Evidence-Based Path to Newborn Screening for Duchenne Muscular Dystrophy

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Objective: Creatine kinase (CK) levels are increased on dried blood spots in newborns related to the birthing process. As a marker for newborn screening, CK in Duchenne muscular dystrophy (DMD) results in false-positive testing. In this report, we introduce a 2-tier system using the dried blood spot to first assess CK with follow-up *DMD* gene testing.
Methods: A fluorometric assay based upon the enzymatic transphosphorylation of adenosine diphosphate to adenosine triphosphate was used to measure CK activity. Preliminary studies established a population-based range of CK in newborns using 30,547 deidentified anonymous dried blood spot samples. Mutation analysis used genomic DNA extracted from the dried blood spot followed by whole genome amplification with assessment of single-/multiexon deletions/duplications in the *DMD* gene using multiplex ligation-dependent probe amplification.
Results: *DMD* gene mutations (all exonic deletions) were found in 6 of 37,649 newborn male subjects, all of whom had CK levels >2,000U/l. In 3 newborns with CK >2,000U/l in whom *DMD* gene abnormalities were not found, we identified limb-girdle muscular dystrophy gene mutations affecting *DYSF*, *SGCB*, and *FKRP*.
Interpretation: A 2-tier system of analysis for newborn screening for DMD has been established. This path for newborn screening fits our health care system, minimizes false-positive testing, and uses predetermined levels of CK on dried blood spots to predict *DMD* gene mutations.

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Over the past 3 decades, creatine kinase (CK) testing on dried blood spots has been attempted as a method of newborn screening (NBS) for Duchenne muscular dystrophy (DMD),[1–9] because CK is elevated at birth in individuals with this condition.[10–12] CK elevation is then validated by retesting of venous blood at 4 to 6 weeks of age with subsequent *DMD* gene analysis employed to establish a definitive diagnosis. Presently, this approach survives only in Antwerp, Belgium[9] (NBS was stopped in Wales on November 30, 2011). It has been difficult for programs to justify NBS for DMD because of the lack of evidence that early treatment improves the outcome of affected newborns.[13,14] In addition, the Wales/Antwerp DMD NBS model, requiring extensive follow-up through retesting of venous blood several weeks after birth for CK with subsequent DNA testing, is impractical to implement in the United States.

Nevertheless, recent advances in diagnostic testing methods and promising molecular-based therapies for DMD have rekindled interest in establishing a pathway

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for NBS for DMD.[15–19] Especially relevant is clinical improvement following the systemic administration of antisense oligonucleotide (AON) PRO051 to induce skipping of exon 51 during premessenger RNA splicing of the *DMD* gene.[15] Patients enrolled in this exon-skipping trial upregulated dystrophin at the sarcolemma and also showed functional improvement in the 6-minute walk distance. In another study, using a morpholino-based AON to skip exon 51 (AVI-4658; eteplirsen), dystrophin expression was increased in a dose-dependent manner at the sarcolemma.[16,17] Additionally, long-term evidence suggests that glucocorticoid treatment prolongs ambulation, reduces the need for spinal surgery, and increases both survival and quality of life.[20–27] The current recommendation for initiation of corticosteroids is to start treatment when boys with DMD have stopped gaining motor skills and not to wait until motor skills have begun to decline.[28] Considering the mean age of DMD diagnosis to be 5 years of age,[29] and that loss of function can begin before this time, an earlier diagnosis could result in an earlier corticosteroid start time, resulting in potential long-term benefits.

In 2004, a workshop sponsored by the Centers for Disease Control and Prevention (CDC) was held to review experiences, benefits, and risks in conducting NBS for DMD. The workshop participants concluded that there was inadequate evidence showing medical benefit from early identification, but that early diagnosis of DMD could have other advantages for the family (http://www.cdc.gov/ncbddd/duchenne/documents/nbs_lay_report.pdf). Following the CDC workshop, funds were made available to explore the potential for establishing a model for DMD NBS in the United States and to address ethical issues identified by the workgroup. Through this funding, we implemented a voluntary DMD NBS program in Ohio, initially through a pilot study in several birthing hospitals in Columbus and Cincinnati, followed by expansion to birthing hospitals throughout the state. Here we describe a 2-tiered method for conducting DMD NBS with initial screening for CK followed by DNA isolation and *DMD* gene analysis on the same dried blood spot. The addition of DNA analysis provides information useful in reducing the number of false positives based on CK alone and a path for initial follow-up of newborns with positive CK screening results. This study provides a model for conducting newborn screening for DMD.

