Friday, September 05, 2025

Dystonia: Bridging Theory and Hands-On Expertise

Genetic basis of dystonia

Michael Zech, MD

Institute of Neurogenomics, Helmholtz Center Munich

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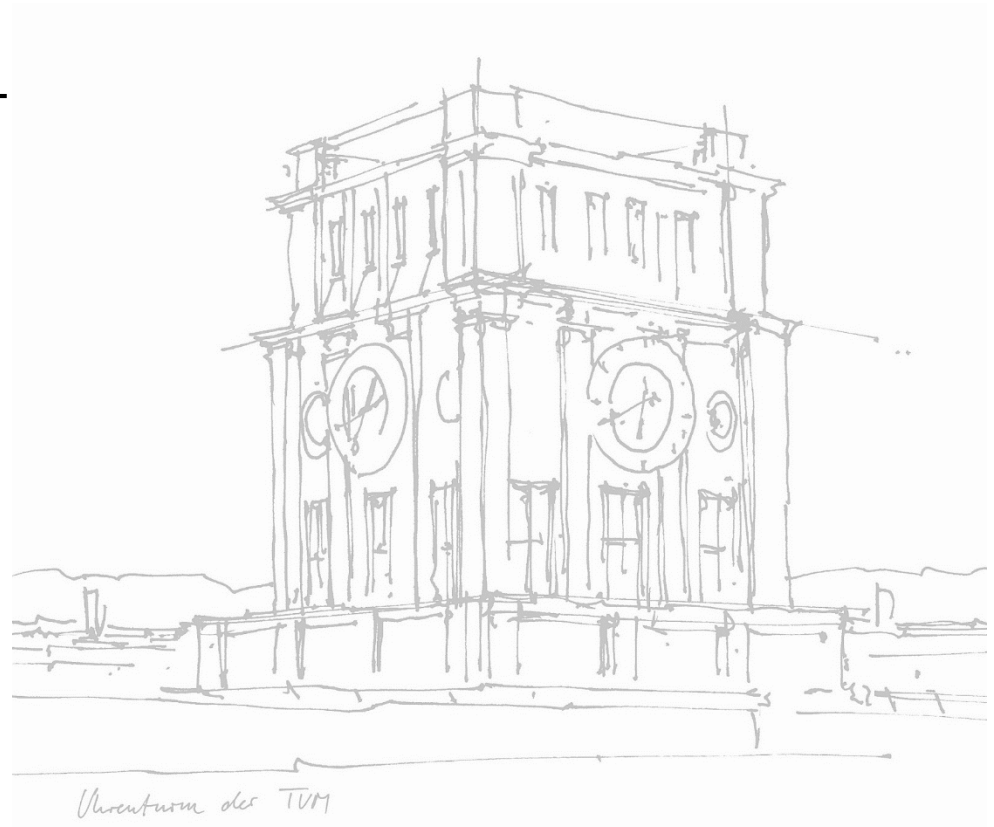
Institute for Advanced Study, Technical University of Munich



Genetic basis of dystonia

Dystonia is a very heterogeneous disorder

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Axis I: clinical characteristics
Age at onset
• Infancy (<2 y)
• Childhood (>2–12 y)
• Adolescence (>12–20 y)
• Early adulthood (>20–40 y)
• Late adulthood (>40 y)
Family history
• Sporadic
• Familial
• Unknown
Body distribution
• Focal
• Segmental
• Multifocal
• Hemidystonia
• Generalized
Temporal dimensions
Onset
• Acute
• Subacute
• Gradual
Course
• Static
• Progressive
• Fluctuating
Variability
• Paroxysmal
• Diurnal variability
• None

Phenomenology
Relationship with voluntary movement
• Task-specific (occurs only with one specific voluntary motor task)
• Action-induced (occurs with a variety of voluntary actions)
• Occurs also at rest (unrelated to voluntary movements)
• Fixed (it is continuous and unalleviated)
Additional characteristics
• Alleviating maneuvers (sensory trick, *geste antagoniste*)

Isolated or combined
• Isolated
• Combined
• With another movement disorder
• With other neurological features
• With systemic features

Clinical heterogeneity

REVIEW

Definition and Classification of Dystonia

Alberto Albanese, MD,[1,2*] Kailash P. Bhatia, MD, DM, FRCP,[3] Victor S.C. Fung, PhD, FRACP,[4] Mark Hallett, MD,[5] Joseph Jankovic, MD,[6] Christine Klein, MD,[7] Joachim K. Krauss, MD,[8] Anthony E. Lang, MD, FRCPC,[9,10] Jonathan W. Mink, MD, PhD,[11] Sanjay Pandey, DM,[12] Jan K. Teller, MA, PhD,[13] Marina A.J. Tijssen, MD,[14,15] Marie Vidailhet, MD,[16,17,18] and H.A. Jinnah, MD, PhD[19,20]

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Genetic basis of dystonia

Dystonia is a very heterogeneous disorder

Axis II: etiology and pathogenesis
Genetic
• Autosomal dominant
• Autosomal recessive
• X-linked recessive
• Maternal
• Unknown*
Acquired
• Medications
• Toxins
• Trauma
• Other acquired cause
• Unknown*
Neuroanatomical
• Focal lesion
• Multifocal lesions
• Diffuse lesions
• Unknown[a]
Pathogenesis
• Developmental
• Degenerative
• Metabolic
• Immune or inflammatory
• Unknown

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Etiological heterogeneity

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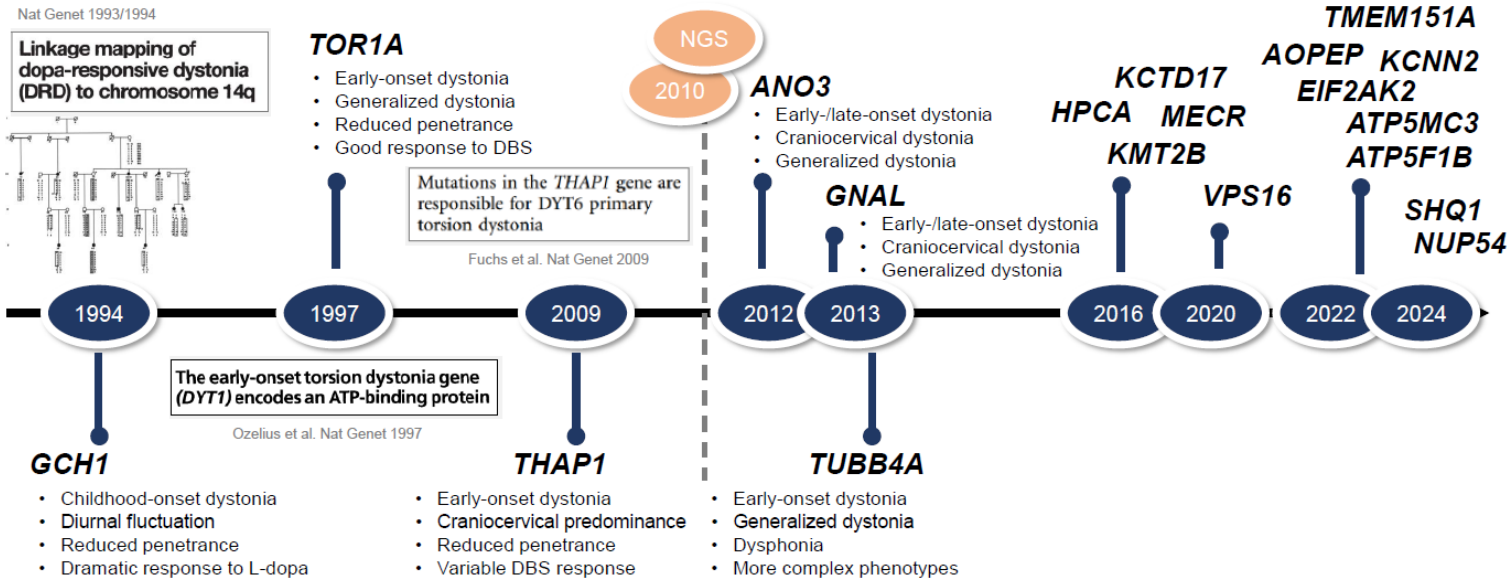
Etiological heterogeneity

Genetic basis of dystonia

Gene discovery timeline in dystonia and DYT nomenclature OMIM® DYT1-DYT37

https://omim.org/



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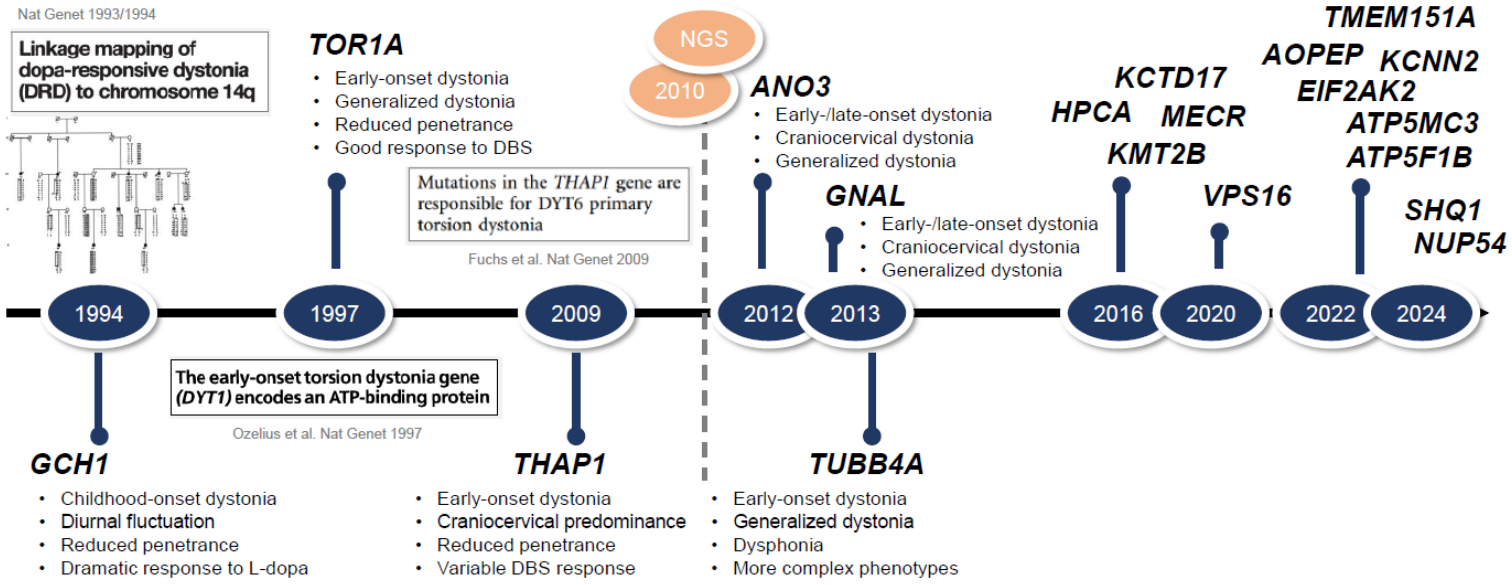

