Integrating Multi-omic perspectives for individualized treatment in Autism Spectrum Disorder

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Introduction

- Autism Spectrum Disorder (ASD) affects 1 in 66 Canadian children.
- Three of four of those are male.
- > 3.2 million dollars/ person for social services, education, and healthcare , emotional burden
- >100 genes implicated, no SNV or CNV genomic micro-deletion or -duplication > 1-2% of ASD cases.
- Patient phenotypic features are often in clusters.

Characteristics of ASD

Restricted, repetitive patterns of behavior, interests, or activities.

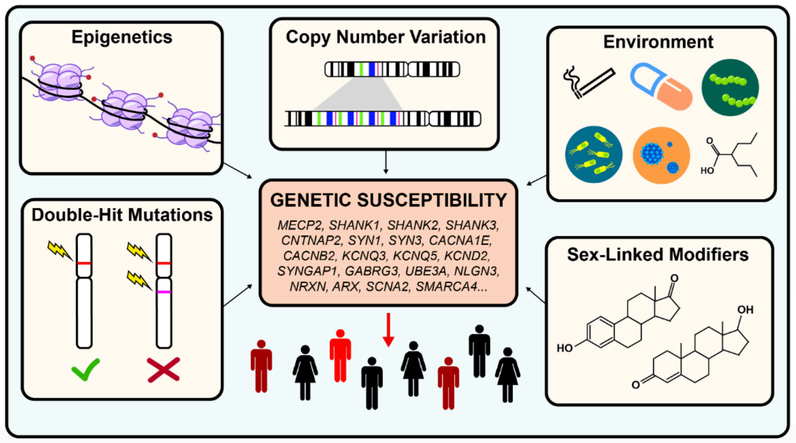
Persistent deficits in social communication and social interaction across multiple contexts.

Co-morbidities

Motor abnormalities (79%), Gastrointestinal (70%)
Epilepsy (30%), Intellectual disability (45%),
Sleep disorders (50–80%), Language disorders.

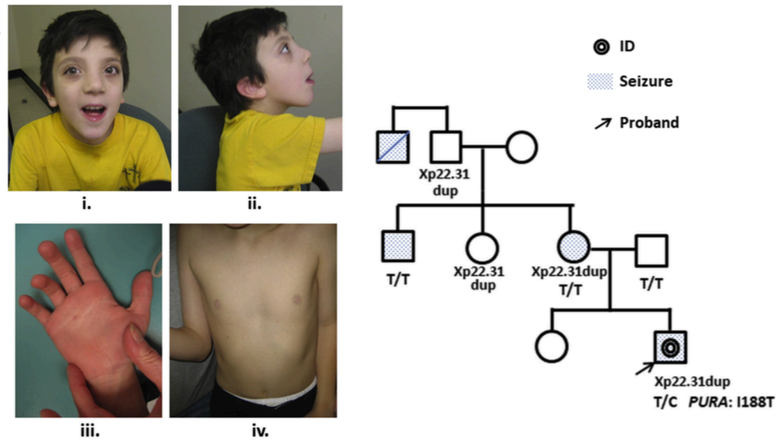
- Early intervention improves Intelligence Quotient , language skills, adaptive behaviour, and reduced severity of autism diagnosis.

Genetic and environmental causes



The project goal is to integrate the phenome and genome of participants with ASD to provide a method for earlier, more stable diagnosis and individualized treatment that will improve patient quality of life.

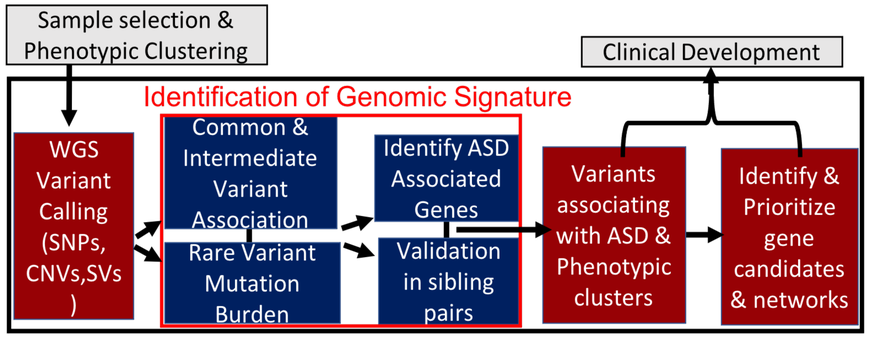
Methods



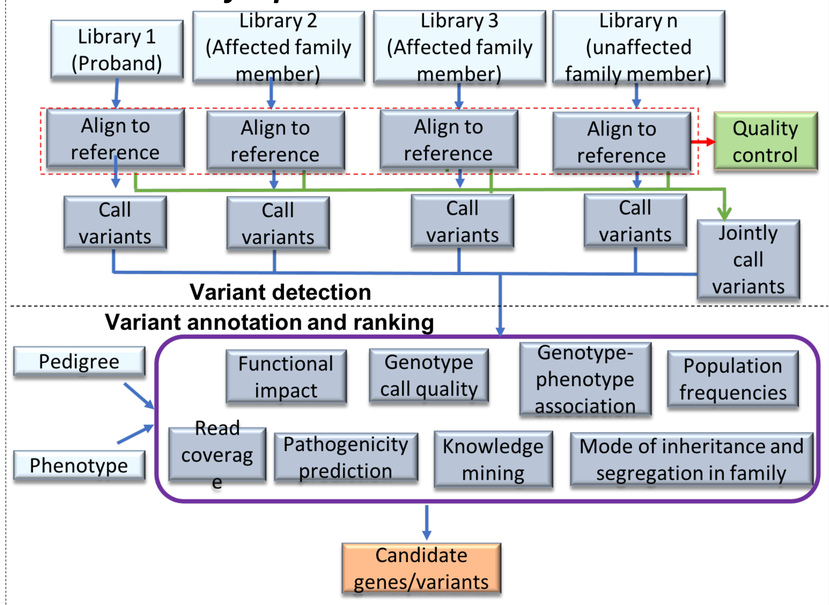
Above: Male diagnosed with ASD with inherited Xp22.31 microduplication and de novo *Pura* Missense mutation

WGS 500 participants and their parents (n=1418)

individualized **T**reatments for **A**utism **R**esponse using **G**enetic-**E**nvironment **T**argets



Methods of Pipelines and Tools



- Metabolic, Proteomic, and Microbiome data are available for some patients for pipeline integration.
- An ensemble of supervised and unsupervised methods will determine the features clustering.
- Statistics specific to polygenic disease and sex.

Conclusion

Whole genome sequencing can be used in conjugation with phenotype to derive common and rare variants in the ASD population, as well as within groups of people with ASD experiencing similar clusters of phenotypic features. Additionally, metabolic, proteomic, and microbiome data can be used to further inform the participants' diagnosis. Ultimately, this will allow for earlier and greater diagnosis, as well as individualized treatment.

Acknowledgement

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References

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