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The Harms of Carrier Status Identification: A Cautionary Warning Against Newborn Sequencing



Two articles by Farrell et al in this volume of *The Journal* explore the potential psychosocial complications of carrier status notification for sickle cell hemoglobinopathy (SCH) and cystic fibrosis (CF) after newborn screening (NBS). Both articles stem from the Wisconsin Project on Improvement of Communication and Process Outcomes after Newborn Screening. In the first, qualitative telephone interviews with parents were conducted after NBS carrier status was disclosed by a primary care provider to evaluate for effectiveness of results communication, misconception of the child's risk for disease, and parental anxiety.¹ The second assessed parents' perceptions of child vulnerability after being informed of carrier result for SCH or CF, and both groups were compared with a control group using an adapted version of the Vulnerable Baby Scale.² Notably, the data collected by Farrell et al in both studies was gathered between 2008 and 2012, and the findings reported in these 2 articles have been corroborated in other studies for these same diseases: (1) parental misunderstanding of carrier status for children with SCH or CF, even in a state that offers genetic counseling; (2) parental anxiety or stress from receiving incidental information; and (3) increased parental assessment of child vulnerability after carrier identification.³⁻⁶ And yet, despite reaffirming the potential harms of carrier status identification in NBS, Farrell et al expect it to expand, concluding that they "suspect that genome sequencing on blood spots will be routine within the coming generation, regardless of ELSI [ethical, legal, and social implications] concerns." Below, we explore why the data from Farrell et al further strengthen the ethical, legal, and social concerns and reject the inevitability of universal adoption of genomic sequencing into NBS programs.

NBS has traditionally focused on conditions and disorders, like CF and SCH, that present early in infancy for which early diagnosis can prevent morbidity or mortality. Although most screening currently uses tandem mass spectrometry, the appeal of whole genome sequencing is the potential to screen

and diagnose even more conditions using a single platform. However, genomic sequencing without phenotypic information still misses many cases of conditions that are currently identified in NBS. In 2014, Bhattacharjee et al attempted to identify the conditions included in state NBS panels.⁷ They wrote: "It is typically assumed that, at least for monogenic disorders, the genotype-phenotype relationship would be simple." Instead the authors found their "ability to pinpoint the clinical phenotype of an individual on the basis of 'genotype' alone is still in its infancy; in our case, only 27 of 36 NBS disease cases were classified correctly without phenotype information."⁷

But imagine that sequencing was better able to identify the conditions included in state NBS panels and could be implemented as the primary platform for NBS. Screening for more conditions would also mean identifying many more carriers. Although broad professional consensus in the US in the early 1990s led to the decision to disclose carrier status when identified in NBS, all US professional statements argue against routine carrier identification in children.⁸⁻¹¹ In BabySeq, a study exploring genomic sequencing of both infants in the neonatal intensive care unit and healthy infants, the researchers demonstrated that >90% of infants screened had ≥ 1 carrier status variant, with an average of 2 carrier status variants and a range from 0 to 7.¹² This finding is lower than data from Bell et al, who found the average participant (noninfant) on whom genomic sequencing was performed was a carrier for 2.8 conditions (range, 0-7).¹³ Primary care physicians are already ill-equipped to discuss NBS carrier results with parents.^{14,15} The identification of more carrier status variants in infants through sequencing will only exacerbate these issues; more information about newborns is not always better, particularly when the information is nonactionable for the health of the infant. Farrell et al have demonstrated the possibility of harm to parents and their children from returning these ancillary results—particularly to parents of lower health literacy.^{1,2} The failure to effectively counsel a significant number of parents about carrier status

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CF Cystic fibrosis
IRT Immunoreactive trypsinogen
NBS Newborn screening
SCH Sickle cell hemoglobinopathy

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for SCH and CF questions our readiness to implement a platform technology that identifies significantly more carriers.

Methodology matters: CF screening using immunoreactive trypsinogen (IRT) with reflex DNA methodology rather than IRT/IRT is more likely to miss minority infants.¹⁶ Today, all US programs use IRT/DNA with few using an expanded DNA panel, which could improve equity for Black and Hispanic children with less common CF DNA variants.¹⁷ As a public health program, NBS should be designed to decrease health care disparities.¹⁸ Incorporating whole genome sequencing into NBS may exacerbate healthcare disparities and should be avoided until we have more diverse racial and ethnic genomic data for conditions included in state NBS panels and a pediatric workforce prepared to counsel families about the actionable and nonactionable findings.¹⁸⁻²¹ ■

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