslini, Genoa, Italy.











RAC3-related disorders of cortical development in human neurodevelopmental phenotypes

Marcello Scala, MD, PhD^{1,2} Pediatrician, Researcher in Medical Genetics

¹ University of Genoa, Department of Neurosciences (DINOGMI) ² IRCCS Giannina Gaslini Children's Hospital and Research Institute, Department of Medical Genetics and Pediatric WebsNeurologys





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Marcello Scala, MD, PhD



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Declaration of conflict of interest I have no commercial disclosure



Neurodevelopmental disorders



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What are NDDs?

NDDs are a **spectrum** of disorders sharing genetic aetiology, pathophysiological mechanisms, and clinical manifestations

However, subgroups are identifiable based on distinctive biological and clinical properties

The **most common NDDs** are:

- Autism spectrum disorders (ASD)
- Attention deficit hyperactivity disorder (ADHD)
- Intellectual disability (ID)
- Epilepsy
- Adult-onset NDDs (Schizophrenia, depression, etc.)

Condition	Prevalence	Common	Commonly
	worldwide	comorbidities	affected brain
			regions
ASD – inc. autistic	1 % [5]	ADHD, ID, SCZ,	Frontal
disorder, Rett		epilepsy,	cortex and
syndrome, childhood		developmental delay,	cerebellum
disintegrative		depression, anxiety,	
disorder, pervasive		bipolar disorder	
developmental			
disorder not otherwise			
specified			
ADHD – inc.	2–6 % [<mark>6</mark>]	ASD, epilepsy, ID,	Frontal
predominantly		bipolar disorder	cortex
inattentive,			
hyperactive-impulsive			
Epilepsy – inc. partial,	0.7 % [7]	ASD, ADHD, ID, SCZ,	Frontal and
focal, general		psychosis	temporal
			cortex
ID - inc. Down's	1–3 % [<mark>8</mark>]	ASD, ADHD,	Frontal
syndrome		developmental delay	cortex
Developmental delay	1–3 % [9]	ASD, ID	Frontal
			cortex
SCZ - inc.	0.3–0.7 %	ASD, ADHD, epilepsy,	Frontal
schizoaffective	[10]	bipolar disorder,	cortex
disorder		depression	
Depression – inc. major	3–6 % [11]	ASD, anxiety, SCZ,	Frontal
depressive disorder		bipolar disorder	cortex

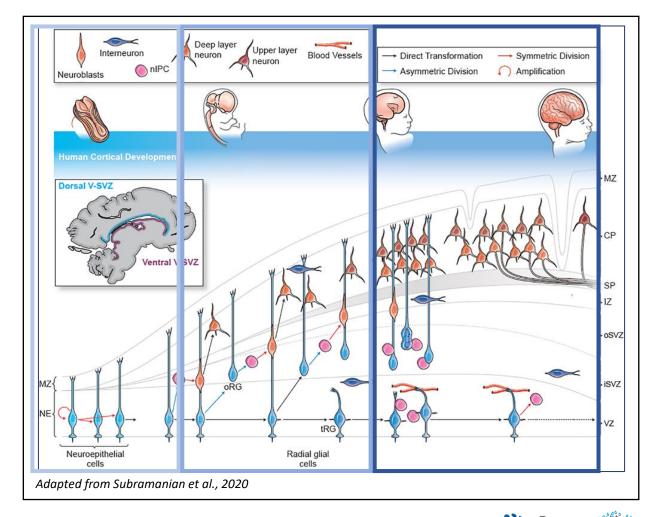




From development to disease

Typically, NDDs are caused by the disruption of the tightly coordinated events regulating **brain development and morphogenesis**:

- First trimester -> neurogenesis
- Second trimester -> more neurogenesis + migration -> corticogenesis (gyri formation)
- Third trimester -> differentiation + cortical axonogenesis -> neural networks/circuitry generation





THAKA

From development to disease

The disruption of each phase may result in distinctive features:

First trimester ->

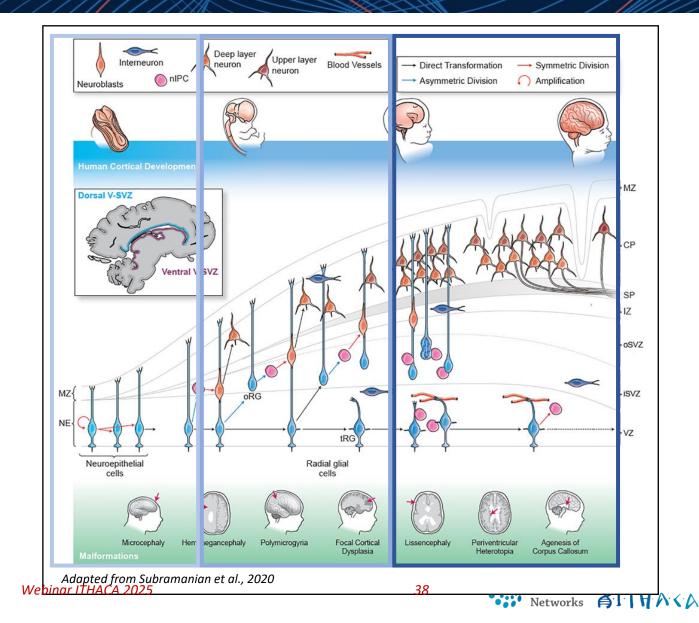
□ Microcephaly (OFC < -2SDs)

Second trimester ->

- Microcephaly
- Lissencephaly (no gyri);
- Polymicrogyria or pachygyria
- Somatic mutation --->
 - Focal Cortical Dysplasia (FCD)
 - Hemimegalencephaly (HME)
 - Megalencephaly (ME)

Third trimester ->

- □ Heterotopias (grey in white)
- □ Lissencephaly (milder)
- □ Agenesis of corpus callosum



Subramanian et al., 2020; Parenti et al., 2020





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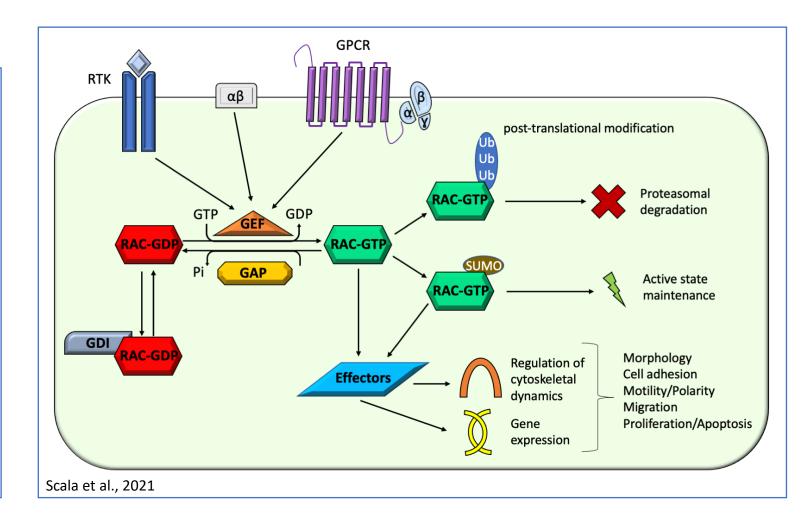
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Rho GTPases in brief

Twenty different Rho GTPases families are present in human, classified in 8 subfamilies based on structure and biological properties

These proteins are crucial regulators of dynamic cytoskeletal rearrangement and intracellular signaling:

- Cell cycle progression
- Transcription
- Cell morphology, motility, and polarity





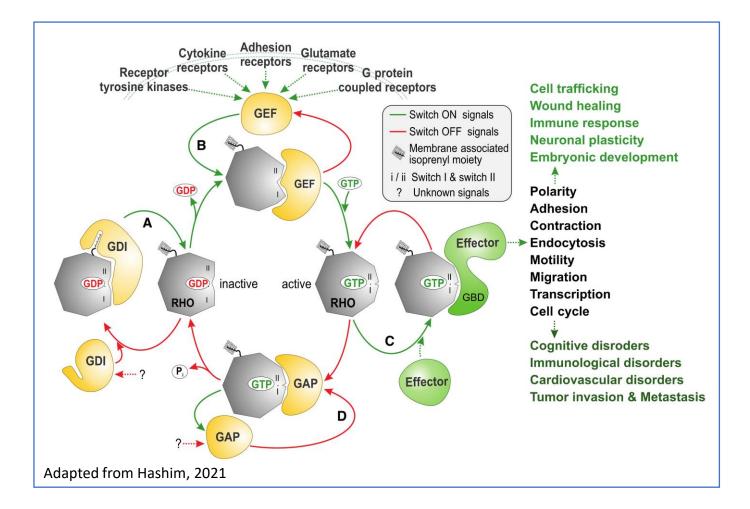
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RAC subfamily

The RAC subfamily consists of four members: RAC1, RAC2, **RAC3** AND RHOG

In the classic **GTPase cycling**, they swing between a GDP-bound (inactive) and a GTP-bound (active) status

GTP hydrolysis and GDP/GTP exchange are mediated by the <u>G domain</u>, composed of **Switch I and Switch II regions**, under the influence of ancillary regulatory proteins (GEFs, GAPs, GDIs)



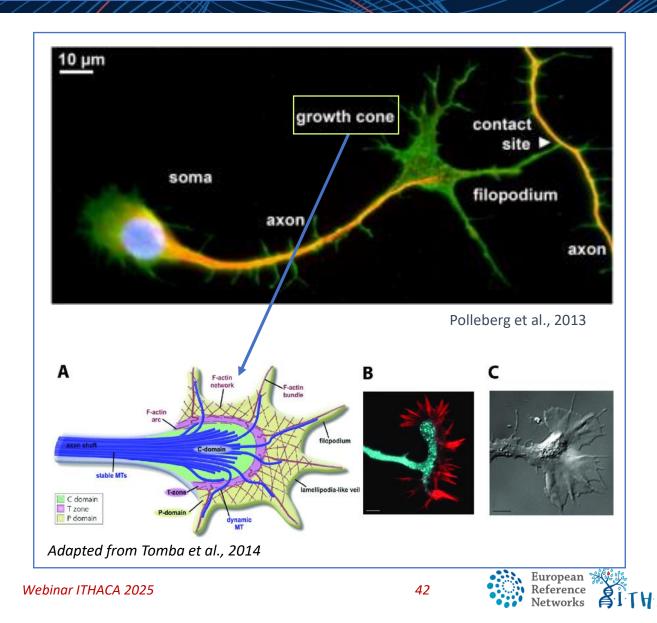
RAC3: biology and function in the brain

The **RAC3 gene** (MIM *602050) maps to 17q25.3 and encodes a 21.4 kDa protein with 92% overlap to RAC1 and 89% overlap to RAC2

RAC3 is specifically expressed in the brain during its development and, together with RAC1, it is fundamental to regulate the formation of the **lamellipodia**, cytoskeletal structures critical for cell movement and polarity

As such, RAC3 is crucial for:

- Neuronal migration
- Growth cone-mediated neuronal development/maturation



RAC3 in human disease



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NEURODEVELOPMENTAL DISORDER WITH STRUCTURAL BRAIN ANOMALIES AND DYSMORPHIC FACIES; NEDBAF, OMIM # 618577

BRIEF COMMUNICATION © American College of Medical Genetics and Genomics

Genetics in Medicine

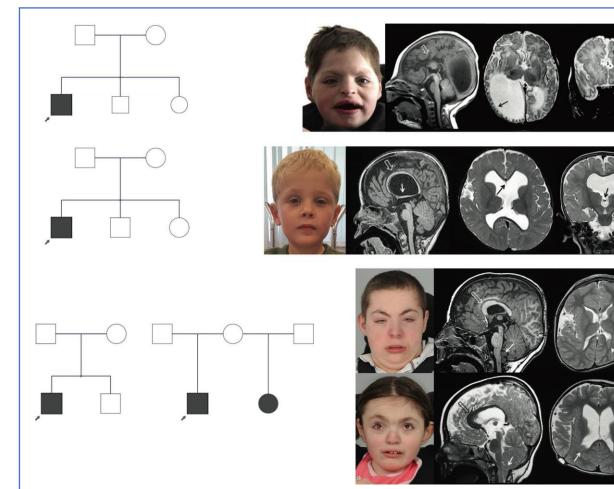
De novo missense variants in RAC3 cause a novel neurodevelopmental syndrome

