

IALP Genetics in speech pathology


Through the lens of childhood apraxia of speech

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Murdoch Children's Research Institute



What do families want to know in clinic?

Prognosis: will
speech get better?



The diagram consists of three stacked, rounded rectangular boxes. The top box is purple and contains the text 'Prognosis: will speech get better?'. The middle box is red and contains the text 'Treatment: what are best therapies?'. The bottom box is teal and contains the text 'Aetiology: why this speech disorder?'. Each box has a corresponding arrow pointing to the right. Additionally, there are two vertical teal arrows pointing upwards: one starts from the bottom of the teal box and points to the bottom of the red box, and the other starts from the bottom of the red box and points to the bottom of the purple box.

Treatment: what are
best therapies?

Aetiology: why this
speech disorder?

Symptom based approach to clinical management

Speech & language - motor speech, phon/linguistic, resonance, grammar, receptive vs expressive

Any co-occurring neurodevelopmental disorders

Careful history - other developmental challenges, cognition

Issues in pregnancy or around time of birth

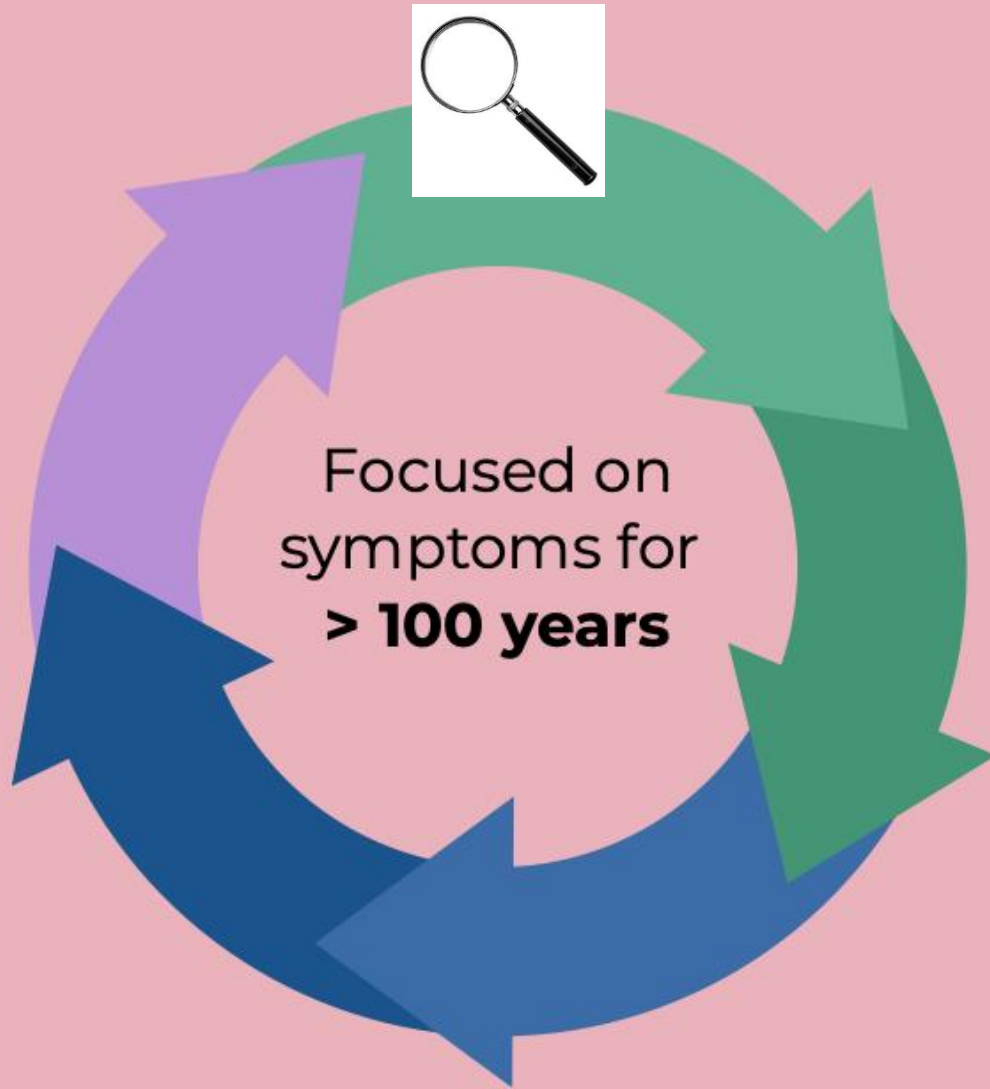
Other health & medical aspects. Hearing? MRI scan?

Family history, languages spoken at home, other

Targeted speech therapy

– limited or no ability to identify aetiology or prognosis

Symptom-based approach to speech pathology



Genetic
advances



Field is moving at a rapid pace
re: aetiology - a new window
into speech development

