Reversible molecular pathology of skeletal muscle in spinal muscular atrophy

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Low levels of full-length survival motor neuron (SMN) protein cause the motor neuron disease, spinal muscular atrophy (SMA). Although motor neurons undoubtedly contribute directly to SMA pathogenesis, the role of muscle is less clear. We demonstrate significant disruption to the molecular composition of skeletal muscle in pre-symptomatic severe SMA mice, in the absence of any detectable degenerative changes in lower motor neurons and with a molecular profile distinct from that of denervated muscle. Functional cluster analysis of proteomic data and phospho-histone H2AX labelling of DNA damage revealed increased activity of cell death pathways in SMA muscle. Robust upregulation of voltage-dependent anion-selective channel protein 2 (Vdac2) and downregulation of parvalbumin in severe SMA mice was confirmed in a milder SMA mouse model and in human patient muscle biopsies. Molecular pathology of skeletal muscle was ameliorated in mice treated with the FDA-approved histone deacetylase inhibitor, suberoylanilide hydroxamic acid. We conclude that intrinsic pathology of skeletal muscle is an important and reversible event in SMA and also suggest that muscle proteins have the potential to act as novel biomarkers in SMA.

INTRODUCTION

Proximal autosomal spinal muscular atrophy (SMA) is a predominantly childhood form of motor neuron disease and is the most common genetic cause of infant mortality, with an incidence of 1:6000–10 000 and a carrier frequency of 1:35 (1,2). SMA is caused by low expression levels of full-length survival motor neuron (SMN) protein, resulting from disruption of the SMN (SMN1) gene (3,4). There are two nearly identical copies of this gene in humans; the telomeric SMN1 gene and the centromeric SMN2 gene. The SMN2 gene, however, produces only 10% of full-length SMN protein due to a defective splicing pattern (4,5). Retention of at least one copy of SMN2 in SMA patients therefore leads to low residual levels of SMN protein. Although SMN protein is ubiquitously expressed, the major pathological hallmarks of SMA are focused on the neuromuscular system, including a loss of lower motor neurons from the ventral horn of the spinal cord and atrophy of skeletal muscle (6–9).

Most research to date has focused on examining how low levels of SMN lead to pathological changes in motor neurons, so the contribution of muscle to the pathogenesis of SMA remains unclear. Although pathological changes in SMA muscle, including evidence of increased levels of apoptosis, are a well-established hallmark of SMA (10–14), it has generally been assumed that changes in muscle occur simply as a secondary consequence of the degeneration of innervating lower motor neurons, rendering muscle fibres denervated. Studies have shown that restoring SMN protein levels in neurons can significantly ameliorate disease progression in

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We validated the absence of any degenerative pathology in lower motor neurons innervating the rostral LAL in Smn<sup>/−;SMN2</sup> mice at a pre-symptomatic age (postnatal day 1; P1; Fig. 1B): >98% of neuromuscular junctions were fully innervated by intact motor axon collaterals in both Smn<sup>/−;SMN2</sup> mice and littermate controls and there was no evidence of abnormal neurofilament accumulations in motor nerve terminals in any of the muscles examined (n > 5 mice per genotype). Similarly, we found no evidence for denervation-induced muscle fibre shrinkage in the rostral LAL from Smn<sup>/−;SMN2</sup> mice at P1 (Fig. 1C). Taken together with the previously published studies, we concluded that the rostral LAL at P1 represents a muscle preparation from an SMA mouse where no detectable neuronal degeneration or muscle denervation is present, making it ideal for intrinsic molecular studies of muscle in SMA. As expected, however, there was still a 70–80% reduction in expression levels of SMN protein in the rostral LAL from Smn<sup>/−;SMN2</sup> mice at P1 compared with control littermates (Fig. 1D).

**RESULTS**

The rostral band of levator auris longus allows examination of intrinsic changes to skeletal muscle in SMA

In order to isolate and identify molecular changes occurring specifically in skeletal muscle during SMA, it is necessary to have an experimental system where low levels of SMN protein are present in muscle, but denervation due to degeneration of innervating lower motor neurons is absent. The homogeneous fast-twitch levator auris longus (LAL) muscle has two distinct bands (rostral and caudal) (28). Motor neurons innervating the caudal band in the Smn<sup>/−;SMN2</sup> mouse model of severe SMA (27) are susceptible to SMA pathology (even at late-symptomatic stages), whereas those innervating the rostral band are resistant (Fig. 1A) (28–30). Importantly, our group and others have previously demonstrated that motor neurons innervating the rostral LAL develop normally in the pre-symptomatic period (30), with genetic and electrophysiological studies similarly indicating an absence of lower motor neuron pathology or neuromuscular junction dysfunction in the rostral LAL from early-symptomatic SMA mice (31,32).