Gregory Costain, MD, PhD¹, Bert Callewaert, MD, PhD², Heinz Gabriel, MD³, Tiong Y. Tan, MBBS, PhD⁴, Susan Walker, PhD^{5,13}, John Christodoulou, MBBS, PhD^{4,6}, Tamas Lazar, MSc⁷, Björn Menten, PhD², Julia Orkin, MD, MSc^{8,9,10}, Simon Sadedin, PhD⁴, Meaghan Snell, MS^{1,11}, Arnaud Vanlander, MD¹², Sarah Vergult, PhD², Susan M. White, MBBS⁴, Stephen W. Scherer, PhD^{5,13,14}, Robin Z. Hayeems, PhD^{10,11}, Susan Blaser, MD¹⁵, Shoshana J. Wodak, PhD⁷, David Chitayat, MD^{1,16}, Christian R. Marshall, PhD^{5,11,17,18} and M. Stephen Meyn, MD, PhD^{1,8,11,14,19}

In 2018, Costain et al. reported the first four **RAC3 families**, cosisting of 5 affected individuals

All subjects harbored *de novo* missense variants in RAC3 and showed developmental delay, hypotonia, and brain abnormalities

However, no functional investigation was performed



Adapted from Costain et al., 2018

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NEURODEVELOPMENTAL DISORDER WITH STRUCTURAL BRAIN ANOMALIES AND DYSMORPHIC FACIES; NEDBAF, OMIM # 618577

Journal of Human Genetics (2019) 64:1127-1132 https://doi.org/10.1038/s10038-019-0656-7

BRIEF COMMUNICATION



A *de novo* variant in *RAC3* causes severe global developmental delay and a middle interhemispheric variant of holoprosencephaly

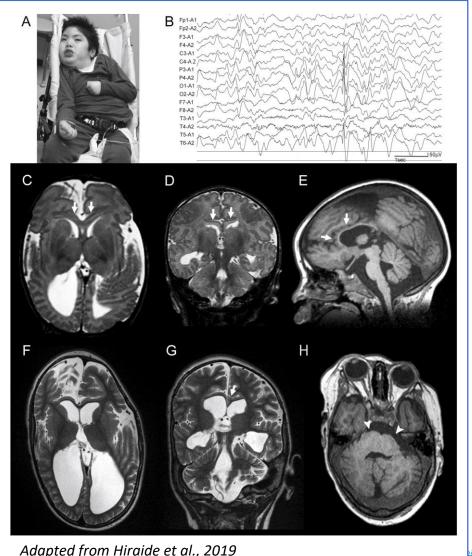
Takuya Hiraide¹ · Hikari Kaba Yasui² · Mitsuhiro Kato³ · Mitsuko Nakashima¹ · Hirotomo Saitsu¹

Received: 23 May 2019 / Revised: 22 July 2019 / Accepted: 4 August 2019 / Published online: 16 August 2019 © The Author(s), under exclusive licence to The Japan Society of Human Genetics 2019

In 2019, Hiraide et al. reported **an additional case**

This subject showed severe global **developmental delay**, intellectual disability, **epilepsy**, and laryngeal dystonia

His brain MRI showed **brain dysplasia**, including coexistence of interhemispheric variant of holoprosencephaly and brainstem dysmorphism



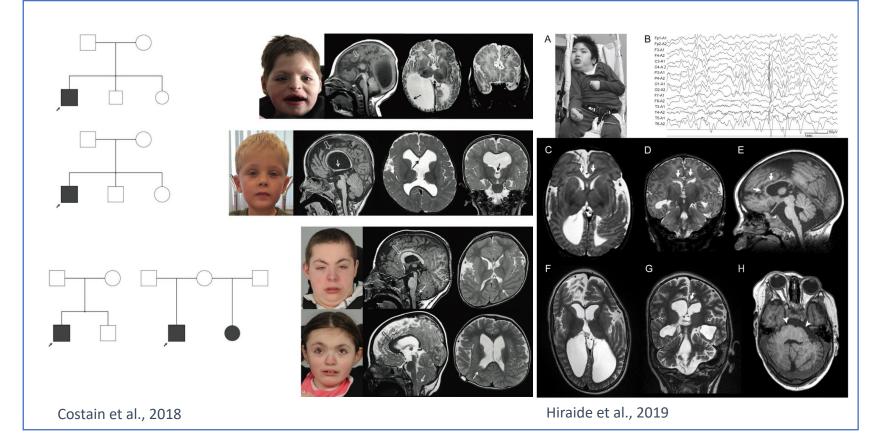


Reference Networks

NEURODEVELOPMENTAL DISORDER WITH STRUCTURAL BRAIN ANOMALIES AND DYSMORPHIC FACIES; NEDBAF, OMIM # 618577

These reports strongly pointed to the relevance of **RAC3 variants** as the cause of a **novel NDD**

However, due to the limited clinical information and the absence of supporting functional evidence, **the actual disease spectrum and its pathophysiology remained largely elusive**





NEDBAF: disease spectrum and pathophysiology



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In this study, we investigated a significant cohort of **ten individuals with NEDBAF**

We dissected the <u>genetic</u> <u>heterogeneity</u> of RAC3 variants, delineated the <u>phenotypic spectrum</u> of NEDBAF, and functionally explored the impact of RAC3 variants on <u>corticogenesis</u> https://doi.org/10.1093/brain/awac106

BRAIN 2022: 00; 1–20 | 1

BRAIN

Variant-specific changes in RAC3 function disrupt corticogenesis in neurodevelopmental phenotypes

 Marcello Scala, ^{1,2,3,†} Masashi Nishikawa, ^{3,†} Hidenori Ito, ^{3,†} Hidenori Tabata, ³ Tayyaba Khan, ⁴ Andrea Accogli, ¹ Laura Davids, ⁵ Anna Ruiz, ⁶ Pietro Chiurazzi, ^{7,8} Gabriella Cericola, ⁹ Björn Schulte, ¹⁰ Kristin G. Monaghan, ¹¹ Amber Begtrup, ¹¹ Annalaura Torella, ^{12,13} Michele Pinelli, ¹² Anne-Sophie Denommé-Pichon, ^{14,15,16}
 Antonio Vitobello, ^{14,15} Caroline Racine, ^{15,16} Maria Margherita Mancardi, ¹⁷ Courtney Kiss, ¹⁸ Andrea Guerin, ¹⁸ Wendy Wu, ^{4,19} Elisabeth Gabau Vila, ²⁰ Bryan C. Mak, ²¹ Julian A. Martinez-Agosto, ^{21,22,23} Michael B. Gorin, ^{21,24,25} Bugrahan Duz, ²⁶ Yavuz Bayram, ^{27,28} Claudia M. B. Carvalho, ^{29,30} Jaime E. Vengoechea, ⁵ David Chitayat, ^{31,32,33} Tiong Yang Tan, ³⁴ Bert Callewaert, ³⁵ Bernd Kruse, ⁹ Lynne M. Bird, ^{36,37} Laurence Faivre, ^{14,16} Marcella Zollino, ^{7,8} Saskia Biskup, ^{10,38} Undiagnosed Diseases Network, Telethon Undiagnosed Diseases Program, Pasquale Striano, ^{1,2} Vincenzo Nigro, ^{12,13} Mariasavina Severino, ³⁹ Valeria Capra, ⁴⁰

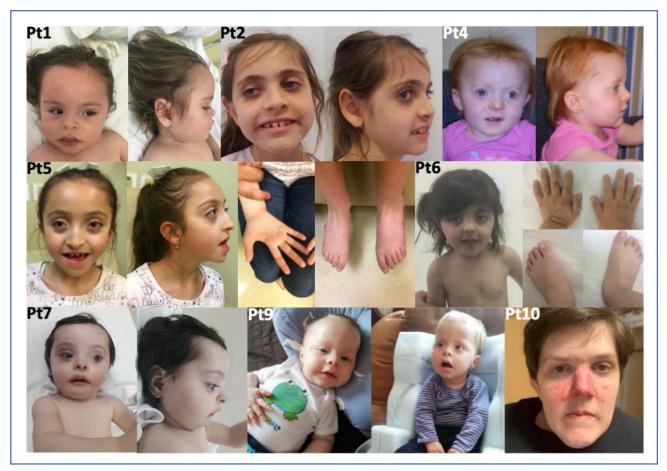
[†]These authors contributed equally to this work.



Study cohort

Affected individuals presented with **neurodevelopmental phenotypes** featuring:

- Developmental delay (global)
- Hypotonia
- Abnormal behavior stereotypies
- Dysmorphism
- Seizures
- Musculoskeletal defects

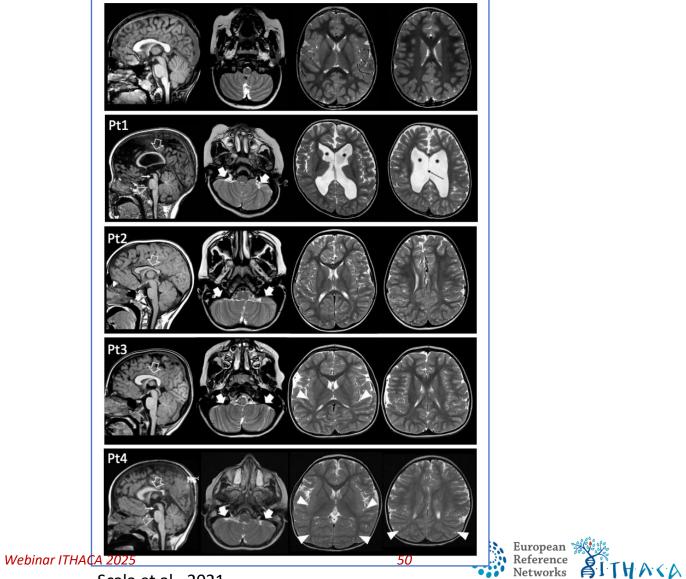




Neuroimaging

Brain MRI revealed a spectrum of brain abnormalities suggestive of malformations of cortical development (MCDs):

- Corpus callosum anomalies
- White matter thinning
- Nodular heterotopia
- Dysgyria/polymicrogyria
- Cerebellar dysplasia



Case study

Case #9, 2 yo

- Developmental delay
- Generalized hypotonia
- Stereotyped movements (mouth and upper limbs)
- Stereotyped deep breathing
- Stereotyped guttural sounds
- Hand mouthing
- Eyelid myoclonia



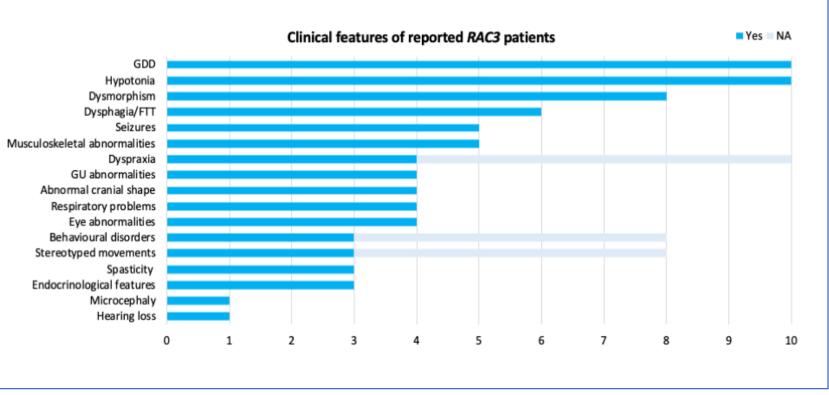




Phenotypic spectrum

Overall, **NEDBAF** is a complex **NDD** characterized by:

- Global psychomotor delay
- Cognitive deficiency (severeprofound)
- Dysmorphism
- Feeding difficulties
- Hypotonia
- Seizures
- MCDs (CCH, dysgyria/PMG, heterotopia, etc.)