MDSGene database

https://www.mdsgene.org/

Monogenic forms of dystonia

Isolated dystonia	Combined dystonia	Complex dystonia	
• DYT-ANO3	• DYT-COX20	• DYT-ACTB	• DYT/CHOR-ACAT1
• DYT-EIF2AK2	• DYT-DNAJC12	• DYT-ATP7B	• DYT/CHOR-ADAR1
• DYT-GNAL	• DYT-SLC39A14	• DYT-BCAP31	• DYT/CHOR-FOXG1
• DYT-HPCA	• DYT/PARK-ATP1A3	• DYT-DCAF17-(NBIA)	• DYT/CHOR-GCDH
• DYT-KMT2B	• DYT/PARK-GCH1	• DYT-DDC	• DYT/CHOR-HPRT
• DYT-PRKRA	• DYT/PARK-TAF1	• DYT-FITM2	• DYT/CHOR-MUT
• DYT-THAP1	• DYT/PARK-TH	• DYT-IRF2BPL	• DYT/CHOR-PCCA/PCCB
• DYT-TOR1A	• DYT/CHOR-GNAO1	• DYT-MECR	• DYT/PARK-CP-(NBIA)
• DYT-VPS16	• MYC/DYT-KCTD17	• DYT-mt-ND6	• DYT/PARK-GLB1
• DYT-AOPEP	• MYC/DYT-SGCE	• DYT-OPA1	• DYT/PARK-PLA2G6-(NBIA)
		• DYT-PANK2-(NBIA)	• DYT/PARK-PTS
		• DYT-SERAC1	• DYT/PARK-QDPR
		• DYT-SLC19A3	• DYT/PARK-SLC6A3
		• DYT-SUCLA2	• DYT/PARK-SLC30A10
		• DYT-TIMM8A	• DYT/PARK-SPR
		• DYT-TUBB4A	• ATX/DYT-SQSTM1
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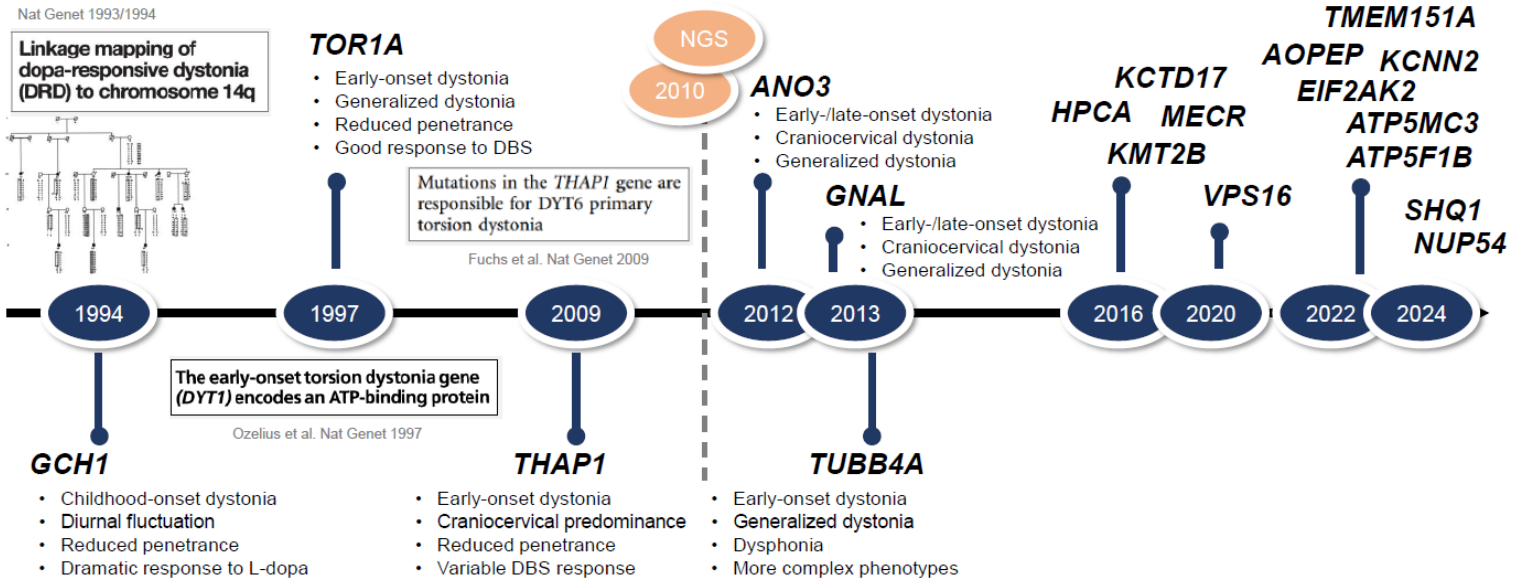

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		• DYT-VAC14	

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First generation sequencing

Targeted single gene testing

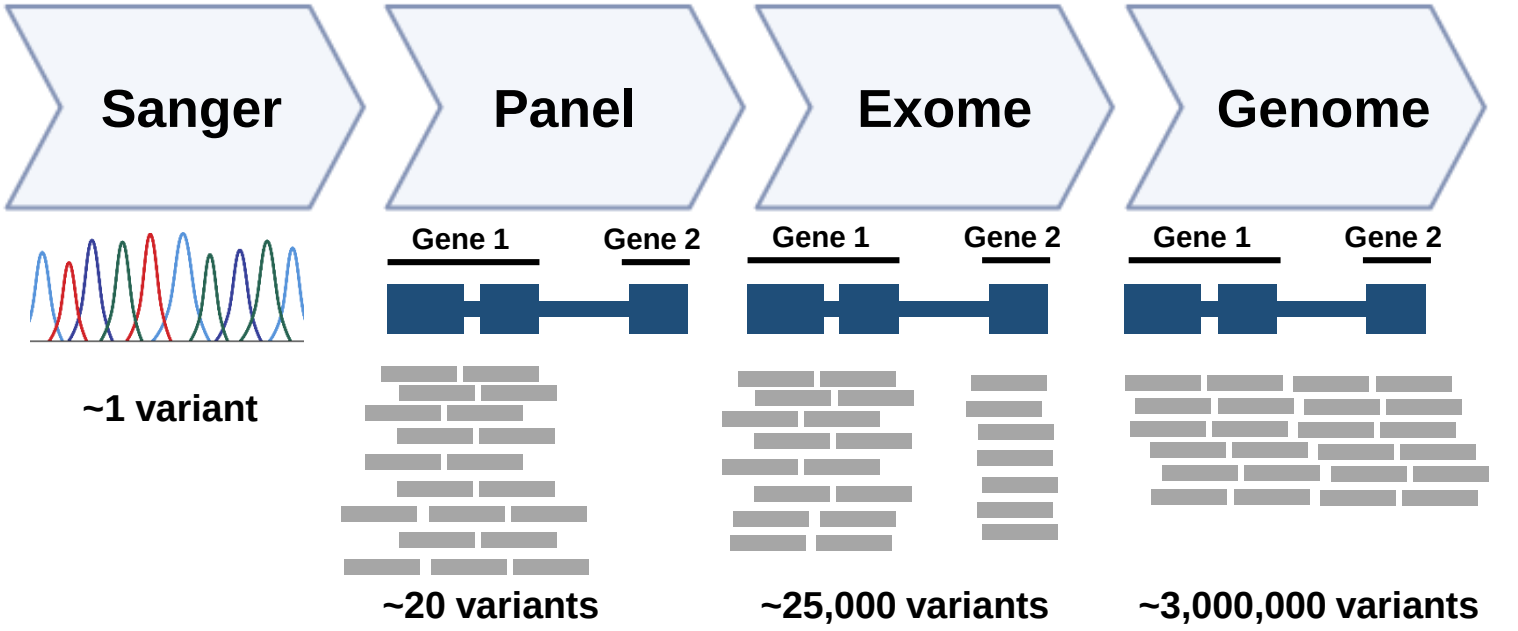
Next generation sequencing (NGS)

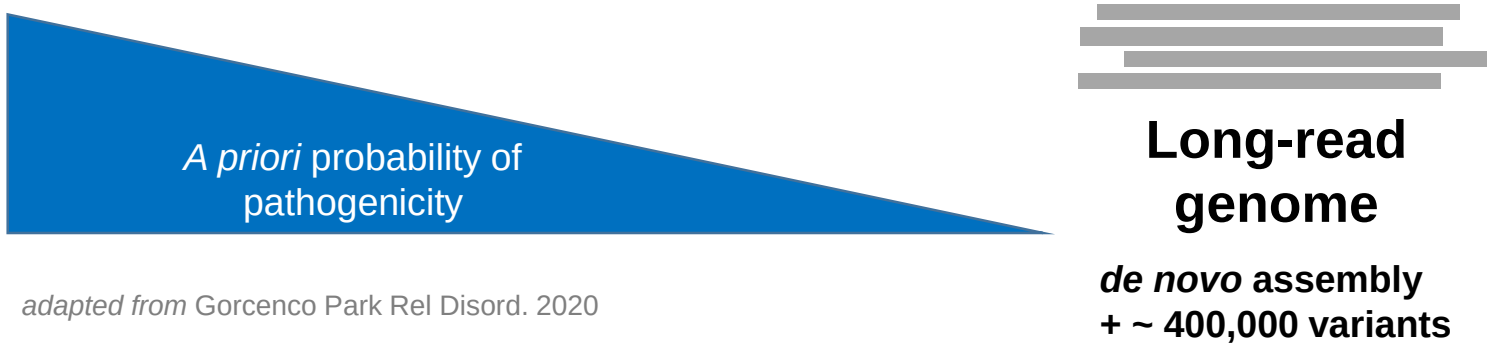
Short-read sequencing
Panels – whole-exome – whole-genome

Long-read genome sequencing

Genetic basis of dystonia

Development of genetics analysis technologies





adapted from Gorcenco Park Rel Disord. 2020

Genetic basis of dystonia

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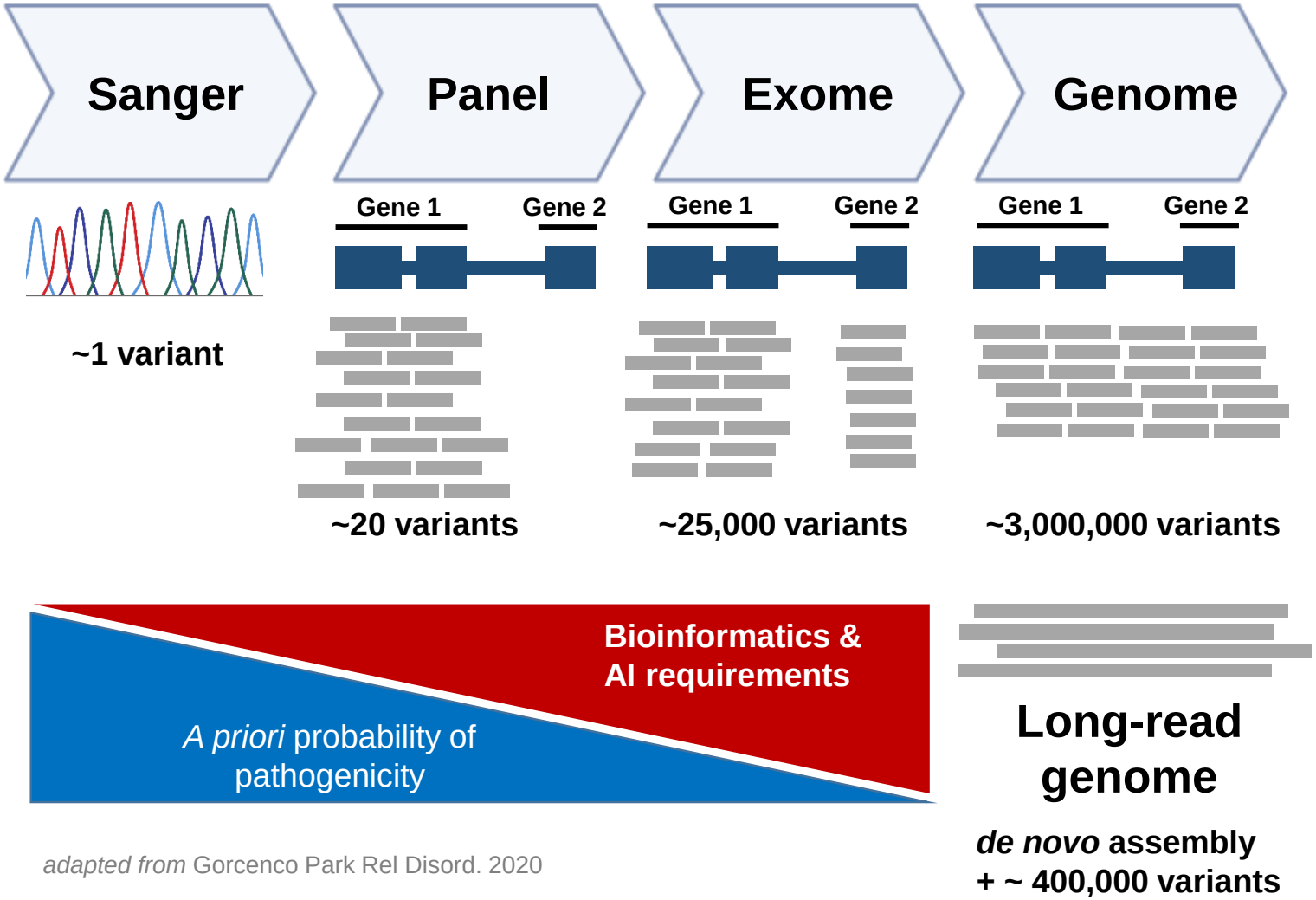

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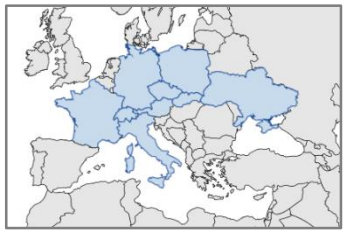
Genetic basis of dystonia

Example of a collaborative dystonia research cohort
>1,800 index patients, dystonia and dystonia plus other movement disorders and/or developmental features



2012-14 → 2015 → 2016 → 2017 → 2018 → 2019 → 2020 → 2021 → 2022 → 2023 → 2024 → 2025

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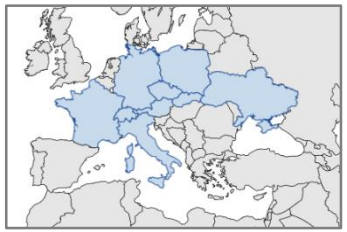