Subjects and Methods

Study Populations

This study included 4 phases. Phase 1 efforts were devoted to creating a population-based range of CK to serve as the first tier of analysis, establishing a threshold that would trigger second-tier *DMD* gene mutation analysis. These studies were carried out at the Ohio Department of Health (ODH) using anonymous dried blood spots from male and female newborns. In phase 2 of this study, parents of newborn males were invited to participate in a pilot NBS study conducted at 1 of 4 major birthing hospitals in Columbus and Cincinnati, Ohio between March 2007 and September 2008. Newborn male infants born at any of the participating hospitals were eligible for the study. In phase 3, the DMD NBS program was expanded to include a total of 43 hospitals throughout the state of Ohio, with recruitment starting in October 2008 and extending through September 2010. In phase 4, the final phase of the study, deidentified blood spots from the newborn screening cards of males and females were again anonymously screened through the ODH (June 2010–January 2011). The goal in the final phase was to increase the number of male samples and to include females. We included both genders, not with the expectation of identifying carriers of an X-linked disease like DMD, but with the specific intent of enhancing our chances of identifying mutations of autosomal genes validating the 2-tier method of screening (CK on dried blood spot followed by DNA testing) to address the issue of elevated CK levels in subjects not found to have *DMD* gene mutations. Considering that false-positive CK elevation is a potential concern of NBS, we wanted to determine if mutations in other muscular dystrophy genes could be found in cases without *DMD* mutations.

Study Design

POPULATION-BASED CK ANALYSIS ON ANONYMOUS DRIED BLOOD SPOTS. In phase 1 of the study, a population-based range of CK was built upon CK testing of 30,547 consecutive anonymous dried blood spot samples (Table 1, Fig 1). Previous concerns had been raised regarding variability related to gender, neonatal weight, and age at time of sample collection. The current study is important in establishing future guidelines for CK, because we found no significant difference in the mean values between males (251.52 $\pm$ 113.85U/l) and females (246.39 $\pm$ 113.86U/l), with a minimal effect related to birth weight. Another point of interest is that although our target group for NBS focuses on dried blood spots collected within the first 48 hours, concerns have also been raised that CK activity diminishes over time. The data we collected show little effect out to 5 days (>120 hours). From this database, we were able to design our protocol for the 2-tier testing protocol. Initially, we chose to launch DNA testing for the *DMD* gene at a CK level of $\geq$600U/l, 3 standard deviations from the mean (0.75 % of screened population; see Table 1, Fig 1).

IMPLEMENTATION OF CK TESTING ON NEWBORNS. For phases 2 and 3, NBS was voluntary and required signed consent by a parent or guardian based on approved protocols by the institutional review board (IRB) at Nationwide Children's Hospital, Cincinnati Children's Hospital Medical Center, the ODH, University of Utah, the CDC, and every

TABLE 1: Population-Based Creatine Kinase in Anonymous Newborns

Group	Count (n)	Mean, U/l	SD	Mean + 1 SD	Mean + 2 SD	Mean + 3 SD	Mean + 4 SD	Mean + 5 SD
All infants	30,547	247.92	109.40	357.36	471.21	585.06	698.91	812.76
Gender								
Male	15,446	251.52	113.85	365.37	479.22	593.07	706.92	820.77
Female	14,983	246.39	113.56	359.95	473.51	587.07	700.63	814.19
Weight								
>2,500g	27,506	250.61	115.99	366.60	480.16	593.72	707.28	820.84
>2,000 to 2,500g	1,555	231.68	87.78	319.46	433.02	586.58	660.14	773.70
1,500 to 2,000g	538	210.41	71.01	281.41	394.97	508.53	622.09	735.65
<1,500g	573	226.36	75.88	302.24	415.80	529.36	642.92	756.48
Total	30,172							
Age at collection								
≤48 hours	27,065	253.37	116.99	370.36	483.92	597.48	711.04	824.60
>48 to 120 hours	2,572	207.56	68.51	276.07	389.63	503.19	616.75	730.31
>120 hours	596	201.64	63.54	265.18	378.74	492.30	605.86	719.42
Total	30,233							

Data are from creatine kinase testing of dried blood spots of 30,547 deidentified newborn samples (broken down by gender, weight, and age at sample collection).
SD = standard deviation.