Scala et al., 2021

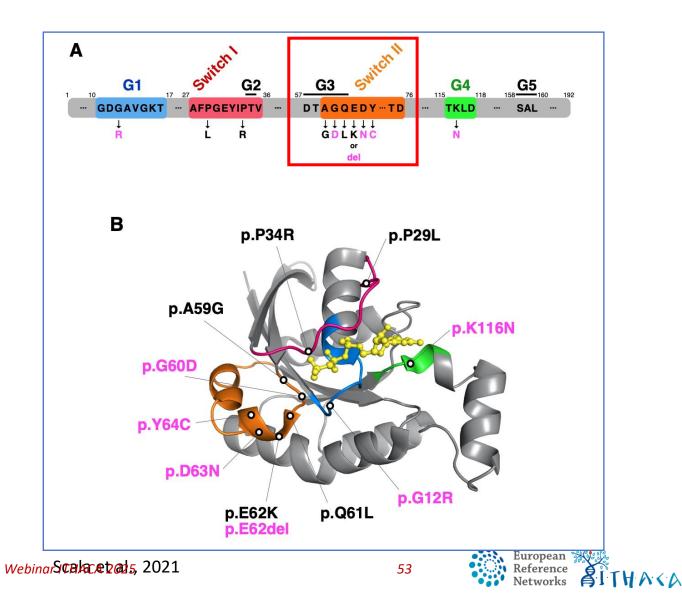


Genotype spectrum

Through ES, we identified **8 different** *de novo RAC3* variants (NM_005052.3), of which **6 were novel (purple in the** *figure)*

Seven changes affected the **Switch II region**, that is important for interactions with RAC3 effectors

This region is also a **mutational hot spot** in *RAC1-, RAC3-* e *CDC42-*related disorders (Reijnders *et al.,* 2017; Martinelli *et al.,* 2018)



Functional investigation: lamellipodia

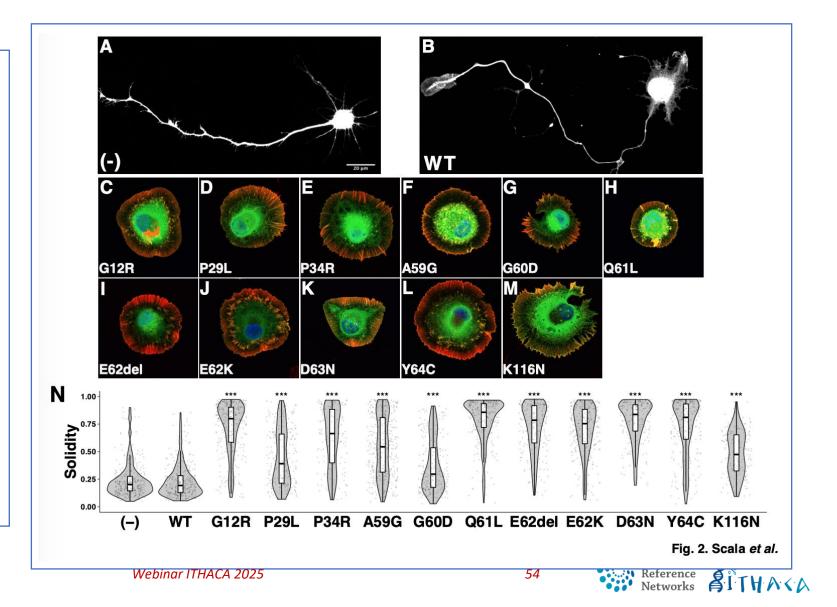
Transfected hippocampal neurons show round shape with lamellipodia, but \checkmark neurite extension

These effects were **variant-specific**, with P29L, -A59G, -G60D, and -K116N occasionally showing neurite extension

All variants facilitate lamellipodia formation and cytoskeletal reorganization (gain of function – GoF)



Structural and functional neuronal defects



Functional investigation: GTPase activity

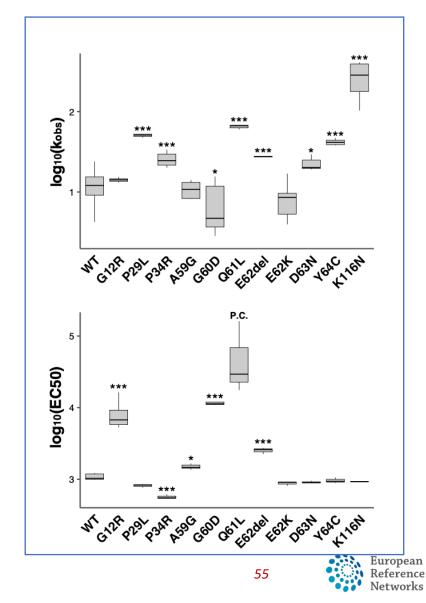
Different variants cause different defects in the **GDP/GTP exchange**, allowing us to classify them in **three subgroups**:

1) <u>Group I</u> (P29L, P34R, Q61L, E62del, D63N, Y64C, K116N): ↑ exchange activity

2) <u>Group II</u> (G12R, A59G, and E62K): normal exchange activity

3) <u>Group III</u> (G60D): preference for GTP binding due to \downarrow GTP hydrolysis and exchange activity rate

	wт	G12R	P29L	P34R	A59G	G60D	Q61L	E62del	E62K	D63N	Y64C	K116N
GTP- loading	→	→	††	Ť	→	ţ	† †	t	→	t	††	† ††
GTPase	→	ţţ	→	Ť	Ļ	ţţţ	ţţţ	Ļ	→	→	→	→

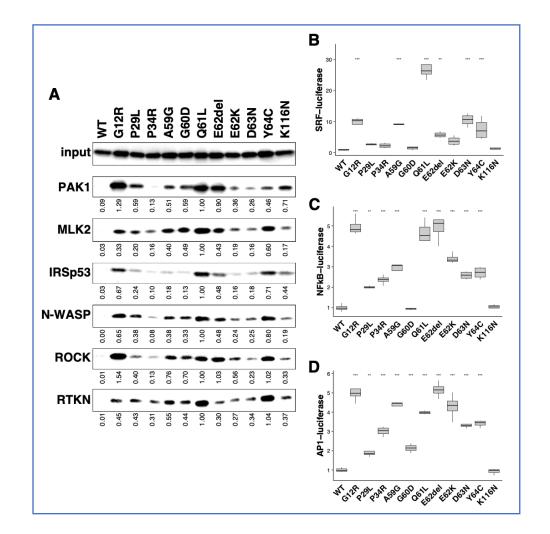


Functional investigation: downstream effectors

Clinical heterogeneity is reflected into **molecular heterogeneity**

Each variant affects the interactions with RAC3 **downstream signaling pathways** in a distinct way

Each variant may affect **similar or different** signaling pathways

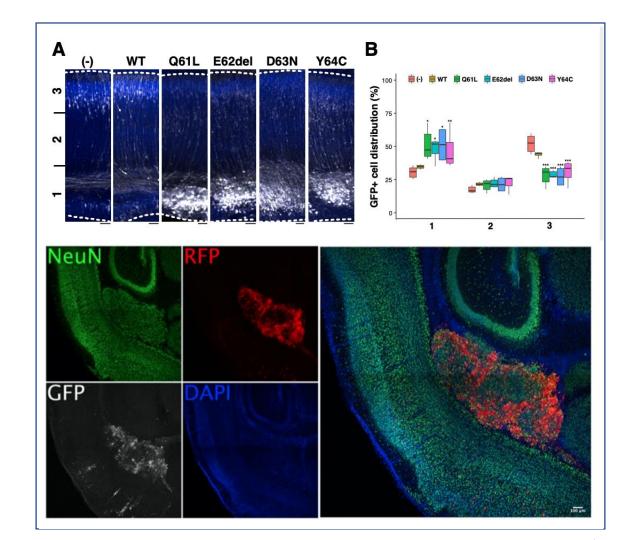




Functional investigation: cortical migration

RAC3 plays a pivotal role in the physiological **migration** of neuronal progenitors during corticogenesis, from VZ to cortical plate

RAC3 mutant neurons are **not able to migrate properly**, leading to the formation of clusters in the VZ/SVZ and IZ

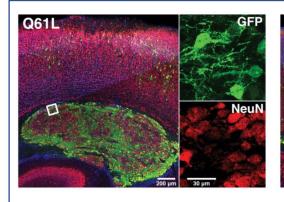


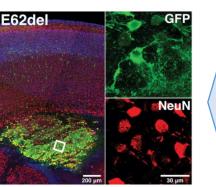


Functional investigation: cortical migration

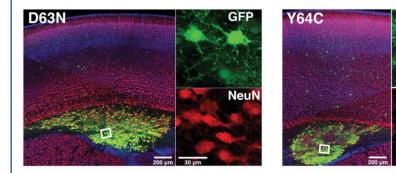
Clinically, this reflects into the spectrum of MCDs observed in NEDBAF:

- Dysgyria
- > Polymicrogyria
- Nodular heterotopia

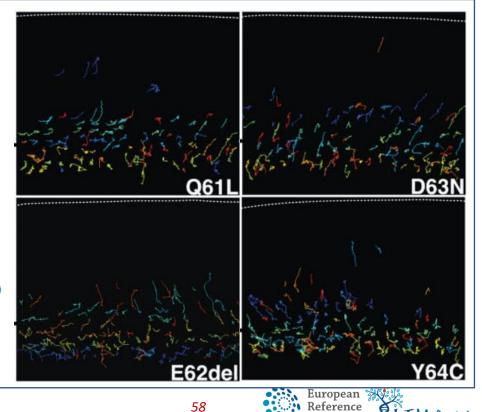




Retained islets of neuronal progenitors (heterotopia)



Time-lapse imaging analyses of migration of mutant cortical neurons



ALTHAKA

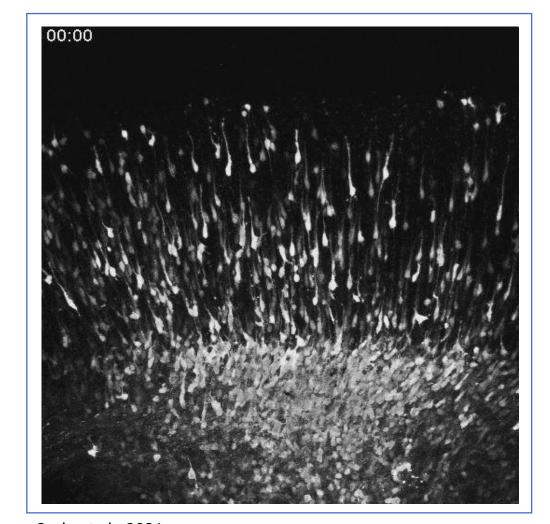
Webinar ITHACA 2025

Corticogenesis: neuronal migration

Newborn **wildtype cortical neurons** in the ventricular zone (VZ) show multipolar shape in the lower intermediate zone (IZ), with:

- Slow and irregular movement (multipolar movement)
- Bipolar shaping (upper IZ)
- Radial migration with saltatory movement*

*extension of the leading process and translocation of the cell body (Tabata and Nakajima, 2003)



Scala et al., 2021 Webinar ITHACA 2025



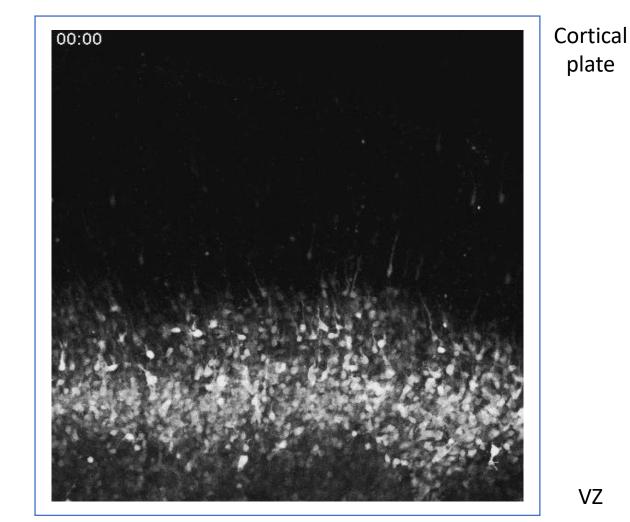
VZ

European `

RAC3 variants affect neuronal maturation

Instead, *RAC3* mutant neurons show **significant abnormalities in their maturation**:

- Q61L, E62del, D63N, and Y64C mutants remain stuck in the IZ
- E62del and D63N mutants
 fail to acquire multipolar
 shape and remain round



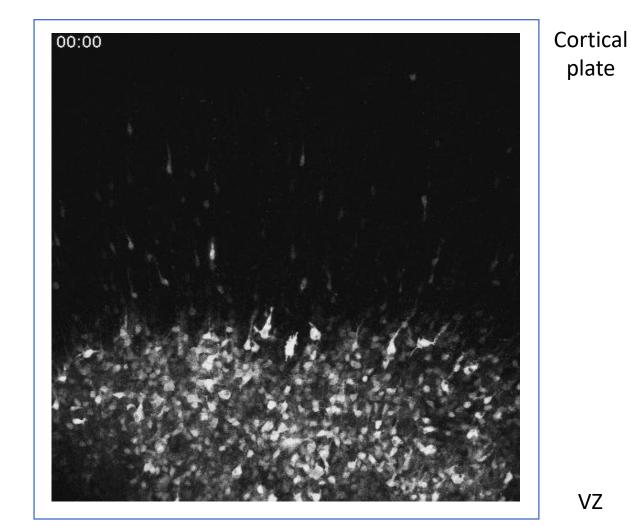
Scala et al., 2021 Webingr ITHACA 2025



RAC3 variants affect neuronal maturation

The effects of RAC3 variants on neuronal maturation are also **variant-specific**

Neurons transfected with Q61L or Y64C variants become multipolar but **fail the transition to bipolar shape**



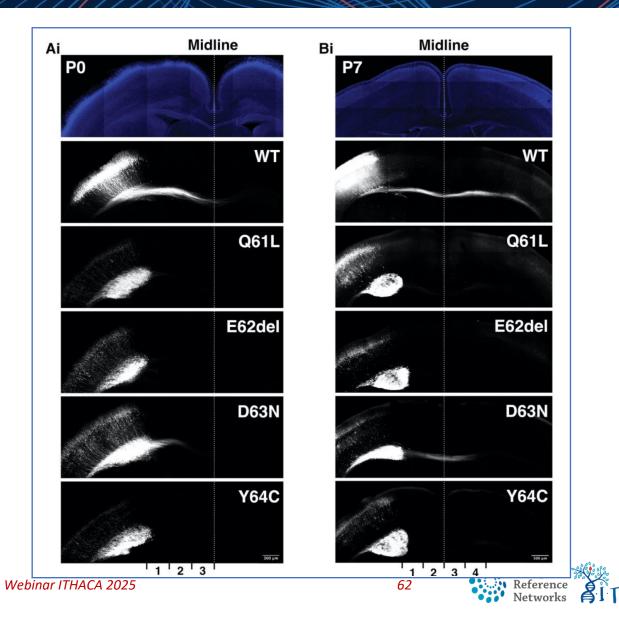


Functional investigation: Axonogenesis

RAC3 is important for **axonal elongation**, which underlies the development of white matter

RAC3 mutant neurons are **unable to project** their axons or can only project a thin bundle

Abornmalities in controlateral axon bundle projection explain the **white matter disorders** observed in NEDBAF, especially **corpus callosum dysgenesis**



Characterizing single variants: why?



