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International assessment of newborn screening for spinal muscular atrophy using advanced sequencing and artificial intelligence

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BACKGROUND

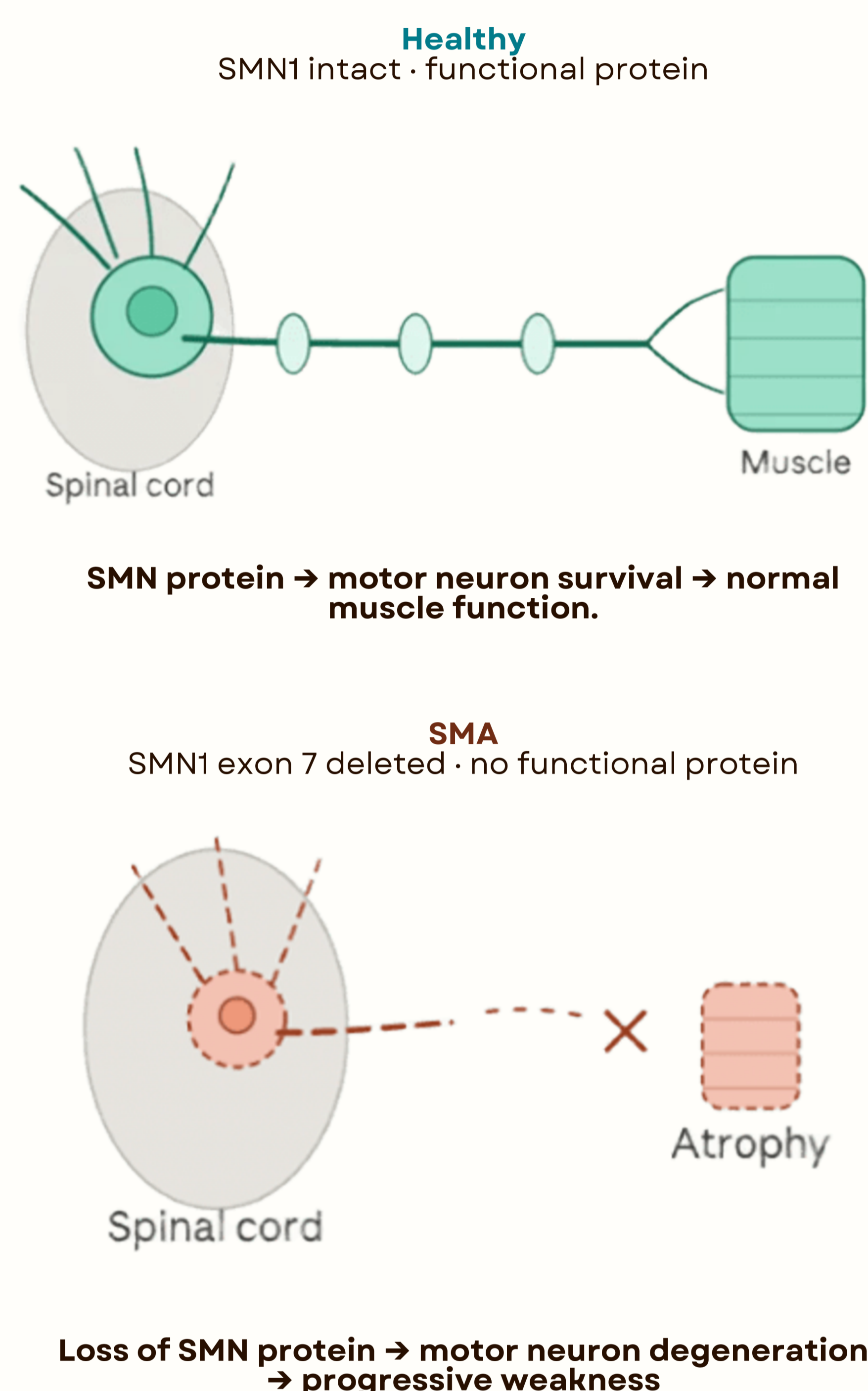
SMA is an autosomal recessive neuromuscular disease (1/10,000 births) caused by homozygous deletions in *SMN1* exon 7.

Clinical severity is modulated by *SMN2* copy number. Early diagnosis is critical: disease-modifying therapies are available, and newborn screening (NBS) enables presymptomatic identification.

MATERIAL AND METHODS:

As part of a pilot study conducted in collaboration with Paraguay and Denmark, 92 anonymous dried blood samples were received. After excluding low-quality samples, 71 samples (41 diagnosed SMA cases, 19 carriers, and 11 healthy donors) were analysed along with 3 controls.

The Phivea® platform (gMendel Test - SMA), based on long-read sequencing and artificial intelligence (AI), was used. The analysis allowed classification of samples into homozygous deletion of *SMN1* exon 7, heterozygous status, or normal genotype, and the number of *SMN2* copies was also assessed.



Early presymptomatic diagnosis via NBS enables treatment before irreversible motor neuron loss

RESULTS:

100%

Analytical sensitivity
No SMA case missed

96.8%

Analytical specificity
Very low false-positive rate

98.6%

Overall accuracy Across all 71 samples

97.6%

Diagnostic sensitivity Clinical confirmation

100%

Diagnostic specificity Zero false positives

0.024

Negative likelihood ratio
Excellent rule-out power

CONCLUSION:

The gMendel-SMA test demonstrates high robustness and reliability for population-based NBS. International collaboration between Spain, Paraguay, Denmark and North Macedonia confirms its feasibility in resource-limited settings.