Chromosome
analysis

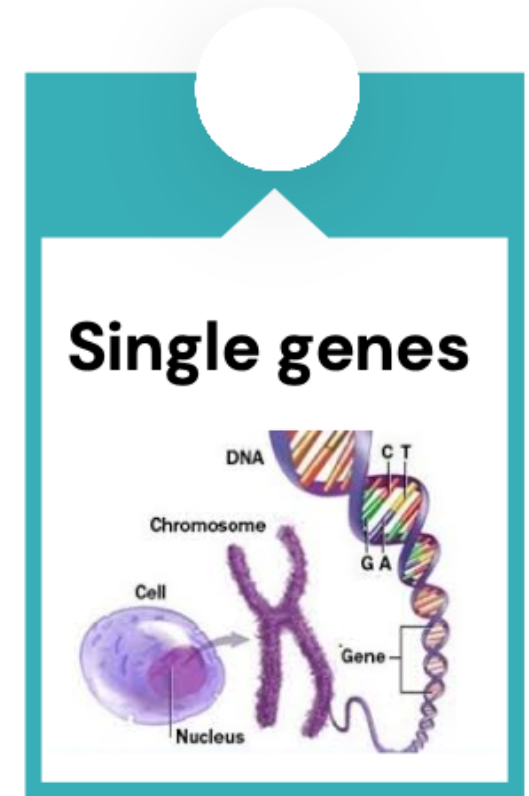
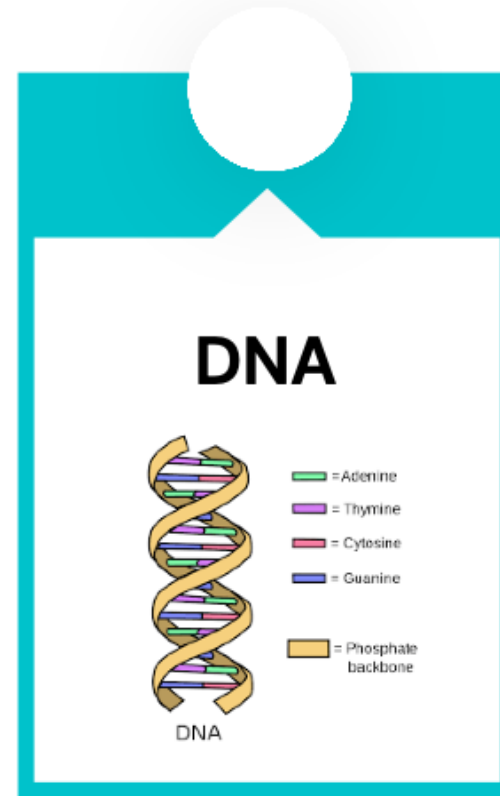
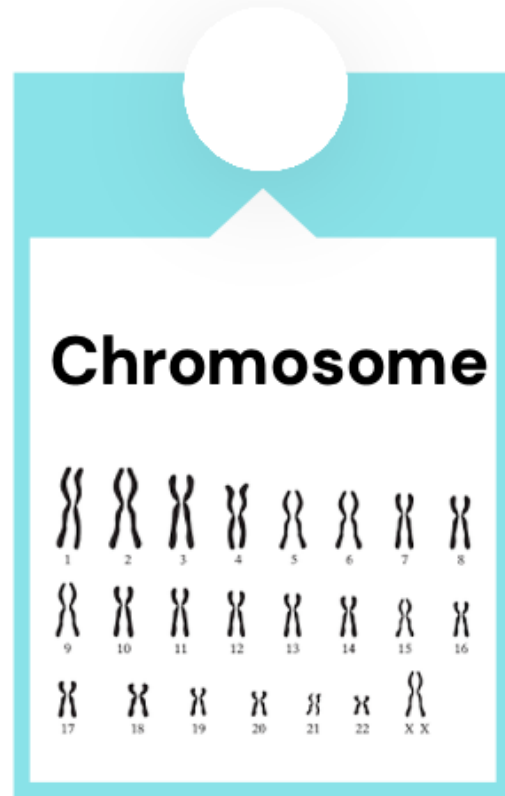
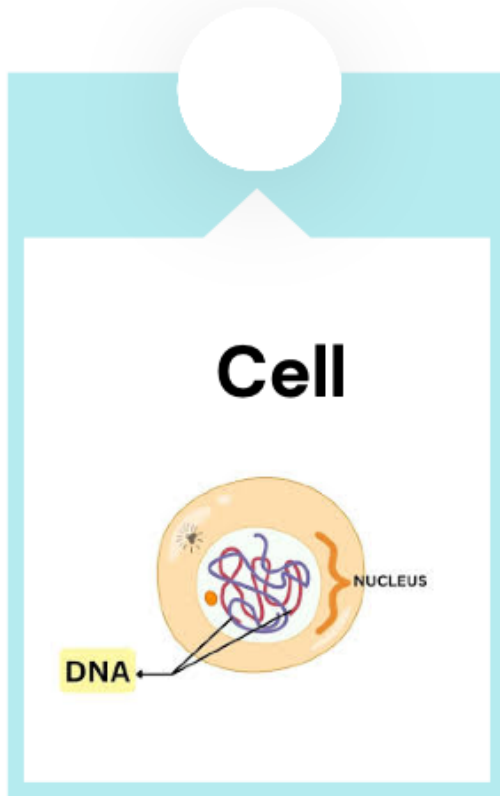
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Recent gains in
understanding
genetic
aetiologies due to
advances in
technology &
analysis

2

Single gene
analysis

Refresher – chromosomes & genes



Hundreds to thousands of genes arranged on each chromosome
Each gene has its own unique position like a street address (16p11.2)