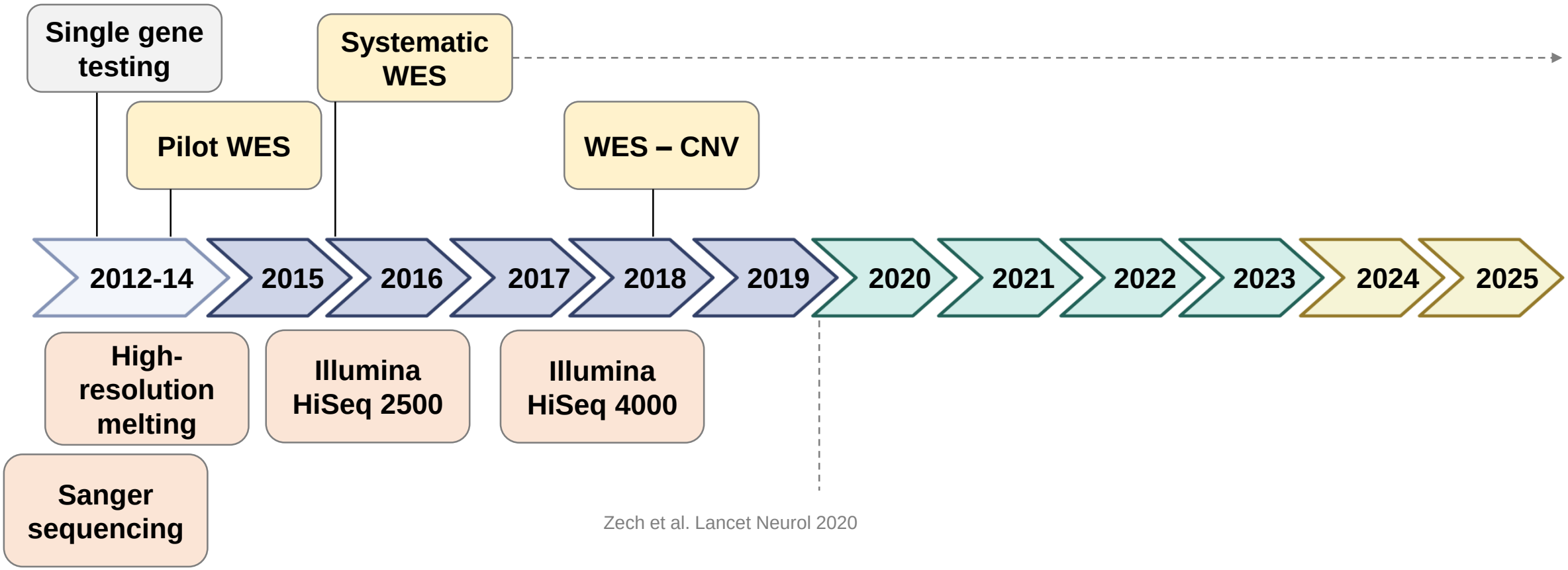

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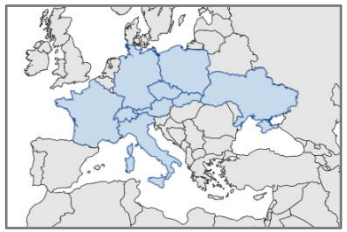
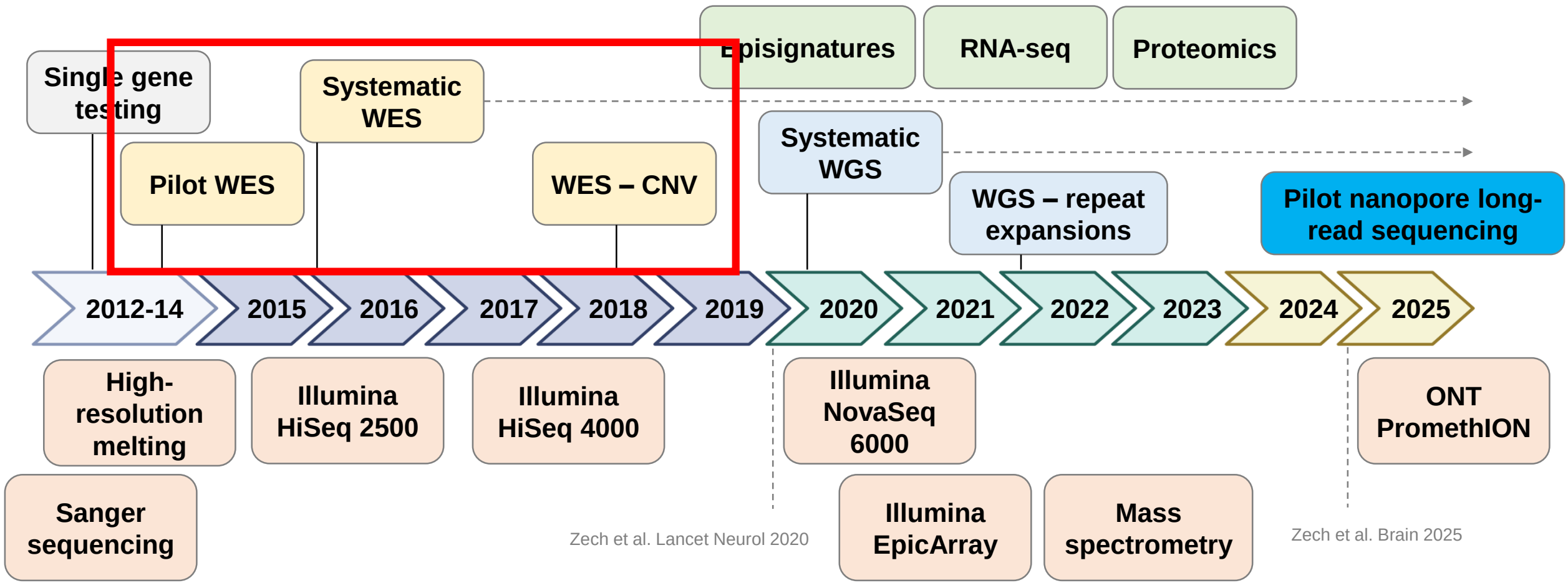
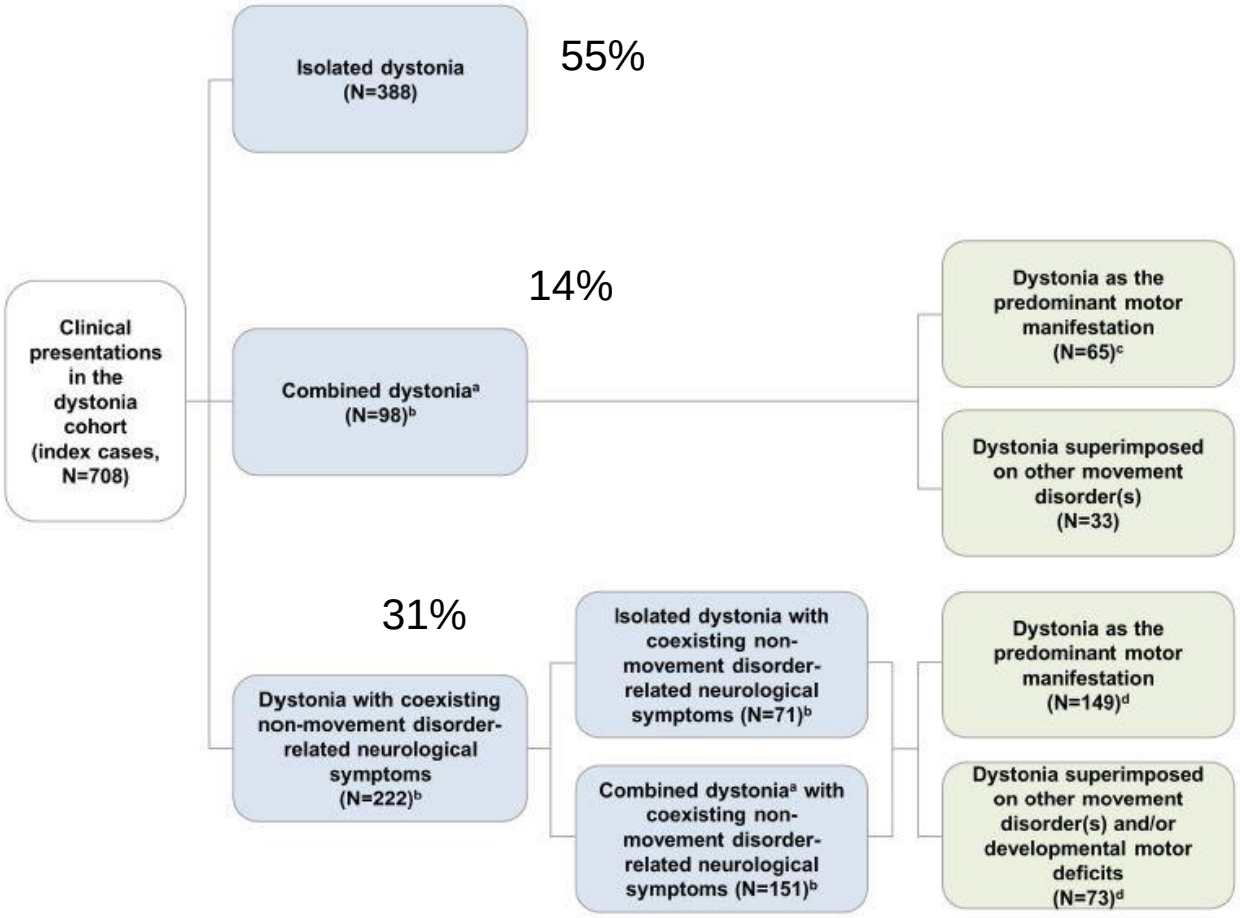




Genetic basis of dystonia

Which patients should be tested by unbiased genetic diagnostics?



708 index cases with various types of dystonia studied by WES

Articles

Monogenic variants in dystonia: an exome-wide sequencing study

Michael Zech, Robert Jech, Sylvia Boesch, Matej Škorvánek, Sandrina Weber, Matias Wagner, Chen Zhao, Angela Jochim, Ján Necpál, Yasemin Dincer, Katharina Vill, Felix Distelmaier, Małgorzata Stoklosa, Martin Krenn, Stephan Grunwald, Tobias Bock-Bierbaum, Anna Fečíková, Petra Havránková, Jan Roth, Iva Přihodová, Miriam Adamovičová, Olga Ulmanová, Karel Bechyně, Pavlína Danhofer, Branislav Veselý, Vladimír Haň, Petra Pavelekova, Zuzana Gdovinová, Tobias Mantel, Tobias Meindl, Alexandra Sitzberger, Sebastian Schröder, Astrid Blaschek, Timo Roser, Michaela V Bonfert, Edda Haberlandt, Barbara Plecko, Birgit Leineweber, Steffen Berweck, Thomas Herberhold, Berthold Langguth, Jana Švantnerová, Michal Minár, Gonzalo Alonso Ramos-Rivera, Monica H Wojcik, Sander Pajusalu, Katrin Õunap, Ulrich A Schatz, Laura Pölsler, Ivan Milenkovic, Franco Laccone, Veronika Pilshofer, Roberto Colombo, Steffi Patzer, Arcangela Iuso, Julia Vera, Monica Troncoso, Fang Fang, Holger Prokisch, Friederike Wilbert, Matthias Eckenweiler, Elisabeth Graf, Dominik S Westphal, Korbinian M Riedhammer, Theresa Brunet, Bader Alhaddad, Riccardo Berutti, Tim M Strom, Martin Hecht, Matthias Baumann, Marc Wolf, Aida Telegrafi, Richard E Person, Francisca Millan Zamora, Lindsay B Henderson, David Weise, Thomas Musacchia, Jens Volkmann, Anna Szuto, Jessica Becker, Kirsten Cremer, Thomas Sycha, Fritz Zimprich, Verena Kraus, Christine Makowski, Pedro Gonzalez-Alegre, Tanya M Bardakjian, Laurie J Ozelius, Annalisa Vetro, Renzo Guerrini, Esther Maier, Ingo Borggraefe, Alice Kuster, Saskia B Wortmann, Annette Hackenberg, Robert Steinfeld, Birgit Assmann, Christian Staufner, Thomas Opladen, Evžen Růžička, Ronald D Cohn, David Dyment, Wendy K Chung, Hartmut Engels, Andres Ceballos-Baumann, Rafal Płoski, Oliver Daumke, Bernhard Haslinger, Volker Mall, Konrad Oexle, Juliane Winkelmann