Label-free proteomic analysis of the rostral LAL reveals molecular alterations to skeletal muscle in pre-symptomatic Smn<sup>/−;SMN2</sup> mice

Label-free proteomic techniques were used to quantify and compare the molecular composition of the rostral LAL from P1 Smn<sup>/−;SMN2</sup> mice compared with littermate controls (Smn<sup>/++;SMN2</sup>; n = 9 mice per genotype; see Materials and Methods). Direct comparison of rostral LAL proteomes revealed that 65 out of the 345 identified individual proteins (19%) were upregulated >20% in Smn<sup>/−;SMN2</sup> mice (Table 1 and Supplementary Material, Table S1). Of these, 20 proteins showed a >2-fold increase in expression levels. In addition, 32 out of the 345 identified proteins (9%) were downregulated >20% in Smn<sup>/−;SMN2</sup> mice (Table 2 and Supplementary Material, Table S2). The increased expression profiles of many proteins in Smn<sup>/−;SMN2</sup> tissue confirmed that the changes observed were active responses to low levels of SMN in muscle, and were not simply occurring as a result of a global decrease in protein synthesis. We initially validated the proteomic data by quantifying expression levels of one significantly downregulated protein (parvalbumin) in immunohistochemically labelled muscle preparations (Supplementary Material, Fig. S1).

To identify any functional clustering of proteins found to have modified expression levels in the rostral LAL of SMA mice, we performed a systems level analysis of the proteomic data, using Ingenuity Pathway Analysis software. Eighty-three out of the 97 proteins identified were listed in this software and therefore available for data mining of the existing published literature to determine potential functional clustering. This analysis revealed that many of the proteins with modified expression profiles in muscle from Smn<sup>/−;SMN2</sup> mice are reported to regulate muscle function and pathology (Table 3). For example, the functional cluster most significantly changed in SMA muscle contained proteins known to contribute to skeletal and muscular disorders: 44 of the proteins changed in Smn<sup>/−;SMN2</sup> muscle (53% of the total list) have links to these disorders, 6 of which also directly contribute to myopathies (Table 3). Similarly, modifications were

SMA animal models (15,16). However, these studies could not rule out an additional contribution resulting from restoration of SMN levels in muscle, raising the possibility that intrinsic responses to low levels of SMN in skeletal muscle may also contribute directly to SMA pathogenesis (15,17–24). Moreover, SMN protein is present in muscle sarcomeres from both mice and Drosophila, alongside other associated SMN complex proteins such as gemins (22,25). Establishing whether skeletal muscle directly contributes to SMA pathogenesis therefore remains a critical question for understanding SMA pathogenesis as well as for the successful targeting of future therapeutic strategies. Previous attempts to address this question have been hampered, at least in part, by the fact that it has proved difficult to distinguish secondary pathological changes, induced as a consequence of denervation due to functional and structural deficits in lower motor neurons, from changes intrinsic to muscle. Moreover, studies of isolated muscle fibres from human SMA patients in vitro (20,24,26) are similarly defined by the fact that they are, as a direct result of the experimental protocol, devoid of lower motor neuron innervation and therefore denervated.

Here, we have utilized a skeletal muscle preparation from an established mouse model of severe SMA (Smn<sup>/−;SMN2</sup> <sup>+/−</sup>) (27) where it is possible to examine molecular changes occurring in skeletal muscle in vivo, in the absence of any detectable denervation-inducing changes in corresponding lower motor neurons. We used this preparation to reveal modifications in the molecular composition of skeletal muscle in SMA mice at a pre-symptomatic age, with a molecular profile distinct from that of denervated muscle. Our findings were confirmed in a milder mouse model of SMA and also in muscle biopsies from human SMA patients. Finally, we demonstrate that molecular pathology of skeletal muscle in SMA mice can be ameliorated by treatment with the FDA-approved histone deacetylase inhibitor (HDACi), suberylanilide hydroxamic acid (SAHA).

![Image](https://example.com/image1.png)

![Image](https://example.com/image2.png)
observed in clusters of proteins contributing to cell death pathways and morphological development (Table 3). A different analysis at the systems level also highlighted disruption of two protein interaction networks (identified by known direct or indirect interactions between individual proteins) implicated in development and function of the skeletal and muscular systems (Supplementary Material, Fig. S2).

