

presence of a critical period when a sufficient amount of SMN protein is required during motor neuron development. In addition, the maturation of the blood brain barrier may hamper the transport of the SMN-expressing vectors to the target neurons, suggesting a finite period for efficient gene therapy.

In 2011, Dominguez and colleagues reported that they used postnatal day 1 systemic injection of self-complementary adeno-associated virus (scAAV9) vectors carrying a codon-optimized *SMN1* sequence and a chimeric intron placed downstream of the strong phosphoglycerate kinase (PGK) promoter (SMNopti) to overexpress the human SMN protein in a mouse model of severe SMA (*Smn*^{-/-}*SMN2*^{+/+}*SMNΔ*^{7+/+}) (Dominguez et al., 2011). Codon optimization is a gene optimization technology that can alter both naturally occurring and recombinant gene sequences to achieve the highest possible levels of productivity in any given expression system. This treatment increased life expectancy from 27 to over 340 days (median survival of 199 days) in mice that normally survive about 13 days. The systemic scAAV9 therapy mediated complete correction of motor function, prevented motor neuron death and rescued the weight loss. This study also showed sex differences in the responsiveness to the treatment. Male SMA mice displayed a lower body weight gain than age-matched control mice, whereas the body weight of females was not statistically different from the controls.

As for stem cell therapy, it has been shown that “spinal cord-derived stem cells” and “embryonic stem cell-derived neural stem cells” can differentiate into motor neurons in vivo (Corti et al., 2008; Corti et al., 2010). In addition, following intrathecal transplantation into SMA mice (*Smn*^{-/-}*SMN2*^{+/+}*SMNΔ*^{7+/+}), the administered neural stem cells survived and migrated extensively to appropriate areas. Here, the transplanted embryonic stem cells were found to work by secreting soluble neuroprotection factors, such as glial-cell derived neurotrophic factor (GDNF), brain derived neurotrophic factor (BDNF), and tumor growth factor (TGF)- α . These growth factors were confirmed to play a role in the improved functional recoveries of SMA mice following transplantation, showing an increase in myofiber number and size, axon length and body weight gain, suggesting that neural stem cell transplantation resulted in successful amelioration of behavioral end points and life span extension in SMA mice (Corti et al., 2010).

Gene and stem cell therapies may be very promising treatments for SMA patients, especially for pre-symptomatic patients. However, the efficacy of such therapies should further be tested in non-human primates before such approaches are applied to the patients, especially in considering if blood brain barrier function may hinder the delivery of therapeutic agents to the neurons (Tsai, 2012). Foust and colleagues investigated whether scAAV9 can traverse the blood-brain barrier in a nonhuman primate, *cynomolgus macaque* (Foust

et al., 2010). They intravenously injected scAAV9 carrying the green fluorescent protein (GFP) gene on postnatal day 1, and demonstrated that scAAV9 crossed the blood brain barrier and reached motor neurons in the nonhuman primate model, suggesting that gene therapy targeting motor neurons can also be done in human.

Non-SMN-Targeting Strategies

Protection of motor neurons

Neuroprotection therapy with riluzole and gabapentin, which had originally been used for the patients with amyotrophic lateral sclerosis (ALS), was also applied to SMA patients (Russman et al., 2003; Merlini et al., 2003). Glutamate excitotoxicity may be an important factor in the pathogenesis of ALS since the cell bodies of motor neurons receive afferent innervation from glutamate neurons. Hence, pharmacologic agents that rescue glutamate excitotoxicity may be effective in slowing disease progression in ALS (van den Bosch, 2006). Similarly, glutamate excitotoxicity may also be an important factor in the pathogenesis of SMA. Riluzole inhibits the presynaptic release of glutamate, while gabapentin reduces the pool of releasable glutamate in the pre-synaptic neurons. Russman et al. (2003) reported the outcome of a clinical trial of riluzole in 10 patients with SMA type 1 (phase 1 trial with randomization of 2:1, i.e., 2 riluzole to 1 placebo). None of the subjects in this study experienced adverse effects. Even though the study sample size was small, some benefits of riluzole were suggested in the treated patients: three of the seven patients taking riluzole lived to more than 5, 4, and 2 years of age respectively with only BiPAP respiratory assistance at night. On the contrary, the placebo-controlled trials of gabapentin showed no significant benefit in motor function of the patients with SMA type 2/3 (Miller et al., 2001; Merlini et al., 2003).

Another group of compounds, β -lactam antibiotics, can also provide neuroprotection against glutamate-mediated excitotoxicity by increasing the expression level of the glutamate transporter EAAT2/GLT-1. However, to date these observations have only been demonstrated using model mice. A treated ALS mouse model showed a delay in loss of neurons and muscle strength, and increase in survival rate (Rothstein et al., 2005). Nizzardo and colleagues demonstrated that a β -lactam antibiotic, ceftriaxone, also ameliorated the neuromuscular phenotype in SMA mice (*Smn*^{-/-}*SMN2*^{+/+}*SMNΔ*^{7+/+}) (Nizzardo et al., 2011). Treatment with ceftriaxone increased general weight, muscle size, motor neuron numbers and NMJs, which are likely the reasons for the increased life span and muscle strength of the SMA mice. According to them, the neuroprotective effect of the β -lactam antibiotic in the SMA mice seems to be mediated not only through the process of increasing

EAAT2/GLT-1, but also by other mechanisms that increase transcription factor Nrf2 and SMN.