participating hospital. Prior to the start of recruitment for phases 2 and 3, we provided an in-service teaching session to the staff of the delivery suites so that they could appropriately obtain consent from parents of newborn males. Within 48 hours of birth, trained staff members approached parents of newborn boys about participation in the study. A brochure describing the NBS was provided describing benefits and risks. Consenters than proceeded to answer questions and obtain consent from parents who wanted to participate. Ohio currently mandates testing (http://www.odh.ohio.gov/odhprograms/phl/newbrn/nbrn1.aspx) of all newborns for 35 disorders through dried blood spots obtained 24 to 48 hours after delivery (extenuating circumstances can permit testing up to 5 days of age). The blood spot cards supplied by the ODH include demographic information, the date and time of collection, and five 100μl blood samples obtained by heel stick imprinted in separate circles on a piece of filter paper attached to the top of the collection card. Two of the circles are used for the mandated

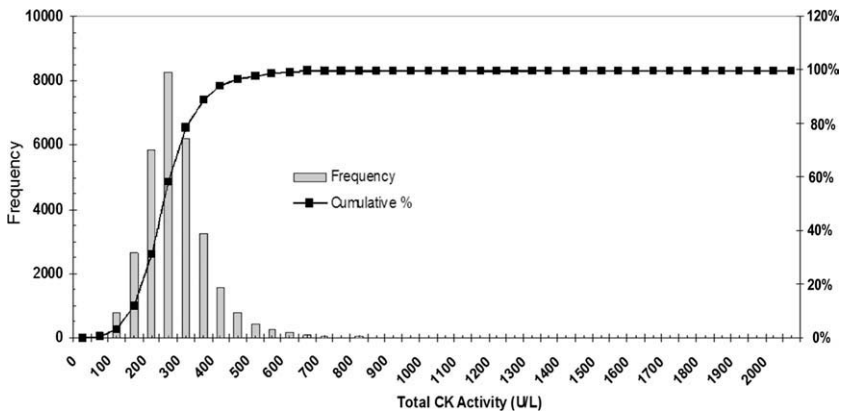

FIGURE 1: A normal distribution of creatine kinase (CK) on dried blood spots was obtained during a phase 1 population-based study of 30,547 deidentified male and female newborns. Based on this study, we used CK 600U/l as the threshold to trigger DNA testing for phase 2 newborn screening. In phase 3 testing, we increased the threshold to CK 750U/l.

NBS tests, and 2 of the 3 remaining circles were used for DMD NBS as part of this research study. A sticker was applied to those cards with parental consent for *DMD* testing. Nationwide Children's Hospital used a cross-referencing system to confirm parental approval.

All results were reported through the mail to the primary care physician or directly to the family if requested at the time of consent. In the case of a positive *DMD* mutation, telephone contact was made with the family to schedule a face-to-face conference to include the primary care physician and a neuromuscular specialist from our team. For CK results on dried blood spots above the threshold for DNA testing but negative for *DMD* gene mutations, the primary care physician was notified by telephone, and a repeat venous blood CK was requested at the expense of the research study. In cases where CK elevations were again found on repeat testing, our staff offered to make an appointment with the nearest Muscular Dystrophy Association clinic for further testing.

Materials

CK TESTING. CK testing was performed on the dried blood spots obtained for all 4 phases performed at the ODH laboratory using a previously published methodology.[1,2,7,30,31] Dried blood spots were punched using a Wallac DBS Puncher (Perkin Elmer, Boston, MA) and placed in wells of a filter plate with the addition of diadenosine pentaphosphate (USB Corporation, Cleveland, OH). Following incubation at room temperature to inhibit red blood cell enzyme activity, the supernatant was removed permitting N-acetyl-L-cysteine to reactivate CK activity (Reagent Kit; Thermo Electron Corporation, Waltham, MA). CK enzymatic activity catalyzed the transphosphorylation of adenosine diphosphate (ADP) to adenosine triphosphate (ATP). A series of coupled reactions produced a reduced form of nicotinamide adenine dinucleotide (NADH) at a rate directly proportional to the CK activity, measured at an excitation wavelength of 355nm and emission wavelength of 460nm by a fluorometer (Victor ^{2}D with Stacker; Perkin Elmer). For each sample, 5 measures were taken over 5 seconds (kinetic method), and the difference between the first and last reading of each sample was used to normalize differences in incubation time between samples. CK levels (in units per liter) were calculated for each sample by a linear formula generated independently for each plate using internal controls, with predefined CK concentrations loaded on each plate.

