

Diagnostic Exome Sequencing in Adolescents with Neurological and Neurodevelopmental Disorders

Kirsten Blanco, BS, Zöe Powis, MS, CGC, Kelly D.F. Hagman, MS, CGC, Elaine C. Weltmer, MS, CGC, Sha Tang, Ph.D.,DABMG

BACKGROUND

- Diagnostic exome sequencing (DES) is increasingly utilized to identify genetic etiologies of neurological and neurodevelopmental disorders (NDD) in pediatric patients.
- Traditional testing guidelines typically recommend microarray, fragile X, karyotype, single gene, and multi-gene panel testing (MGPT) in individuals with NDD, resulting in a lengthy “diagnostic odyssey” with often inconclusive or negative results (1).
- Adolescents provide a unique opportunity within the pediatric population to evaluate the clinical utility of DES in undiagnosed individuals with NDD, yet little is known about genetic testing in this cohort.
- Herein, we report the characteristics and detection rates of adolescent patients with NDD.

FIGURE 1. DETECTION RATES (n = 568)

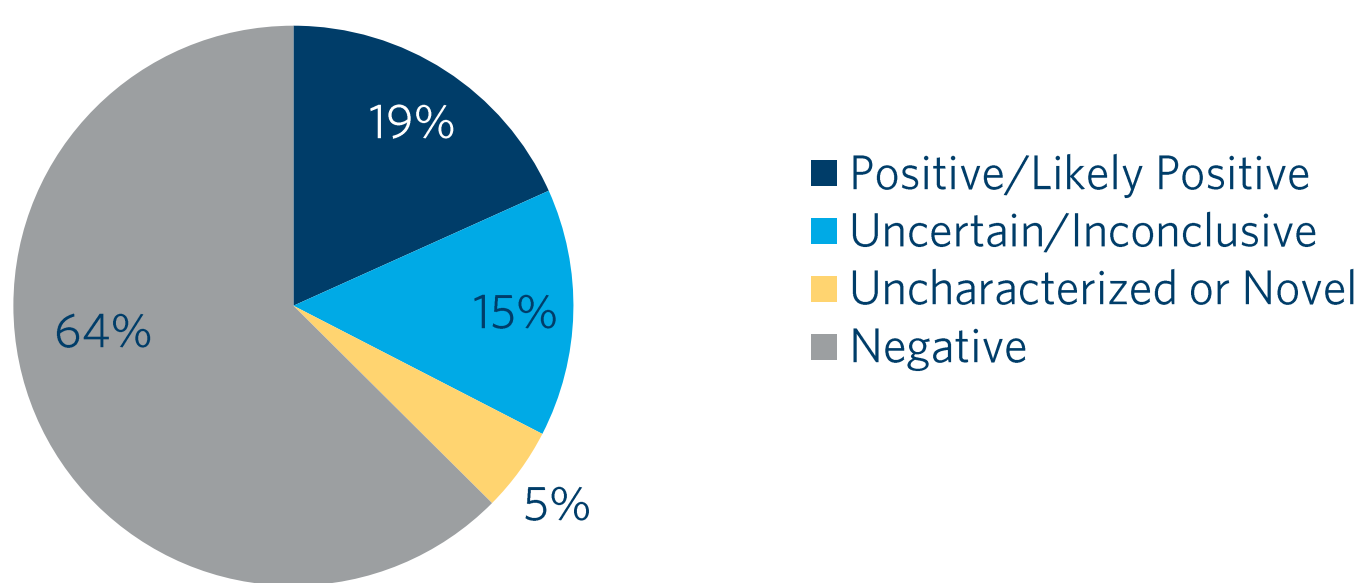
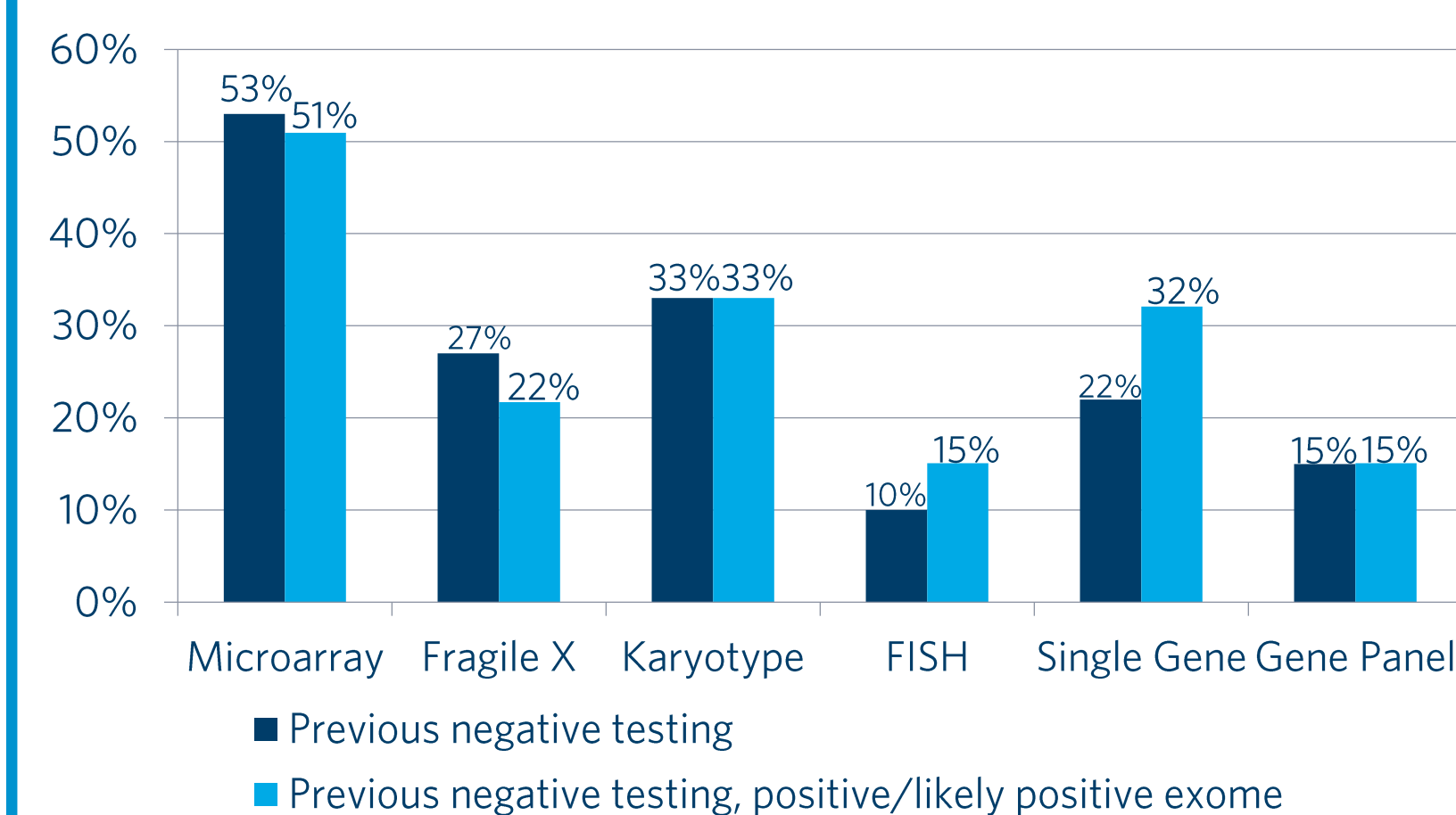