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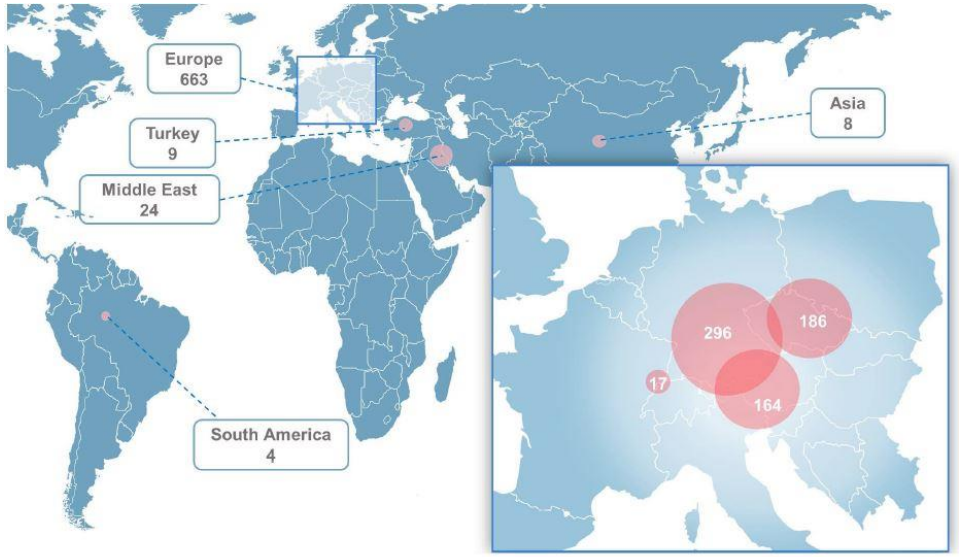
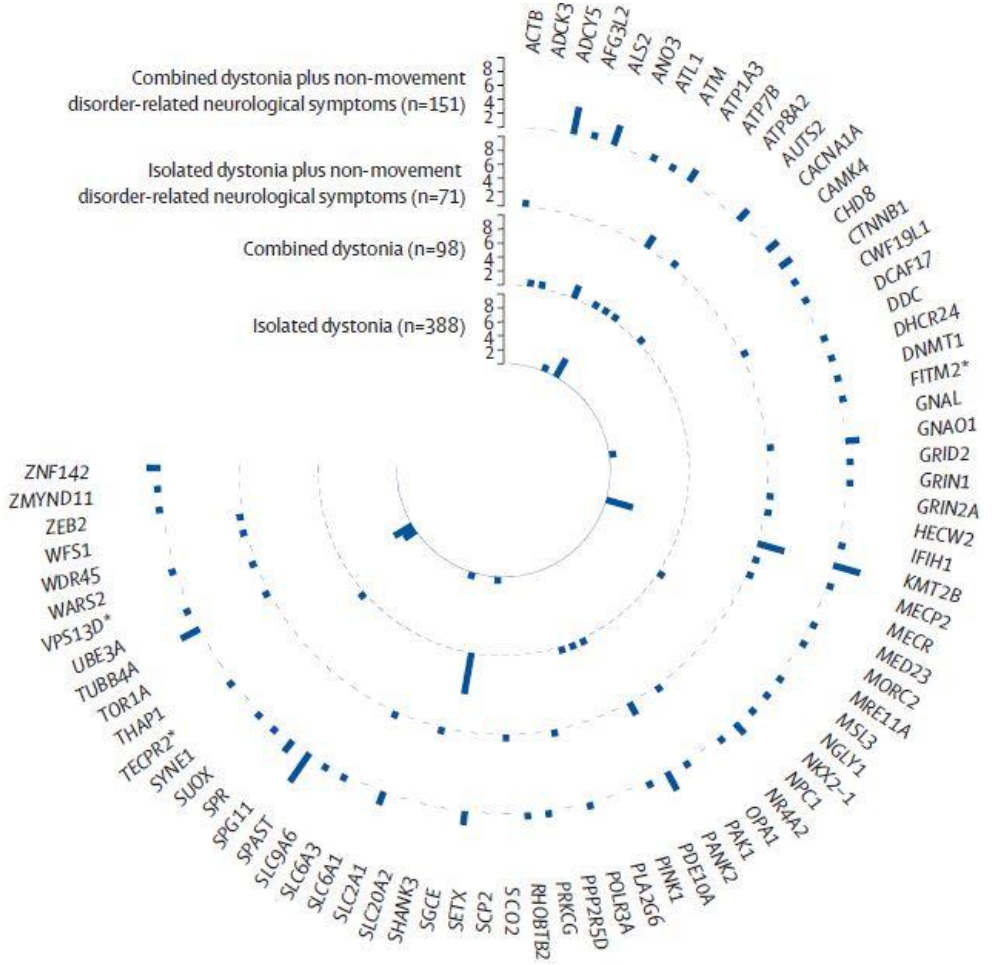


Genetic basis of dystonia

Which patients should be tested by unbiased genetic diagnostics?

- Overall diagnostic rate: 19% (135/708)
- 78 distinct molecular diagnoses



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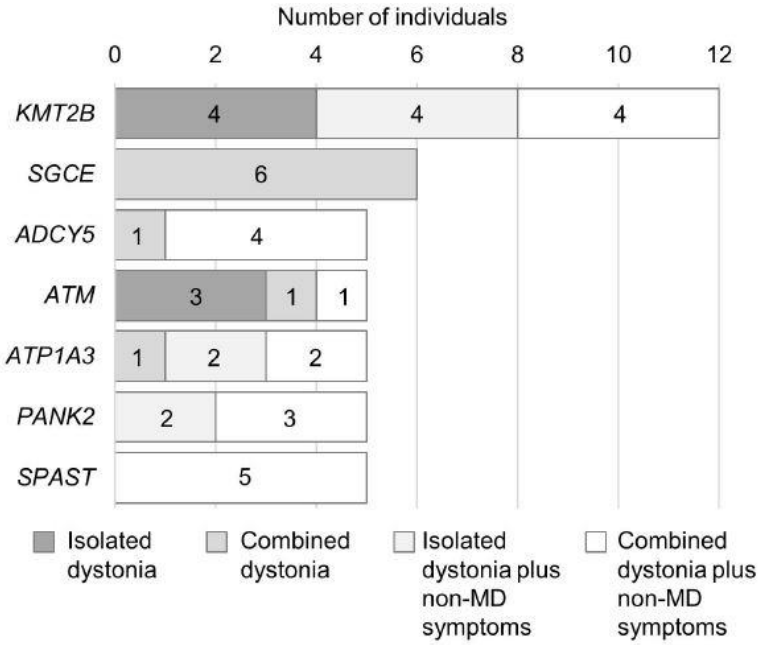
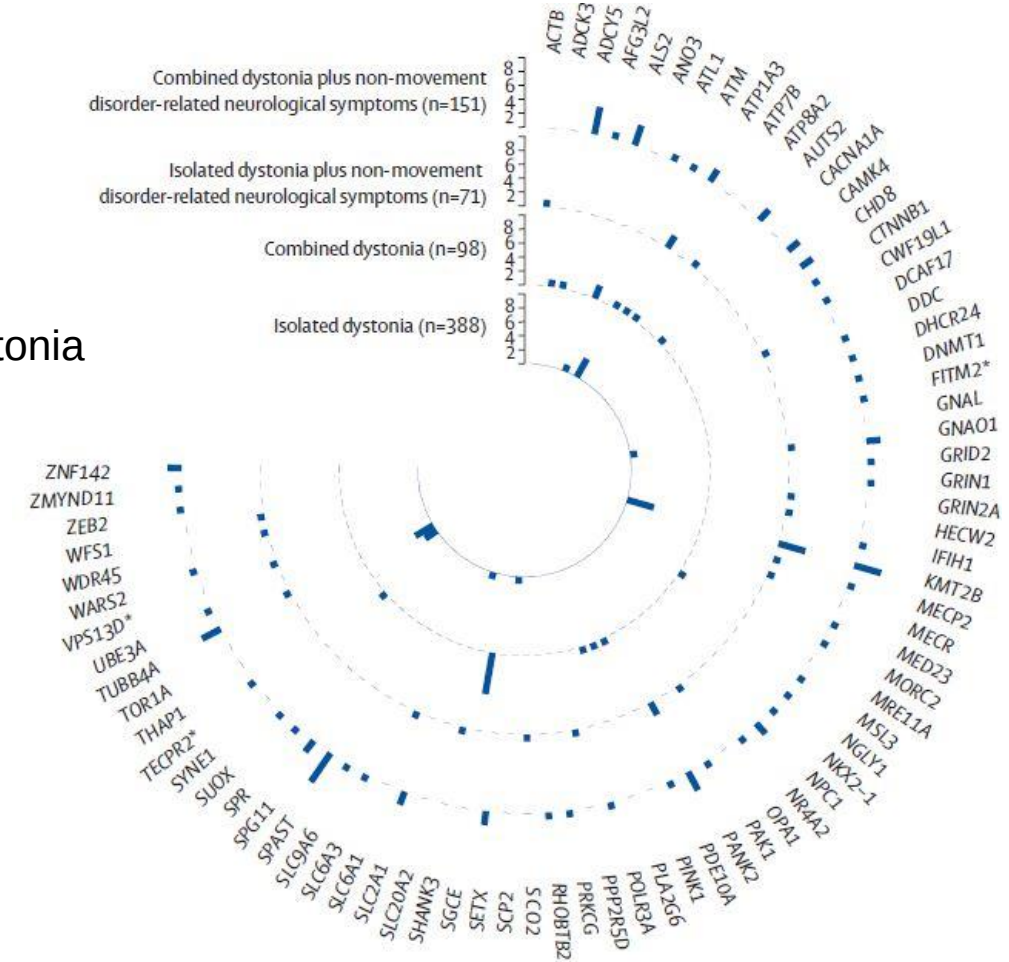
- 78 distinct molecular diagnoses
- Most frequent diagnosis: *KMT2B*-related dystonia





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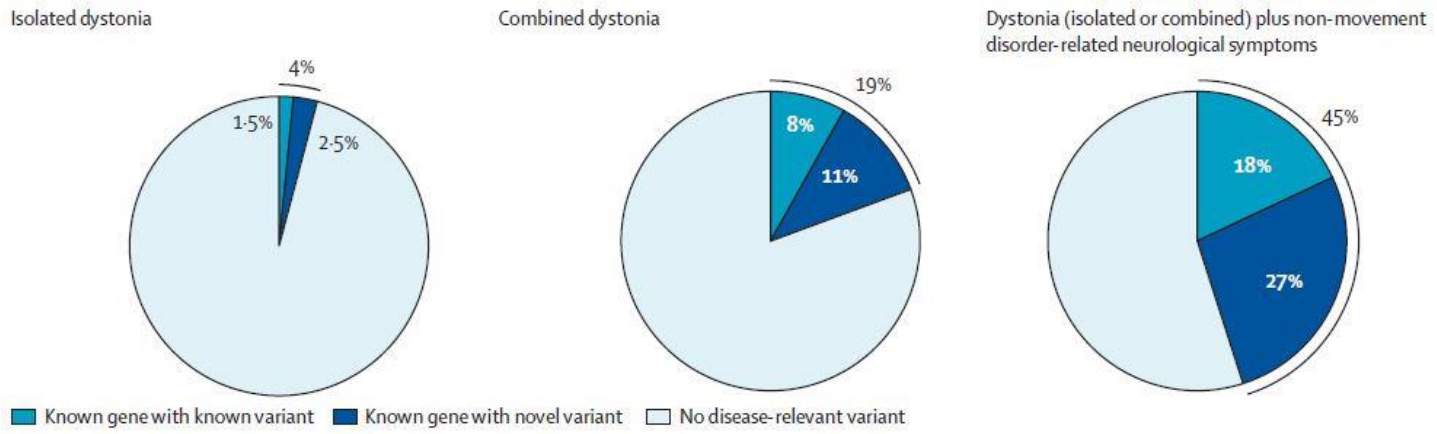

Diagnostic rates differ substantially between dystonia subgroups:

- Early-onset dystonia > late-onset dystonia
- Generalized dystonia > focal dystonia
- Complex dystonia > isolated dystonia

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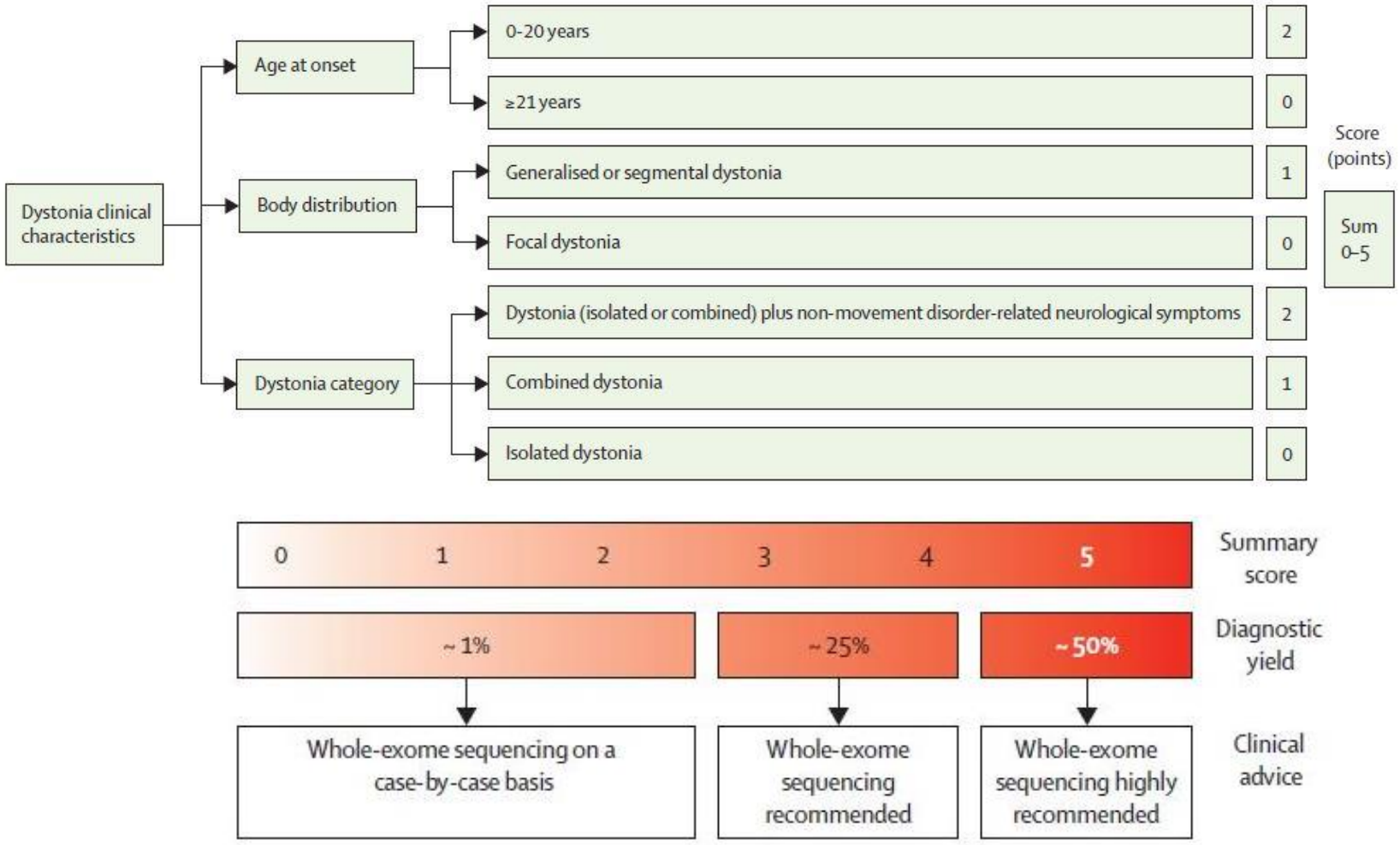

