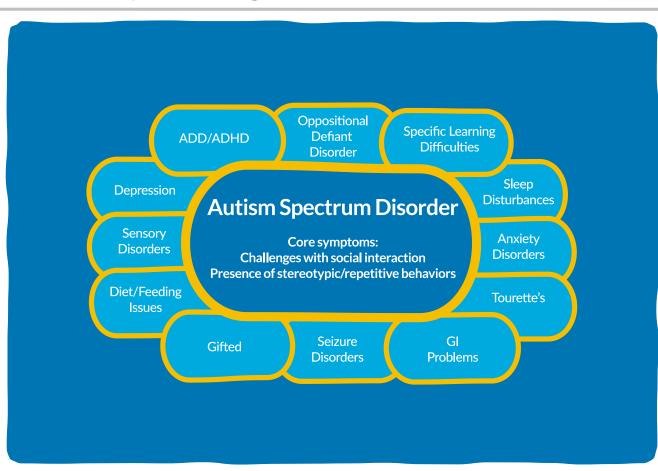
SPARK: a large-scale genomic resource of 99,000 individuals

Pamela Feliciano, PhD

Scientific Director, SPARK

March 12, 2018

ASD is extremely heterogeneous



ASD risk is also complex

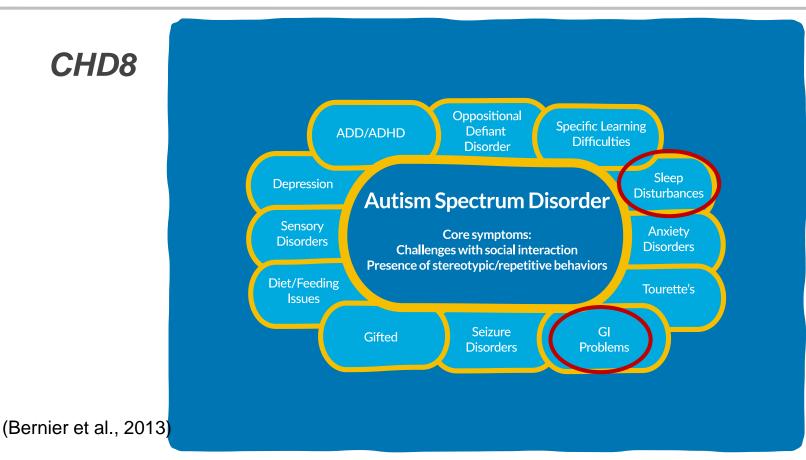
Inherited variants ~50%?

De novo LGD & missense variants ~10-30%?

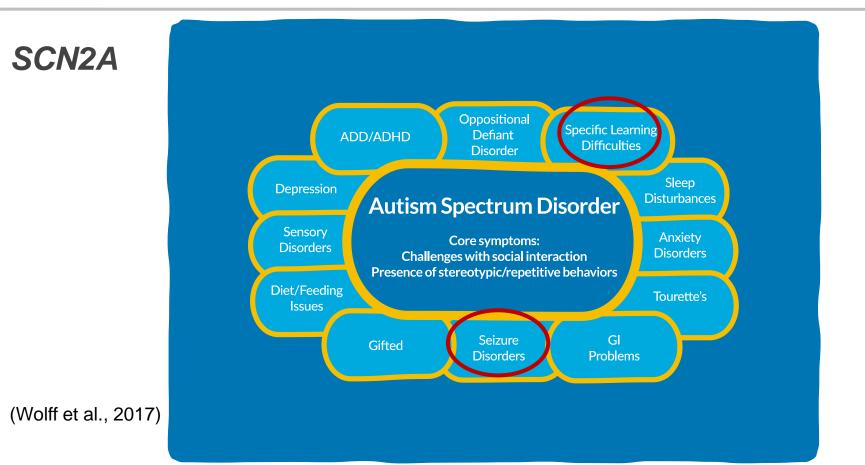
Somatic variants 1%?

Environment 17%

Genes define more homogeneous subtypes



Variants can inform treatment



Why SPARK?

• Hundreds of genes still unknown

• Clinical research is important, but participant recruitment is challenging

• Genotype/pathway-driven clinical research even more difficult

	SSC			
Size	2,517 families Some			
Recontactable				
Return of results	Some In clinic			
ASD Dx & Phenotyping				
Emphasis on partnership	Some			
Central IRB	No			

Scaling research to tens of thousands





Enroll Online SPARKforAutism.org Saliva by mail

Recruitment through clinical site network



Recruitment via social media



SPARK for Autism

September 15 · 🚱

Let's have some fun! Add your response to the comments below. Then visit our website to learn more about how you can accelerate autism research. https://goo.gl/eVptNH

Describe yourself or your loved one with autism using emojis.					
SPARK Initing autism research Improving lives					
SPARK for Autism Organization	Learn More				
🖬 Like 📕 Comment					