DNA TESTING

DNA Extraction and Whole Genome Amplification. DNA testing off the initial dried blood spot was performed for samples with elevated CK. The dried blood spot was sent to the clinical DNA sequencing laboratory at the University of Utah. Genomic DNA was purified using the MasterPure Genomic DNA Extraction Kit (Epicentre, Madison, WI; catalog No. MC89010). A punch (2mm^2) from each blood spot card was submerged in 300μl of cell lysis solution containing 50μg of proteinase K, and incubated at 50°C for 16 hours; 160μl of MasterPure^{TM} Protein Precipitation Reagent was added, the samples were vortexed, and placed on ice for 30 minutes. The debris was pelleted by centrifugation for 10 minutes at 10,000 $\times$ *g* in a microcentrifuge. The supernatant was transferred to a fresh tube containing 600μl of isopropanol, mixed, and placed at −20°C for 30 minutes. DNA was pelleted by centrifugation at 4°C for 10 minutes at 10,000 $\times$ *g*, rinsed with 70% ice-cold ethyl alcohol, air dried, and resuspended in 20μl of TE buffer, pH 7.6. Whole genome amplification (WGA) of this purified DNA from each blood spot was performed with the REPLI-g kit (Qiagen, Valencia, CA; catalog No. 150045). Five microliters of genomic DNA was denatured for 3 minutes at room temperature and neutralized according to the manufacturer's specifications, and a 50μl final volume reaction containing REPLI-g DNA Polymerase was incubated at 30°C for 16 hours, followed by heating at 65°C for 3 minutes to inactivate the enzyme.

MUTATIONAL ANALYSIS. Deletion and sequencing analysis of the *DMD* gene was performed on WGA template DNA using the 2-step SCAIP method, as described in detail elsewhere.[32] This method uses polymerase chain reaction (PCR) amplification and capillary-based fluorescent DNA sequencing to screen for deletions and point mutations in all 79 coding exons and approximately 50 nucleotides of flanking intronic sequences of the major mRNA transcript isoform in muscle plus the 5′ untranslated region (UTR), 3′ UTR, and 6 alternate promoters. PCR was carried out in 10μl reactions using Platinum *Taq* DNA Polymerase (Invitrogen, Carlsbad, CA). Each PCR reaction contained 0.14μl of WGA template, and 93 total PCR reactions were analyzed per sample. Enzymatic cleanup was performed with the ExoSAP-IT reagent (Affymetrix, Santa Clara, CA), and the treated samples were sequenced using ABI (Applied Biosystems, Foster City, CA) BigDye Terminator v.3.1 chemistry. Samples were run on an ABI 3730xl sequencer, and analyzed using the base-calling sequence software described previously.[32] Nucleotide positions were determined according to the standard reference *DMD* sequence used for mutation analysis (GenBank accession number NM_004006.2). Nucleotide numbering reflects cDNA numbering, with +1 corresponding to the A of the ATG translation initiation codon in the reference sequence, according to established guidelines (www.hgvs.org/mutnomen).

All samples were analyzed for single-/multiexon deletions/duplications in the dystrophin gene using multiplex ligation-dependent probe amplification (Salsa multiplex ligation-dependent probe amplification [MLPA] kit P034/P035 DMD/Becker MLPA; MRC-Holland, Amsterdam, the Netherlands) as described.[33] One microliter of WGA template in 5μl of TE buffer was fragmented at 98°C for 5 minutes, cooled, and split between 2 separate tubes; 1.5μl of Salsa P034 and P035 primers were added to the tubes, respectively, incubated at 95°C for 1 minute, followed by annealing at 60°C for 20 hours. DNA ligase buffer and enzyme were added to each reaction in a total volume of 20μl and incubated at 54°C for 15 minutes, followed by 5-minute incubation at 98°C. Five microliters was

subsequently used in a 25μl PCR reaction that consisted of 35 cycles: 95°C for 30 minutes, 60°C for 30 minutes, and 72°C for 1 minute, followed by a final incubation at 72°C for 20 minute; 1.5μl of the sample was run on an ABI 3730xl instrument and analyzed for fragment size, peak height, and peak area using GeneMapper software (Applied Biosystems). *DMD* exon copy number was determined by dosage quotient analysis generated for each MLPA peak by using 10 individual flanking peaks as reference peaks. Control ratios were calculated from MLPA assays using WGA genomic DNA from 3 non-DMD controls, and the mean of these ratios formed the denominator in the dosage quotient formula.[34] The diagnostic accuracy of the MLPA assay on WGA template purified from dried blood spots was validated by blinded analysis of blood spots obtained from consenting DMD patients and parents with known mutations, including 7 exonic deletions and 6 exonic duplications, and showed 100% accuracy on these samples.

