

Newborn Screening for Type 1 Diabetes Risk Using Genome Sequencing: The Early Check Experience

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Disclosures

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The findings and conclusions in this presentation are those of the authors and do not necessarily represent the views of the North Carolina Department of Health and Human Services, Division of Public Health.





Early Check – A Newborn Screening Program in North Carolina

- Researching the feasibility and acceptability of using genome sequencing to screen newborns for monogenic and complex conditions
- Mothers of babies born in North Carolina visit the Early Check website to sign-up
- Uses the state-collected dried blood spot (no additional sample collection needed)





Welcome to Early Check! Let's get started.

Early Check is a voluntary research study that provides free health tests to new babies.

The goal of Early Check is to find serious health conditions in babies so they can get help sooner.





Early Check: A Voluntary Newborn Screening Program

Screened ~ 27,000 newborns in N.C. since 2018





Selected a Published and Validated GRS



Luckett et al., 2023



Formative Research and Community Engagement Activities





Set GRS Reporting Thresholds

Table 1—Simulated population-based prediction of T1D using HLA screening, the original T1D GRS, and the T1D GRS2									
T1D centile*	Population centile**	GRS2	Specificity (%)	Sensitivity (%)	1-Specificity (%)	Youden index (j)	T1D risk (%)***		
5	70.2	11.68	69.5	94.8	30.5	0.643	0.9		
10	79.4	12.36	78.9	89.4	21.1	0.683	1.3		
25	90.6	13.45	90.4	77.5	9.6	0.679	2.4		
50	96.8	14.60	96.7	53.7	3.3	0.505	4.7		
75	99.1	15.65	99.1	30.2	0.9	0.293	9.1		
90	99.8	16.54	99.8	13.2	0.2	0.130	15.7		
95	99.9	17.06	99.9	7.2	0.1	0.072	22.8		

Sharp et al, 2019



Set GRS Reporting Thresholds





T1D Screening Process Overview

Early Check

- Obtain consent in portal
- Match consent to dried blood spot (DBS) specimens at state lab
- Obtain punches from DBS card



Laboratory Partner

- DNA extraction
- Genome sequencing
- Prepare genome data and send to RTI

Early Check

- Extract SNPs from genome data
- GRS calculation
- Results reported in portal



Screening flow: T1D cohort of first ~ 2,000 babies screened





Characteristics: first ~2,000 babies screened 9/2023 – 6/2024

	Screened Newborns (N=1979)	Screened for T1D Risk (N=1605)
Sex		
Girl	1006 (50.8%)	807 (50.3%)
Воу	973 (49.2%)	798 (49.7%)
Group Identity		
American Indian or Alaska Native	4 (0.2%)	2 (0.1%)
Asian	98 (5.0%)	71 (4.4%)
Black, African American or African	145 (7.3%)	99 (6.2%)
Hispanic, Latino, or Spanish	103 (5.2%)	74 (4.6%)
Middle Eastern or North African	5 (0.3%)	5 (0.3%)
Native Hawaiian or Pacific Islander	0 (0.0%)	0 (0.0%)
White	1164 (58.8%)	986 (61.4%)
Two or more groups	438 (22.1%)	355 (22.1%)
Unknown	22 (1.1%)	13 (0.8%)

Genetic risk scores: first T1D cohort (N=1605)

	T1D Results
	n (%)
Low concern (<2% risk)	1425 (88.8%)
Moderate concern (2-5% risk)	118 (7.4%)
Higher concern (5-10% risk)	51 (3.2%)
Higher concern (>10% risk)	11 (0.7%)
Total	1605



Distribution of PRS Scores (N=1605)



Mean GRS Scores by Self-reported Group Identity (N=1605)

	PRS			
	N	Mean	Std	
African American/Black	99	9.09	2.19	
American Indian or Alaska Native	2	11.78	1.57	
Asian	71	10.22	2.07	
Hispanic/Latino or Spanish	74	10.70	2.28	
Middle Eastern/North African	5	10.99	3.78	
Two or more	355	10.45	2.30	
Unknown	13	10.57	1.88	
White	986	10.63	2.32	



Return of Results in the Portal



Follow-up for Higher Concern or Moderate + 1º relative







Psychosocial assessments

- Consenting parent for 17 of 27 (63%) newborns completed the Patient Health Questionnaire (PHQ-2) and General Anxiety Disorder (GAD-2) after completion of genetic counseling
- 1 scored above clinical cutoffs and was administered the PHQ-9 and GAD-7
- 1 remained above clinical cutoffs
 - Follow-up by study psychologist
 - Parent was actively in comprehensive treatment



Conclusions

- Demonstrates feasibility of using genome data to screen for complex conditions
- Evaluation surveys and interviews with parents and providers will assess acceptability, clinical utility and psychosocial outcomes



Early Check Team



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Grier Page

Powell







Why Screen for T1D?



Besser et al., 2022

Developed SNP Missingness Thresholds

- SNPs contributing to T1D GRS2 calculation fall into 3 main classes:
 - HLA-DQ (n=14)
 - \circ HLA other (n=21)
 - Non-HLA (n=32)
- Different missingness thresholds used for different classes of SNPs
 - $_{\odot}$ $\,$ HLA-DQ: No tolerance for missing SNPs $\,$
 - Other SNPs: Tolerance for up to 2 missing SNPs