Evidence for increased cell death in SMA muscle

The finding that 35% of the proteins submitted for functional clustering analysis contribute to cell death pathways (Table 3) was of particular interest given that apoptotic cell death has previously been reported in SMA muscle (10–14). Indeed, several of the protein expression changes identified in the rostral LAL of SMA mice have previously been implicated in activation of apoptotic and non-apoptotic cell death pathways (e.g. Vdac2, voltage-dependent anion-selective channel protein 2) (33,34). We therefore asked whether markers of cell death were increased in the rostral LAL of SMA mice compared with littermate controls (Smn+/+;SMN2) at P1. There was no denervation-induced muscle fibre atrophy in the SMA mice (P > 0.05; unpaired, two-tailed t-test; n > 3 mice per genotype). (D) Representative western blot showing reduced expression levels of SMN protein in the rostral band of the LAL from SMA mice compared with littermate controls. Beta-V-tubulin was used as a loading control. Scale bars = 20 μm.

Changes in the molecular composition of skeletal muscle in SMA mice are distinct from those elicited following acute or chronic denervation

To confirm that the molecular changes observed in SMA muscle were not occurring as a result of acute or chronic denervation subsequent to motor neuron pathology, we compared our proteomic data with similar data from proteomic studies of chronically denervated muscle (>1 week following nerve injury; Fig. 3A). The profile of expression changes observed in the rostral LAL of SMA mice was clearly distinct from those modified following denervation (Fig. 3A) (37–39). As these previous studies were all performed on chronically denervated muscle, we also quantified expression levels of two proteins significantly altered in SMA muscle (Vdac2 and parvalbumin) in acutely denervated muscles. We
lesioned the sciatic nerve in wild-type mice and isolated the denervated flexor digitorum brevis (FDB) and deep lumbrical muscles from the hind-foot 24 h later. As expected, morphological evaluation of neuromuscular junctions confirmed complete denervation in all muscles examined (data not shown). However, levels of both Vdac2 and parvalbumin remained unchanged (Fig. 3B).

**Molecular pathology of muscle is also present in human SMA patients**

We next examined whether molecular changes observed in pre-symptomatic SMA mice were also present in skeletal muscle from human SMA patients. Quantitative fluorescent western blotting was performed on human SMA patient quadriceps femoris muscle biopsy samples, to establish expression levels of Vdac2 and parvalbumin (Fig. 4). Biopsies were obtained from type II/III SMA patients (aged between 3 and 25 years old; see Materials and Methods), with genetic diagnosis of SMA confirmed by a homozygous deletion of the SMN1 gene. Three age-matched control samples, genetically confirmed to have no mutations in the SMN1 gene, were used for comparison. As expected, SMN protein expression levels were significantly decreased in SMA patient samples compared with control samples (Fig. 4A and B). Quantitative western blotting revealed that both Vdac2 and parvalbumin showed similar alterations in expression levels to those previously observed in Smn−/−;SMN2 mice: Vdac2 was significantly upregulated >3-fold in SMA patient muscle (Fig. 4C), and parvalbumin was significantly downregulated >4-fold (Fig. 4D).

**Molecular pathology of skeletal muscle is reversed by treatment with the FDA-approved HDACi, SAHA**

The finding that levels of full-length SMN protein produced by the SMN2 gene can be modulated by small molecules and drugs has raised the possibility of a therapy for SMA. For example, epigenetic modulation using HDACis appears to be successful (40), with the HDACi SAHA (also known as Vorinostat or Zolinza) elevating full-length SMN protein levels in SMA mouse models by treatment with the FDA-approved HDACi, SAHA.

**Table 1. Proteins upregulated >2-fold with peptide count >1 in the rostral band of LAL from SMA mice compared with littermate controls at P1**