Mutation analysis was performed on 9 anonymous samples from 2 females and 7 males who had CK levels >2,000 and did not have a mutation identified in the *DMD* gene. The 7 most common genes causing limb-girdle muscular dystrophy (LGMD) were selected and prioritized for analysis according to the following hierarchy (*DYSF, CAPN3, SGCA, SGCB, SGCG, SGCD*, and *FKRP). DYSF* and *CAPN3* were sequenced with 15μl of WGA template using SCAIP methodology.[32] These tests surveyed for point mutations in the *DYSF* gene (reference mRNA transcript, National Center for Biotechnology Information [NCBI] accession No. NM_003494.3, 55 exons encoding the 237kDa dysferlin protein) and in the *CAPN3* gene (reference mRNA transcript, NCBI accession No. NM_000070.2, 24 exons encoding the calpain-3 isoform of a 94kDa protein). In samples not found to have *DYSF* or *CAPN3* mutations, sequence analysis on coding exons was performed on the following genes: *SGCA* (NM_000023.2), *SGCB* (NM_000232.4), *SGCD* (NM_000337.5), *SGCG* (NM_000231.2), and *FKRP* (NM_024301.4).

Results

Newborn Screening CK Studies: Phase 2 and Phase 3 Analyses

A phase 2 pilot study screening 6,928 newborns was done at the major birthing hospitals in Columbus and Cincinnati, Ohio. In this phase of the study, we tracked the number who declined consent and found it to be 6.0% (n = 478) of those authorized to give approval. We found that 110 subjects exceeded the CK ≥600U/l testing threshold, requiring DNA analyses. Only the 2 subjects with CK ≥2,000U/l (2,461 and 2,675) were found to have proven *DMD* gene mutations. The false-positive rate for this phase was 1.6% (108 of 6,926).

The pilot study provided the impetus to move the CK threshold for the statewide, phase 3 program to ≥750U/l. The CK data collected from enrollment of an additional 10,937 newborn males led to the identification of 58 with elevated CK. One newborn was found to harbor a *DMD* mutation, and his CK was again >2,000U/l (2,003U/l). The false-positive rate for phase 3 was 0.52% (57 of 10,936). Increasing the CK threshold from 600U/l to 750U/l reduced the number of newborn males requiring DNA testing by 68%. The number declining enrollment in this phase of the study was not accurately tracked. Forty-three individual birthing sites were responsible for obtaining consent in the statewide program, exceeding our tracking capabilities.

Of additional interest regarding a frequently expressed concern of CK testing in the newborn period is the potential contribution of enzyme elevation from trauma as the neonate progresses through the birth canal.[35–37] We have examined this by checking CK levels on follow-up venous blood samples obtained through the primary care physician for participants in phase 2 and phase 3 studies. We were able to obtain samples for only 43 of 165 subjects who were negative for *DMD* gene mutations and in whom CK was elevated on dried blood spots (distributed as follows: 35 between 600 and 999U/l; 6 between 1,000 and 1,499U/l; and 2 between 1,500 and 1,999U/l). In most cases, the follow-up venous CK was lower compared to the blood spot-derived CK (Fig 2). Of particular note, the highest of the non-DMD group was 1,700U/l yet the repeat venous blood showed a CK level of 46U/l. In only 2 cases, the venous CK remained slightly elevated >500U/l on follow-up (888 reduced to 672, 809 reduced to 656). This confirms that CK elevation on dried blood spots can be attributed to birth trauma and accounts for most values above normal, findings similar to previous reports.[35–37] A point of interest is that 1 of the infants with a documented *DMD* gene mutation, whose dried blood spot CK was 2,462U/l, had a repeat venous blood sample at 6 weeks showing a dramatic elevation to 8,888U/l.

Phase 4 Newborn Screening CK Study

In the fourth and final phase of this study, to increase the sample size to further validate the 2-tier approach for DMD identification in the newborn period, we screened a large cohort of deidentified newborn samples anonymously. This increased our sample size by 19,884 newborn males (total 37,649). Based on results of phase 2 and phase 3 studies, we limited DNA screening on dried blood spots to those males with CK ≥750U/l. There were 308 CK levels found to be >750U/l, and ten >2,000U/l. In this final phase of the study, we also included anonymous CK analysis on dried blood spots of 18,763 newborn females. For the females, CK was ≥750U/l in 242, with CK ≥2,000 on 2 anonymous dried blood spots.