Clinical score for prediction of positive genetic finding from WES

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• Action-induced (occurs with a variety of voluntary actions)
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Additional characteristics
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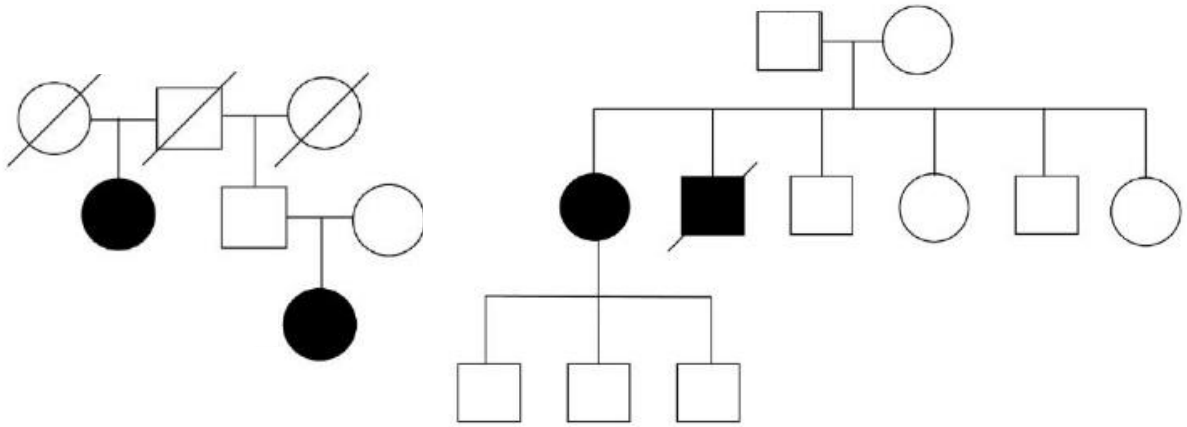
Genetic basis of dystonia

New genetic causes are being identified continously



Isolated generalized dystonia with variable onset

Example *VPS16*-related dystonia

Steel et al. Ann Neurol 2020

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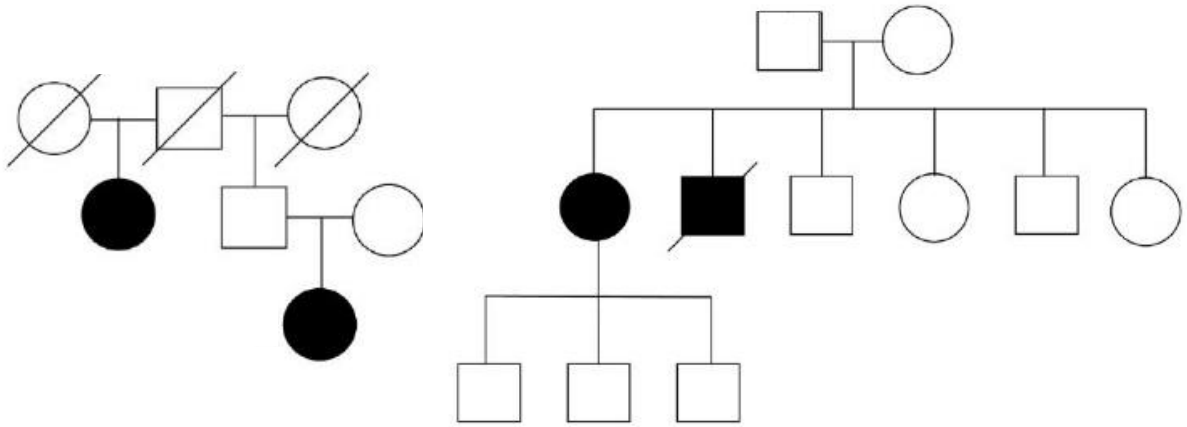

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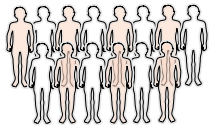
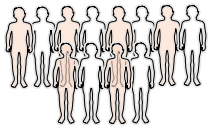
Burden testing with WES data



Cases

138 index patients with early-onset generalized dystonia

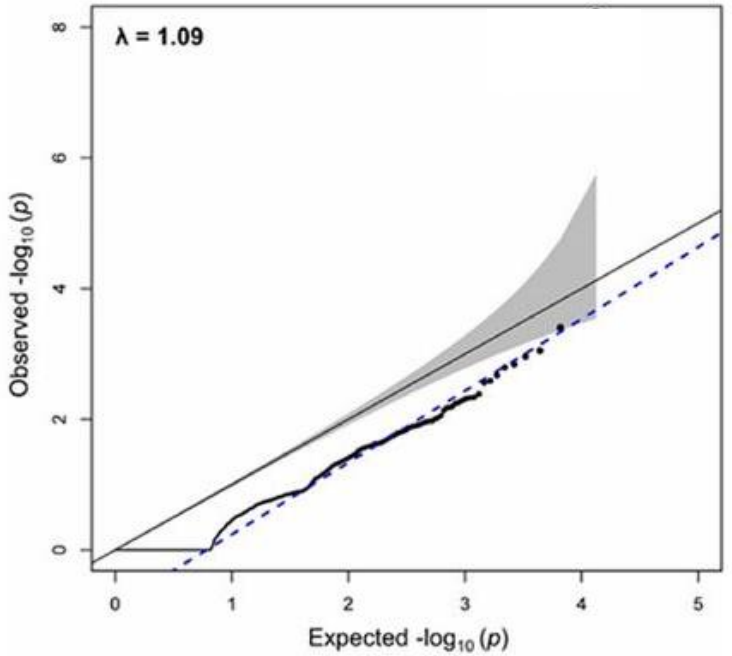


Controls

65,000 European-descent population controls from gnomAD

Autosomal-dominant model

- All ~20,000 protein-coding genes
- Loss-of-function variants
- MAF < 0.0005
- Exome-wide significance



Steel et al. Ann Neurol 2020

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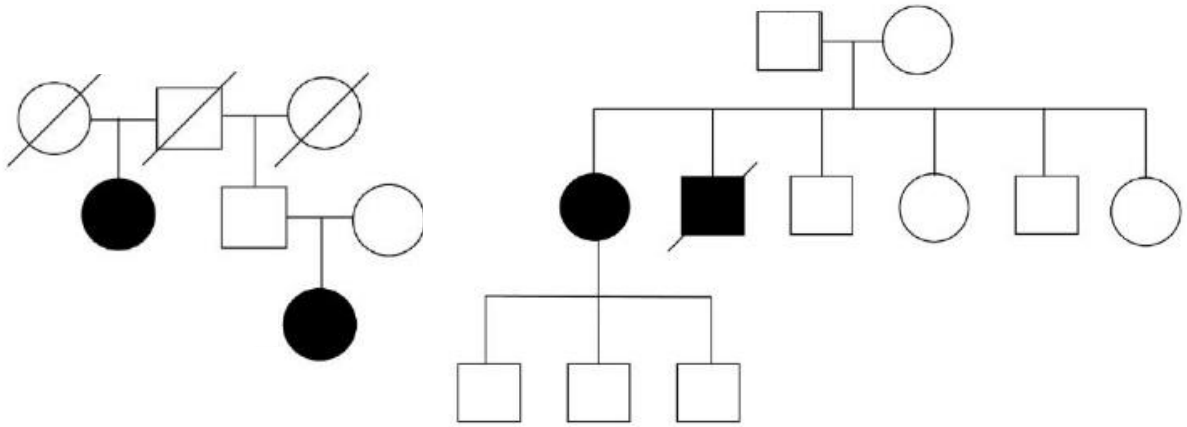

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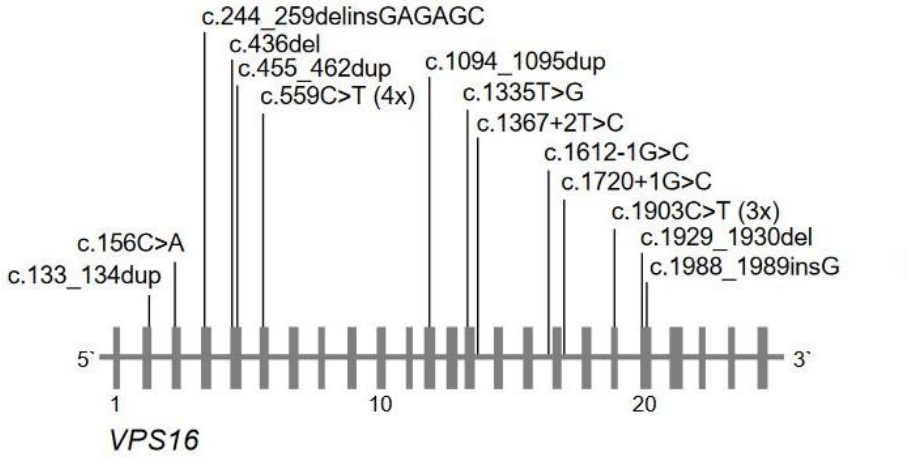

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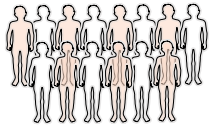

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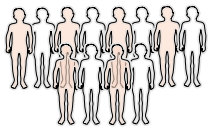

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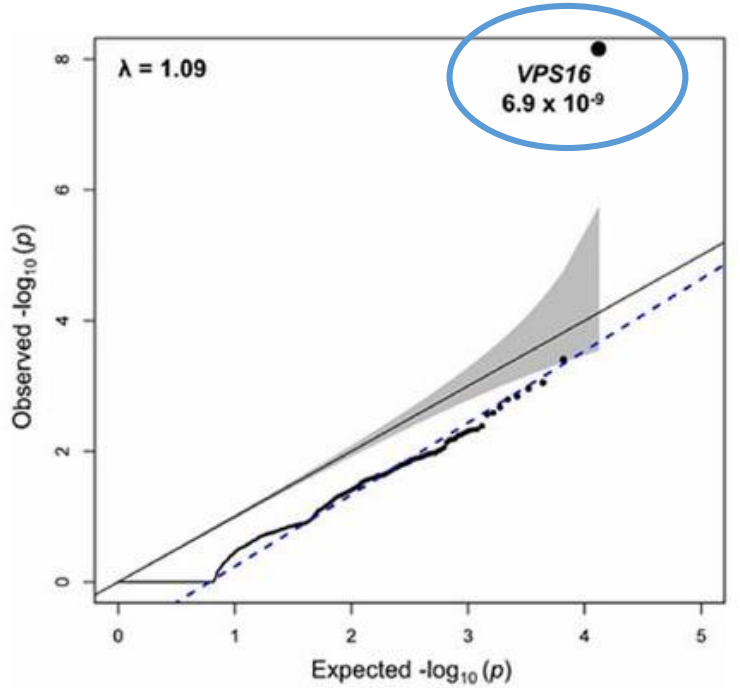


Genetic basis of dystonia

New genetic causes are being identified continously

VPS16-related dystonia

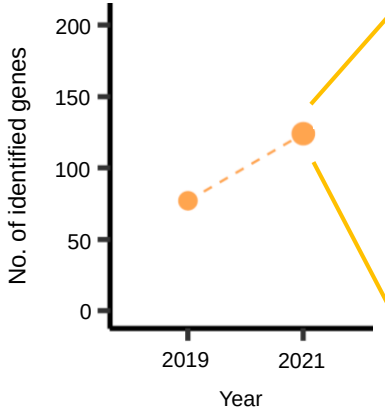
- **Inherited mutations associated with variable penetrance**
- **Adolescence-onset generalized dystonia**
- **Mostly isolated dystonia, mild neurodevelepmental comorbidity**
- **Among most common monogenic causes in isolated dystonia**
- **DBS response in 75% of patients (GPi DBS), approx. 50% have improvement over 50% in BFMDRS**

(Svorenova et al. Ann Neurol 2025)

