

Spinal Muscular Atrophy Diagnosis and Dried Saliva Spots

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Spinal muscular atrophy (SMA) is a lower motor neuron disease, once considered incurable. The main symptoms are muscle weakness and muscular atrophy. More than 90% of cases of SMA are caused by homozygous deletion of survival motor neuron 1 (*SMN1*). Emerging treatments, such as splicing modulation of *SMN2* and *SMN* gene replacement therapy, have improved the prognoses and motor functions of patients. However, confirmed diagnosis by *SMN1* testing is often delayed, suggesting the presence of diagnosis-delayed or undiagnosed cases. To enable patients to access the right treatments, a screening system for SMA is essential. Even so, the current newborn screening system using dried blood spots is still invasive and cumbersome. Here, we developed a completely non-invasive screening system using dried saliva spots (DSS) as an alternative DNA source to detect *SMN1* deletion. In this study, 60 DSS (40 SMA patients and 20 controls) were tested. The combination of modified competitive oligonucleotide priming-polymerase chain reaction and melting peak analysis clearly distinguished DSS samples with and without *SMN1*. In conclusion, these results suggest that our system with DSS is applicable to SMA patient detection in the real world.

Keywords: dried saliva spot ; spinal muscular atrophy ; melting peak analysis ; nested PCR

1. Introduction

Spinal muscular atrophy (SMA) is one of the most devastating neuromuscular disorders, characterized by motor neuron degeneration^[1]. The patients present with muscle weakness and muscular atrophy^[1]. Clinically, SMA is divided into five subtypes: Type 0 (the most severe form, prenatal onset, death within weeks of birth); Type I (Werdnig–Hoffmann disease, severe form, onset < 6 months, non-sitter); Type II (Dubowitz disease, intermediate form, onset < 18 months, sitter); Type III (Kugelberg–Wielander disease, mild form, onset > 18 months, walker); and Type IV (the mildest form, onset > 30 years)^{[2][3]}.

The majority of SMA cases (~95%) involve homozygous deletion of survival motor neuron 1 (*SMN1*), while some others (~5%) carry a deleterious *SMN1* mutation, thus *SMN1* is considered the disease-causing gene^{[4][2]}. The homologous gene, *SMN2*, serves as an SMA-modifying gene because a high *SMN2* copy number is generally associated with a milder phenotype^{[4][5]}.

SMN1 and *SMN2* are identical except for five nucleotides located in intron 6, exon 7, intron 7, and exon 8^[1]. Molecular diagnosis of SMA requires the detection of *SMN1*-specific nucleotides, especially the one located in exon 7. Several methods have been developed to achieve this, including single-stranded conformation polymorphism (SSCP) analysis^[1], restriction enzyme digestion analysis^[6], modified competitive oligonucleotide priming-polymerase chain reaction (mCOP-PCR)^{[7][8]}, multiplex ligation-dependent probe amplification (MLPA)^[9], digital droplet PCR (ddPCR)^[10] and next-generation sequencing (NGS)^[11].

SMA has long been thought an incurable disease because of the absence of effective drugs. However, three new and effective drugs for SMA are now available: nusinersen^[12], onasemnogene abeparvovec-xioi^[13], and risdiplam^[14]. These drugs give better outcomes when treatment is initiated at an early stage, before the onset of symptoms^{[12][13][14]}. Therefore, there is a growing implementation of newborn screening programs for SMA (NBS-SMA) worldwide^{[7][15][16][17][18][19][20][21]}. Technically, the current NBS-SMA program can detect all SMA patients with a homozygous deletion regardless of the clinical subtype.

Even though NBS-SMA has begun in many countries, there remain many older children or adults with SMA in the population who were not detected in early infancy. The majority of them may be diagnosed with SMA in a timely fashion, but the rest may be diagnosed late or may not be diagnosed, particularly those with a later onset of the disease^{[22][23][24][25]}. Undiagnosed patients cannot access treatment with the new drugs. Therefore, to complement NBS-SMA, it is

desirable to establish a screening system that covers older children and adults. The samples for that purpose should be collected at schools, workplaces, or homes. However, one potential hurdle is the invasiveness of blood-based templates such as dried blood spots (DBS), which may require health care visitation of the individuals or blood collection by health care workers.