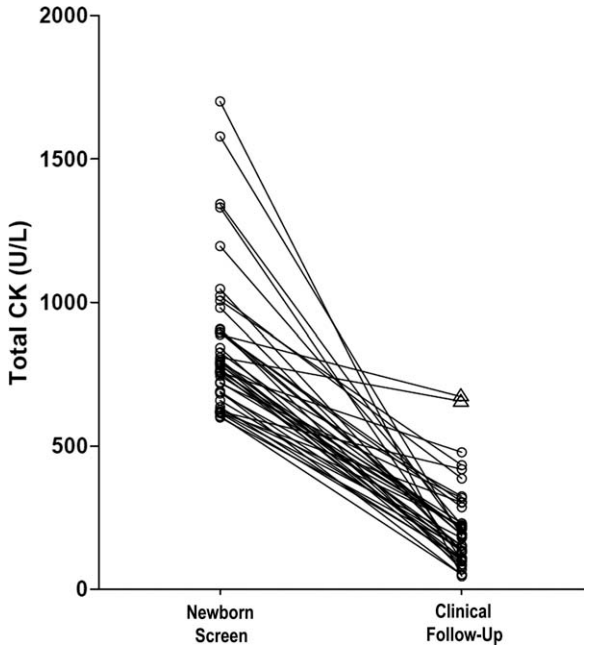

FIGURE 2: Forty-three subjects who were not found to have Duchenne muscular dystrophy (DMD) mutations, but had elevated creatine kinase (CK) levels on dried blood spots, agreed to be retested using venous blood at 6 weeks after birth. CK was found to be lower in all cases (clinical follow-up); 2 were slightly elevated (>500U/l) at 672 and 656 (Δ). These were far below the CK >2,000U/l found in all those identified with DMD.

DNA Analysis on Dried Blood Spots

Among a total of 37,649 newborn males screened for DMD (phase 2, 3, 4), 6 males were found to have *DMD* gene mutations. All were single-exon or multiexon deletions, 5 out-of-frame and 1 in-frame mutation (Table 2); no point mutations or duplications were found. These exon deletion mutations followed a typical distribution seen from large cohorts, although the in-frame deletion, exons 5–41, has been reported only once previously (http://www.leiden.nl), and was associated with DMD, likely due to a deletion that encompasses critical actin-binding domains.

A striking finding in the mutation analysis was that all samples with *DMD* mutations had CK values ≥2,000U/l. Our attention was therefore drawn to subjects (7 males and 2 females) with CK ≥2,000 in whom we did not find *DMD* mutations. We therefore extended the study to include analysis of mutations in the most common LGMD genes (*DYSF, CAPN3*, *SGCA, SGCB, SGCC, SGCD*, and *FKRP*). Mutations were found in 1 female (a *DYSF* point mutation) and 2 males (1 with a point mutation in *SGCB*, and the other with a point mutation in *FKRP*; see Table 2). In none of these 3 instances was a second mutant allele detected.

Discussion

CK testing on dried blood spots to identify DMD cases in the newborn period was validated in 1979 and relies on enzyme activity to catalyze the transphosphorylation of ADP to ATP.[1] As initially introduced, a luciferase-based bioluminescence assay established enzyme intensity; later modifications (as used here) utilized an NADH-based fluorometric readout as a measure of CK activity.[31] Table 3 tracks the sequential history of NBS for DMD from its early introduction in New Zealand[1] through programs in Edinburgh,[2] Germany,[3] Canada,[4] France,[5] the USA (western Pennsylvania),[6] Wales,[7] Cyprus,[8] and Belgium.[9] Antwerp is the only program that maintains NBS for DMD to this day. In this program, samples with elevated CK are retested through venous blood samples taken at about 6 weeks after birth. Their nationalized health care system is positioned to accommodate

TABLE 2: Mutations Found in Newborns with CK Levels >2,000U/l

Gender	CK value, U/l	Gene	Mutation	cDNA	Frame
Male	2,462	*DMD*	Deletion ex50	[c.7201-?_7309+?del]	Out
Male	2,675	*DMD*	Deletion ex5–41	[c.265-?_5922+?del]	In
Male	2,003	*DMD*	Deletion ex8–9	[c.650-?_960+?del]	Out
Male	2,466	*DMD*	Deletion ex45	[c.6439-?_6614+?del]	Out
Male	2,791	*DMD*	Deletion ex45–48	[c.6439-?_7095+?del]	Out
Male	2,688	*DMD*	Deletion ex4–7	[c.187-?_649+?del]	Out
Female	2,731	*DYSF*	Frameshift ex39	[c.4200dupC]	Out
Male	2,735	*SGCB*	3 nt dup, ex1	c.21_23dup	In
Male	2,984	*FKRP*	p.R143S missense	c.427C>A	In

CK = creatine kinase.