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Protein name</th>
<th>Accession number</th>
<th>Fold</th>
<th>Peptides</th>
<th>Score</th>
<th>Anova (P-value)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vdac2</td>
<td>Voltage-dependent anion-selective channel protein 2</td>
<td>IP000122547.1</td>
<td>5.12</td>
<td>2</td>
<td>113.23</td>
<td>4.05E−04</td>
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<tr>
<td>RpL32 60S</td>
<td>Ribosomal protein L32</td>
<td>IP000230623.8</td>
<td>3.33</td>
<td>2</td>
<td>77.74</td>
<td>5.92E−03</td>
</tr>
<tr>
<td>Acta1</td>
<td>Actin, alpha cardiac muscle</td>
<td>IP000654242.1</td>
<td>3.07</td>
<td>6</td>
<td>420.13</td>
<td>1.52E−06</td>
</tr>
<tr>
<td>Acta2</td>
<td>Actin, alpha skeletal muscle</td>
<td>IP000110827.1</td>
<td>3.01</td>
<td>6</td>
<td>447.06</td>
<td>1.61E−06</td>
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<tr>
<td>Atp5c1</td>
<td>ATP synthase subunit gamma</td>
<td>IP000313475.1</td>
<td>2.95</td>
<td>2</td>
<td>116.18</td>
<td>1.59E−04</td>
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<tr>
<td>−11 kDa protein</td>
<td>N/A</td>
<td>IP000329998.3</td>
<td>2.58</td>
<td>2</td>
<td>117.08</td>
<td>4.67E−06</td>
</tr>
<tr>
<td>Alb</td>
<td>Serum albumin</td>
<td>IP000131695.3</td>
<td>2.51</td>
<td>13</td>
<td>615.81</td>
<td>1.07E−05</td>
</tr>
<tr>
<td>MylLf</td>
<td>Myosin regulatory light chain 2, skeletal muscle isoform</td>
<td>IP000224549.3</td>
<td>2.5</td>
<td>6</td>
<td>372.77</td>
<td>5.08E−04</td>
</tr>
<tr>
<td>RpL8 60S</td>
<td>Ribosomal protein L8</td>
<td>IP000137779.3</td>
<td>2.48</td>
<td>2</td>
<td>92.06</td>
<td>9.31E−05</td>
</tr>
<tr>
<td>Pgk1</td>
<td>Phosphoglycerate kinase 1</td>
<td>IP000555006.3</td>
<td>2.36</td>
<td>5</td>
<td>326.18</td>
<td>9.71E−08</td>
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<tr>
<td>Atp5b</td>
<td>ATP synthase subunit beta</td>
<td>IP000468412.1</td>
<td>2.35</td>
<td>3</td>
<td>271.15</td>
<td>3.17E−05</td>
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<tr>
<td>Dcn</td>
<td>Decorin</td>
<td>IP000123196.1</td>
<td>2.33</td>
<td>2</td>
<td>50.99</td>
<td>1.41E−04</td>
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<tr>
<td>Apoa1</td>
<td>Apolipoprotein A-I</td>
<td>IP000121209.1</td>
<td>2.24</td>
<td>2</td>
<td>93.53</td>
<td>2.01E−04</td>
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<tr>
<td>Lgals1</td>
<td>Galectin-1</td>
<td>IP000229517.5</td>
<td>2.23</td>
<td>3</td>
<td>174.29</td>
<td>5.17E−04</td>
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<tr>
<td>Mdh2</td>
<td>Malate dehydrogenase, mitochondrial</td>
<td>IP000323592.2</td>
<td>2.21</td>
<td>3</td>
<td>143.52</td>
<td>6.59E−06</td>
</tr>
<tr>
<td>Cs</td>
<td>Citrate synthase</td>
<td>IP000113141.1</td>
<td>2.17</td>
<td>2</td>
<td>85.12</td>
<td>3.66E−05</td>
</tr>
<tr>
<td>Atp5o</td>
<td>ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit</td>
<td>IP000118986.1</td>
<td>2.08</td>
<td>2</td>
<td>85.41</td>
<td>5.84E−04</td>
</tr>
<tr>
<td>Acsl2</td>
<td>Acyl-CoA oxidase</td>
<td>IP000116074.1</td>
<td>2.05</td>
<td>5</td>
<td>219.6</td>
<td>9.84E−06</td>
</tr>
<tr>
<td>Trf</td>
<td>Serotransferrin</td>
<td>IP000139788.2</td>
<td>2.02</td>
<td>11</td>
<td>645.3</td>
<td>9.07E−05</td>
</tr>
<tr>
<td>Afp</td>
<td>Alpha-fetoprotein</td>
<td>IP000113163.1</td>
<td>2</td>
<td>5</td>
<td>288.77</td>
<td>1.20E−04</td>
</tr>
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</table>

**Table 2. Proteins downregulated >2-fold with peptide count >1 in the rostral band of LAL from SMA mice compared with littermate controls at P1**