Thyrotropin-releasing hormone (TRH, L-pyroglutamyl-L-histidyl-L-prolinamide) has trophic effects on spinal motor neurons, and it has also been tried for ALS and SMA patients. TRH was administered intravenously (Takeuchi et al., 1994; Tzeng et al., 2000) or orally (Kato et al., 2009) to SMA patients in small clinical trials but only transient improvement was observed in some patients.

Olesoxime (TRO19622), a small molecule with a cholesterol-like structure, has protective properties for motor neurons. It targets proteins associated with the mitochondrial permeability pore (Bordet, 2007). Olesoxime has been granted orphan drug status for the treatment of ALS and SMA, and clinical trials for ALS and SMA have been started in the US and Europe (<http://clinicaltrials.gov/ct2/show/NCT01285583>; <http://clinicaltrials.gov/ct2/show/NCT01302600>). In December 2011, Trophos SA announced the results from the phase 3 study of olesoxime in 512 patients with ALS; olesoxime was well tolerated but did not demonstrate a significant increase in survival of patients receiving riluzole (Rilutek®). Olesoxime trials for SMA are still ongoing and the results are to be expected in 2013 (<http://www.trophos.com/news/pr20111213.htm>).

IGF-1 is reported to modulate multiple fundamental cellular processes, such as cellular growth, proliferation, and survival (Vardatsikos et al., 2009). Most recently, Tsai and colleagues reported that CNS-directed IGF-1 delivery could reduce motor neuron death in SMA mice ($Smn^{-/-}SMN2^{+/+}$) (Tsai et al., 2012). Murdocca and colleagues also reported the effects of IPLEXTM [recombinant human insulin-like growth factor 1 (rhIGF-1) combined with recombinant human IGF-1 binding protein 3 (rhIGFBP-3)] on a severe SMA mouse model ($Smn^{-/-}SMN2^{+/+}SMN\Delta 7^{+/+}$) (Murdocca et al., 2012). According to them, perinatal administration of IPLEXTM results in reduced degeneration of motor neurons, increased muscle fiber size and in amelioration of motor functions in SMA mice, suggesting this compound as a plausible therapeutic candidate to hinder the progression of the neurodegenerative process in SMA. However, it should be noted that CNS-directed IGF-1 delivery could not improve motor function in SMA mice (Tsai et al., 2012) and that IPLEXTM did not improve lifespan and body weight gain of the treated mice (Murdocca et al., 2012). IGF-1 may provide at least some beneficial effects on the survival of motor neurons. However, it is necessary to further study the systemic effect of IGF-1 administration before clinical application, because IGF-1 has multiple functions in various organs.

Protection of non-neuronal tissues

Nutrition may be critical for the care of SMA patients, especially SMA type 1 patients (Oskoui et al., 2007). The improved survival of SMA type 1 patients observed in recent

years can be attributed to noninvasive pulmonary support and aggressive nutrition with gastrostomy feedings. Butchbach and colleagues observed that maternal diet can significantly modify survival and the motor neuron disease phenotype in SMA mice ($Smn^{-/-}SMN2^{+/+}SMN\Delta 7^{+/+}$). According to them, SMA mice from dams that were fed a higher fat diet survived longer than those from dams on a lower fat diet (Butchbach et al., 2010a). The effect of nutritional support on survival of SMA patients and model animals indicates that improvement of pathological conditions of non-neuronal tissues including muscles should be considered in SMA therapy.

Treatments that directly target muscles and improve muscle mass have been reported: inhibition of myostatin by overexpression of follistatin (Sumner et al., 2009) and expression of IGF-1 (Bosch-Marcé et al., 2011). Although inhibition of myostatin did not ameliorate motor function or survival of severe SMA mice ($Smn^{-/-}SMN2^{+/+}SMN\Delta 7^{+/+}$) (Sumner et al., 2009), overexpression of IGF-1 resulted in enlarged myofibers, but not in improvement of motor function (Bosch-Marcé et al., 2011). Murine IGF-1 administration had been proven to give different positive effects when it was expressed locally in muscle of SMA mice ($Smn^{-/-}SMN2^{+/+}SMN\Delta 7^{+/+}mIGF-1^{+/-}$) (Bosch-Marcé et al., 2011) or in motor neurons (Murdocca et al., 2012).

Recently, there has been emerging evidence that the RhoA/ROCK pathway may play an important role in the pathogenesis of SMA (Bowerman et al., 2009; Nölle et al., 2011) since SMN depletion leads to an increased activation of ROCK, a major regulator of actin dynamics. Bowerman et al. (2010) reported that ROCK inhibitors, Y-27632 and Fasudil, dramatically improved the survival of the $Smn^{2B/-}$ mice, an intermediate SMA mouse model. They emphasized that lifespan extension in SMA mice with ROCK inhibitors was accompanied by an improvement in the maturation of NMJs and an increase in muscle fiber size (Bowerman et al., 2010; Bowerman et al., 2012). However, Bowerman and colleagues showed that administration of Y-27632 had no beneficial effect on the $Smn^{-/-}$ mouse model with the most severe SMA phenotype. Here, they suggested that there may be a need for differential therapies for the different types of SMA severities and that the “one size fits all” approach may not be tenable (Bowerman et al., 2010).