TABLE 3: History of Newborn Screening

Year of Report	Investigators/ Country	Observations	Incidence
1975[12]	USA	Introduced CK testing on DBS in normal newborns	Established proof of principle
1979[1]	New Zealand	10,000 newborns screened; 2 DMD cases identified	1:5,000
1982[2]	Edinburgh, UK	2,336 newborns screened; no DMD cases identified	0
1986[3]	West Germany	358,000 screened (10% <4 weeks of age; 65% 4–6 weeks of age; 23% 6 weeks to 6 months; 2% 6 months to 1 year); 78 had DMD	1:4,589
1988[4]	Manitoba, Canada	54,000 screened; 10 DMD cases identified	1:5,400
1989[5]	Lyon, France	37,312 newborns screened; 7 DMD cases identified	1:5,330; an earlier report showed 1:5,929
1991[6]	Western Pennsylvania, USA	49,000 screened; 10 DMD identified	1:4,900
1993[7]	Wales, UK	34,219 screened; 9 DMD cases found	1:3,802[a]
1998[8]	Cyprus	30,014 screened; 5 DMD cases found	1:6,002
2006[9]	Antwerp, Belgium	281,214 newborns screened at 4–6 weeks; 51 DMD cases found	1:5,500[b]

[a]Presentation in London, UK, March 18, 2011, reported 335,045 screened, with an incidence of 1:5,266.
[b]Only newborn screening program that continues to actively screen subjects for DMD.
CK = creatine kinase; DBS = dried blood spot; DMD = Duchenne muscular dystrophy.

multiple rounds of testing, concluding with *DMD* gene analysis if indicated. This approach can be challenging, as evidenced by the recent closure in Wales of the longest-running DMD NBS program in history.

From its inception, our goals included creating a DMD NBS program that would fit the obstetrics practice in the USA, where mother and child are discharged within 24 to 48 hours following uncomplicated deliveries, and developing a method to readily distinguish false and true positives. Fulfillment of this task required a 2-tier system of analysis permitting CK testing followed by DNA analysis on the same dried blood spot. The design introduced has similarities to the NBS program for cystic fibrosis based on 2-tier molecular genetics testing that was first introduced in a pilot program in the state of Wisconsin.[38] Prior to implementing a newborn screening program for DMD, 2 components had to be put in place. A validated method was required for extraction of genomic DNA from a small punch of the dried blood spot, followed by whole genome amplification with analysis of single-/multiexon deletions/duplications in the dystrophin gene using SCAIP combined with MLPA.[31,33,39] Preparatory trials provided confidence in the methodology based upon 100% accuracy in the blinded identification of 7 exonic deletions and 6 exonic duplications taken from DMD patients with known mutations (voluntary and IRB approved) placed on newborn screening cards at Nationwide Children's Hospital and sent to the clinical DNA sequencing laboratory at the University of Utah. It was also necessary to establish a population-based range of CK on anonymous dried blood spots. This important undertaking was enabled by the full cooperation of the laboratories of the ODH, facilitating a path forward for newborn screening. Through anonymous CK analysis on >30,000 newborns (see Fig 1), we established a starting point for DNA testing at a CK level 3 standard deviations above the mean. Adding CK testing to the full battery of tests performed on dried blood spots at the ODH was not overly burdensome, and the cost for adding this 1 assay (to 35 others) was minimal (approximately $1.00 of raw materials). For those exceeding the CK threshold requiring

DNA testing, the cost at the University of Utah laboratory was an additional $150.00 in raw materials.