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Protein name</th>
<th>Accession number</th>
<th>Fold</th>
<th>Peptides</th>
<th>Score</th>
<th>Anova (P-value)</th>
</tr>
</thead>
<tbody>
<tr>
<td>P4hb</td>
<td>Prolyl 4-hydroxylation, beta polypeptide</td>
<td>IP000122815.3</td>
<td>2.66</td>
<td>3</td>
<td>111.53</td>
<td>6.29E−05</td>
</tr>
<tr>
<td>Pvalb</td>
<td>Parvalbumin alpha</td>
<td>IP000230766.4</td>
<td>2.65</td>
<td>2</td>
<td>90.44</td>
<td>3.72E−05</td>
</tr>
<tr>
<td>Rcn3</td>
<td>Reticulocalbin-3</td>
<td>IP000221798.1</td>
<td>2.28</td>
<td>2</td>
<td>173.67</td>
<td>1.35E−05</td>
</tr>
<tr>
<td>Rps7 40S</td>
<td>Ribosomal protein S7</td>
<td>IP000136984.1</td>
<td>2.15</td>
<td>2</td>
<td>63.7</td>
<td>4.38E−04</td>
</tr>
<tr>
<td>Anxa5</td>
<td>Annexin A5</td>
<td>IP000317309.5</td>
<td>2.05</td>
<td>2</td>
<td>98.22</td>
<td>8.74E−03</td>
</tr>
<tr>
<td>Hist1h1d</td>
<td>Histone H1.3</td>
<td>IP00031597.6</td>
<td>2.03</td>
<td>4</td>
<td>168.92</td>
<td>0.03</td>
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</table>
Table 3. Systems level analysis of functional pathway changes in the rostral band of LAL muscle in SMA mice at P1

