Progress of newborn screening for spinal muscular atrophy

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Spinal muscular atrophy (SMA) ~95% due to SMN1 deletion



-Copy number of SMN2 correlate with the onset age

 Because of the high incidence of SMA, rapid loss of motor neurons in the spinal cord and the brainstem, and there are several promising treatment options, newborn screening for SMA is considered.

Screening principle detect SMN1 deletion

- Lack of IVS7+100 a (first-tier test by qPCR)
- Lack of c.840 C (second-tier test by

SMN-specific PCR/Sequencing and ddPCR)



Example results



Rn: normalized reporter signal the fluorescence of the reporter dye divided by

the fluorescence of a passive reference dye ΔRn :

Rn (post-PCR read) – Rn (pre-PCR read)

Algorithm



Pilot SMA newborn screening program

- National Taiwan University Hospital (NTUH) Screening center screened 35~37% of populations in Taiwan
- Incorporated into routine metabolic screening
 - 1st sample at 3-days-old
 - Informed consent required



NTUH SMA NBS Timeline



Current progress an incidence as ~1 in 14,500 live births

In true positive patients, *SMN1* gene and *SMN2* gene copy numbers were denoted as 0:4, 0:3, and 0:2.



False positive in 1st- tier Screening

 One newborn with lower amplification at the target sequence (IVS7+100) in SMN1, and second-tier test showed presence of SMN1 at c.840



Amplification curve

False positive in 1st- tier Screening

• Two newborns with a nucleotide change at IVS7+100, but second-tier test showed presence of SMN1 at c.840



Amplification curve of this false positive case

Frequency of recombination between Exon7 and Intron7

• Risk of false negative due to IVS7+100 variation is low, only when both SMN1 del homozygous and one SMN2 T-a

genotype of c.840 - IVS7+100	n
SMN1 (represent by ASP-C) (Ca)	Totally 1463 NB samples
Ca	1458
Ca/g	5
SMN2 (represent by ASP-T) (Tg)	
Tg	1401
Ta/g	5
No SMN2 PCR product	62

Proposed mechanism for recombination between Exon7 and Intron7 (after verifying exon8 polymorphism)



Conclusion

- The incidence of SMA in our newborn population is 1 in 14,500 (95% Confidence interval 1 in 6,176~33,849).
- Doing only 1st-tier has very low false positive, and the positive prediction rate is 62.5%.
 - Combining with 2nd-tier test, such as assay at c.840 either by Genotyping assay or ddPCR, can largely improve the screening performance
 - The theoretically false negative rate was 5% since we only detect SMN1 deletion homozygous patients.



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