Steel et al. Ann Neurol 2020

Genetic basis of dystonia

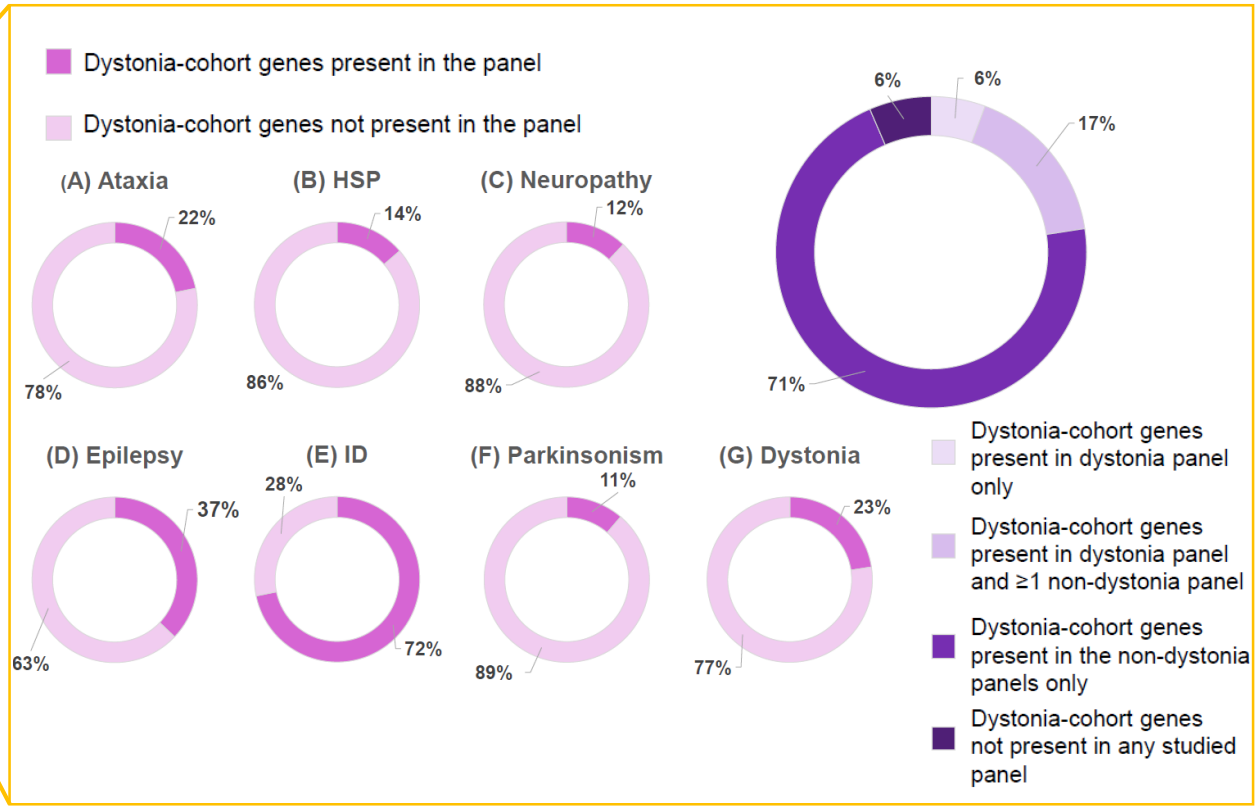
Genetic overlap of dystonias with other neurological disorders



n = 1,100 index cases

20% diagnostic yield

124 distinct genes



Dzinovic et al. Park Rel Disord 2022

Genetic basis of dystonia

Too many patients remain genetically unresolved

Exome
34% (11/32) diagnosed patients
Mostly complex dystonia

Wirth et al. Park Rel Disord 2020

Exome
19% (135/708) diagnosed patients
Different dystonia types

Zech et al. Lancet Neurol 2020

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21% (9/43) diagnosed patients
Different dystonia types

Ahn et al. Park Rel Disord 2023

Exome
23% (15/65) diagnosed patients
Different dystonia types

Dhar et al. Park Rel Disord 2024

Exome
36% (15/42) diagnosed patients
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Atasu et al. J Med Genet 2024

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64% to 88% of patients undiagnosed

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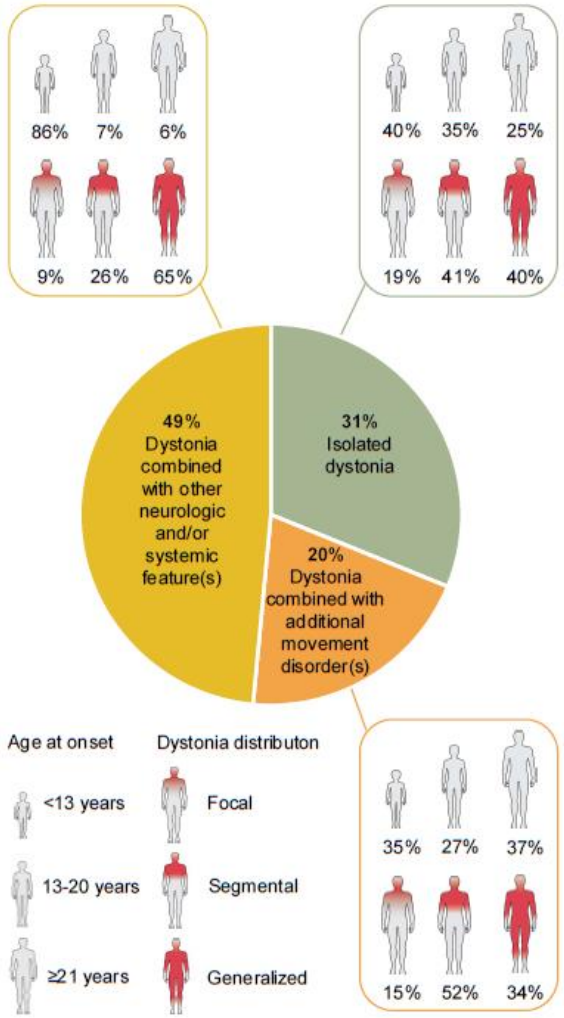
Genetic basis of dystonia

Second-line whole-genome sequencing (WGS) to find unexplored and unidentified variant types

80% WES-negative families

High ongoing suspicion of monogenic etiology



N = 305 families
564 total individuals
305 index patients, 259 relatives

Short read-whole genome sequencing
>100 Gb sequencing data per sample
Average coverage >40x across genome

Comprehensive bioinformatic annotation & variant analyses
3 – 4 million variants per sample
Coding & non-coding regions
Copy number variants
Structural variants
Repeat expansions
Mitochondrial DNA mutations

Zech et al. Brain 2025

Genetic basis of dystonia

Second-line whole-genome sequencing (WGS) increases the diagnostic yield

4 additional diagnoses

Variants not captured by exome analysis:
non-covered coding regions, intronic mutations, RNA gene variants

Copy number variants
Structural variants

14 additional diagnoses

4 additional diagnoses

Mitochondrial DNA mutations

Repeat expansions

7 additional diagnoses

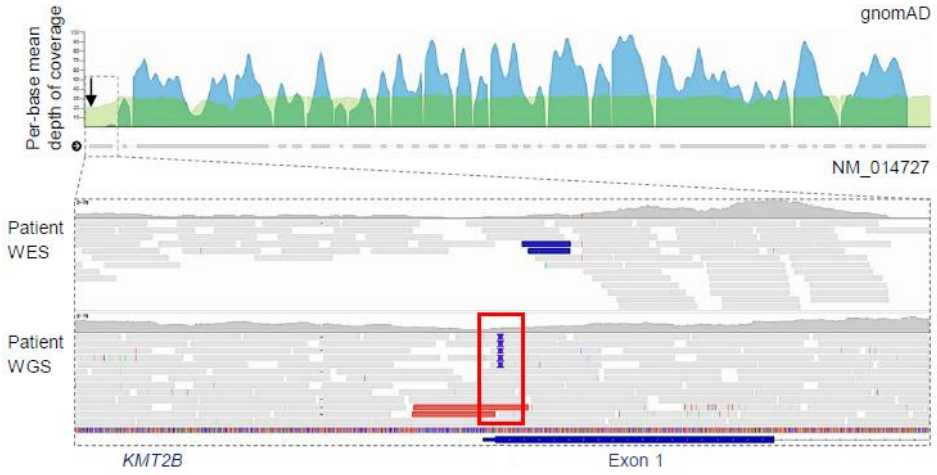
Σ 10%

Zech et al. Brain 2025

Genetic basis of dystonia

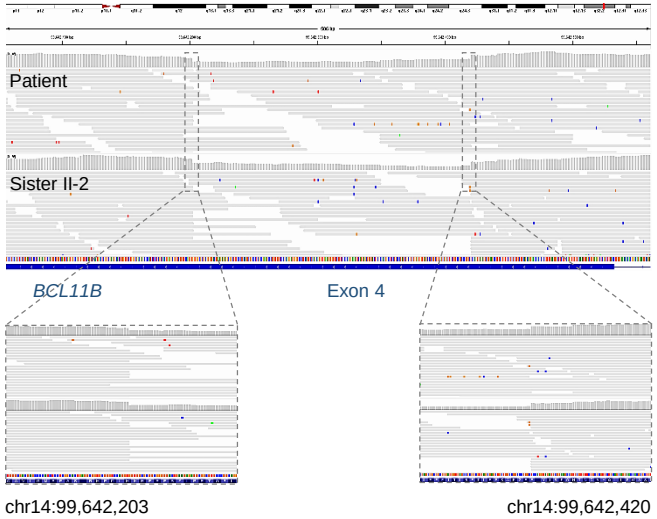
Second-line whole-genome sequencing (WGS) increases the diagnostic yield

Coding mutation not covered by exome



c.17_23dup (p.Ser9Argfs*109)

Difficult-to-detect copy number variant



218 bp deletion in exon 4

Diagnosis of *KMT2B*-related dystonia

Diagnosis of *BCL11B*-related dystonia

Zech et al. Brain 2025

Genetic basis of dystonia

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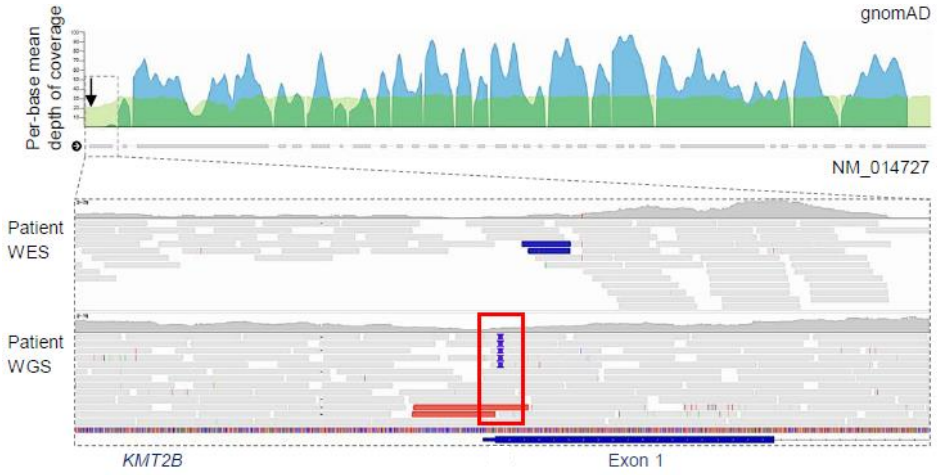

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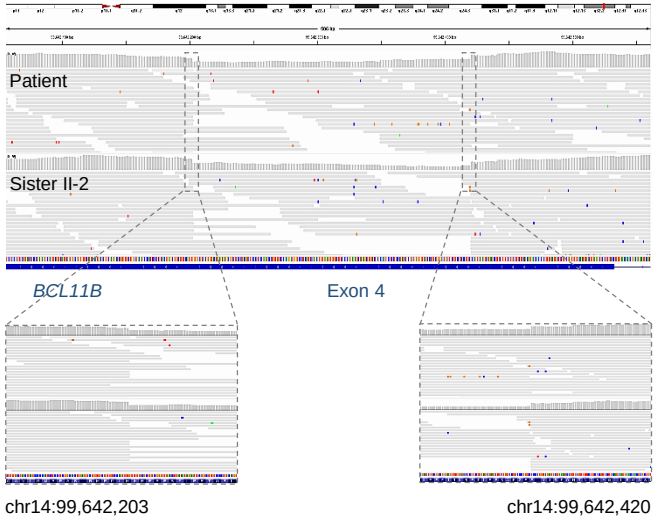

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Zech et al. Brain 2025

Genetic basis of dystonia

Insights into pathogenesis

Axis II: etiology and pathogenesis
Genetic
• Autosomal dominant
• Autosomal recessive
• X-linked recessive
• Maternal
• Unknown*
Acquired
• Medications
• Toxins
• Trauma
• Other acquired cause
• Unknown*
Neuroanatomical
• Focal lesion
• Multifocal lesions
• Diffuse lesions
• Unknown[a]
Pathogenesis
• Developmental
• Degenerative
• Metabolic
• Immune or inflammatory
• Unknown