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The F28S variant

Neurogenetics

Original research

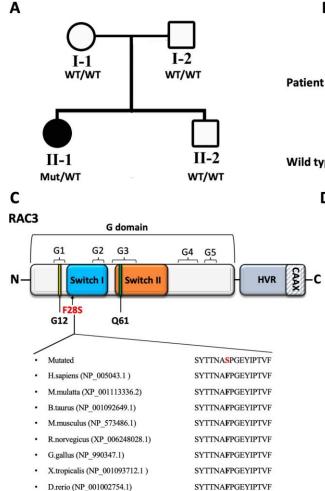
Gain-of-function p.F28S variant in *RAC3* disrupts neuronal differentiation, migration and axonogenesis during cortical development, leading to neurodevelopmental disorder

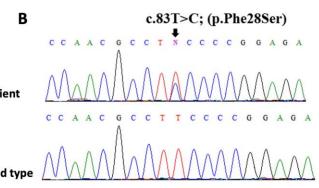
Masashi Nishikawa,¹ Marcello Scala,^{2,3} Muhammad Umair ⁽¹⁾, ^{4,5} Hidenori Ito,¹ Ahmed Waqas,⁶ Pasquale Striano ⁽¹⁾, ^{2,3} Federico Zara,⁷ Gregory Costain ⁽¹⁾, ⁸ Valeria Capra,⁷ Koh-ichi Nagata ⁽¹⁾, ¹

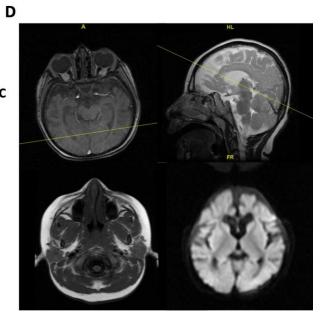
In this study, we identified and characterized a novel *RAC3* variant in the **Switch I domain**

The switch I and II domains contain the consensus binding sites for regulatory proteins and effectors

This 13yo patient had **NEDBAF** with delayed myelination, cerebral volume loss (WM++), and hypoplasia of the corpus callosum







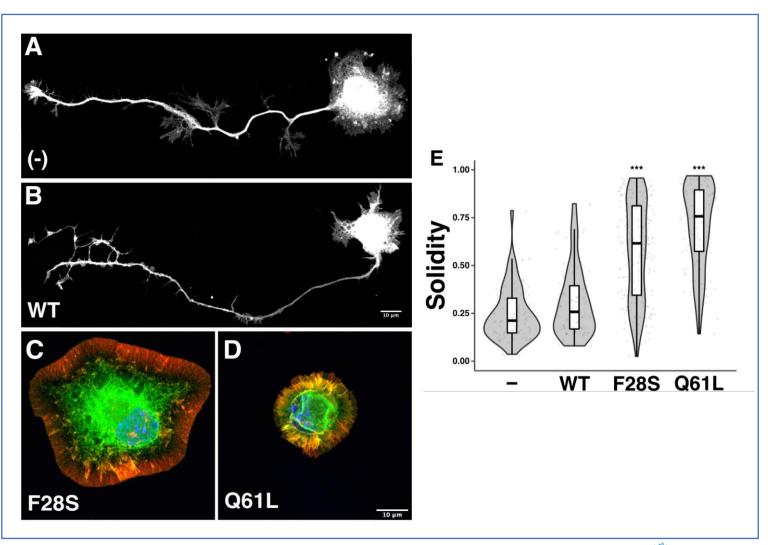


Lamellipodia formation

Hippocampal neurons electroporated with RAC3-F28S displayed cell rounding and lamellipodia formation, with increased solidity and defective differentiation

Compared to RAC3-Q61L, RAC3-F28S only **moderately facilitate** cytoskeletal reorganisation to form **lamellipodia**

However, **this mild impact is sufficient** to disrupt cell-signalling and impair neuronal morphology and function



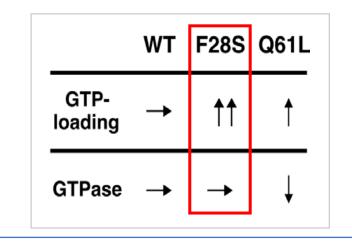


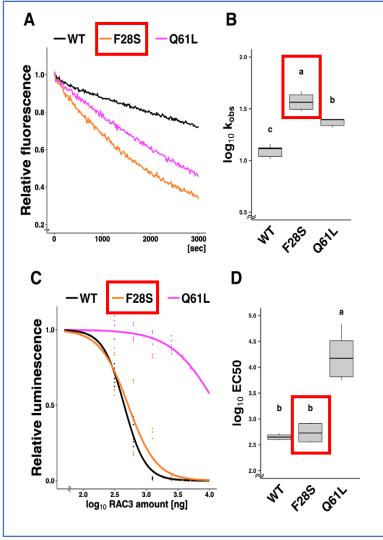
Biochemical activity

We then measured intrinsic GTP/GDPexchange and GTP- hydrolysis activities:

- RAC3-F28S significantly accelerates GDP/GTP-exchange (> Q61L)
- RAC3-F28S slightly affects GTP hydrolisis (<< Q61L)</p>

Thus, **RAC3-F28S** acts as a **GOF** variant through a higher GTP/GDP-exchange activity, despite normal intrinsic GTP-hydrolysis





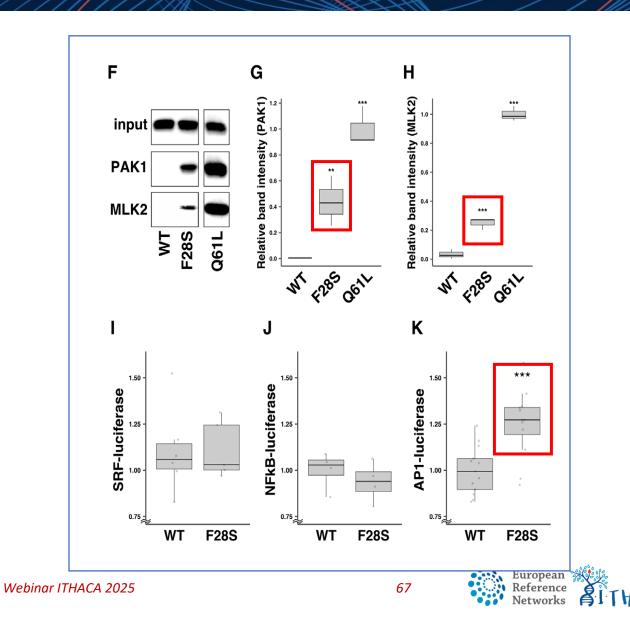
Impact on effectors

PAK1 (crucial for neuronal migration and mutated in NDDs) and **MLK2** (activator of JNK-MAP kinase downstream signalling pathways) are downstream effectors of RAC3

RAC3-F28S hyperactivates PAK1-mediated and/or MLK2-mediated signalling

Rho-family proteins contribute to regulate SRF-mediated, NF- B-mediated, and AP1-mediated gene expression

RAC3-F28S dysregulates AP1-mediated signalling pathways

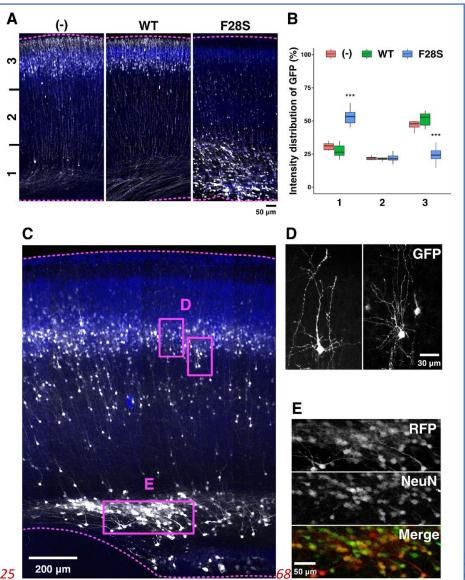


Impaired migration

The majority of RAC3-F28S-expressing cells **remain** in the ventricular and subventricular zones (VZ/SVZ) and the intermediate zone (IZ) (bin 1)

Cells incorporating high amount of the expression vector remained in the IZ and were positive for <u>NeuN</u>, indicating that they were **differentiate at abnormal posi-tions and extended neurites**

These results strongly suggest that RAC3-F28S dysregulates neuronal migration and development during corticogenesis

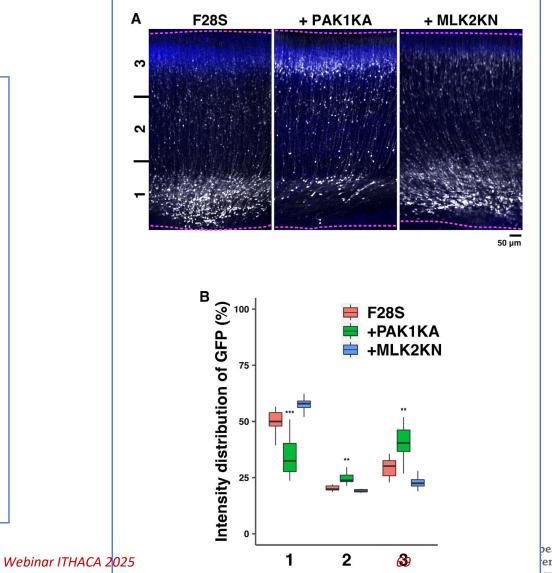


Role of PAK1 in NEDBAF

Since **RAC3-F28S** interacts with **PAK1**, which is also associated with an NDD, we analysed the possible involvement of PAK1 in the migration defects caused by RAC3-F28S

Co-electroporation with kinase-negative PAK1 (but not MLK2) **rescued** the positional defects of mutants

Thus, the **hyperactivation of PAK1 signalling** by RAC3-F28S is **responsible** for the neuronal migration defects and contributes to determine the NDD phenotype

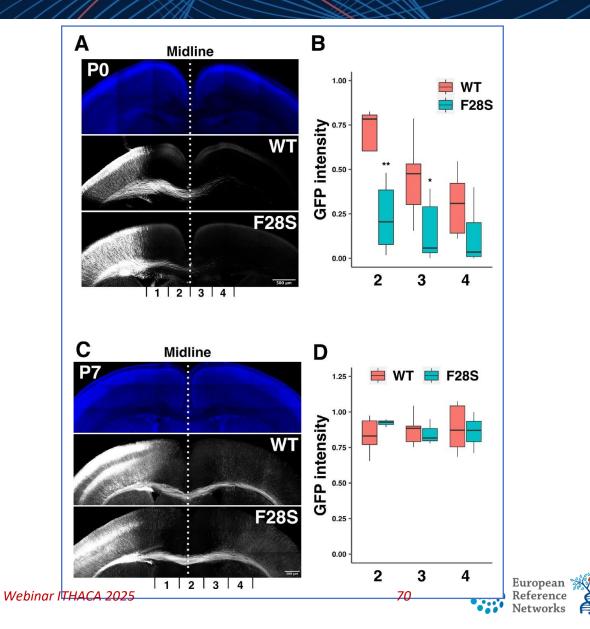


Axon elongation defect

Axon elongation was significantly <u>delayed</u> in neurons expressing RAC3-F28S

When we analysed the long-term effects at P7, control neurons as well as RAC3-F28S-expressing cells extended the axon efficiently into the contralateral cortex