Challenges in Clinical Trials

Despite the large number of candidate compounds evaluated, there has yet to be any effective drug treatment reported for all types of SMA (Wadman et al., 2012a; Wadman et al., 2012b). A number of clinical trials for SMA have already been conducted in the past decade, some of which are still ongoing (Miller et al., 2001; Mercuri et al., 2007; Pane et al., 2008;

Swoboda et al., 2009; Tiziano et al., 2010; Kissel et al., 2011). However, all clinical trials reported so far failed to show significant effectiveness of the therapeutic approaches, which may indicate the difficulties of designing clinical trials for this disorder. An adequate design should take into account the rarity of the patients, clinical disease heterogeneity (subtypes, onset age, sex, stage of disease progress, timing of enrollment, and intervention relative to disease progression), treatment plans (selection of the drug with possible ameliorating effects on the clinical symptoms, sufficient dose, and duration to see some measurable effects) and outcome measures [laboratory biomarkers including *SMN* transcript and *SMN* protein amounts, muscle mass and strength, motor function testing, respiratory function testing, MUNE, questionnaires for quality of life (QOL)] (Swoboda et al., 2007; Kissel et al., 2011). Clinical endpoints, i.e., the target outcome of the clinical trials: such as extension of the survival period in the patients with SMA type 1 (which will be discussed again below), improvement of motor function in the patients with SMA type 2, and extension of the walking period in the patients with SMA type 3, need to be specified. However, great subtlety may be required for the accurate evaluation of these outcomes. Even if a therapeutic approach could ameliorate the symptoms in some patients, these outcomes may not be detected if the trials are not adequately designed.

To address the challenges due to the rarity of SMA, Mercuri's group (2012) called for clinical trials to be carried out as large multicenter international trials. Such large-scale collaborations would increase the numbers of patients enrolled and would enable randomized placebo studies to be carried out. This approach could also overcome the problems due to clinical heterogeneity as a stratification method could be used to provide a fair evaluation of the treatments (Mercuri et al., 2012).

The selection of appropriate outcome measures to test the efficacy of a therapy remains one of the most difficult problems to be resolved. As for laboratory biomarkers, only *SMN* transcript or *SMN* protein levels have been established. However, determination of *SMN* transcript or *SMN* protein levels may not be enough, because these cannot be used to evaluate treatments targeting biochemical reactions downstream of *SMN*-related signaling (Crawford et al., 2012). Recently, metabolomics studies have suggested that some proteins and metabolites can be used as laboratory biomarkers to reflect responsiveness to treatment (Finkel et al., 2012). Further studies are still required for future clinical usage.

The Hammersmith Functional Motor Scale (HFMS) (Main et al., 2003), Modified HFMS (MHFMS) (Krossschell et al., 2006), and gross motor function measure (GMFM) (Nelson et al., 2006) have been established as standard measures of functional ability in children with SMA types 2 and 3 for use in longitudinal multicenter clinical trials. The Children's

Hospital of Philadelphia Infant Test of Neuromuscular Disorders (CHOP INTEND) may also be used for the evaluation of children with SMA type 1 (Glanzman et al., 2010). However, it is difficult to evaluate the actual change in motor scales in SMA patients with any motor function measurements. Thus, it is necessary for investigators in multicenter networks to share the test skills and scoring criteria in order to improve inter-rater reliability and objectivity. For that purpose, training of test skills and collaboration in the scoring criteria should be implemented across centers with different expertise (Mercuri et al., 2012).

In an SMA mouse model, extension of lifespan has been considered to reflect the effectiveness of therapeutic approaches. However, lifespan cannot be simply applied to evaluate the therapeutic approaches in human SMA patients because not only the administered therapy, but the type of supportive care including respiratory management can also change the lifespan of patients. In addition, the use of an artificial respirator in SMA type 1 management is still controversial. Such differences in clinical care may hamper simple comparison using lifespan outcomes in international clinical trials. The occurrence of death and the requirement for an artificial respirator may be considered as equivalent events when evaluating the efficacy of clinical trials in patients with SMA type 1 because improvement of motor scale cannot be expected from these patients (Oskoui et al., 2007; Mercuri et al., 2012). Currently, using lifespan as the only available outcome measure, is not ideal anymore. If it is possible to measure improvements in respiratory function or restoration of motor function, alternative outcome measures for SMA type 1 may become achievable. Highly effective therapies which will improve motor scale of patients with SMA type 1 can then be sought.

Conclusions

SMA is an incurable motor neuron disease with autosomal recessive inheritance. Molecular biology studies of SMA have been greatly advanced in two directions, namely diagnostic applications and pathophysiological studies, since the discovery of the *SMN* genes in 1995. Molecular diagnostics has enabled us not only to diagnose SMA in patients, but has also provided the ability to carry out carrier and newborn screening of SMA for populations. Pathophysiological studies have provided an improved understanding of the underlying pathogenesis of SMA, including alternative splicing of *SMN2*, aberrant splicing due to the defect of snRNPs, impairment of motor circuit formation and/or NMJ development, and dysregulation of cytoskeleton dynamics. To date, there has been no successful therapy for SMA, but an in-depth understanding of the pathophysiology underlying the disease

can offer useful insights for development of effective treatment approaches. Some therapeutic strategies have already been devised based on current pathophysiological knowledge of the disease, namely *SMN2*-targeting, *SMN1*-introduction and non-*SMN* targeting strategies. With multiple approaches in therapeutic strategies for SMA being pursued, some of which are already in clinical trials, it is expected that some candidate compounds may emerge as potential therapeutic agents in the near future. These exciting developments offer promising outcomes for SMA patients in overcoming this debilitating disease.