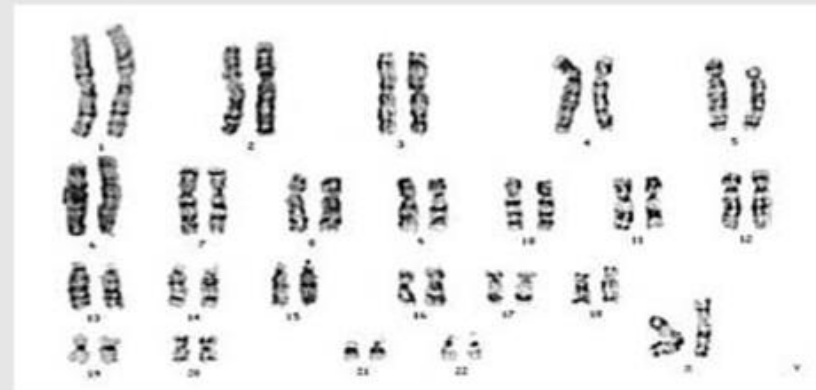
Detecting chromosomal changes

Outdated and early genetic methods - karyotype 1959

Trisomy 21



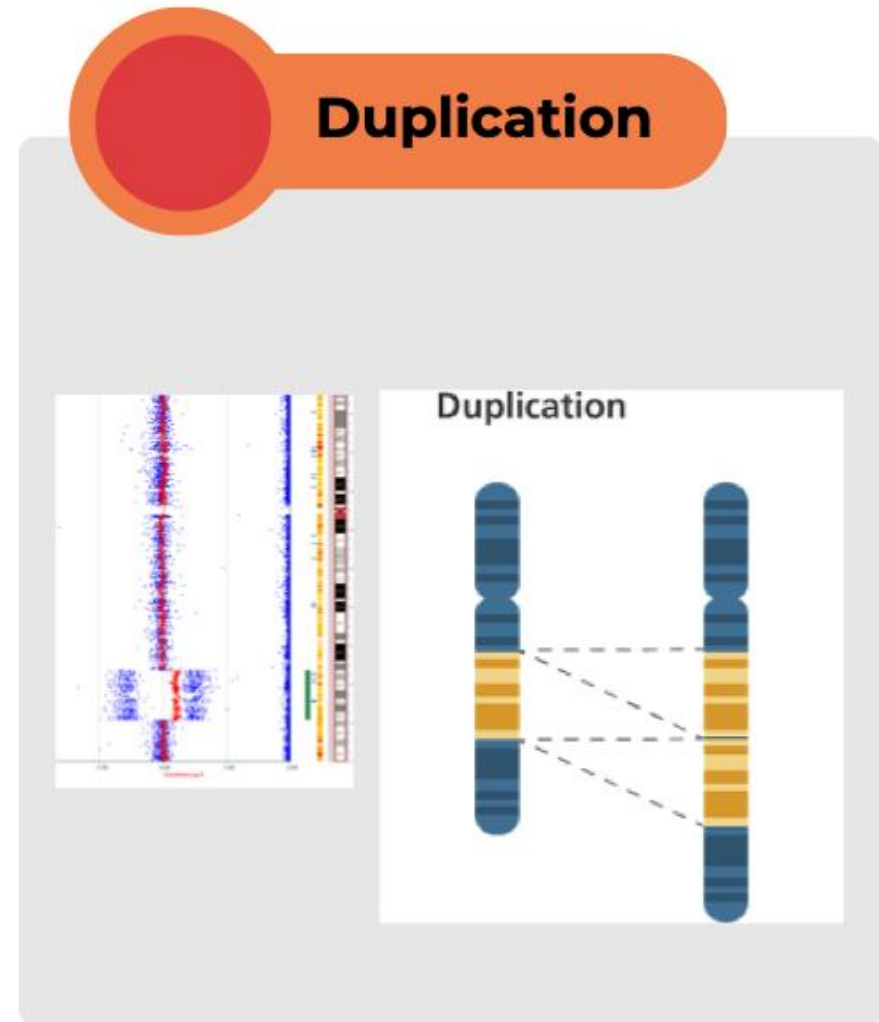
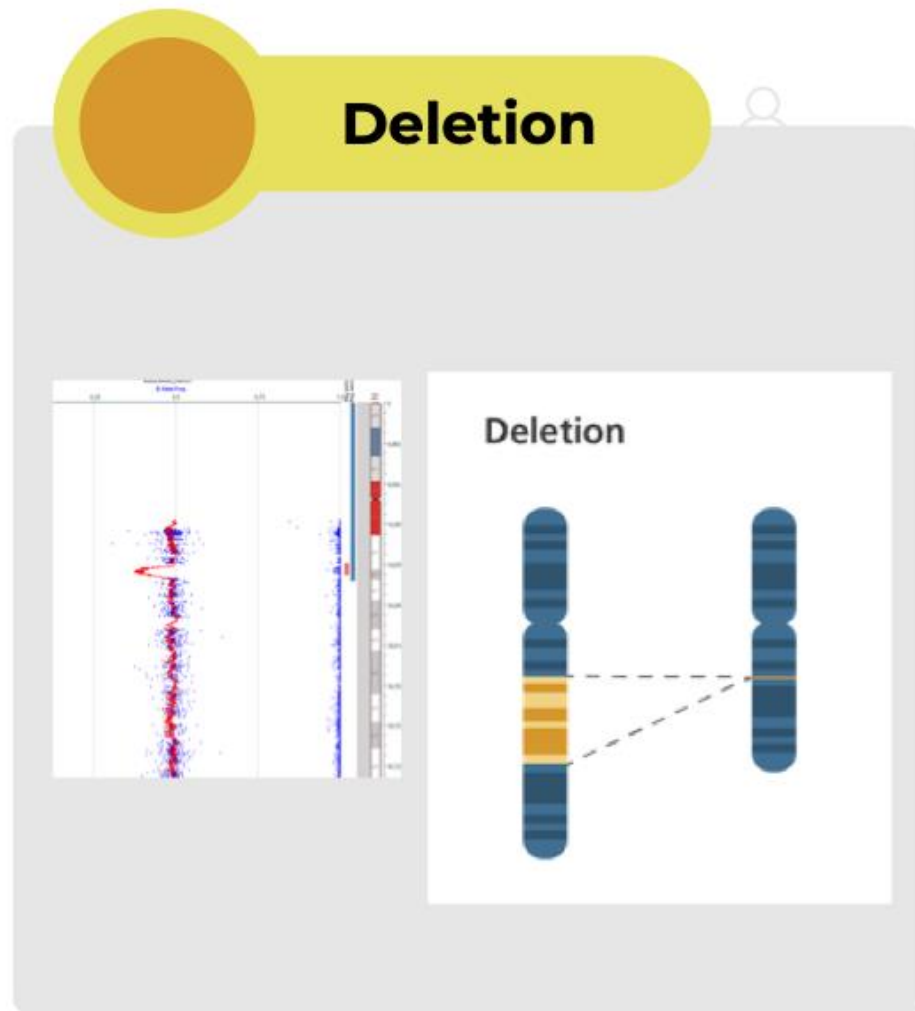
Cri du chat 6p deletion

