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A FIBROBLAST GROWTH FACTOR 14 (FGF14) DELETION UNDERLIES A VESTIBULOCEREBELLAR DISORDER PRESENTING AS EARLY ONSET NYSTAGMUS – AN OLD PEDIGREE REVISITED

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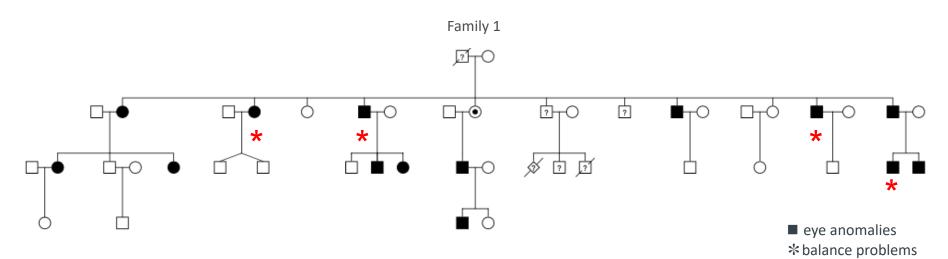
FAMILY 1

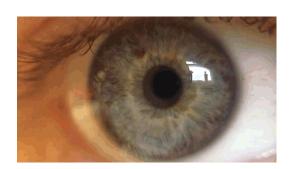
- Nystagmus: involuntary and periodic oscillations of the eye
- Harris *et al.*, 1993:

Large pedigree with a dominant vestibulo-cerebellar disorder:

- gaze evoked and upbeat nystagmus
- absent/poor smooth pursuit
- poor vestibulo-ocular reflex
- normal vision
- normal electroretinograms (ERG), attenuated visually-evoked potentials
- Ragge *et al.*, 2003:

Linkage study: locus on chromosome 13q31-q33 (NYS4)

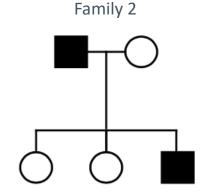


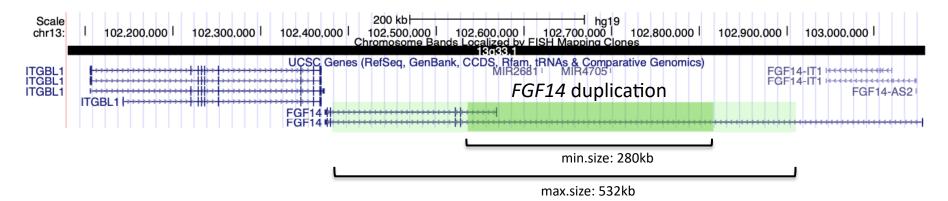




FAMILY 2

- o Phenotype:
 - -eye movement anomalies (gaze evoked and upbeat nystagmus, poor smooth pursuit)
 - -early onset tremor
 - -poor balance and fine motor difficulties
 - -mood disorder
- Affected:proband and father (mild)
- aCGH: intragenic duplication of *FGF14* (chr13q33.1)