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COMMENTARY

PLS3 expression and SMA phenotype: a commentary on correlation of PLS3 expression with disease severity in children with spinal muscular atrophy

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MODIFIERS OF SMA PHENOTYPE

Spinal muscular atrophy (SMA; OMIM 253300) is an autosomal recessive neuromuscular disorder characterized by the loss of motor neurons.¹ It is clinically heterogeneous and can be classified into three subtypes depending on the age of onset and achievement of motor milestones: SMA type 1 (a severe type with onset before the age of 6 months, patients are unable to sit without support), SMA type 2 (an intermediate type with onset before the age of 18 months, patients are unable to stand or walk without support) and SMA type 3 (a mild type with onset after the age of 18 months, patients are able to stand and walk independently until the disease progresses).¹

Causative mutations of SMA are mainly homozygous deletions of the *SMN1* gene located on chromosome 5q13. The gene product, the SMN protein, has critical roles in a variety of cellular activities.¹ The *SMN2* gene, an almost identical homolog of *SMN1*, is retained in all SMA patients and produces low levels of SMN protein, but does not fully compensate for mutated *SMN1*. *SMN2* is now considered to be a modifier of the SMA phenotype, as high copy numbers of *SMN2* ameliorate the clinical severity in SMA patients.¹ However, some asymptomatic individuals inherit the same *SMN* genotype (homozygous *SMN1* deletion and identical *SMN2* copy numbers) as their affected siblings. The presence of such SMA-discordant families suggests the influence of modifier genes other than *SMN2*.²

PLS3 EXPRESSION IN FEMALE SMA PATIENTS

Oprea *et al.*³ identified six SMA-discordant families with eight fully asymptomatic females who shared the same *SMN* genotype as their affected siblings. The authors found that *PLS3*, a gene encoding the actin-bundling protein plastin 3 (PLS3, T-plastin or T-fimbrin; MIM300131, Xq23), was highly expressed in lymphoblastoid cell lines from unaffected female siblings. They also obtained experimental evidence that the overexpression of *PLS3* rescues the axonal growth defect associated with low-SMN levels in motor neurons of SMA-mouse embryos and zebrafish. They concluded that *PLS3* (or *PLS3*) may be a gender-specific SMA modifier.

To examine whether *PLS3* is a gender-specific modifier, Stratigopoulos *et al.*⁴ analyzed 88 SMA patients (41 males and 47 females), and found that in postpubertal female patients, the amount of the *PLS3* transcript was highest in type 3 patients, followed by type 2 patients and lowest in type 1 patients. In these SMA patients, *PLS3* expression was related to *SMN2* copy number, gross motor function measure and clinical subtype. Interestingly, *PLS3* expression in either pre- or postpubertal male patients or prepubertal female patients did not correlate with clinical subtype or *SMN2* copy number. The authors concluded that *PLS3* is an age- and/or puberty-specific and sex-specific modifier of the SMA phenotype.

In this issue of the journal, Cao *et al.*⁵ also suggested that *PLS3* is a gender-specific modifier for SMA phenotype, based on their analysis of 65 SMA patients (36 males

and 29 females) and 59 healthy controls (31 males and 28 females). According to this study, among the older female patients (>3 years of age), *PLS3* expression was significantly higher in type 3 than type 2, which is consistent with the results of Stratigopoulos *et al.*, although the age cut-off levels differed between the two studies. Cao *et al.* demonstrated two important findings in this article. The first was that *PLS3* expression is age-dependent and decreases in type 1–2 SMA patients and healthy controls above 3 years of age, suggesting that the patient's age should always be considered when evaluating *PLS3* expression. The second was that *PLS3* expression of type 3 patients who can walk is higher than in patients unable to do so, suggesting that it could be used as a biomarker of disease progression. However, as stated in the report, this will be necessary to verify in a larger sample.

PERSPECTIVE ON SMA TREATMENT

The relationships between Smn protein levels (or *SMN2* copy number) and Pls3 protein levels (or *PLS3* expression) in motor neurons are still poorly understood and studies have shown conflicting results. For example, *PLS3* was suggested to be expressed independently of SMN (or *SMN2* copy number) in the report by Oprea *et al.*,³ which described unaffected siblings of the patients, and that by Ackermann *et al.*⁶ using SMA mice. By contrast, the study of Hao *et al.*⁷ on zebrafish showed that Pls3 levels were dependent on Smn levels.

Hao *et al.* demonstrated that human *PLS3* overexpression was able to rescue neuromuscular junction defects in SMA mutants

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of transgenic zebrafish, suggesting that decreased PLS3 contributes to SMA motor phenotypes. Indeed, when Smn protein levels were severely decreased in SMA mutants, they found that PLS3 translation was compromised, leading to SV2 presynaptic defects at the neuromuscular junction. In addition, as human SMN expression increased the Pls3 level in SMA mutants, this led them to conclude that Pls3 levels are dependent on Smn levels.

Ackermann *et al.* generated a conditional PLS3-overexpressing mouse bred into an SMA background to show that PLS3 overexpression restored defects in motor neurons and neuromuscular junctions. In this study, they also observed that Pls3 was not decreased in the brain and spinal cord of SMA mice compared with controls. This finding suggests that Pls3 levels are not regulated by Smn levels. Thus, it was postulated that PLS3 has an Smn-independent ameliorative action on the phenotype of SMA mice.

As PLS3 expression restores the motor neuron and rescues neuromuscular junction defects, it could be a potential therapeutic target for SMA treatment.^{3,6} This has already been hypothesized by Bowerman *et al.*⁸ who have suggested possible treatment strategies including the upregulation of PLS3 to target actin cytoskeletal dynamics.