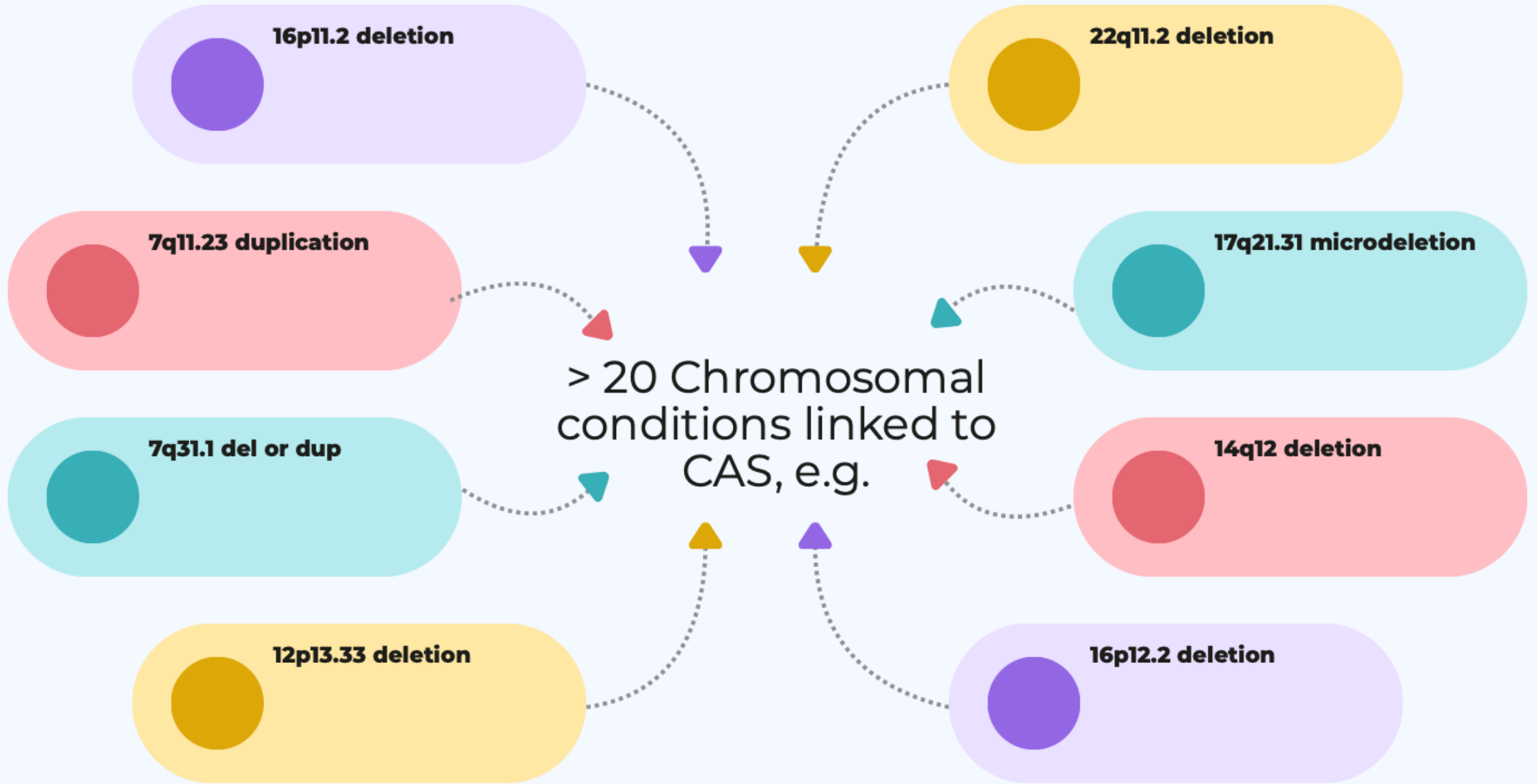


Karyotype: number & appearance of chromosomes

Detecting chromosomal changes

Chromosomal microarray karyotyping - modern day approach





16p11.2 deletion

Phenotype



Prevalence of 1/5,000-10,000
Autism spectrum disorder (ASD)*
Mild-mod intellectual impairment
Mild-mod language impairment
Epilepsy (20%)
Macrocephaly (large head)
Obesity
Childhood apraxia of speech

*16p11.2 deletion explains 1/150 cases with ASD

16p11.2 deletion

 **Phenotype**

7;7 year old Australian male

CAS

Mild-moderate expressive & receptive
language impairment

Low average non-verbal IQ

Mainstream school

Hearing WNL

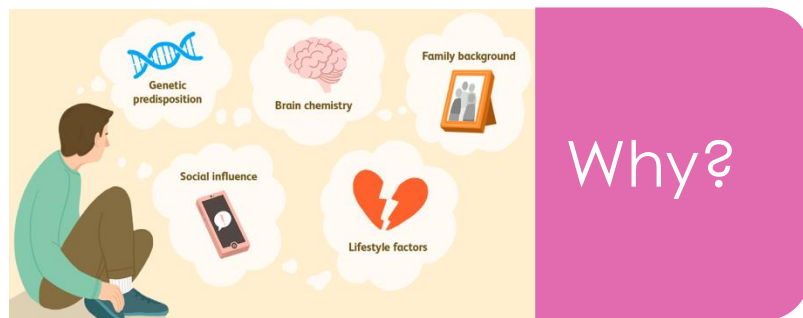
Detecting chromosomal changes in childhood apraxia of speech How does this help in the clinic?

Dear Speech Pathology,

Thankyou for seeing 3;5 year old male with 17q21.31 microdeletion.

Family are keen for support with communication development.

Kind regards,



Detecting chromosomal changes in childhood apraxia of speech

How does this help in the clinic?

Early speech development in Koolen de Vries syndrome limited by oral praxis and hypotonia - PubMed

PubMed.gov

17q21.31 microdeletion speech language

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Found 1 result for 17q21.31 microdeletion speech language

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> Eur J Hum Genet. 2018 Jan;26(1):75-84. doi: 10.1038/s41431-017-0035-9. Epub 2017 Dec 11.

Early speech development in Koolen de Vries syndrome limited by oral praxis and hypotonia

Abstract

Communication disorder is common in Koolen de Vries syndrome (KdVS), yet its specific symptomatology has not been examined, limiting prognostic counselling and application of targeted therapies. Here we examine the communication phenotype associated with KdVS. Twenty-nine participants (12 males, 4 with KANSL1 variants, 25 with 17q21.31 microdeletion), aged 1.0-27.0 years were assessed for oral-motor, speech, language, literacy, and social functioning. Early history included hypotonia and feeding difficulties. Speech and language development was delayed and atypical from onset of first words (2; 5-3; 5 years of age on average). Speech was characterised by apraxia (100%) and dysarthria (93%), with stuttering in some (17%). Speech therapy and multi-modal communication (e.g., sign-language) was critical in preschool. Receptive and expressive language abilities were typically commensurate (79%), both being severely affected relative to peers. Children were sociable with a desire to communicate, although some (36%) had pragmatic impairments in domains, where higher-level language was required. A common phenotype was identified, including an overriding 'double hit' of oral hypotonia and apraxia in infancy and preschool, associated with severely delayed speech development. Remarkably however, speech prognosis was positive; apraxia resolved, and although dysarthria persisted, children were intelligible by mid-to-late childhood. In contrast, language and literacy deficits persisted, and pragmatic deficits were apparent. Children with KdVS require early, intensive, speech motor and language therapy, with targeted literacy and social language interventions as developmentally appropriate. Greater understanding of the linguistic phenotype may help unravel the relevance of KANSL1 to child speech and language development.