<table>
<thead>
<tr>
<th>Function annotation</th>
<th>Number of proteins</th>
<th>Percentage of candidate list</th>
<th>P-value</th>
<th>Proteins</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Skeletal and muscular disorder</strong></td>
<td>44</td>
<td>53.0</td>
<td>2.31E−08</td>
<td>ACTA1, ACTB, ACTN2, ALB, ANXA2, ANXA5, APOA1, ATP5C1, BIN1, CA3, CASQ2, Ckap4, CLTC, CRyAB, DES, EE2F, EE1F1G, FH, FLH1, FLNA, GPI, HNRNPAP1, HNRNPAP3, HSP90B1, HSPA8, HSPB1, LGALS1, MDH1, MYH8, MYL1, MYOM1, MYOM2, NONO, PDAIA, PKFM, PGK1, PKM2, PPiA, PVAlB, RPL3, RPL32, TNCC2, TPM2, VIM</td>
</tr>
<tr>
<td><strong>tumorigenesis</strong></td>
<td>41</td>
<td>49.4</td>
<td>5.12E−06</td>
<td>ACTB, ACTC1, Afp, ALB, ANXA2, ANXA5, APOA1, ATP5C1, CA3, CKM, CRyAB, CSRPI, Dcn, EF4A1, FH, FLNA, FSCN1, GPI, Hbb, HBD, HNRNPAP1, HNRNPAP3, HSP90B1, HSPA8, HSPB1, LGALS1, MDH1, MYH8, MYL1, MYOM1, MYOM2, NONO, PDAIA, PKFM, PK, PKM2, PPiA, PVAlB, RPL3, RPL32, TNCC2, TPM2, VIM</td>
</tr>
<tr>
<td><strong>Cell death</strong></td>
<td>29</td>
<td>34.9</td>
<td>9.60E−04</td>
<td>ACTB, ACTC1, AFP, ALB, APOA1, BIN1, CCT7, CCTL, CRyAB, DCN, FLNA, GPI, HIST1H1C, HNRNPAP1, HSPA8, HSPB1, LGALS1, MDH1, NME2, P4HB, PDIA3, PKM2, PPiA, PpID, TF, TPM1, VCL, VDAC2, VIM</td>
</tr>
<tr>
<td><strong>Inflammatory disorder</strong></td>
<td>29</td>
<td>34.9</td>
<td>2.32E−02</td>
<td>ACTB, ACTA1, ALB, ANXA5, APOA1, CA3, CLTC, CRyAB, EE2F, EE1F1G, GPI, Hbb, HNRNPAP1, HNRNPAP3, HSP90B1, HSPA8, LGALS1, NONO, P4HB, PDIA3, PGK1, PpID, RPL32, TF, TPM2, VDAC2, VIM</td>
</tr>
<tr>
<td><strong>Growth of cells</strong></td>
<td>24</td>
<td>28.9</td>
<td>1.18E−04</td>
<td>ACTB, AKR1IB1, ALB, ANXA2, ATP5B, BIN1, CA3, CCT7, CRYAB, Dcn, Ds, Efi4A1, HNRNPAP1, LGALS1, NME2, PA2G4, PDIA3, PKG1, PKM2, SERPINH1, TF, TPM1, TPM2</td>
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<tr>
<td><strong>Cardiovascular disorder</strong></td>
<td>24</td>
<td>28.9</td>
<td>2.01E−02</td>
<td>ACTA1, ACTC1, ACTN2, ALB, ANXA2, ANXA5, APOA1, BIN1, CA3, CASQ2, Ckap4, CKM, CRyAB, CS, CSRPI, Dcn, FH1L, GPI, MYH8, MYOM1, SERPINH1, TF, TPM1, TPM2</td>
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<tr>
<td><strong>Proliferation of cells</strong></td>
<td>23</td>
<td>27.7</td>
<td>1.10E−02</td>
<td>AFP, AKR1IB1, ANXA2, APOA1, BIN1, CLTC, CRyAB, DCN, FH1L, Fscn1, Gpi, HNRNPAPK, HSP90B1, LGALS1, NME2, PA2G4, PGK1, PPiA, SPTAN1, TPM1, VCL, VIM</td>
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<td><strong>Connective tissue disorder</strong></td>
<td>21</td>
<td>25.3</td>
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</tr>
<tr>
<td><strong>Developmental disorder</strong></td>
<td>15</td>
<td>18.1</td>
<td>9.47E−04</td>
<td>ACTC1, ALB, APOA1, CA3, CASQ2, CRyAB, CSRPI, Ds, FLNA, Hbb, MYOM1, SEC23A, TF, TPM1, VCL</td>
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<tr>
<td><strong>Progressive motor neuropathy</strong></td>
<td>15</td>
<td>18.1</td>
<td>8.09E−03</td>
<td>ACTB, ANXA2, ANXA5, CA3, CRyAB, FH, HSPB1, MDH1, MYOM1, PDIA3, PDLIM5, PGK1, PVAlB, RPL3, VIM</td>
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<td><strong>Contraction of muscle</strong></td>
<td>14</td>
<td>16.9</td>
<td>6.26E−12</td>
<td>ACTA1, ACTC1, ACTN2, ANXA6, CASQ2, CRyAB, Ds, FLH1, GPI, MYOM1, MYOM2, MYOM3, TPM2, TPM1, TPM2</td>
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<td><strong>Cell movement</strong></td>
<td>13</td>
<td>15.7</td>
<td>5.28E−03</td>
<td>ACTB, ANXA2, APOA1, FLNA, FSCN1, GPI, HSPB1, LGALS1, PA2G4, PKM2, TPM1, VCL, VIM</td>
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<td><strong>Formation of filaments</strong></td>
<td>10</td>
<td>12.0</td>
<td>1.07E−05</td>
<td>ACTA1, ACTC1, DES, FH1L, GPI, MYOM1, SERPINH1, TPM1, TPM2, VIM</td>
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<tr>
<td><strong>Metabolic process of carbohydrate</strong></td>
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<td>AKR1IB1, APOA1, CRyAB, CS, GPI, PKFM, PKG1, PKM2, PYGM</td>
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<td>12.0</td>
<td>2.73E−02</td>
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<td><strong>Developmental process of muscle</strong></td>
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<td>10.8</td>
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<td>Dcn, GPI, LGALS1, PA2G4, PKG1, TF</td>
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<td>ACTB, DES, FLNA, FSCN1, TPM1</td>
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<td>APOA1, LGALS1, PDIA3, PPiA, SPTAN1</td>
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this model is better for testing potential therapeutic agents than the more severe Smn<sup>−/−</sup>;SM2 model (41). We first confirmed that molecular pathological changes similar to those observed in Smn<sup>−/−</sup>;SM2 mice were also present in untreated late-symptomatic (P10) Taiwanese-SMA mice. As expected, SMN protein levels in the gastrocnemius muscle were reduced to ~25% of those in littermate controls (Fig. 5A and B). Vdac2 levels were increased (Fig. 5C) and parvalbumin levels were decreased (Fig. 5D) in Taiwanese-SMA mice, and increased cell death was confirmed by an increase in levels of H2AX (Fig. 5E). Importantly, it has previously been demonstrated that neuronal pathology is present in the gastrocnemius muscle of Taiwanese-SMA mice at P10 (including denervation of muscle fibres) (41). Thus, the molecular changes initially observed in the LAL muscle of severe SMA mice at P1 in the absence of neuronal pathology were also present in anatomically distinct muscles susceptible to denervation in SMA.
Taiwanese-SMA mice and littermate controls were treated with SAHA from birth via oral administration of 25 mg/kg SAHA (dissolved in DMSO) twice daily (41). For control experiments, mice were dosed with DMSO alone. As previously reported (41), SAHA treatment significantly increased SMN protein expression levels in the gastrocnemius muscle (Fig. 5). Importantly, however, SAHA treatment significantly ameliorated SMN-induced changes in levels of Vdac2, parvalbumin and H2AX (Fig. 5).