CONCLUSIONS

Cao *et al.*⁵ confirmed that PLS3 expression modifies the phenotype of female SMA patients and suggested that its expression in peripheral blood cells will be a useful biomarker of disease progression in female patients with SMA. Investigation of the modifiers including PLS3 expression, SMN2

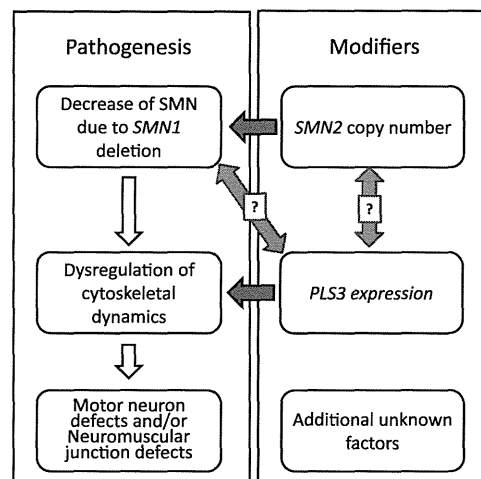


Figure 1 Modifiers of phenotype in female SMA patients. SMN2 copy number and PLS3 expression are recognized as phenotype modifiers in female SMA patients. Both the SMN and PLS3 proteins are involved in the regulation of cytoskeleton dynamics. However, the relationship between SMN protein levels (or SMN2 copy number) and PLS3 protein levels (or PLS3 expression) remain to be elucidated. A full color version of this figure is available at the *Journal of Human Genetics* journal online.

copy numbers and additional unknown factors will help our understanding of the mechanism underlying SMA pathology (Figure 1), and lead to the establishment of new treatments for SMA.

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Original article

Intragenic mutations in *SMN1* may contribute more significantly to clinical severity than *SMN2* copy numbers in some spinal muscular atrophy (SMA) patients

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Abstract

Background: Spinal muscular atrophy (SMA) is an autosomal recessive neuromuscular disorder caused by deletion or intragenic mutation of *SMN1*. SMA is classified into several subtypes based on clinical severity. It has been reported that the copy number of *SMN2*, a highly homologous gene to *SMN1*, is associated with clinical severity among SMA patients with homozygous deletion of *SMN1*. The purpose of this study was to clarify the genotype-phenotype relationship among the patients without homozygous deletion of *SMN1*. **Methods:** We performed molecular genetic analyses of *SMN1* and *SMN2* in 112 Japanese patients diagnosed as having SMA based on the clinical findings. For the patients retaining *SMN1*, the PCR or RT-PCR products of *SMN1* were sequenced to identify the mutation. **Results:** Out of the 112 patients, 106 patients were homozygous for deletion of *SMN1*, and six patients were compound heterozygous for deletion of one *SMN1* allele and intragenic mutation in the retained *SMN1* allele. Four intragenic mutations were identified in the six patients: p.Ala2Val, p.Trp92Ser, p.Thr274TyrfsX32 and p.Tyr277Cys. To the best of our knowledge, all mutations except p.Trp92Ser were novel mutations which had never been previously reported. According to our observation, clinical severity of the six patients was determined by the type and location of the mutation rather than *SMN2* copy number. **Conclusion:** *SMN2* copy number is not always associated with clinical severity of SMA patients, especially SMA patients retaining one *SMN1* allele.

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1. Introduction

Spinal muscular atrophy (SMA) is a common neuromuscular disease characterized by degeneration of lower motor neurons, leading to the axial and limb weakness associated with muscle atrophy. The incidence of the disease has been estimated at 1 in 10,000 newborns, with an expected carrier frequency of 1 in 50 [1]. Based on molecular epidemiological analysis using *SMN1* copy number, the worldwide carrier frequency of SMA is 1 in 40–70, suggesting a disease incidence of 1 in 6000–20,000 [2].

SMA is classified into four subtypes depending on the age of disease onset and the achievement of motor milestones [3]: namely, type 1 (severe form; onset age of 0–6 months old, unable to sit unaided), type 2 (intermediate form; onset age of <18 months old, unable to stand or walk unaided), type 3 (mild form; onset age of >18 months old, able to stand or walk unaided), and type 4 (milder form; onset age of >21 years old, able to stand or walk unaided).

All SMA subtypes have been mapped to chromosomal region 5q11.2–13.3 [4–7] and the survival motor neuron gene (*SMN*) and neuronal apoptosis-inhibitory protein gene (*NAIP*) were cloned as SMA-causing gene candidates [8,9]. The *SMN* gene exists as two highly homologous copies, *SMN1* (the telomeric copy) and *SMN2* (the centromeric copy) [8]. It is now established that SMA is caused by deletions or intragenic mutations of *SMN1*. *SMN1* is homozygously deleted in more than 90% of SMA patients [8,10], and deleteriously mutated in the remaining patients [8,11]. On the other hand, *NAIP*-deletion has been found only in 50% of type 1 patients, and much less frequently in type 2 and 3 patients. The presence or absence of *NAIP* may be associated with the clinical severity of SMA [9,10].

Increased *SMN2* copy number is related to improved survival outcomes and maintenance of motor function [12–16]. Both *SMN* genes, *SMN1* and *SMN2*, differ by only five nucleotides [8]. Of the five nucleotide differences between the two *SMN* genes, only one is present in the coding region at position +6 of exon 7 in *SMN1* (c.840C) and *SMN2* (c.840T). Although this mutation is translationally silent, the C-to-T transition alters the splicing pattern in *SMN2* exon 7 [17]. *SMN1* exclusively produces full-length (FL) *SMN1* transcripts, while *SMN2* produces ~90% of exon7-lacking (Δ 7) *SMN2* transcripts and ~10% of FL-*SMN2* transcripts [18]. It is expected that high *SMN2* copy number may

produce a large amount of FL-*SMN2* to compensate for the loss of *SMN1* to some degree.