Bert de Vries, David Koolen

diagnosis

KDVS Koolen de Vries Syndrome Foundation

About Us KDVS Community Events Get Involved Shop DONATE

20 Feb Colby

Colby was diagnosed with Koolen-de Vries Syndrome in 2007. He makes friends with everyone he meets and makes his family so proud!

20 Feb Emma Leann Kuenz

Emma was diagnosed with the KANSL1 mutation and received the Koolen-de Vries Syndrome diagnosis in 2013. She wakes up every morning with a smile on her face and ready to face the day.

Support group - quality of life & wellbeing

Chromosome
analysis

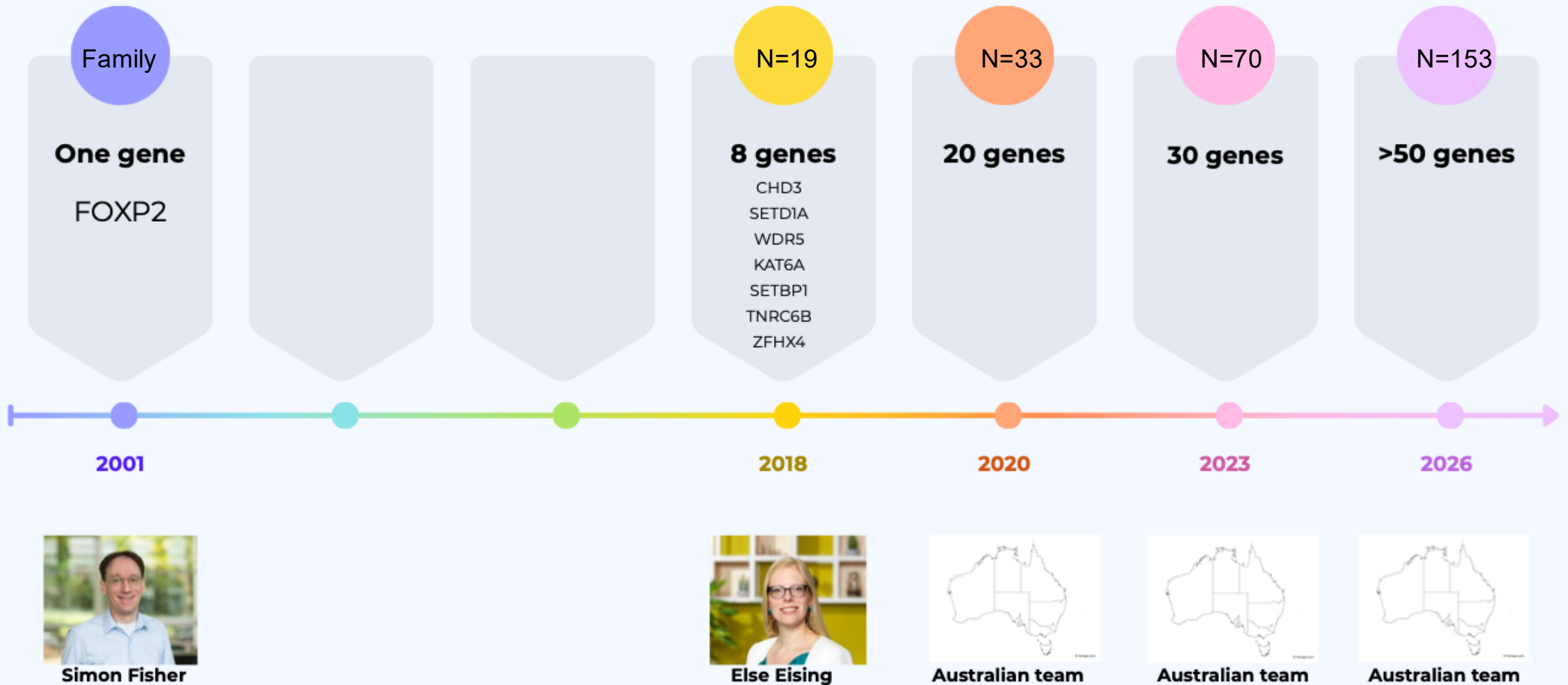
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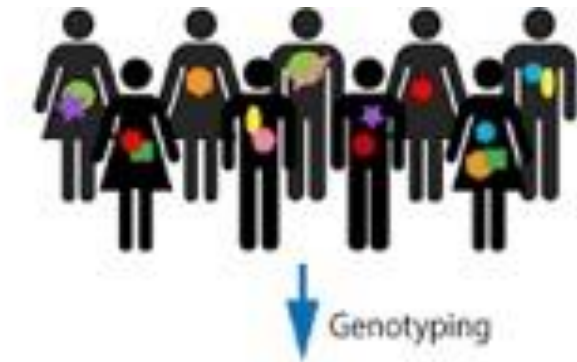
Single genes for childhood apraxia of speech 2001-2026



Also work and further genes identified in the US by Beate Peter, presented next! and Marisa Mitchell

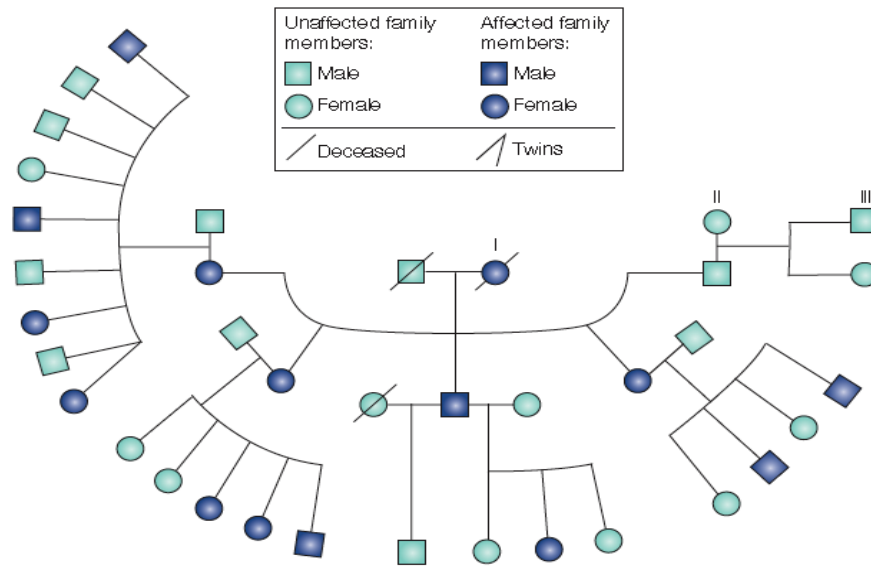
Childhood apraxia of speech is genetically heterogeneous –
(as for all neurodevelopmental disorders)