FIGURE 2. PERCENTAGE OF PATIENTS WITH PREVIOUS NEGATIVE TESTING



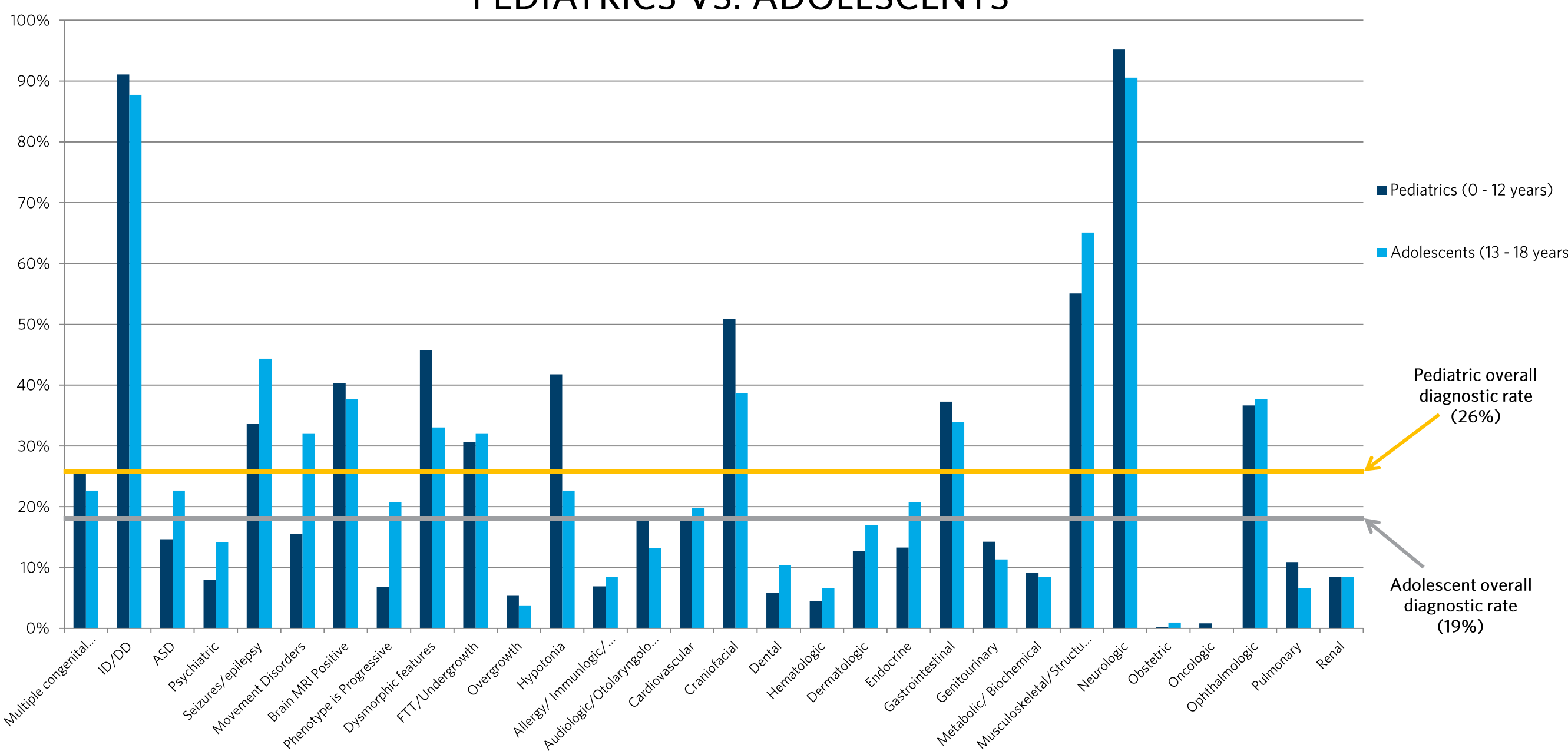
METHODS

- Available clinical and genetic testing histories were reviewed for an unselected cohort of 568 adolescents (ages 13 – 17 years) referred for DES at one commercial company with neurological indications, including intellectual disability (ID)/developmental delay (DD), autism spectrum disorder (ASD), and seizures/epilepsy.
- All probands underwent characterized gene analysis; if negative, novel candidate gene analysis was performed if requested and an informative family trio was provided. Overall result categories were determined according to predefined diagnostic variant assessment criteria (2). Diagnostic rates are defined by a positive or likely positive overall report.