These results suggest that RAC3-F28S **delayed, but not prevented**, axon elongation of cortical neurons



Atypical NEDBAF: the current borders of RAC3 research



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The N92K variant

Child's Nervous System (2024) 40:1597–1602 https://doi.org/10.1007/s00381-024-06285-z

CASE REPORT



An unusual presentation of *de novo RAC3* variation in prenatal diagnosis

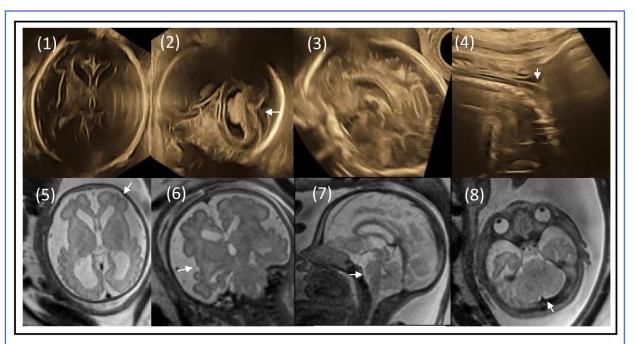
Colombine Meunier¹ · Marie Cassart² · Karole Kostyla³ · Nicolas Simonis¹ · Olivier Monestier¹ · Aude Tessier¹

Received: 5 December 2023 / Accepted: 6 January 2024 / Published online: 12 January 2024 $\ensuremath{\textcircled{}}$ The Author(s) 2024

Before this study, a single *RAC3* **prenatal case** was known, featuring midline and posterior fossa anomalies

Very recently, an **atypical clinical presentation** associated with a novel *RAC3* variant (**p.(Asn92Lys)**) was reported

This **second prenatal NEDBAF case** displayed ventriculomegaly and polymicrogyria, **without** callosal, cerebellar, or brainstem malformations



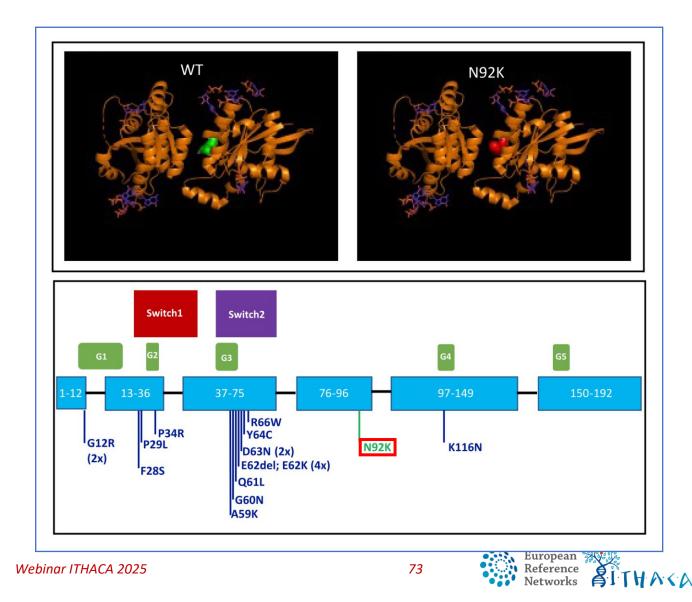
Sonographic and MRI examinations performed respectively at 28 and 31 WG showing:

- Ventriculomegaly
- Square shape of the frontal horns
- Enlarged pericerebral spaces
- Hypoplastic frontal lobes
- Abnormal Sylvian operculization

The N92K variant

The **p.(Asn92Lys)** variant affects a conserved residue within a poorly characterized region of RAC1, **outside** of the mutational hotspots for classic NEDBAF

This suggests that variants localized in different regions of the protein may lead to **atypical** clinical presentations, leading to the concept of 'NEDBAF spectrum'



The N92K variant

Work in progress

Pathophysiological significance of a neurodevelopmental disorder-causative *RAC3* p.N92K variant located outside the functional regions

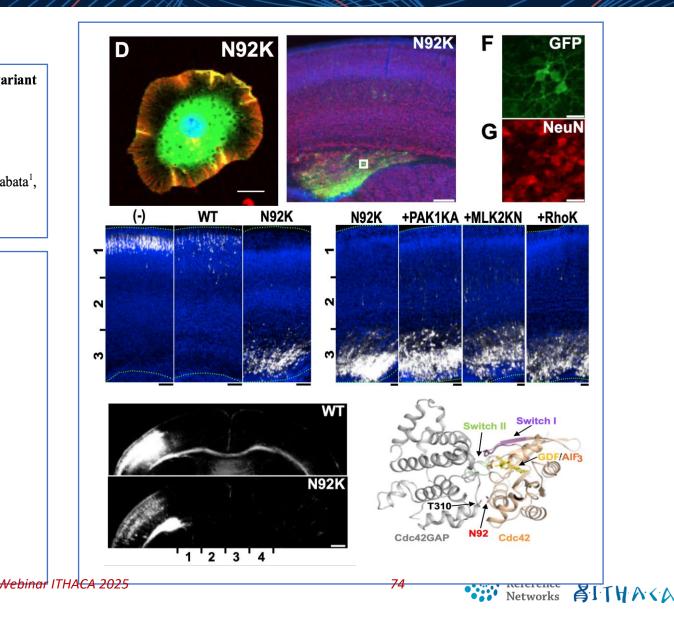
Ryota Sugawara^{1,2}*, Keisuke Hamada³*, Hidenori Ito¹, Marcello Scala^{4, 5}, Hiroshi Ueda², Hidenori Tabata¹,

Kazuhiro Ogata³, and Koh-ichi Nagata^{1,6}

In this study, we are exploring the functional properties of the N92K variant in search for mechanisms underlying **atypical NEDBAF**

We found that N92K:

- Is constitutively activated (GoF)
- Destabilize the interaction with GAPs (GoF)
- Is independent of PAK1, MLK2, Rho (vs Q61L!)
- Causes defects in cell migration -> heterotopia
- Impairs axon elongation



The R66W variant

Received: 15 September 2021 | Revised: 15 January 2022 | Accepted: 22 January 2022

DOI: 10.1002/pd.6106

RESEARCH NOTE

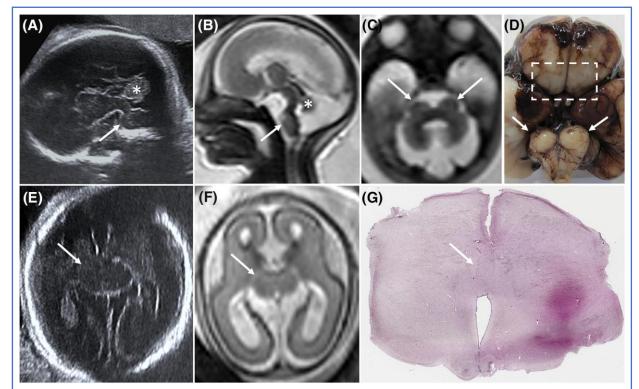
PRENATAL DIAGNOSIS WILEY

Prenatal imaging features related to RAC3 pathogenic variant and differential diagnoses

Sara Cabet^{1,2} | Alexandre Vasiljevic^{3,4} | Audrey Putoux^{2,5} | Audrey Labalme⁶ | Damien Sanlaville^{2,6} | Nicolas Chatron^{2,6} | Gaetan Lesca^{2,6} | Laurent Guibaud^{1,4} |

Aside from a variability in imaging patterns, likely reflecting a variability in NDD phenotypes, new research suggests that **atypical NEDBAF may embrace a much larger spectrum** of *RAC3*-related disorders

Surprisingly, a novel *RAC3* variant (**p.(Arg66Trp)**) was associated with a <u>fetal akinesia deformation sequence</u>, also featuring and <u>complex brain malformations</u> including corpus callosum agenesis, diencephalosynapsis, kinked brainstem, and vermian hypoplasia



Sonographic and MRI images at 24 WG showing:

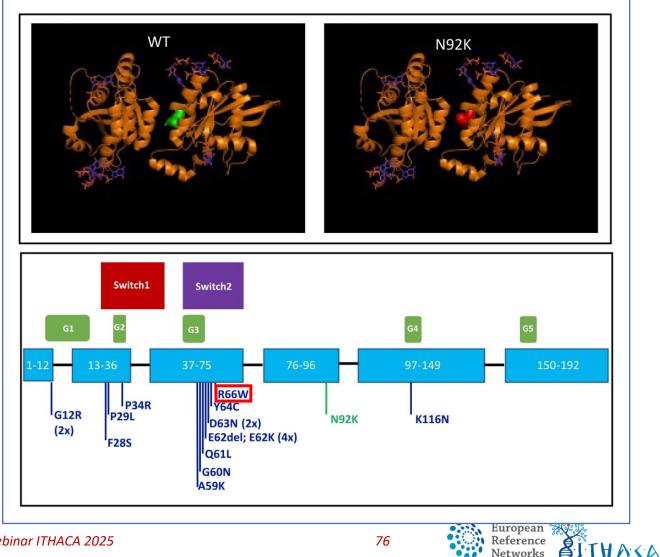
- Kinked brainstem with bifid pons
- Vermian hypoplasia
- Corpus callosum agenesis
- Arhinencephaly
- Diencephalosynapsis

The R66W variant

The **p.(Arg66Trp)** variant affects a conserved residue within the Switch II domain, crucial to mediate RAC3 interactions

Switch II is a **mutational hotspot** in classic NEDBAF

Despite this, the phenotype associated with R66W is pretty unique





The R66W variant



MDPI

Article

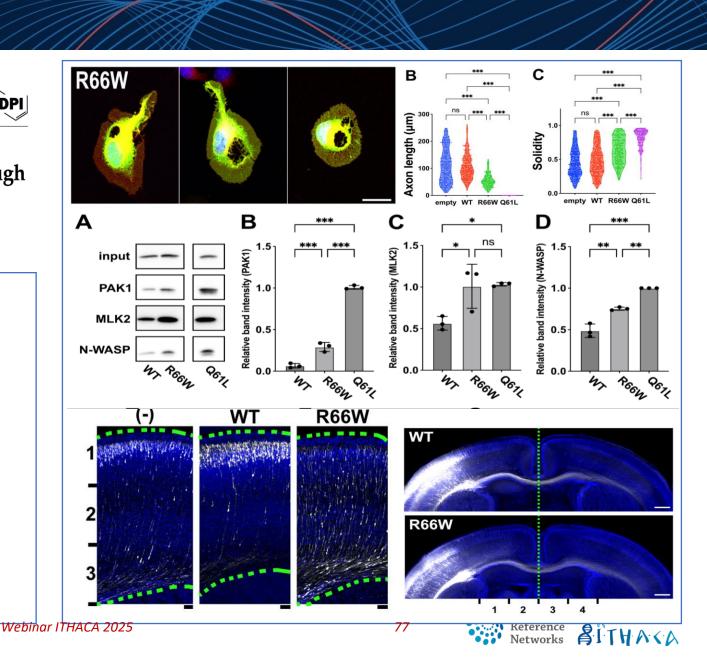
The p.R66W Variant in RAC3 Causes Severe Fetopathy Through Variant-Specific Mechanisms

Ryota Sugawara ^{1,2}, Hidenori Ito ¹, Hidenori Tabata ¹, Hiroshi Ueda ^{2,3}, Marcello Scala ⁴ and Koh-ichi Nagata 1,5,*0

In this study, we delved into the **pathophysiology of R66W**, showing that this variant:

- Is only mildly activated (mild GoF)
- Preferentially interact with MLK2 vs PAK1
- Does not activate transcription (SRF, AP1, NFkB)
- Impairs neuronal differentiation
- Impairs cortical migration
- Impairs axon elongation





Sara Cabet^{1,2} | Alexandre Vasiljevic^{3,4} | Audrey Putoux^{2,5} | Damien Sanlaville^{2,6} | Nicolas Chatron^{2,6} | Gaetan Lesca^{2,6} |

Received: 15 September 2021 Revised: 15 January 2022 Accepted: 22 January 2022

Child's Nervous System (2024) 40:1597-1602

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PRENATAL DIAGNOSIS WILEY Article

Audrey Labalme⁶

Laurent Guibaud^{1,4}

The p.R66W Variant in RAC3 Causes Severe Fetopathy Through Variant-Specific Mechanisms

Ryota Sugawara ^{1,2}, Hidenori Ito ¹, Hidenori Tabata ¹, Hiroshi Ueda ^{2,3}, Marcello Scala ⁴ and Koh-ichi Nagata 1,5,*0

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Pathophysiological significance of a neurodevelopmental disorder-causative RAC3 p.N92K variant

located outside the functional regions

Ryota Sugawara^{1,2*}, Keisuke Hamada^{3*}, Hidenori Ito¹, Marcello Scala^{4,5}, Hiroshi Ueda², Hidenori Tabata¹,