Group of children with CAS

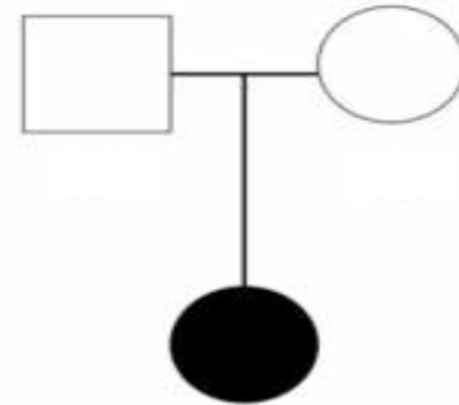


Genetic does NOT always mean inherited

More often sporadic – than inherited

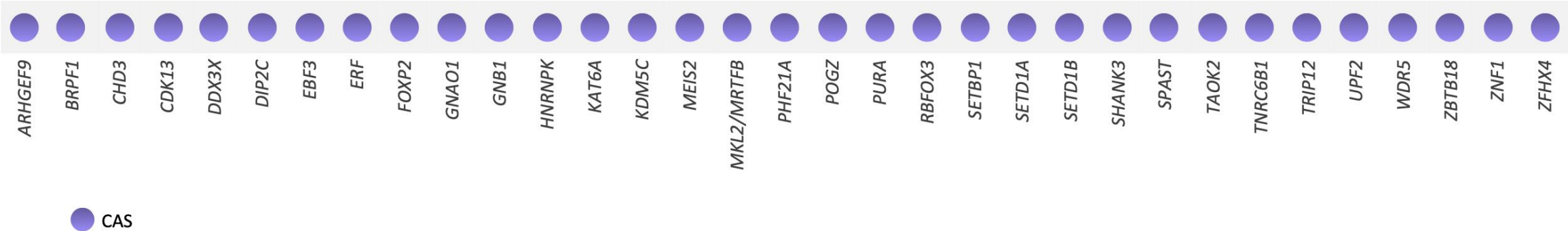


Inherited model
– multi generational



Sporadic – ‘de novo’
(occurring for the first
time in the family)

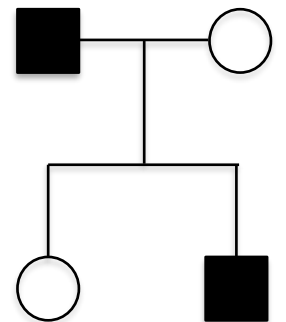
Broadening phenotype of known neurodevelopmental disorders (IQ>70 for CAS cases)



CAS candidate genes and co-occurring conditions (> seen in general population)

CACNA1A-related condition

- Paternal history speech delay, subclinical autism traits
- First words at age 2 years
- Mild delays in receptive language & academic skills
- Motor milestones slightly delayed; walked at 16 months
- Some autism traits noted
- Staring spells, EEG normal
- No dysmorphism noted
- c.3829C>T; p.(Arg1277*) (ClinVar 8506)