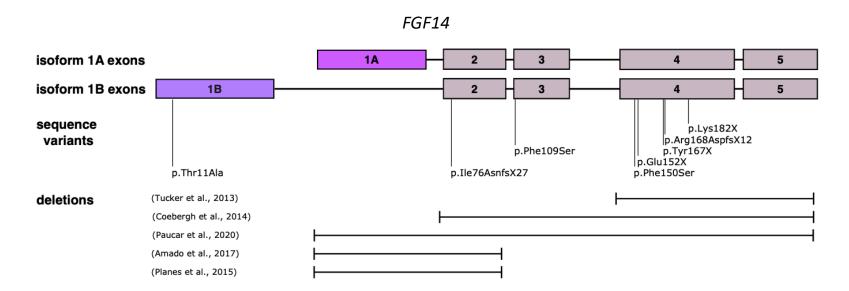






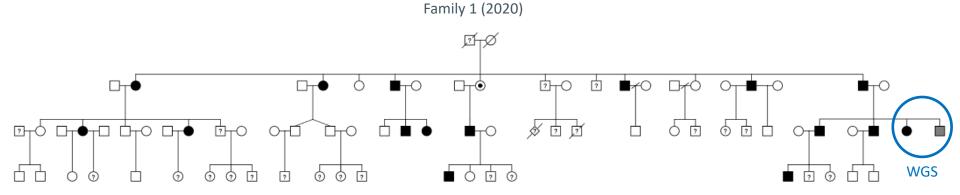
FGF14

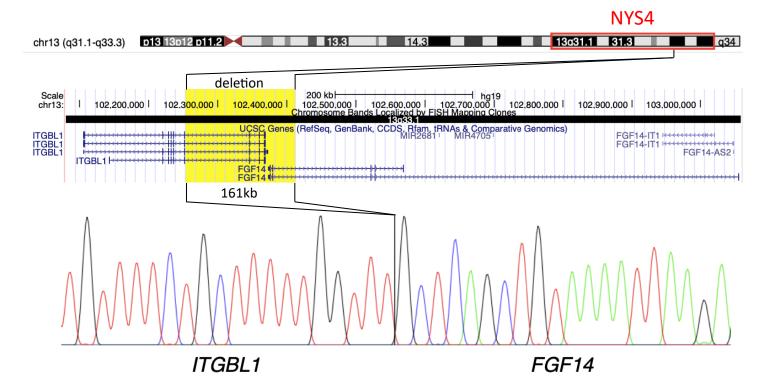
- Intracellular fibroblast growth factor involved in multiple neuronal processes: channel gating, neuronal excitability, synaptic transmission and plasticity
- Heterozygous FGF14 variants:
 - Spinocerebellar Ataxia type 27 (SCA27)
 - Episodic Ataxia
 - Paroxysmal non-kinesigenic dyskinesia
 - → phenotypes consistent with mouse models
- <20 variants have been reported in families with these phenotypes</p>





FAMILY 1

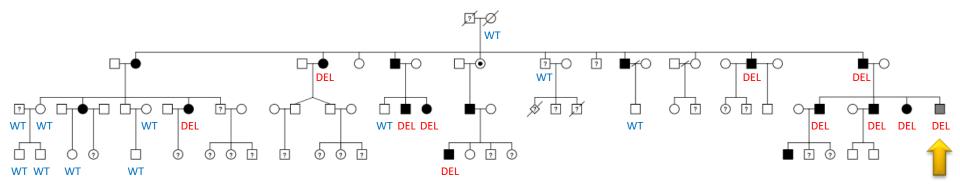




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FAMILY 1



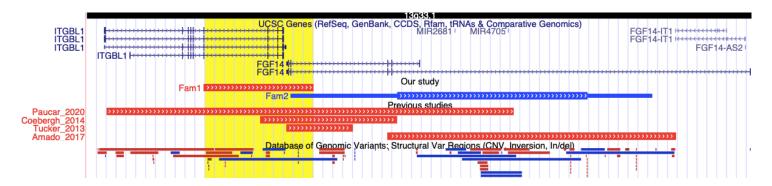


Segregation analysis: long range PCR

- Present in 10 affected + 1 mildly affected
- Absent in 8 unaffected

Literature: heterozygous FGF14 deletions previously reported in cases with SCA27

→ Pathogenic variant





CONCLUSIONS

- Family 1
 FGF14 heterozygous deletion → underlying cause of NYS4
- Family 2
 FGF14 heterozygous duplication → first duplication reported in SCA27
- FGF14 spectrum: from isolated nystagmus to SCA27
 - -early onset
 - -slow progression
 - -inter- and intra-familial variability
- Importance of FGF14 screening in cases with childhood nystagmus
 - -both sequence and structural variants



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