DISCUSSION

In this study, we have identified and characterized molecular pathology of skeletal muscle in an established mouse model of severe SMA. These changes were present during the earliest stages of disease and occurred in the absence of any detectable degeneration of lower motor neurons. The molecular profile of muscle pathology in SMA was distinct from that of denervated muscle, with functional cluster analysis of proteomic data and H2AX labelling highlighting increased activity of cell death pathways. We confirmed the robust upregulation of Vdac2 and downregulation of parvalbumin in mouse FDB muscles before (control) or 24 h after (denervated) tibial nerve lesion. Neither protein showed a significant change in expression in denervated muscle (P > 0.05; unpaired, two-tailed t-test; n = 3 mice per genotype).

Figure 2. Increased levels of cell death in the rostral LAL from SMA mice. (A) Representative fluorescence micrographs of rostral LAL muscle preparations from an Smn<sup>−/−</sup>;SMN2 mouse (bottom panels) and a littermate control (top panels) immunohistochemically labelled for the cell death marker H2AX (green). Nuclei were labelled with TOPRO-3 (red). Almost all muscle nuclei in muscles from littermate control mice showed no, or weak, labelling (A), whereas strong H2AX labelling was easily identified in SMA muscles. Images were taken with identical settings on the confocal microscope (e.g. laser intensity, gain, zoom, z-stack depth, etc). (B) Bar chart (mean ± SEM) showing a significant increase in the numbers of cells with intense H2AX labelling in the rostral LAL of Smn<sup>−/−</sup>;SMN2 mice (SMA) compared with littermate controls (Control) (*P < 0.05, unpaired two-tailed t-test, n = 3 muscles). Scale bar = 10 μm.

Figure 3. Molecular pathology of SMA skeletal muscle is molecularly distinct from changes elicited following chronic or acute denervation. (A) Comparison of expression profiles of individual proteins identified in SMA muscle, with expression changes observed in chronically denervated rodent muscle. Note that the molecular profile of SMA muscle was distinct from that in denervated muscle. NC, no change; NR, not reported; UP, increased expression; DOWN, decreased expression. (B) Bar chart (mean ± SEM) showing expression levels of Vdac2 and parvalbumin in mouse FDB muscles before (control) or 24 h after (denervated) tibial nerve lesion. Neither protein showed a significant change in expression in denervated muscle (P > 0.05; unpaired, two-tailed t-test; n > 3 mice per genotype).
studies of SMN protein expression and localization have identified the SMN complex in muscle from both mice and Drosophila, as well as in C2C12 cells in vitro (21,22,25). Moreover, in vitro studies have shown that muscle cells derived from SMA patients can inhibit neuronal outgrowth and development when co-cultured with wild-type healthy motor neurons (12,17,42) and a recent study of myotubes from human SMA fetuses also revealed a delay in growth and maturation in vitro (24). Moreover, fibroblast growth factor signalling in muscle can ameliorate SMN-associated abnormalities at the neuromuscular junction in Drosophila (43), and increased levels of insulin-like growth factor in muscle modulate SMA phenotype in mice (44). Taken together, these findings suggest SMN levels are critical for the establishment and maintenance of molecular homeostasis in skeletal muscle. Thus, direct disruption of muscle resulting from low levels of SMN is likely to be a significant contributor to SMA pathogenesis, alongside pathological changes in motor neurons.

Interestingly, many of the proteins shown to have altered expression profiles in skeletal muscle during SMA have previously been implicated in other neuromuscular diseases where intrinsic muscle pathology occurs. For example, decorin is associated with modified proliferation and differentiation of myogenic cells in X-linked muscular dystrophy (45), and reticulocalbin 1 expression is altered in dystrophic muscles (46). Galectin 1 has been implicated in myoblast differentiation, skeletal muscle development and muscle regeneration (47,48). Similarly, proteins such as serpin H1 (a.k.a. HSP47) and vinculin (through its interaction with dysferlin) have been implicated in muscle fibre repair and maintenance of the muscle membrane, respectively (49,50). Thus, the proteins we identified as having altered expression profiles in SMA muscle are consistent with those that might be expected to regulate intrinsic muscular pathology based on findings from other neuromuscular disorders.