ESHG

www.nature.com/ejhg

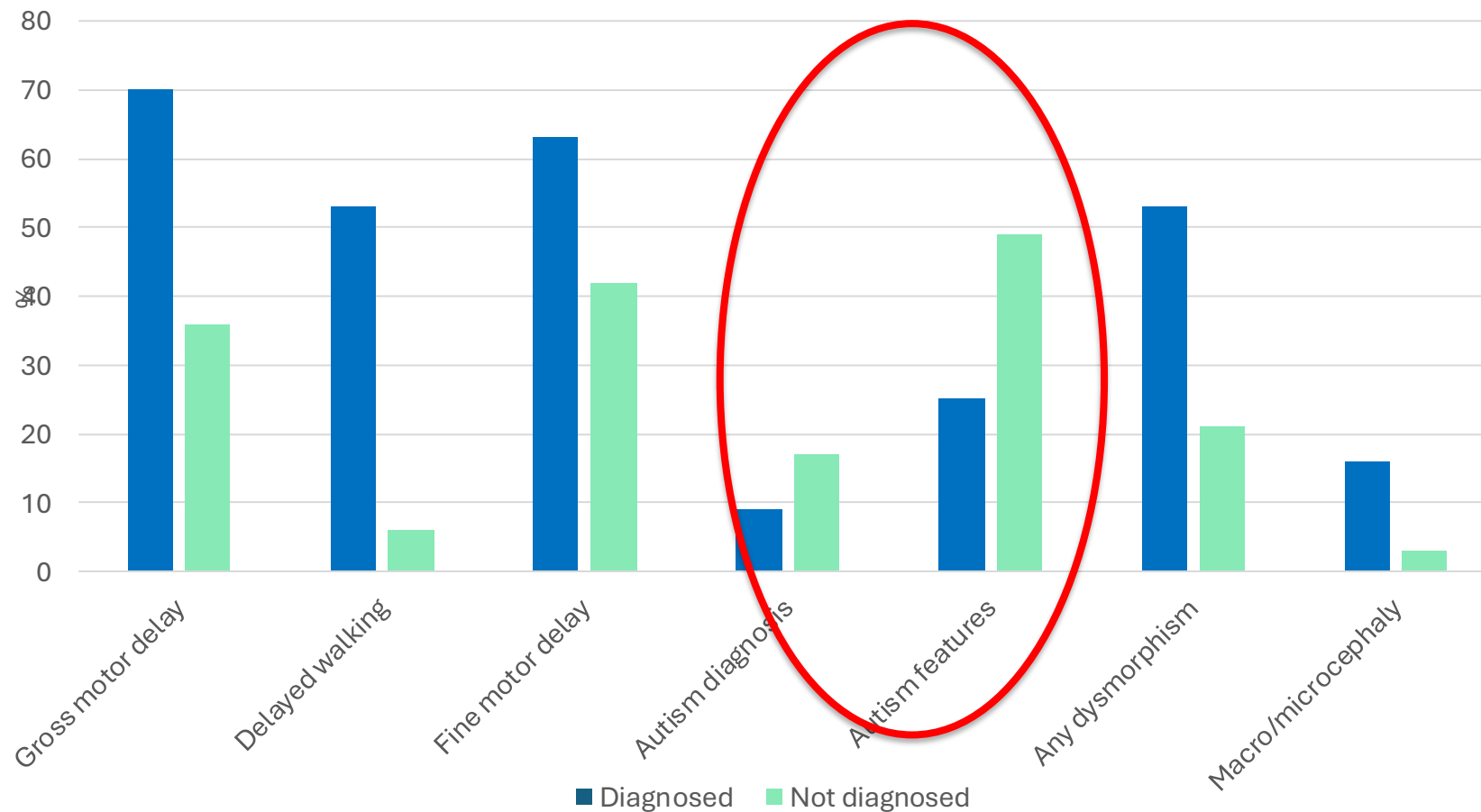
ARTICLE OPEN

Check for updates

Childhood motor speech disorders: who to prioritise for genetic testing

Halianna Van Niel^{1,13}, Mariana Lauretta^{1,2,13}, Emma Baker^{1,2}, Lorraine O'Donnell^{1,2}, Charlotte Boulton^{1,2}, Cella Brencley^{1,2}, David Coman^{1,2}, Evyenia Michellis¹, Himanshu Goel³, Geoff Thompson⁴, Richard Webster⁷, Georgia Paxton^{5,8}, Zornitza Stark⁹, Ingrid E. Scheffer^{6,10}, Michael S. Hildebrand^{6,10,11}, David J. Amor^{2,4,14} and Angela T. Morgan^{1,2,4,14}

Can we predict who will receive a single gene diagnosis?



ARTICLE OPEN

Check for updates

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Single genes for apraxia - translating research into the clinic

Value of genetic testing in the clinic?

www.nature.com/ejhg



ARTICLE OPEN

Check for updates

The value of genomic testing in severe childhood speech disorders

Yan Meng¹, Stephanie Best^{1,2,3,4}, David J. Amor^{1,5,6}, Ruth Braden⁵, Angela T. Morgan^{1,5,6,7} and Ilias Goranitis^{1,2,5,7}

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Marginal utilities & willingness to pay - general public N=950

	Marginal WTP (AU\$) ^c
Number of children who receive genetic diagnosis	45
Knowledge gained from a genomic diagnosis (some knowledge)	1478
Knowledge gained from a genomic diagnosis (a lot of knowledge)	3092
Chance of improving the process of the child's medical care now	90
Time between now and when your child does the test	-201
Cost of testing to you	
Allowing access to educational support services	1140
Enabling access to relevant genetic-based family support groups	520

Marginal utilities & willingness to pay – apraxia families N=54

	Marginal WTP (AU\$) ^c
Number of children who receive genetic diagnosis	49
Knowledge gained from a genomic diagnosis (some knowledge)	2352
Knowledge gained from a genomic diagnosis (a lot of knowledge)	4207
Chance of improving the process of the child's medical care now	93
Time between now and when your child does the test	-169
Cost of testing to you	
Allowing access to educational support services	3094
Enabling access to relevant genetic-based family support groups	658

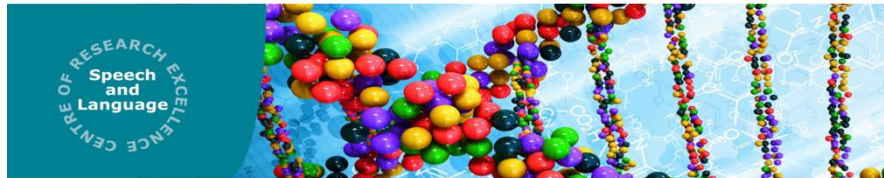
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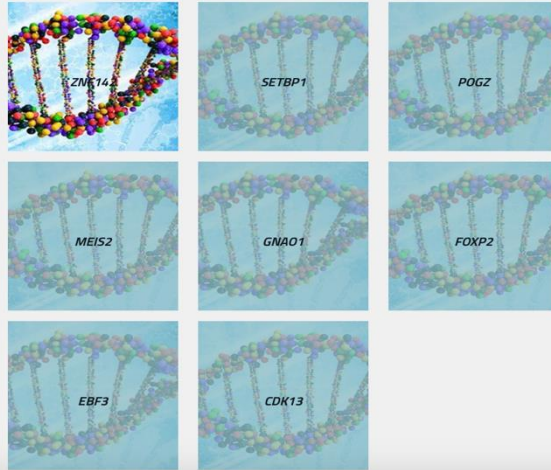
Genetics in the clinic – impacts for clinical practice?

Supporting families, consumer groups



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Genetic conditions associated with childhood apraxia of speech candidate genes



Genes

Genetic conditions associated with childhood apraxia of speech candidate genes

Other conditions we have studied that include speech and language disorder presentations



Lottie Morison Olivia van Reyk Ruth Braden Miya St. John Elana Forbes Sarah Horton

Frequently asked questions

What are the associated health or developmental conditions seen in children with *SETBP1* haploinsufficiency disorder?

At what age to children with *SETBP1* haploinsufficiency disorder begin speaking?

When children start speaking – what are the main features of their speech?

[How does speech develop over time?](#)

Do the children attend mainstream schools?

What are the best-evidenced speech and language therapies?

What happens to communication during adolescence and into early adulthood?

What do children with *SETBP1* haploinsufficiency disorder sound like across the lifespan?