Kazuhiro Ogata³, and Koh-ichi Nagata^{1,6}

MDPI

DOI: 10.1002/pd.6106 **RESEARCH NOTE** Prenatal imaging features related to RAC3 pathogenic variant and differential diagnoses

Taken together, the atypical

The R66W variant

findings observed in prenatal cases suggest the existence of a severe 'RAC3 fetopathy'

This phenotype is part of the extended NEDBAF spectrum and underlain by variantspecific molecular mechanisms

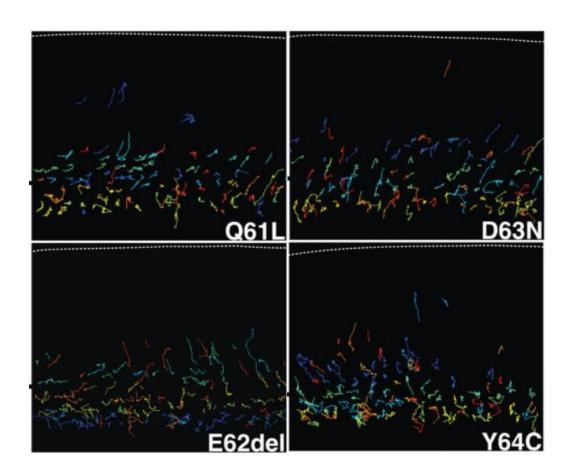
https://doi.org/10.1007/s00381-024-06285-z CASE REPORT Check for An unusual presentation of *de novo RAC3* variation in prenatal diagnosis Colombine Meunier¹ • Marie Cassart² • Karole Kostyla³ • Nicolas Simonis¹ • Olivier Monestier¹ Aude Tessier¹0 Received: 5 December 2023 / Accepted: 6 January 2024 / Published online: 12 January 2024

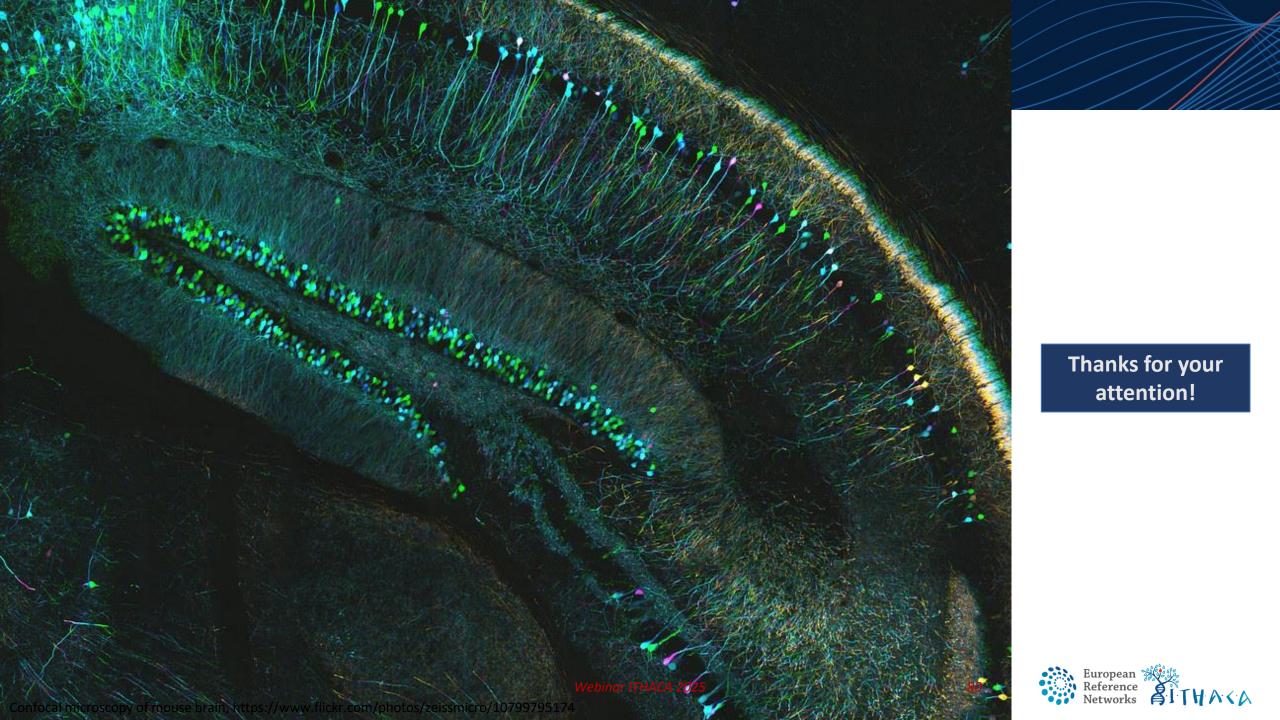


cells

Conclusive remarks

- > **RAC3** is a crucial for **brain development**, regulating:
 - Neuronal maturation
 - Neuronal migration
 - Axon elongation
- De novo variants in RAC3 cause a severe NDD (NEDBAF) featuring autistic features, cognitive deficiency, and a spectrum of brain malformations
- Generally, disease-causing variants cause RAC3 hyperactivation (GoF)
- However, recent research suggests the existence of variant-specific mechanisms -> NEDBAF spectrum
- This has significant impact on the diagnosis and management of affected individuals





3.Mechanistic analysis of RAC1 related neurodevelopmental disorders

Tom H. Millard, PhD - Division of Developmental Biology and Medicine, Faculty of Biology, Medicine and Health, University of Manchester M13 9PL, UK.







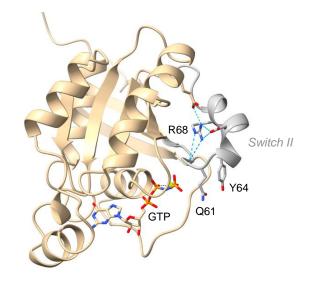
Mechanistic analysis of RAC1-related neurodevelopmental disorders

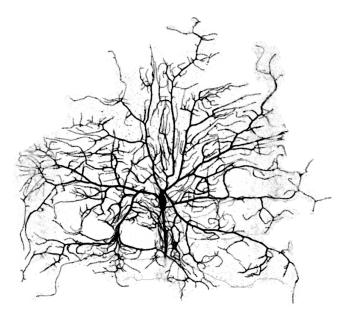
Tom Millard

University of Manchester, U.K.

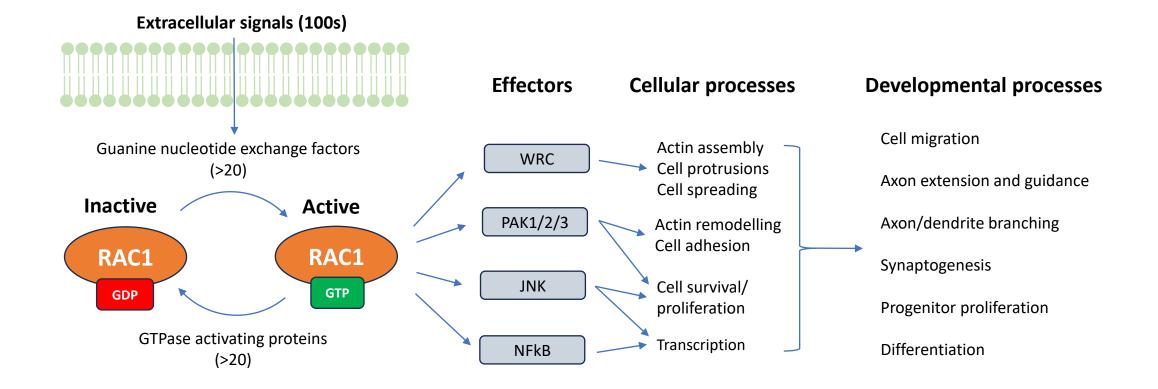


Siddharth Banka





RAC1: A key regulator of diverse cellular and developmental processes



2017: De novo missense variants in RAC1 cause a developmental disorder with diverse phenotypes



Variant

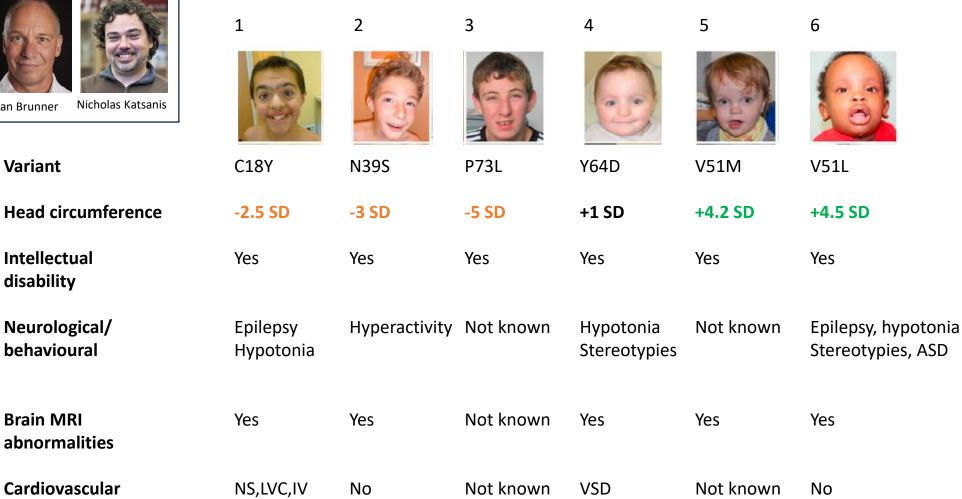
Intellectual

disability

Brain MRI

Margot Reijnders Han Brunner

Nicholas Katsanis

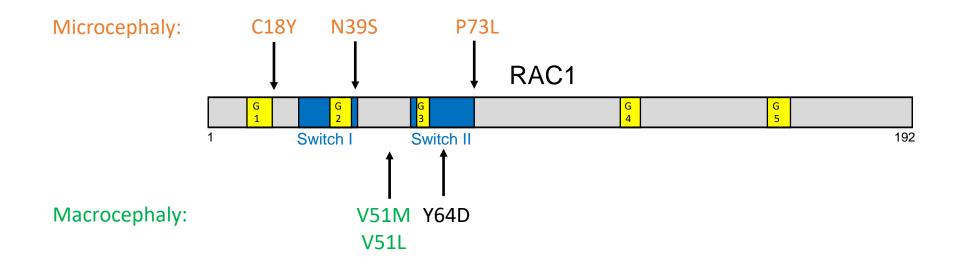


2017: De novo missense variants in RAC1 cause a developmental disorder with diverse phenotypes



Margot Reijnders Han Brunner Nicholas Katsanis	184	-102				a al
Variant	C18Y	N39S	P73L	Y64D	V51M	V51L
Head circumference	- 2.5 SD	-3 SD	-5 SD	+1 SD	+4.2 SD	+4.5 SD
Intellectual disability	Yes	Yes	Yes	Yes	Yes	Yes
Neurological/ behavioural	Epilepsy Hypotonia	Hyperactivity	Not known	Hypotonia Stereotypies	Not known	Epilepsy, hypotonia Stereotypies, ASD
Brain MRI abnormalities	Yes	Yes	Not known	Yes	Yes	Yes
Cardiovascular	NS,LVC,IV	No	Not known	VSD	Not known	No
Reijnders <i>et al.</i> 2017 AJHG	Mi	Webinar ITH Crocephal	ACA 2025		Mac	rocephaly

Does head circumference correlate with location of variant in RAC1 protein?

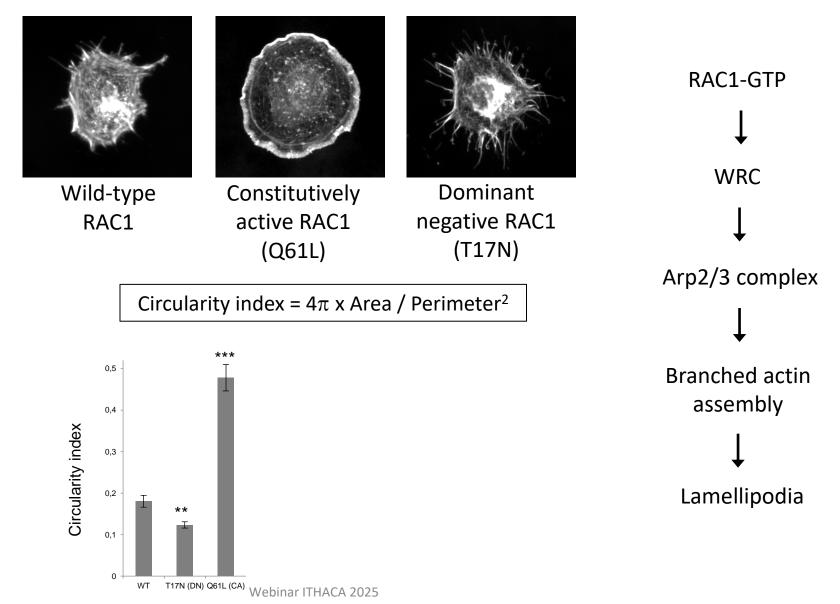


Switch domains: Different conformations in GTP and GDP bound states. Main interaction sites for upstream regulators and downstream effectors

G1-5 motifs: Collectively form the GTP/GDP binding site

Does head circumference correlate with effect on RAC1 activity?