REVIEW

Definition and Classification of Dystonia

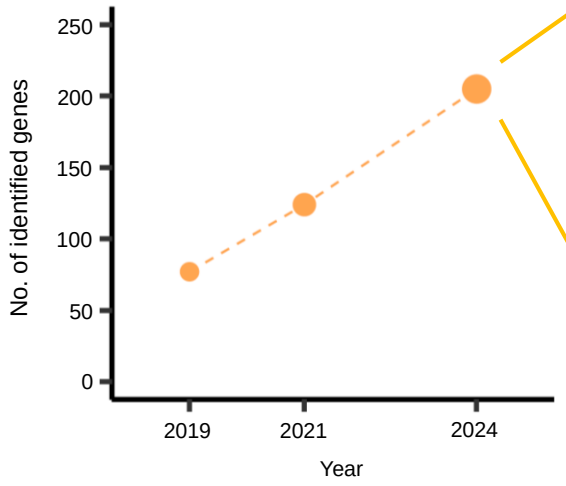
Alberto Albanese, MD,[1,2*] Kailash P. Bhatia, MD, DM, FRCP,[3] Victor S.C. Fung, PhD, FRACP,[4] Mark Hallett, MD,[5] Joseph Jankovic, MD,[6] Christine Klein, MD,[7] Joachim K. Krauss, MD,[8] Anthony E. Lang, MD, FRCPC,[9,10] Jonathan W. Mink, MD, PhD,[11] Sanjay Pandey, DM,[12] Jan K. Teller, MA, PhD,[13] Marina A.J. Tijssen, MD,[14,15] Marie Vidailhet, MD,[16,17,18] and H.A. Jinnah, MD, PhD[19,20]

Albanese et al. Mov Disord 2025

Etiological heterogeneity

Genetic basis of dystonia

Insights into pathogenesis



AARS1, *ACTB*, *ADAR*, *ADCY5*, *AFG3L2*, *ALS2*, *ANK2*, *ANO3*, *AOPEP*, *ARHGEF9*, *ARSA*, *ASXL3*, *ATL1*, *ATM*, *ATP1A3*, *ATP2B2*, *ATP5F1A*, *ATP5F1B*, *ATP5MC3*, *ATP7B*, *ATP8A2*, *AUTS2*, *BCL11B*, *BRAF*, *BRPF1*, *C19orf12*, *CACNA1A*, *CACNA1E*, *CAMK4*, *CAMTA1*, *CASK*, *CD40LG*, *CHD3*, *CHD4*, *CHD8*, *CNTNAP1*, *COQ8A*, *CP*, *CSDE1*, *CTNNB1*, *CUL3*, *CUX1*, *CWF19L1*, *DCAF17*, *DDC*, *DHCR24*, *DHDDS*, *DLG4*, *DLL1*, *DNAJC6*, *DNM1L*, *DNMT1*, *EBF3*, *ECHS1*, *EEF1A2*, *EFTUD2*, *EIF2AK2*, *EIF4A2*, *ERCC4*, *ERCC8*, *FA2H*, *FBXO31*, *FGF14*, *FITM2*, *FOXG1*, *FOXP2*, *FRMD5*, *FRYL*, *FTL*, *GABBR2*, *GABRA1*, *GAD1*, *GCH1*, *GJA1*, *GJC2*, *GNAL*, *GNAO1*, *GNB1*, *GRIA2*, *GRIA3*, *GRID2*, *GRIN1*, *GRIN2A*, *HECW2*, *HEXA*, *HIBCH*, *IFIH1*, *IMPDH2*, *INTS11*, *IRF2BPL*, *KCNA2*, *KCNB1*, *KCNJ10*, *KCNMA1*, *KCTD17*, *KIF1A*, *KIF5A*, *KMT2B*, *LIG4*, *LRRK2*, *MAG*, *MATR3*, *MECP2*, *MECR*, *MED23*, *MICU1*, *MMAA*, *MORC2*, *MRE11*, *MSL3*, *NAA15*, *NARS2*, *NAV3*, *NEFL*, *NFIX*, *NGLY1*, *NKX2-1*, *NPC1*, *NR4A2*, *NUP54*, *OPA1*, *PAK1*, *PANK2*, *PARK7*, *PCDH12*, *PDE10A*, *PDHA1*, *PINK1*, *PLA2G6*, *PNKD*, *PNPLA6*, *POGZ*, *POLG*, *POLR1A*, *POLR3A*, *PPP2R5D*, *PPT1*, *PRKCG*, *PRKN*, *PRRT2*, *PSEN1*, *PTS*, *PURA*, *RALA*, *RARB*, *RERE*, *RHOBTB2*, *SATB1*, *SCN2A*, *SCO2*, *SCP2*, *SERAC1*, *SETX*, *SGCE*, *SHANK3*, *SHQ1*, *SLC16A2*, *SLC19A3*, *SLC20A2*, *SLC2A1*, *SLC6A1*, *SLC6A3*, *SLC9A6*, *SNAP25*, *SNX14*, *SON*, *SOX2*, *SOX6*, *SPAST*, *SPG11*, *SPG7*, *SPR*, *SPTBN1*, *SRRM2*, *SUCLG1*, *SUOX*, *SYNE1*, *TBC1D24*, *TBCD*, *TBX1*, *TCF20*, *TECPR2*, *TFE3*, *TH*, *THAP1*, *TMEM240*, *TOR1A*, *TTPA*, *TUBB4A*, *UBE3A*, *UBTF*, *VLDLR*, *VPS16*, *WAC*, *WARS2*, *WASHC5*, *WDR45*, *WDR73*, *WFS1*, *YY1*, *ZC4H2*, *ZEB2*, *ZMYND11*, *ZNF142*, *ZNF335*

n = 1,825 index cases

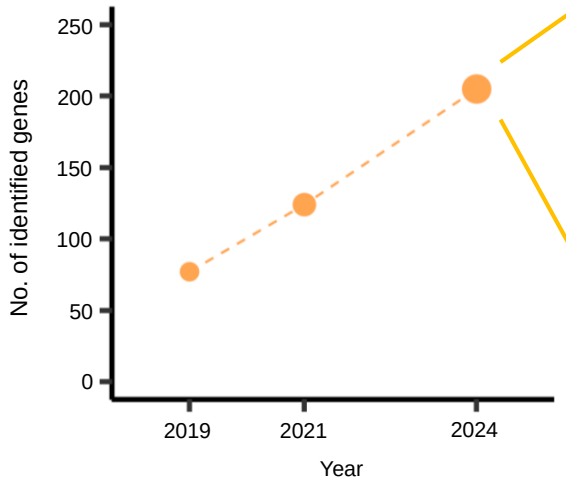
21.7% diagnostic yield

205 distinct genes

Zech et al. Brain 2025

Genetic basis of dystonia

Insights into pathogenesis



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73.2% (150/205) involved in brain development

Curated list of ~2,000 neurodevelopmental disorder genes

SysNDD v0.1.0

https://sysndd.dbmr.unibe.ch/

Kochinke et al. Am J Hum Genet 2016

Zech et al. Brain 2025

Genetic basis of dystonia

“Autism“ gene – CHD8

Cell Reports

Article

CHD8 haploinsufficiency links autism to transient alterations in excitatory and inhibitory trajectories

Villa et al. Cell Rep 2022

615032

INTELLECTUAL DEVELOPMENTAL DISORDER WITH AUTISM AND MACROCEPHALY; IDDAM

Alternative titles; symbols

AUTISM, SUSCEPTIBILITY TO, 18, FORMERLY; AUTS18, FORMERLY

Phenotype-Gene Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key	Gene/Locus	Gene/Locus MIM number
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CHD8-related generalized dystonia

Doummar et al. Ann Clin Trans Neurol 2021, Sorrentino et al. J Neurol 2024

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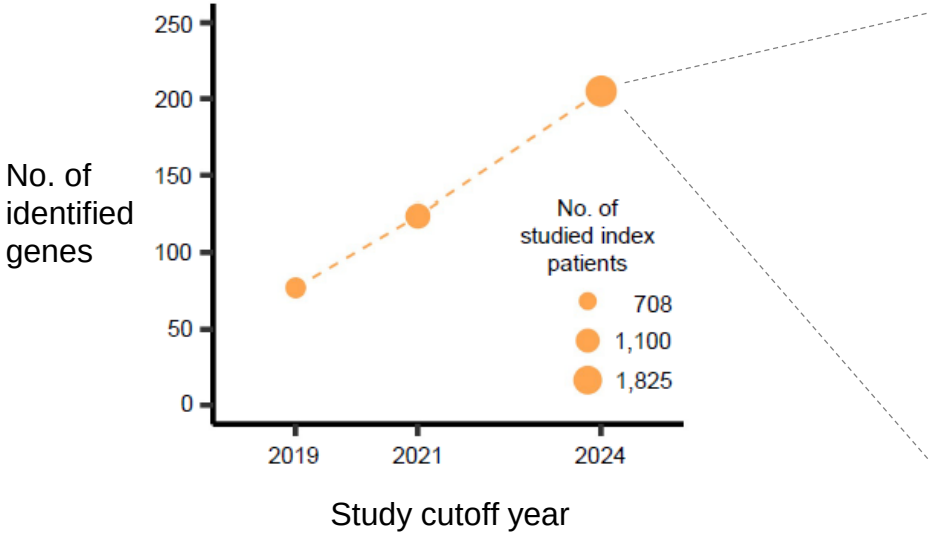
Insights into pathogenesis