However, most phenotype-genotype correlation studies have been conducted only in SMA patients with a complete loss of *SMN1*. The relationship between *SMN2* copy number and clinical severity are yet to be clarified in SMA patients retaining one *SMN1* allele. In this study, to understand the modifying factors in determining the clinical phenotype of SMA patients retaining one *SMN1* allele, we conducted a mutation analysis and investigated the contribution of *SMN2* copy number to the clinical severity in such patients.

2. Patients and methods

2.1. Patients

All 112 Japanese patients (51 males and 61 females) fulfilled the diagnostic criteria defined by the International SMA Consortium [19]. Here, patients with onset before 20 years old was classified into type 3, and those with onset after 21 years old was classified into type 4 [3]. Informed consent was obtained from these patients and/or their parents. This study project including genetic analysis was approved by the Ethical Committee of the Kobe University Graduate School of Medicine, Japan.

In this study, six patients (Patients 1–6) retaining one allele of *SMN1* exon 7, were found to carry intragenic mutations in *SMN1*. Patients 1 (female) and 2 (male) were type 1 patients reported previously to have one *SMN1* allele [20]. Patient 3 was a 19-day-old male with SMA type 1, referred to us because of respiratory insufficiency and swallowing difficulties. Patient 4 was a 7-year-old female with type 2 SMA. She was first diagnosed as having SMA type 2 close to type 3 because she could sit unaided and stand while holding onto something (such as a wall or table) for support. However, she rapidly lost such abilities at 2 years old. Finally, she was bound to artificial ventilator because of respiratory insufficiency at 3 years old. Patient 5 was a 13-year-old male with type 3 SMA, who had pain and heaviness in legs during exercise since the age of 11 years. He later developed symptoms including waddling gait, muscle weakness and atrophy in quadriceps, and attenuated patellar tendon reflex. Patient 6 was a 19-year-old female with type 3 SMA, who had noticed muscle weakness during swimming exercise at the age of 13 years. She gradually lost her running ability and could no

longer run as fast as the other classmates in her high school days.

2.2. *SMN and NAIP deletion test*

Genomic DNA was extracted from 3 ml of whole blood using a DNA extraction kit, SepaGene (Sanko Junyaku, Tokyo, Japan). For the *SMN* and *NAIP* deletion test, PCR and enzyme digestion reactions were performed according to the method of van der Steege et al. [21]. Exon 5 of the *NAIP* gene was detected using the PCR method of Roy et al. [9]. Here we adopted “exon 5” as a widely accepted exon number, although this exon has been denoted as “exon 4” by Chen et al. [22].

2.3. Copy number analysis of the *SMN* genes using real time PCR method

We determined the copy numbers of the *SMN* genes based on the real-time PCR method of Tran et al. [23]. Cystic fibrosis trans-membrane regulator gene (*CFTR* gene) was used as a reference gene for the relative quantification of copy numbers.

2.4. Messenger RNA analysis

For the assignment of the mutation to *SMN1* or *SMN2*, mRNA analysis was performed. Total RNA was extracted from leukocytes using the acid guanidiumthiocyanate-phenol-chloroform method. *SMN1* and *SMN2* mRNA species were amplified by reverse transcriptase (RT)-PCR method [16,24]. A new primer, ex1-F (5'- GCT ATG GCG ATG AGC A GC GGC -3'), was designed for this study. The mRNA species encompassing exons 1–8 were amplified using primers ex1-F and 541C1120 [8], and the mRNA species encompassing exons 1–7 were amplified using primers ex1-F and 541C770 [8].

2.5. Nucleotide sequencing

The amplified PCR or RT-PCR products of *SMN* exons were purified and sequenced directly or after sub-cloning. The sequencing reaction was performed using a dye terminator cycle-sequencing kit (Life Technologies Corporation, Carlsbad, CA). The reaction product was electrophoresed on an ABI PRISM® 310 Genetic Analyzer (Life Technologies Corporation, Carlsbad, CA).

2.6. Computational algorithms

We predicted the mutation effects on the protein function using three computational algorithms: Sorting Intolerant from Tolerant amino acid substitutions (SIFT) [25], Polymorphism Phenotyping-2 (PolyPhen-2) [26], and Grantham score difference (Align-GVGD) [27].

2.7. Statistics

The correlation of copy number of *SMN2* with the clinical subtypes was compared by chi-square test and *t*-test. *P*-value of less than 0.05 was considered to indicate a significant difference. The software used for statistical analysis was Statistical Program for Social Science (SPSS) Version 16 (IBM Corporation, Paulo Alto, US).

3. Results

3.1. *SMN1* and *NAIP* deletion test

SMN1 exon 7-deletion (herein after referred to as *SMN1*-deletion) was found in almost all SMA patients, regardless of clinical subtypes: 106 out of 112 (95%) patients with SMA in this study had *SMN1*-deletion and 6 patients (5%) had subtle mutations in *SMN1*. Out of 106 *SMN1*-deleted patients, 48 (45%) were type 1, 35 (33%) were type 2, 19 (18%) were type 3, and 4 (4%) were type 4 (Table 1).

In our study, 96 of 106 (91%) *SMN1*-deleted patients had deletion of *SMN1* exon 8. However, the other 10 patients (9.0%) retained *SMN1* exon 8. We confirmed that these patients had at least one copy of the hybrid gene with *SMN2* exon 7 and *SMN1* exon 8 using direct sequencing analysis of the PCR fragment amplified with the common primers for *SMN1* and *SMN2*.