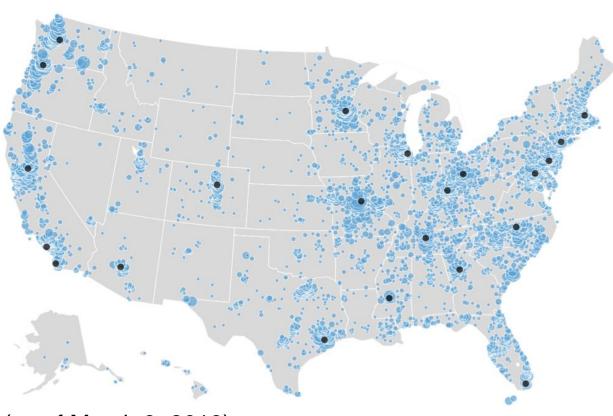


uly 15 · 🚱

Any Dad would wrestle a bear for his child with autism, but we need more Dads to complete saliva kits. Take action! https://goo.gl/tn9JxB #thanksdad #autism



SPARK Participants n = 99,209



Individuals with autism n = 38,248

DNA samples n = 47,083

Complete trios + DNA n = 6,985

(as of March 8, 2018)

8% of probands harbor *de novo* gene-disrupting mutations in constrained genes

Established ASD

**CHD8 *CHD2 *SCN2A **FOXP1 *POGZ **SYNGAP1 *MBD5 *ADNP *SHANK3

Neurodevelopmental

*NBEAAFF3REREAGPS*QRICH1*DPP6*MEIS2GIGYF1HNRNPUIRF2BPLTRERF1PLXNA2FEZF2*SETD1A

Candidate RALGAPB CLASP2 YBX1 SH3RF3 WDR20SF3B2 CBX1 PSMD6 CHD3

(pLI ≥ 0.9; likelihood of intolerance to gene-disrupting mutation) * = validated by Sanger sequencing

SPARK is returning individual genetic results related to ASD

- Pre-define genes that are validated ASD genes
 - 3 independent reports of *de novo* LGD variants in ASD
 - With few exceptions, currently returning *de novo* LGD variants
- Current list has 90 genes and CNV loci
- Variants are confirmed in CLIA lab, Medical Genetics committee review all cases
- If participant chooses to receive result, SPARK returns result through a genetics counselor or we will give report to participant's medical provider

5.5% of individuals with ASD (n=25) have a returnable result

de novo *CHD8 (n =2) * SCN2A SYNGAP1 (n=2) * FOXP1 (n=2) * SHANK3 (n=2) * POGZ * ADNP * CHD2 MBD5 HRNPU

Inherited X-linked * ATRX * MECP2

de novo CNVs 1q21.1 dup 15q13.3 dup 16p11.2 dup 16p11.2 distal dup 17q12 dup 21q21.3 dup

Inherited CNVs

16p11.2 dup *NRXN1* deletion (n =2)

*result returned to family already

SPARK Research Match is a resource for researchers

- Any researcher can apply to use SPARK Research Match (~99K ind with ASD and 1st degree family members) to recruit for their studies
- No cost to researchers
- Requirements: IRB approved protocol, plan to return information back to participants, data sharing with SPARK
- 2017: ~10 studies using Research Match successfully, some with 60% response rate

Launched Research Match studies

#	Short Title (PI _Institution)	Study Type	Families Invited	Indicated Interest	Completed study
1	Genes and environment in ASD (Volk/Fallin_JHSPH)	Online	2,089	64%	60%
2	Understanding non-drug treatment and care (Monz_Roche)	Online	11,514	48%	43%
3	Somatic mutations in ASD – twin study (O'Roak_OHSU)	Remote*	870	27%	not yet available
4	Visual experiments to develop an ASD model (Angelaki_Baylor)	Clinic (observation)	295	32%	not yet available
5	Oxytocin and theory of mind training (Soorya_Rush)	Clinic (intervention)	81	19%	0%
6	Arbaclofen and imaging dose response (Roberts_CHOP)	Clinic (intervention)	108	25%**	not yet available
7	Investigation of Genetic Exome Research-2 (The TIGER-2 Study) (Bernier_UW)	Clinic (observation)		*at least 1 SPARK family that received result from SPARK	not yet available

* Remote - requires online or paper questionnaires plus genetic sample

** Study launched January 10 and still actively recruiting



Why SPARK?

- Hundreds of genes still unknown
- ✓ DNA from thousands of families and individuals with ASD in pipeline.
- Clinical research is important, but participant recruitment is challenging
- Emphasis on participant engagement and Research Match platform should make recruitment more efficient
- Genotype/pathway-driven clinical research even more difficult
- Return of individual genetic results related to ASD should accelerate this type of research

Data & Access to participants: https://www.sfari.org/resource/sfari-base/



Special thanks to

- The SPARK Team
- SPARK's Clinical Site & Genomics Consortium
- Our collaborators & partners at Baylor College of Medicine, Prevention Genetics, and Regeneron

And most importantly, to the incredible community of individuals and families participating in SPARK

SFAR SIMONS FOUNDATION AUTISM RESEARCH INITIATIVE



sfari.org/resources/sfari-base

SPARKforAutism.org