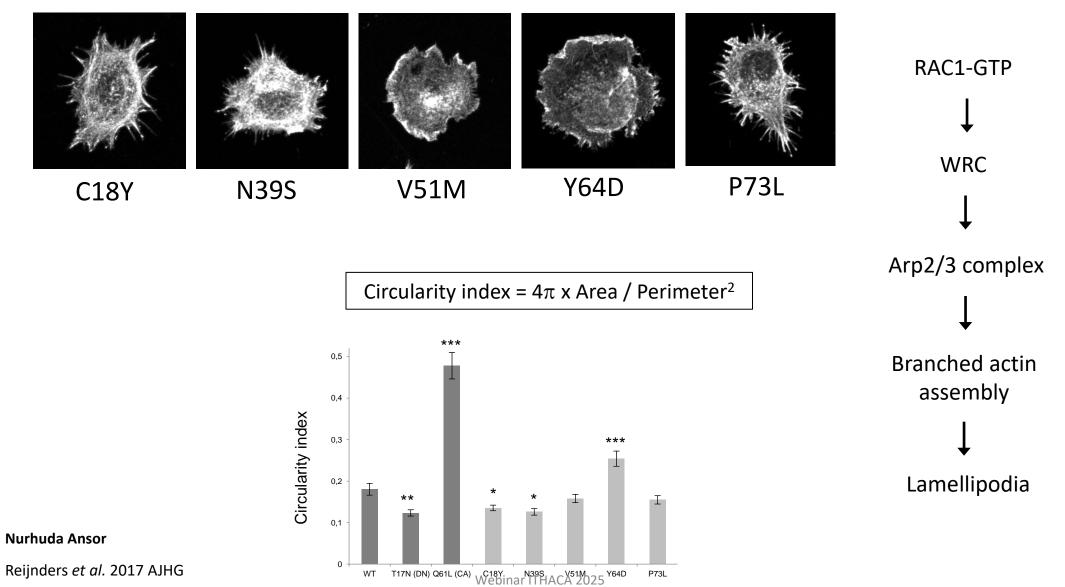
Fibroblast spreading – a simple cellular assay for RAC1 activity



Nurhuda Ansor

Reijnders et al. 2017 AJHG

Fibroblast spreading – a simple cellular assay for RAC1 activity



De novo RAC1 missense variants cause a developmental disorder with extremely diverse phenotypes

3

Macrocephaly

89

6

5

4

Microcephaly

2

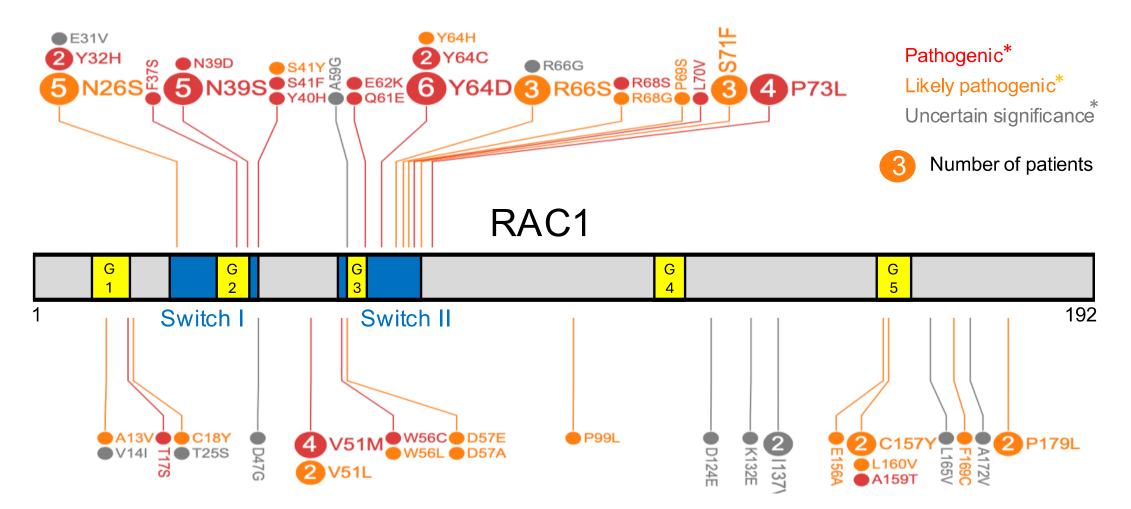
1



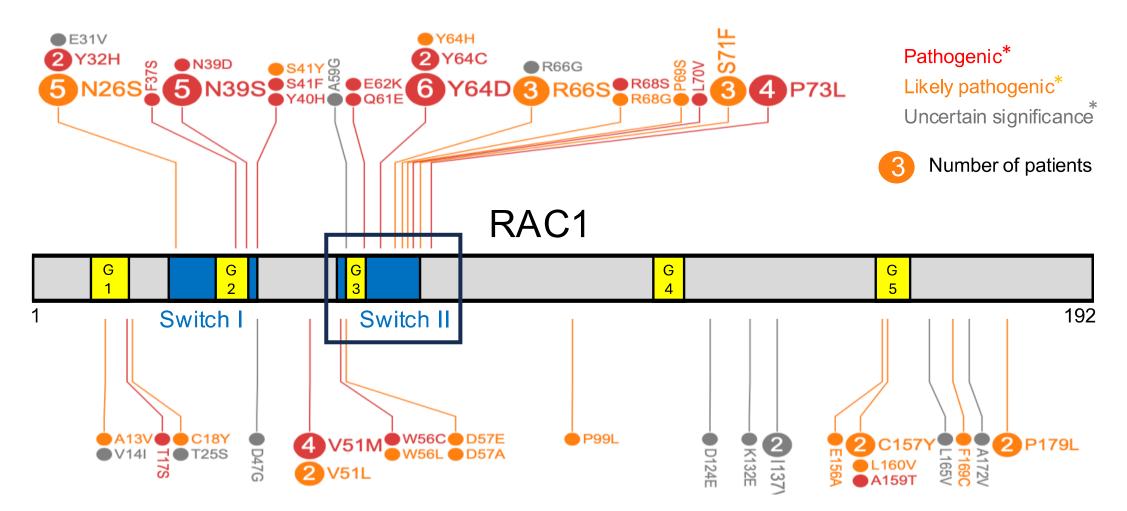
Reijnders et al.

ers Han Brunner Nicholas Katsanis	184	132				a al
Variant	C18Y	N39S	P73L	Y64D	V51M	V51L
Head circumference	-2.5 SD	-3 SD	-5 SD	+1 SD	+4.2 SD	+4.5 SD
Intellectual disability	Yes	Yes	Yes	Yes	Yes	Yes
Neurological/ behavioural	Epilepsy Hypotonia	Hyperactivity	Not known	Hypotonia Stereotypies	Not known	Epilepsy, hypotonia Stereotypies, ASD
Brain MRI abnormalities	Yes	Yes	Not known	Yes	Yes	Yes
Cardiovascular	NS,LVC,IV	No	Not known	VSD	Not known	No
Effect on RAC1 activity I. 2017 AJHG	DN	DN Webinar ITH	Likely DN ACA 2025	Activating	?	?

2025: >80 individuals with >50 distinct variants identified

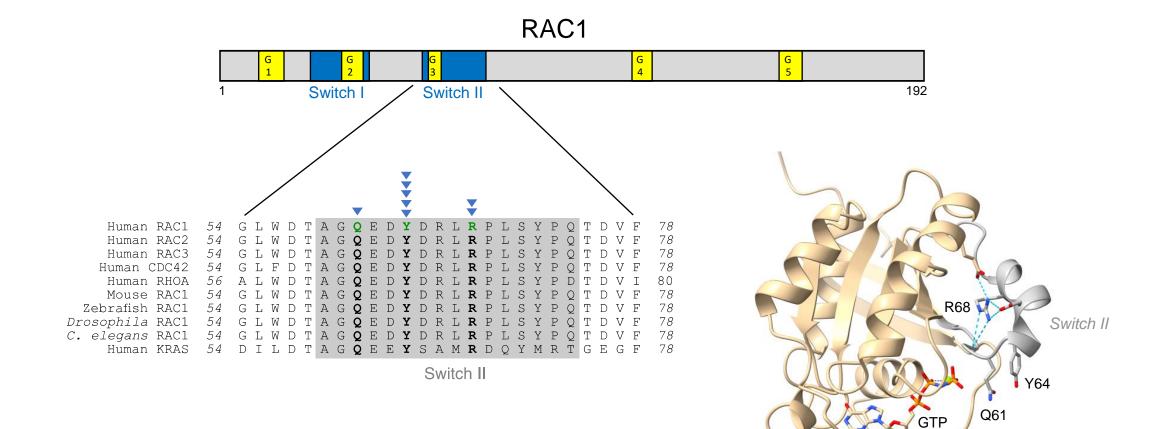


2025: >80 individuals with >50 distinct variants identified



Highest concentration of pathogenic wariants in switch II region of RAC1

Focus on variants affecting switch II



Eight individuals identified with variants affecting Q61-R68 within switch II region

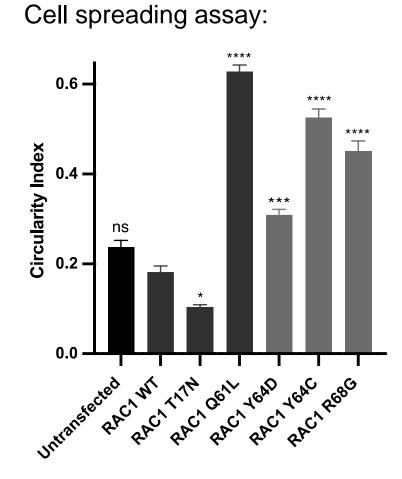
	1	2	3	4	5	6	7	8
Variant	Q61E	Y64D	Y64D	Y64D	Y64D	Y64C	R68S	R68G
Head circumference	-2 SD	+0.7 SD	-0.8 SD	+3.1 SD	+0.2 SD	-1.6 SD	-2.2 SD	-0.8 SD
Intellectual disability	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Neurological/ behavioural	Eating disorder	Stereotypies	Hypotonia	Dyspraxia ADHD	Sleep difficulties	None	Hypotonia	Hypotonia
Brain MRI Abnormalities	None	Yes	Not known	Yes	Not known	Yes	Yes	Yes
Cardiovascular	ASD, VSD	VSD	None	Not known	VSD	None	PDA,PFO,TI	None

Variants affecting Q61-R68 do not cause extreme macro- or microcephaly

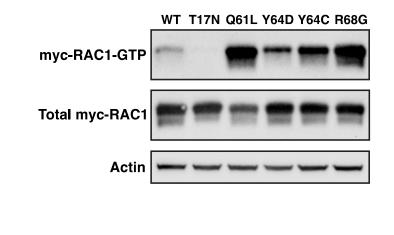
	1	2	3	4	5	6	7	8
Variant	Q61E	Y64D	Y64D	Y64D	Y64D	Y64C	R68S	R68G
Head circumference	-2 SD	+0.7 SD	-0.8 SD	+3.1 SD	+0.2 SD	-1.6 SD	-2.2 SD	-0.8 SD
Intellectual disability	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Neurological/ behavioural	Eating disorder	Stereotypies	Hypotonia	Dyspraxia ADHD	Sleep difficulties	None	Hypotonia	Hypotonia
Brain MRI Abnormalities	None	Yes	Not known	Yes	Not known	Yes	Yes	Yes
Cardiovascular	ASD, VSD	VSD	None	Not known	VSD	None	PDA,PFO,TI	None

Do variants affecting Q61-R68 hrave similar effects on RAC1 activity?