2. Saliva as a Good Source for Genetic Analysis

Saliva has been used for analysis of human DNA by PCR-based HLA typing^[26], microarray SNP genotyping^{[27][28]}, TaqMan SNP genotyping assays^{[27][29]}, loop-mediated isothermal amplification-melting curve (LAMP-MC) analysis^[29], PCR-Sanger sequencing^[28], next generation sequencing^[30], and whole genome or exome sequencing^{[31][32]}.

Saliva has now proved to be a good alternative source for genetic analysis. In the studies mentioned above, saliva was collected using a saliva collection kit with a special container, either in-house-made^[26] or commercially available^{[27][28][29][30][31][32]}. Later, DNA was extracted from the liquid saliva sample in the container^{[26][27][28][29][30][31][32]}.

Some previous studies used a different kind of saliva sample. Instead of a liquid saliva sample, some researchers prepared DSS samples and extracted DNA from them for various purposes^{[33][34][35]}. Kisoi et al. identified insertion/deletion polymorphisms of the angiotensin-converting enzyme (*ACE*) gene by PCR amplification using DNA from DSS samples^[33]. Our study also demonstrated genotyping analysis of *SMN* genes using DSS samples. These findings support the idea that saliva, even if dried, can be a good DNA source for PCR.

Kisoi et al. reported a simple DNA extraction method from the DSS samples: they boiled one DSS punch (4 mm in diameter) and used an aliquot of the supernatant for PCR amplification^[33]. Hayashida et al. reported direct PCR from DSS to detect SNP in alcohol metabolism-related genes (*ADH1B* and *ALDH2*) using a TaqMan probe assay^[36]. In agreement with their results, we provide further evidence that direct PCR amplification is feasible from DSS without boiling or DNA purification procedures.

3. Robustness and Accuracy of Our SMA Screening System

In this study, the basic technology to detect *SMN1*, mCOP-PCR, is a type of allele-specific PCR. Originally, COP-PCR was based on allele-specific amplification, in which two oligonucleotide primers compete for one target DNA sequence in one PCR tube^[37]. The primers are short (10–11 bases) and highly identical except for one nucleotide change in the middle of the primers^{[8][37]}. The modified version adopted in this study, mCOP-PCR, uses one gene-specific oligonucleotide primer (*SMN1*-COP) that preferentially binds the *SMN1* sequence rather than the competitor sequence, *SMN2*^[8].

Here, we employed nested PCR to rescue low quantity and quality genetic material in the DSS. The first-round PCR amplified common regions of the target genes and provided enough template for the second-round PCR, even for quantitative assays^{[7][8][38]}. In addition, the first-round PCR products contained no other sequences similar to the *SMN1*-specific mCOP-PCR primer, which avoids the amplification of unexpected primer binding sites in the second-round PCR and enhances the specificity of our system^{[7][8]}.

4. Limitation of PCR-Based Assays Using DSS

The use of saliva, either liquid or dried, has potential limitations for PCR-based assays. First, the quantity of amplifiable human DNA recovered from liquid saliva is lower than blood (37.3% in saliva versus 87.6% in the blood)^[27]. Second, the DNA quality obtained from saliva does not always meet the quality standard for certain assays, even though the DNA obtained from saliva showed a good A260/A280 ratio^[31]. DNA degradation during the storage period may be related to the quality. Third, PCR inhibitors in the saliva may confound the results^{[27][39]}.

We experienced one case of assay failure out of 61 DSS samples (1.6%) in this study. This failure might be due to the absence of DNA or the presence of PCR inhibitors. The possibility of DNA degradation can be ruled out because the storage period was less than two weeks. In our pilot study of NBS-SMA, there were no cases of assay failure out of 4157 DBS samples (0%)^[7]. Compared with our previous study of DBS, this study with DSS showed a higher rate of assay failure.

5. Conclusions

We demonstrated the potential use of DSS sampling as a good alternative source for SMA detection using nested mCOP-PCR. The sample collection procedure is non-invasive, easy to handle, and requires no hospital visitation. DSS might be preferable for SMA screening for older children or adults. We hope that this will help in overcoming the delay in SMA diagnosis.

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