[Further information and support](#)

Thankyou and acknowledgements

Acknowledgements- co-investigators of the speech genetics team

David Amor, Clinical Geneticist, University of Melbourne, VCGS, MCRI

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Nick Martin, Queensland Institute of Medical Research

Else Eising, MPI

Frederique Liegeois, University College London Institute of Child Health

Sheena Reilly, Speech Pathologist, Griffith University

Stephanie Best, Peter Mac

Anna Jarmolowicz, UoM

Ilias Goranitis, Health economist, University of Melbourne, MCRI

MCRI, RCH speech and language genetics team

Olivia van Reyk, Speech pathologist

Lottie Morison, Speech pathologist

Mariana Laretta, Speech pathologist

Elana Forbes, Psychologist

Miya St. John, Speech pathologist

Sarah Horton, Speech pathologist

Dr. Ruth Braden, Speech pathologist

Dr. Emma Baker, Psychologist

Bronwyn Parry-Fielder, Speech pathologist

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Clinical genetics



Ingrid Scheffer
Neurology



Fred Liegeois
Neuroscience

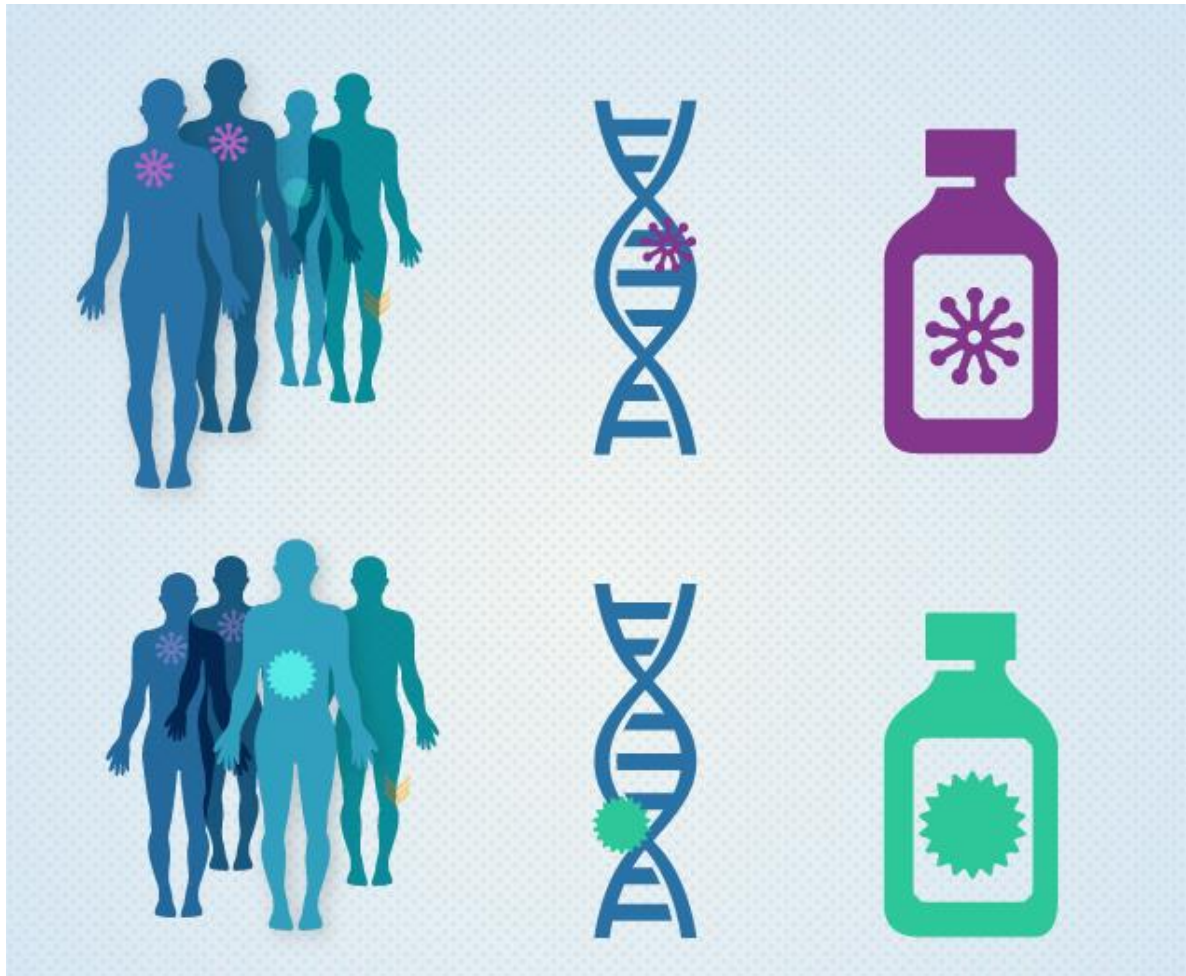


Simon Fisher
Biology



Michael Hildebrand
Molecular genetics

Precision or personalized medicine – biologically targeted therapies

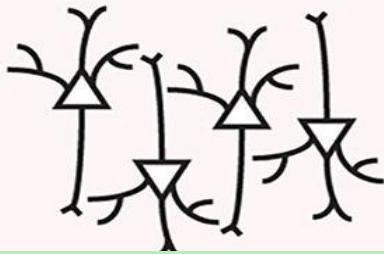


Unique therapies that treat an individual's (speech) disorder based on the specific genetic abnormalities of their condition

Towards precision medicine, biologically targeted therapies

Replicating genetic variants & trialing drug therapies

Cell cultures



SETBP1 variant

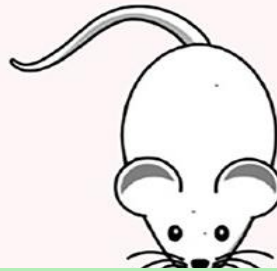
Pros:

- Derivable from patient iPS cells
- Readily available
- Easy to manipulate
- High throughput

Cons:

- Lacks brain cytoarchitecture
- Lacks 3D microenvironment
- Missing many cell types

Animal models



SETBP1 variant

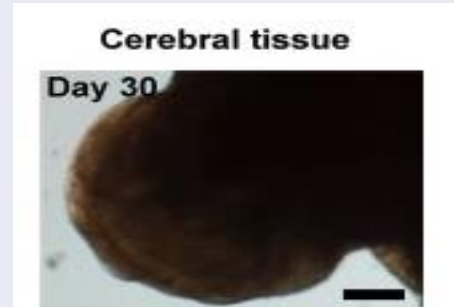
Pros:

- Intact brain structure
- 3D microenvironment
- Behavioral testing

Cons:

- May not generalize to patients
- Low throughput

Brain organoids



SETBP1 variant

Pros:

- Human origin
- Derivable from patient iPS cells
- Brain-like cytoarchitecture
- 3D microenvironment

Cons:

- Limited maturity & size
- Missing certain cell types
- Neural activity not well defined