RESULTS

- Of 568 probands, 258 (45%) were female and 310 (55%) male; average age of testing was 14.8 years.
- 111 positive/likely positive findings were identified in 106 (19%) probands (Figure 1) in 89 characterized genes, 72% (64/89) of which are not included on a large routine neurodevelopmental MGPT (Table 1).
- Of these findings, 35% (39/111) were inherited and 48% *de novo*; 31 (28%) were in autosomal recessive genes, 66 (59%) in autosomal dominant, 6 (5%) in X-linked dominant, 6 (5%) in X-linked recessive, and 1 (1%) in a mitochondrial gene.
- Previous negative testing was reported in 419 (74%) of probands, with 19% (81/419) having a positive or likely positive DES finding (Figure 2).
- Diagnostic rates in adolescents with ASD, seizures/epilepsy, and musculoskeletal indications (Figure 3) were greater than those in an unselected cohort of pediatric patients with NDD (n=3648).

FIGURE 3. DIAGNOSTIC RATES BY CLINICAL CHARACTERISTICS: PEDIATRICS VS. ADOLESCENTS



Gene Findings

Characterized Positive/Likely Positive

Included on Neurodevelopmental MGPT (25 genes)

ADNP (2 cases)	DLG3	IQSEC2	PHF6
ANKRD11 (3 cases)	DYNC1H1	KCNQ2	PLP1
ARID1B (3 cases)	DYRK1A	KDM5C (2 cases)	PNKP
CACNA1A (2 cases)	FOXG1	KIF1A	VPS13B
CHD2	GNAO1	MECP2	
CHD7 (2 cases)	GRIA3	NSUN2	
DDX3X	GRIN1	PACSI	

Not Included on Neurodevelopmental MGPT (64 genes)

ASXL1	FBN1	MED13L	RYR1
ATP1A3	FGFR3	MT-ND6	SBF2
BRAF	FUS	MTOR	SCN3A
CCND2	GBE1	MYO7A	SETX (2 cases)
CFTR	GJC2	NEB	SH3TC2
CHRNA1	HIVEP2	NFIA (2 cases)	SLC26A2
COL4A1	HMGCL	NPC1	SLC37A4
CSF1R	HSD17B10	NR2F1	SOX9
CYP2U1	KCNK3	NUBPL	SPAST
CYP7B1	KMT2A (2 cases)	PDE6A	TANGO2
DEAF1	KMT2B	PIEZO2	TP63
DLAT	KMT2D	PKD1	TRIO
DNM1L	LAMA2	PKD2	TRIT1
DOK7	LDLR*	PMM2 (2 cases)	TRPV4
EBF3	LMNA	PRNP	TUBB
FA2H	MAGEL2	PYCR1	USH2A

Candidate/Suspected Candidate (15 genes)

ADCY5	PKDCC	CLTC	RICTOR
CDC42 (2 cases)	SNAP25	FDXR	RYR3
COQ4	ATP6V1A	PDGFRB	WARS2
ERBB4	CLCN3	RHOA	

TAKE-HOME POINTS

- Positive/likely positive findings were identified in 106 probands (19%); compared to pediatrics, diagnostic rates were higher in patients with ASD, seizures/epilepsy, and musculoskeletal/structural indications.
- As 72% (64/89) of gene findings are not included on a large routine neurodevelopmental MGPT, this study highlights the clinical utility of DES in adolescents with complex NDD phenotypes in which traditional testing strategies have failed to elucidate a genetic etiology.
- Detection of alterations in both characterized and novel genes provides patients with an accurate diagnosis and has important treatment, medical management, and reproductive implications as they transition to adulthood.

REFERENCES

- Xue Y, Ankala A, Wilcox WR, et al. Solving the molecular diagnostic testing conundrum for Mendelian disorders in the era of next-generation sequencing: single-gene, gene panel, or exome/genome sequencing.
- Farwell KD, Shahmirzadi L, El-Khechen D, et al. Enhanced utility of family-centered diagnostic exome sequencing with inheritance model-based analysis: results from 500 unselected families.