NAIP exon 5-deletion (herein after referred to as *NAIP*-deletion) was always accompanied by *SMN1*-deletion (Table 1). In addition, *NAIP*-deletion was much more frequent in SMA type 1 than SMA non-type 1. *NAIP*-deletion was found in 29 out of 48 (60%) patients with *SMN1*-deleted SMA type 1, while it was found in only 8 out of 58 (14%) patients with *SMN1*-deleted SMA types 2, 3 and 4.

3.2. *SMN2* copy number and clinical severity in patients with *SMN1*-deletion

We determined the *SMN2* copy numbers of all the patients enrolled in this study using the real-time PCR method. For the analysis of *SMN2* copy number and clinical severity, the “*SMN2* exon 7-*SMN1* exon 8 hybrid” gene is regarded as *SMN2*.

A significant relationship between *SMN2* copy number and clinical severity was observed in this study (Table 2). 38 out of 48 (79%) patients with *SMN1*-deleted SMA type 1 showed one copy or two copies of *SMN2*, 34 out of 35 (97%) patients with *SMN1*-deleted SMA type 2 showed three copies of *SMN2*, 18 out of 19 (95%) patients with *SMN1*-deleted SMA type 3 showed three or four copies of *SMN2*, and 3 out of 4 (75%) patients with *SMN1*-deleted SMA type 4 showed four copies of *SMN2*.

Table 1
SMN1 and *NAIP* deletion test ($n = 112$).

<i>SMN1</i>		<i>NAIP</i>	Type 1	Type 2	Type 3	Type 4	Total
Exon 7	Exon 8	Exon 5					
Del	Del	Del	29	6	1	1	37
Del	Del	Non-del	17	24	15	3	59
Del	Non-del	Non-del	2	5	3	0	10
Non-del	Non-del	Non-del	3	1	2	0	6
Total			51	36	21	4	112

Table 2
 Clinical severity and *SMN2* copy number in patients with homozygous *SMN1*-deletion ($n = 106$).

	1 copy	2 copies	3 copies	4 copies	Mean	(SD)
Type 1	1	37	10	0	2.18	(0.44)
Type 2	0	1	34	0	2.97	(0.17)
Type 3	0	1	13	5	3.18	(0.51)
Type 4	0	0	1	3	3.80	(0.40)
Total	1	39	58	8		

Table 3
 Clinical severity and *SMN2* copy number in patients retaining one *SMN1* allele ($n = 6$).

	Sex	Onset	Type	<i>SMN2</i> copy number	Nucleotide change (exon)	Amino acid change	Domain	References
Patient 1	F	5m	1	3	c.275 G > C (exon 3)	p.Trp92Ser	Tudor	[20]
Patient 2	M	6m	1	3	c.275 G > C (exon 3)	p.Trp92Ser	Tudor	[20]
Patient 3	M	0m	1	2	c.819_820insT (exon 6)	p.Thr274Tyr fsX32	C-terminal	This study
Patient 4	F	12m	2	1	c.830 A > G (exon 6)	p.Tyr277Cys	C-terminal	This study
Patient 5	M	11y	3	1	c.5 C > T (exon 6)	p.Ala2Val	N-terminal	This study
Patient 6	F	13y	3	1	c.5 C > T (exon 1)	p.Ala2Val	N-terminal	This study

3.3. *SMN2* copy number and clinical severity in patients retaining one *SMN1* allele

In this study, we identified four different intragenic mutations in *SMN1* of six patients without *SMN1*-deletion (Patients 1–6) (Table 3). All of them were compound heterozygous for deletion of one *SMN1* allele and an intragenic point mutation of the other *SMN1* allele. The intragenic mutations included three missense mutations and one frame-shift mutation: c. 5C > T (p.Ala2Val) in exon 1, c. 275G > C (p.Trp92Ser) in exon 3, c.819_820insT (p.Thr274TyrfsX32) in exon 6, and c.830 A > G (p.Tyr277Cys) in exon 6. Three of the mutations, p.Ala2Val, p.Thr274TyrfsX32 and p.Tyr277Cys, are novel ones which have never been previously reported.

We predicted the effect of the missense mutations on the protein function using three computational algorithms: SIFT [25], PolyPhen-2 [26], and Align-GVGD [27]. All three types of missense mutation were predicted to damage the protein function.

Interestingly, the observed phenotype of patients carrying an intragenic mutation deviated from the expected correlations with the *SMN2* copy number (Table 3 and Fig. 1): type 3 patients with p.Ala2Val (Patients 5 and 6) carried only a single copy of *SMN2*, while type 1

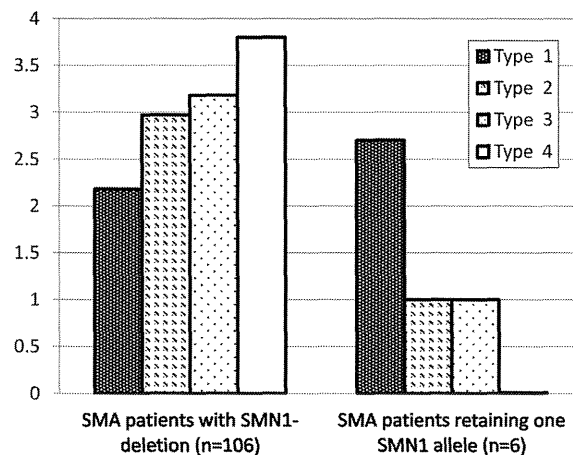


Fig. 1. Mean *SMN2* copy numbers in SMA patients. Patients with *SMN1*-deletion ($n = 106$) carried zero copies of *SMN1*. Patients retaining one *SMN1* allele ($n = 6$) which harbored intragenic mutations: p.Ala2Val, p.Trp92Ser, p.Thr274TyrfsX32 and p.Tyr277Cys.

patients with p.Trp92Ser (Patients 1 and 2) carried as many as 3 copies of *SMN2*. These findings suggested that intragenic mutations in *SMN1* influence the clinical phenotype more significantly than *SMN2* copy numbers in some patients.