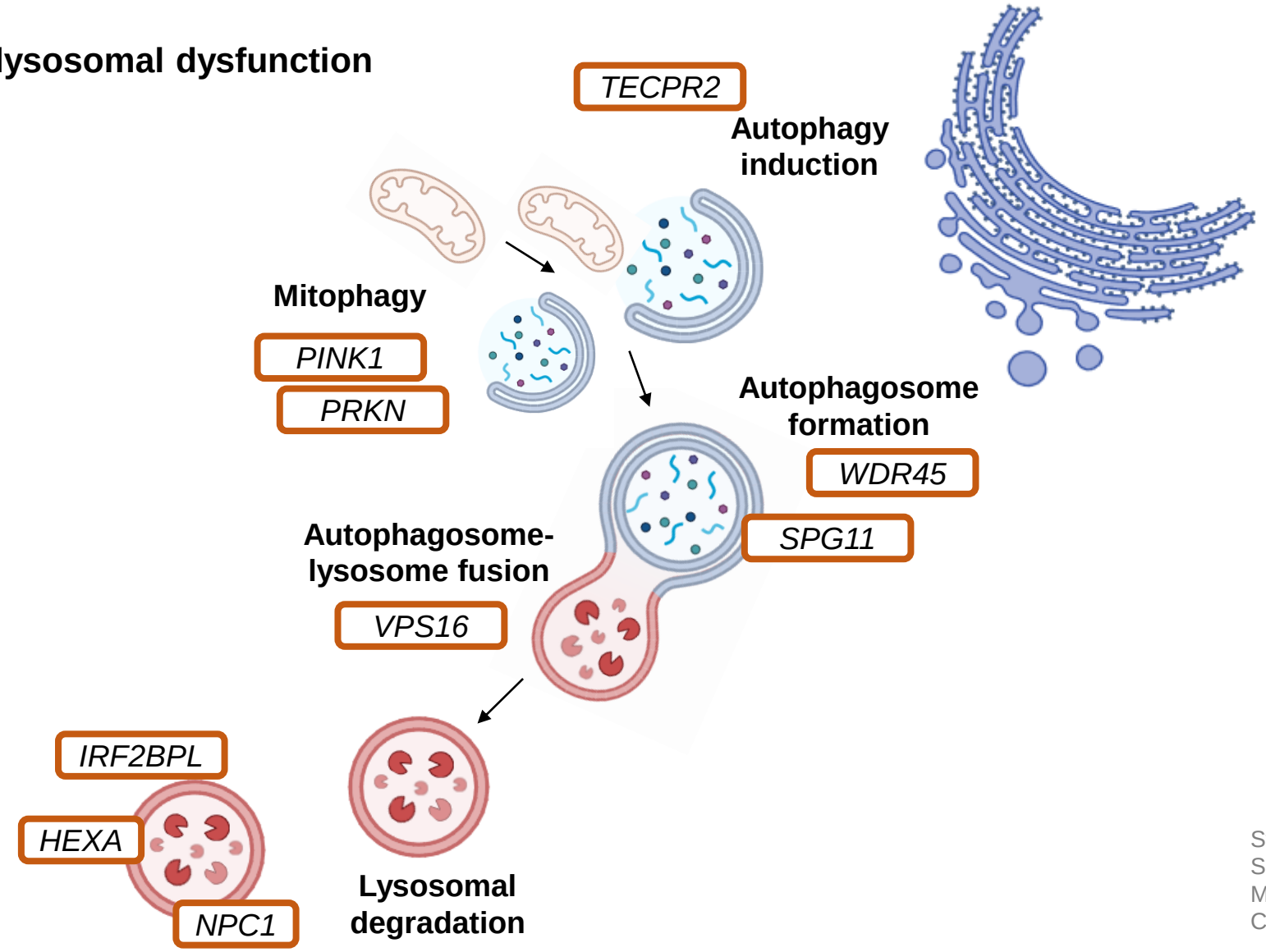


AARS1, *ACTB*, *ADAR*, *ADCY5*, *AFG3L2*, *ALS2*, *ANK2*, *ANO3*, *AOPEP*, *ARHGEF9*, *ARSA*, *ASXL3*, *ATL1*, *ATM*, *ATP1A3*, *ATP2B2*, *ATP5F1A*, *ATP5F1B*, *ATP5MC3*, *ATP7B*, *ATP8A2*, *AUTS2*, *BCL11B*, *BRAF*, *BRPF1*, *C19orf12*, *CACNA1A*, *CACNA1E*, *CAMK4*, *CAMTA1*, *CASK*, *CD40LG*, *CHD3*, *CHD4*, *CHD8*, *CNTNAP1*, *COQ8A*, *CP*, *CSDE1*, *CSTB*, *CTNNB1*, *CUL3*, *CUX1*, *CWF19L1*, *DCAF17*, *DDC*, *DHCR24*, *DHDDS*, *DLG4*, *DLL1*, *DNAJC6*, *DNM1L*, *DNMT1*, *EBF3*, *ECHS1*, *EEF1A2*, *EFTUD2*, *EIF2AK2*, *EIF4A2*, *ERCC4*, *ERCC8*, *FA2H*, *FBXO31*, *FGF14*, *FITM2*, *FOXG1*, *FOXP2*, *FRMD5*, *FRYL*, *FTL*, *GABBR2*, *GABRA1*, *GAD1*, *GCH1*, *GJA1*, *GJC2*, *GLS*, *GNAL*, *GNAO1*, *GNB1*, *GRIA2*, *GRIA3*, *GRID2*, *GRIN1*, *GRIN2A*, *HECW2*, ***HEXA***, *HIBCH*, *HTT*, *IFIH1*, *INTS11* ***IRF2BPL***, *KCNA2*, *KCNB1*, *KCNJ10*, *KCNMA1*, *KCTD17*, *KIF1A*, *KIF5A*, *KMT2B*, *LIG4*, *LRRK2*, *MAG*, *MATR3*, *MECP2*, *MECR*, *MED23*, *MICU1*, *MMAA*, *MORC2*, *MRE11*, *MSL3*, *MT-ATP6*, *MT-ND3*, *MT-ND6*, *MT-TL1*, *NAA15*, *NARS2*, *NAV3*, *NEFL*, *NFIX*, *NGLY1*, *NKX2-1* ***NPC1***, *NR4A2*, *NUP54*, *OPA1*, *PAK1*, *PANK2*, *PABPN1*, *PARK7*, *PCDH12*, *PDE10A*, *PDHA1*, ***PINK1***, *PLA2G6*, *PNKD*, *PNPLA6*, *POGZ*, *POLG*, *POLR1A*, *POLR3A*, *PPP2R5D*, *PPT1*, *PRKCG* ***PRKN***, *PRKRA*, *PRRT2*, *PSEN1*, *PTS*, *PURA*, *RALA*, *RARB*, *RERE*, *RHOBTB2*, *SATB1*, *SCN2A*, *SCO2*, *SCP2*, *SERAC1*, *SETX*, *SGCE*, *SHANK3*, *SHQ1*, *SLC16A2*, *SLC19A3*, *SLC20A2*, *SLC2A1*, *SLC6A1*, *SLC6A3*, *SLC9A6*, *SNAP25*, *SNORD118*, *SNX14*, *SON*, *SOX2*, *SOX6*, *SPAST*, ***SPG11***, *SPG7*, *SPR*, *SPTBN1*, *SRRM2*, *SUCLG1*, *SUOX*, *SYNE1*, *TBC1D24*, *TBCD*, *TBX1*, *TCF20*, ***TECPR2***, *TFE3*, *TH*, *THAP1*, *TMEM240*, *TOR1A*, *TTPA*, *TUBB4A*, *UBE3A*, *UBTF*, *VLDLR*, *VPS13D*, ***VPS16***, *WAC*, *WARS2*, *WASHC5*, ***WDR45***, *WDR73*, *WFS1*, *YY1*, *ZC4H2*, *ZEB2*, *ZMYND11*, *ZNF142*, *ZNF335*

Functionally converging genes unveil causative pathways

Genetic basis of dystonia

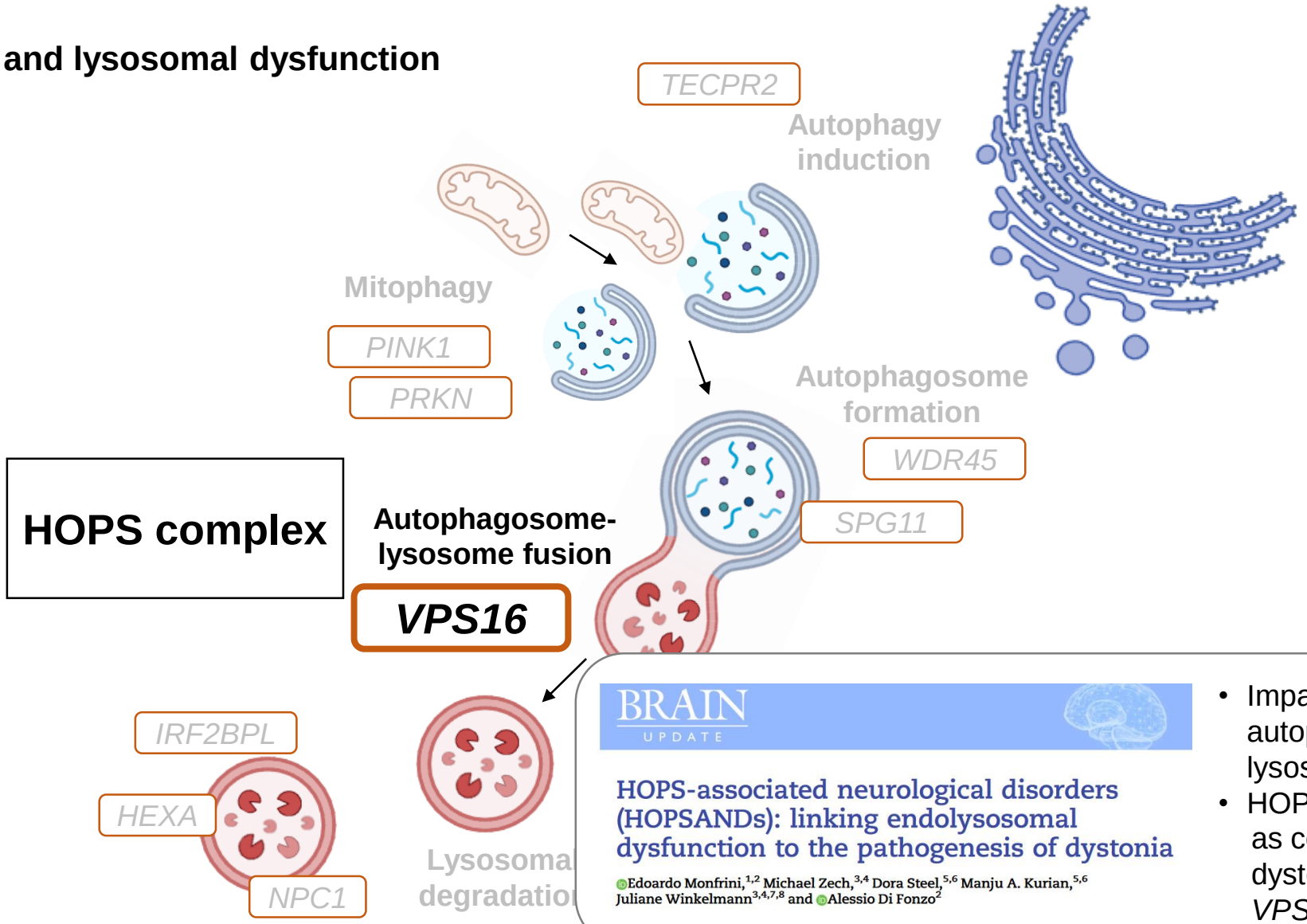
Impaired autophagy and lysosomal dysfunction



Steel et al. Ann Neurol 2020
Sanderson et al. Brain 2021
Monfrini et al. Brain 2021
Calakos & Zech Mov Disord 2024

Genetic basis of dystonia

Impaired autophagy and lysosomal dysfunction



BRAIN UPDATE

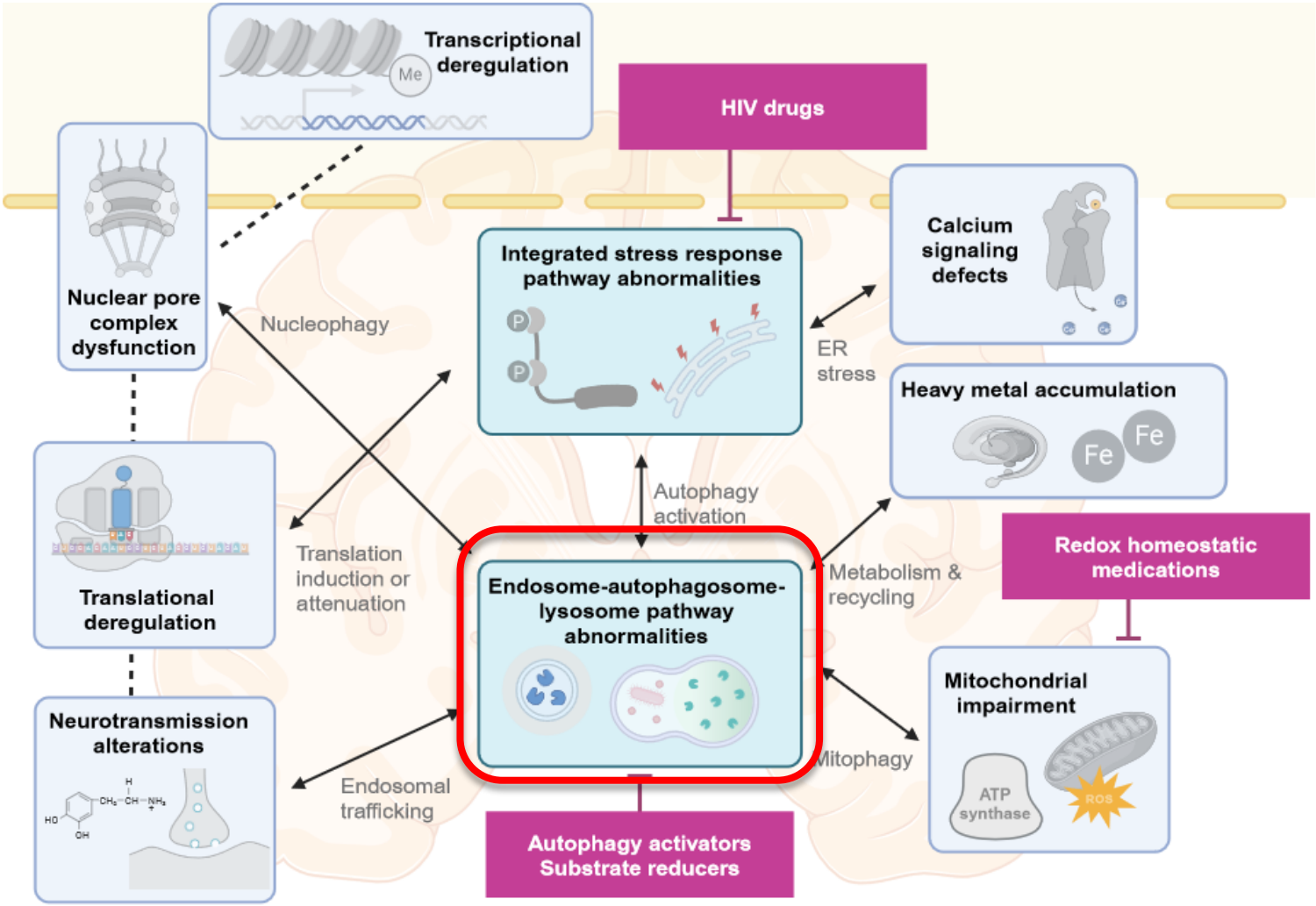
HOPS-associated neurological disorders (HOPSANDs): linking endolysosomal dysfunction to the pathogenesis of dystonia

Edoardo Monfrini,[1,2] Michael Zech,[3,4] Dora Steel,[5,6] Manju A. Kurian,[5,6] Juliane Winkelmann[3,4,7,8] and Alessio Di Fonzo[2]

- Impaired autophagosome/endosome – lysosome fusion
- HOPS complex dysfunction as converging mechanism for dystonia (*VPS16*, *VPS41*, *VPS11*)

Genetic basis of dystonia

Lessons from WES and WGS – identified pathways and their druggable potential



Conclusions – Genetic basis of dystonia

- Genetics informs on heterogeneous causes of dystonia
- Exome/genome testing in dystonia especially useful for patients with early onset, more complex forms of the disease
- Genetic overlap with other disorders (ataxia, epilepsy …)
- Neurodevelopmental etiology
- Transition from WES to even more comprehensive methods (WGS, Omics, long-reads …)
- Gene findings translate into pathophysiology and potential targets for therapy
- More genetic studies need to be done in dystonia in different populations
- Call for collaboration, research exome/genome analysis for dystonia patients

Thank you!

Prof. Sylvia Boesch
Dr. Elisabetta Indelicato

Prof. Robert Jech

Prof. Matej Skorvanek
Dr. Jan Necpal

Patients and families