Variants affecting Q61-R68 increase RAC1 activity



PAK pulldown assay:



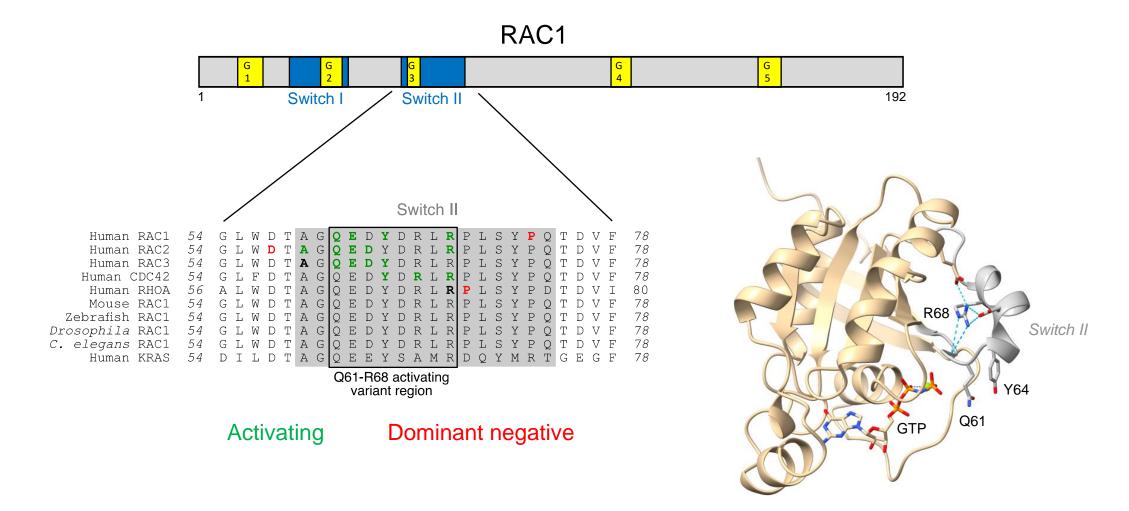
Abi Bennington, Martin Baker

Banka et al (2022) Brain

Downstream PAK and WRC pathways both activated by these variants

Webinar ITHACA 2025

Variants affecting Q61-R68 are activating throughout the Rho GTPase family



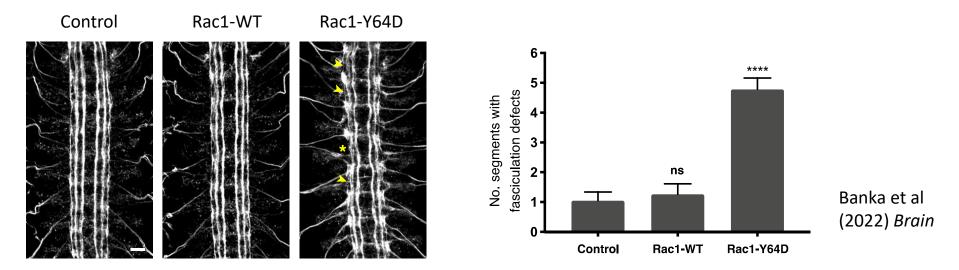
How do activating switch II variants affect neurodevelopment?



Drosophila melanogaster

RAC1 structure and function extremely well conserved

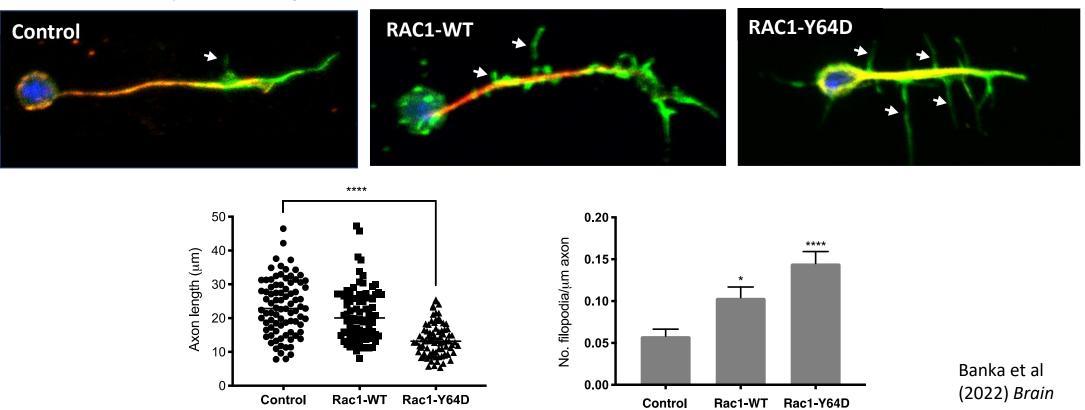
Neurons in developing *Drosophila* embryonic VNC (spinal cord):



Expression of activating RAC1 variant causes neuronal disorganization in embryonic CNS 97

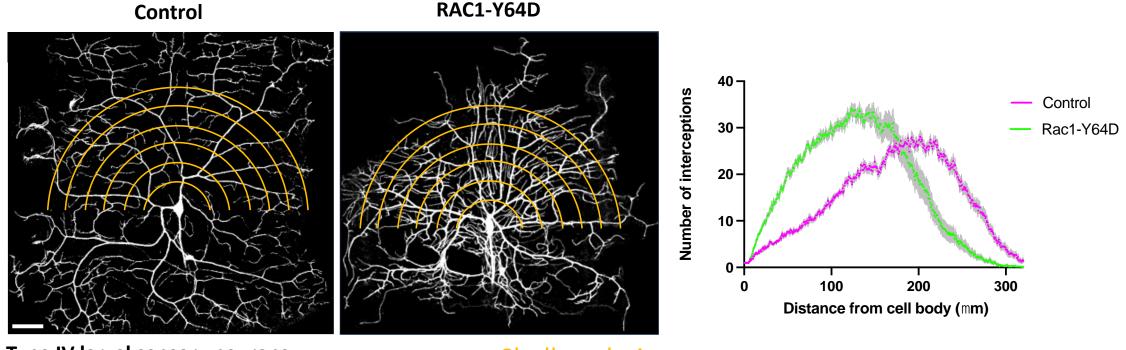
How do activating *RAC1* variants affect the morphology of individual neurons?

Cultured *Drosophila* embryonic neurons



Expression of activating RAC1 variant reduces axonal length and increases lateral filopodia

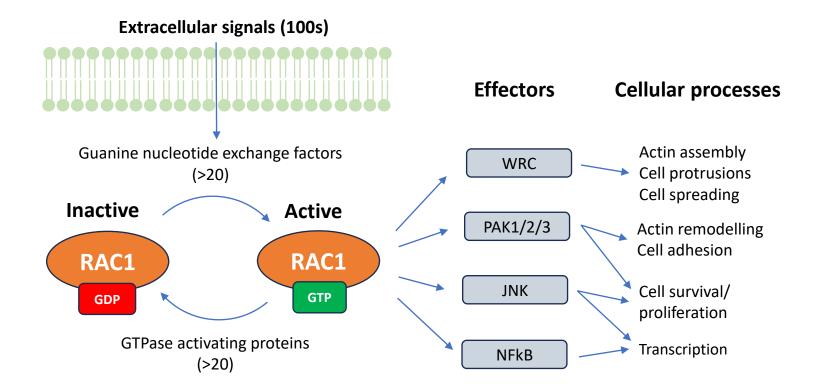
Expression of an activating *RAC1* variant increases dendritic arbor complexity



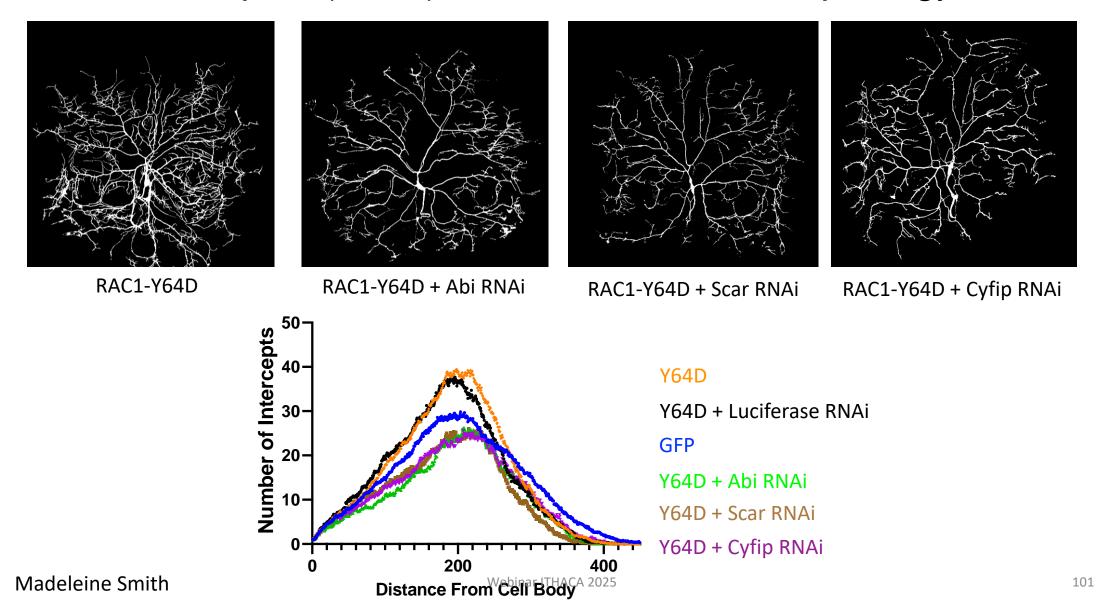
Type IV larval sensory neurons

Sholl analysis

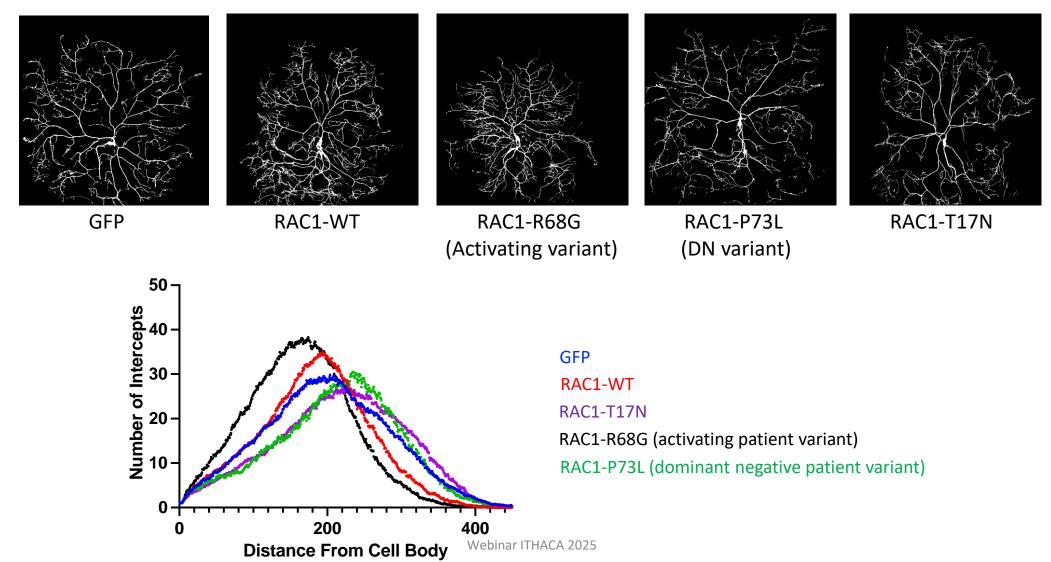
Which effector drives neuronal morphology changes caused by activating variants?



Knocking down components of the WAVE regulatory complex (WRC) rescues neuronal morphology



Dominant negative *RAC1* variants reduce dendritic complexity



Conclusions

Variants in *RAC1* cause complex developmental disorders with a wide phenotypic spectrum

RAC1 variants result in at least 3 mechanistically distinct disorders:

Dominant negative	Microcephaly	Reduced dendritic complexity
Activating	Normocephaly	Increased dendritic complexity
?	Macrocephaly	No effect

Likely to be other mechanistically distinct variant groups/sub-groups



The University of Manchester

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Margot Reijnders Han Brunner Nicholas Katsanis Maria Kousi Wyatt Yue Persiliz Tan Katie Clarkson Jill Clayton-Smith Ken Corning Julie Jones Wayne Lam Grazia Mancini Carlo Marcelis Shehla Mohammed **Rolph Pfundt** Maian Roifman **Ronald Cohn**

+ Patients and their families



tom.millard@Manchester.ac.uk

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David Chitayat Ellen Rijckmans Kwame Anyane-Yeboa Lauren Badalato **Boyan Dimitrov David Fitzpatrick** Anna Hurst Anna Jansen Melissa Kelly Ian Krantz **Claudine Rieubland Meredith Ross** Natasha Rudy Javier Sanz Katrien Stouffs Zhuo Luan



Discussion & Conclusion

Time for questions



- Satisfaction Survey :
 - https://forms.office.com/e/kznh4KWQG9
- Website :
 - https://ern-ithaca.eu



European Reference

ERN ITHACA Satisfaction Survey Webinar jan 21, 2025