4. Discussion

The identification of intragenic mutations, especially missense mutations, may help us to further elucidate the function of SMN and the pathogenic mechanism of SMA. In this study, we identified four different intragenic *SMN1* mutations in six SMA patients without *SMN1*-deletion. These intragenic mutations were p.Ala2Val, p.Trp92Ser, p.Thr274TyrfsX32, and p.Tyr277Cys.

The p.Ala2Val mutation, which is located in the N-terminal domain, has never been reported until now. Our two patients with p.Ala2Val were unrelated. However, another mutation in the same location, p.Ala2Gly, has previously been reported in three SMA patients; these patients were also unrelated individuals, but had the possibility of sharing an ancestral origin [28]. All patients with p.Ala2Gly carried only one *SMN2* copy, and two of them showed mild phenotype (type 3). The mutation effect of p.Ala2Val, as well as p.Ala2Gly, may be much less deleterious than other missense mutations identified in this study. However, *SMN2* may not be dispensable in these patients. The mild SMA mutation, p.Ala2Gly, by itself cannot rescue *Smn*^{-/-} mice, suggesting that homomer of the mutant SMN is not functional [29]. According to the Workman et al. [30], the heteromer of mutant SMN and FL-SMN from a single copy of *SMN2* must have some function.

We previously reported the p.Trp92Ser mutation in two unrelated patients [20]. This mutation is located in the Tudor domain to which other proteins bind. [31]. Many of them are involved in small nuclear ribonucleoprotein (snRNP) biogenesis. SMN Tudor domain preferentially binds symmetric dimethylated arginine (sDMA) of Sm proteins which constitute Sm core of snRNP [32]. We have already reported that the binding ability of the mutated SMN with p.Trp92Ser to SmB and fibrillarin was reduced to half of normal levels [20]. Most recently, Tripsianes et al. [33] examined the relationship between mutated Tudor domain and the binding capacity to sDMA *in vitro*. According to them, p.Trp92Ser mutant was unfolded, as judged by fingerprint NMR spectra analysis, and did not bind sDMA [33].

The p.Thr274TyrfsX32 mutation is a frameshift mutation arising from a single nucleotide insertion in exon 6 and results in a truncated SMN protein lacking the C-terminal domain of *SMN*. A new isoform of SMN, axonal SMN (a-SMN), is expected to be produced in the patient, because a-SMN is a truncated, alternatively spliced isoform of *SMN1*, originating from the retention of intron 3 [37,38]. Although the role of a-SMN in the pathogenesis of SMA has not been clarified yet, the disease severity of the patient with this mutation suggests that a-SMN functions were not enough to fully compensate for the deleterious mutation.

The p.Tyr277Cys mutation is located in the C-terminal domain of SMN known as the YG box, which is essential for oligomerization or self-association of SMN [31]. Oligomerization defect destroys the function of SMN and correlates with clinical severity of SMA [34]. Many other mutations in the same domain have been frequently reported [35,36], although the p.Tyr277Cys mutation has not been reported up to now.

An interesting question arises as to which factor contributes more significantly to clinical phenotype in SMA, *SMN1* intragenic mutation or *SMN2* copy number. According to our analysis of the patients with homozygous *SMN1*-deletion (Table 2 and Fig. 1), increased *SMN2* copy number was associated with milder phenotype, which was compatible with previous reports [12–16]. However, the phenotype of patients without *SMN1*-deletion was not related to their *SMN2* copy number (Table 3 and Fig. 1). In our study, p.Ala2Val was found in two type 3 patients with one *SMN2* copy, p.Trp92Ser in two type 1 patients with three *SMN2* copies, p.Thr274TyrfsX32 in one type 1 patient with two *SMN2* copies, and p.Tyr277Cys in one type 2 patients with one *SMN2* copy. According to our findings, *SMN1* intragenic mutations appear to contribute much more significantly to clinical severity than *SMN2* copy numbers in some patients.

Since our patients carry various intragenic *SMN1* mutations, the next question is whether *SMN2* copy number effect is present or absent among the patients with the same *SMN1* mutation. Using the data of the SMA patients with missense mutations described in a review paper of Sun et al. [36], we analyzed the relationship between *SMN2* copy number and clinical severity in eleven patients with p.Tyr272Cys in *SMN1*. We observed that higher *SMN2* copy number was correlated with reduced disease severity: patients with three *SMN2* copies showed milder phenotype than the patients with one *SMN2* copy number. Thus, we speculate that *SMN2* copy number effect is present when the *SMN1* mutation is the same in the patients.

In conclusion, *SMN2* copy number is not always associated with clinical severity of SMA patients, especially SMA patients without *SMN1*-deletion. In these patients, clinical severity in SMA caused by *SMN1* mutations may be determined by the type and location of the intragenic mutation. Intragenic mutations in *SMN1* may contribute more significantly to clinical severity than *SMN2* copy numbers in some spinal muscular atrophy patients.

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