The results of our study support the 2-tier system of analysis for newborn screening for DMD, perhaps in a way even more satisfying than anticipated. Over the course of this program, we screened 37,649 males and found 6 males with *DMD* gene mutations, an incidence of 1 in 6,291. The comparative incidence of newborn boys with documented DMD is lower than other studies throughout the world, which ranged from 1 in 3,802 to 1 in 6,002 (taking all programs together, 1 in 4,087; see Table 3), and would have to be viewed cautiously based on sample size and location in a single state in the USA. What is particularly notable about our study is that all of our patients with DMD (or dystrophinopathies) had CK levels at birth $\geq$2,000U/l. This margin between documented cases of DMD and those with elevated CK not found to have a *DMD* mutation provides reasonable assurance for circumventing false positives, enabling us to raise the threshold for DNA testing in phase 3 of the study to CK $\geq$750U/l. This reduced the number of newborns requiring *DMD* gene testing by about 68%, representing a significant cost savings for an NBS program. With additional confirmation of our findings, these initial studies suggest that the threshold for DNA testing could be elevated even higher (eg, CK $\geq$1,000U/l), improving the potential cost–benefit ratio for NBS.

As our program evolved, we had more confidence in the identification of the great majority with DMD mutations, but we were aware of limitations. Additional experience would be required to confirm that point mutations, present in approximately 1/4 of DMD patients and not detected in this study, were the result of mutation detection using WGA from DNA isolated from dried blood spots. However, we are confident that appropriate methodology has been applied in this NBS study based on our previous work demonstrating the detection of 506 point mutations (294 nonsense mutations) in the analysis of 1,111 dystrophinopathies representing 46% of subjects (over-represented in this population because of study design).[40] In addition, the group of dystrophinopathies manifesting predominantly as a cardiomyopathy accompanied by relative sparing of skeletal muscle (ie, X-linked cardiomyopathy) will often be missed in any NBS protocol. It is well recognized that many patients in this group have reduced CK levels in venous blood, some even in the normal or near normal range.[41–43] We were also aware of newborns on the other end of the spectrum with elevated CKs and no diagnosis of DMD. For this reason, we extended the study to address this potential limitation. In the final phase of this study, we did DNA testing for the most common LGMD genes if CK was $\geq$2,000U/l in the absence of an identified DMD gene mutation. In this small sample, we found 1 individual with a known single-nucleotide insertion mutation in *DYSF*, 1 with a known missense mutation in *FKRP*, and another with a 3-nucleotide duplication in *SGCB* of unknown pathogenicity that has been reported in 5 sarcoglycanopathy patients (Leiden Database; see Table 2). These findings demonstrate proof of principle illustrating that LGMD gene mutations can be identified as part of the screening process. Only 1 pathogenic allele was detected in each case, a result that is not uncommon for these genes.[44–46] Further characterization of these deidentified samples would be required to evaluate copy number changes indicative of a second, undetected large deletion or duplication.

Our completed study was not intended to address the question of whether NBS for DMD should be introduced but rather to provide a pathway for implementation given the recent reports of therapeutic benefit for DMD.[15–18,20–24] The phase 2 DMD NBS program explored ethical issues involved by assessing parent and provider experiences through questionnaires; however, this topic has been reserved for a future article. The program we have introduced differs from past programs and the current Antwerp approach to NBS for DMD that require a 3-step process: (1) CK testing on dried blood spots, followed by (2) confirmation of elevated CK levels by venous blood obtained at the 4- to 6-week time point, with (3) a final step that requires an additional blood draw for DNA testing. The approach we have developed is a 2-tier approach, with all testing done using the original blood obtained from the heel stick within the first 24 to 48 hours. All testing is done from the same dried blood spot card. A threshold level of CK determines if DNA testing is to be done without additional blood obtained from the neonate. The DNA assay utilizes the most sophisticated technology available[40] (and can be periodically modified if necessary). Whether treatment has advanced to the point of justifying newborn screening for DMD requires assessment through state and federal agencies with appropriate jurisdiction. If and when an early therapy that improves the health outcome for individuals with DMD becomes available, our study serves as a model for implementation of newborn screening for DMD. If the development of promising therapies for DMD continues to proceed at its current pace, newborn screening could be on the horizon for this disease, not only in the USA, but also in other countries. If successful therapy for dystrophinopathies is available for newborns, guidelines will need to be established for referral to an appropriate muscle specialist. In addition, a pathway for referral could be built into the program for

those with CK elevations in the absence of *DMD* mutations, where there is the potential to identify other causative mutations, as we have demonstrated in this report.

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The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

Potential Conflicts of Interest

N.D.L.: board membership, Genzyme; consultancy, Schulman IRB; employment, CCHMC; expert testimony, Wellpoint; grants/grants pending, NIH. K.M.F.: consultancy, GSK, AVI, Prosensa, PTC; grants/grants pending, NIH. J.G.-F.: consultancy, Inova Healthcare; grants/grants pending, National Cancer Institute; travel expenses, European Organisation for Research and Treatment of Cancer.

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