Two proteins of particular interest in the context of this study are Vdac2 and parvalbumin. Both showed modified expression levels in skeletal muscle across two different mouse models of SMA as well as in human patients, and both responded significantly to SAHA treatment. This raises the possibility of their use as novel biomarkers to report directly on the pathological status of the neuromuscular system in human patients. Such biomarkers are urgently required for clinical trials in SMA patient cohorts, where appropriate molecular biomarkers are currently lacking. The observation

![Figure 4. Molecular modifications are also present in skeletal muscle from human SMA patients. (A) Representative fluorescent western blots on quadriceps femoris biopsy samples from SMA patients (type II or type III; aged between 3 and 25 years old) and non-SMA controls showing levels of SMN protein, beta-V-tubulin (loading control), Vdac2 and parvalbumin. (B–D) Bar charts showing expression levels of SMN, Vdac2 and parvalbumin in human SMA patient muscle compared with controls. Data are shown for individual patients (black and white bars to the left of the hashed line) as well as mean ± SEM for each genotype (right of the line). SMN levels were significantly decreased in SMA patients (*P < 0.05; unpaired, two-tailed t-test; B), Vdac2 levels were significantly increased (*P < 0.05; unpaired, two-tailed t-test; C) and parvalbumin levels were significantly decreased (*P < 0.05; B).](https://academic.oup.com/hmg/article-abstract/20/22/4334/637574/4340)
that the expression profiles of these two proteins are changed in opposing directions in SMA further strengthens their potential utility as biomarkers, providing an internal control against any global up- or downregulation of protein expression in individual patients. Vdac2 is a mitochondrial protein associated with formation of channels in the mitochondrial outer membrane, responsible for regulating cell death pathways and calcium signalling (51–53). It is also a core component of the muscle response to ageing (54) and has been implicated in early pathogenic events occurring in the mdx mouse model of muscular dystrophy (55). Parvalbumin is a cytosolic calcium buffer in muscle, breakdown of which similarly contributes to muscular dystrophy (56,57).

Finally, our finding that the altered molecular composition of skeletal muscle in SMA is reversible using the HDACi SAHA highlights the potential to treat SMN-induced muscle changes using small molecules and drugs. SAHA has been shown to penetrate into a range of tissues following administration—including the nervous system and muscle (41,58,59)—and is approved for use in humans by the FDA in the USA. SAHA is a second generation HDACi, so it is likely that future generations will have even higher specificity and potency, increasing their attractiveness for use in SMA patients. Our findings suggest that attempts to develop better HDACi that specifically target SMN levels in skeletal muscle would likely lead to effective therapeutic options for SMA. Testing other currently available HDACi for the potential to rescue muscle pathology in vivo will also be an important next step. The current data do not allow us to ascertain whether raised SMN levels in muscle induced by SAHA also have a secondary impact on pathological changes occurring in other cell types (e.g. motor neurons), due to systemic delivery of the HDACi (41). Thus, the potential for a causal relationship between the rescue of pathological changes occurring in muscle in SAHA-treated SMA mice and the reduction in pathology of motor neurons previously reported (41) remains untested and warrants further investigation. Nevertheless, the current study shows that intrinsic pathological changes in muscle are a significant feature of SMA, regardless of their possible secondary impact on other cell types.

MATERIALS AND METHODS

Mice

Smm<sup>−/−</sup>;SMN2 mice (Jackson Labs strain no. 005024) were maintained as heterozygote breeding pairs under standard SPF conditions in animal care facilities in Edinburgh. Litters produced from SMA colonies were retrospectively genotyped using standard PCR protocols (JAX<sup>®</sup> Mice Resources), as previously described (29). Taiwanese-SMA mice were bred and maintained in micro-isolation chambers in Cologne as previously reported (41). For SAHA experiments, litters of Taiwanese-SMA mice (containing SMA mice and littermate controls) were dosed twice daily from birth with either 25 mg/kg SAHA dissolved in DMSO, or an equivalent
volume of DMSO alone, via oral application with a feeding needle. All animal procedures and breeding were performed in accordance with Home Office guidelines in the UK and according to guidelines established by the Landesamt fur Natur, Umwelt und Verbraucherschutz NRW in Germany.

**Human muscle samples**

Quadriiceps femoris biopsy samples were obtained from Fondazione IRCCS Istituto Neurologico ‘C. Besta’ in Milan, Italy, and Fondazione Ospedale Maggiore Poloclinico Mangiagalli en Regina Elena, IRCCS in Milan, Italy, through EuroBioBank (http://www.eurobiobank.org/).

**Acute nerve degeneration**

Young adult wild-type (C57Bl/6J) mice (n = 4) were anaesthetized by inhalation of isofluorane (2%, 1:1 N2O/O2) before exposing the sciatic nerve in the thigh and removing 1 mm section of the nerve to ensure complete transection. Post-operative mice were kept in standard animal house conditions for 24 h before sacrifice.

**Muscle preparation**

*Mouse.* Neonatal Smm−/−;SMN2 and wild-type (Smm+/+; SMN2) littersmates were sacrificed by chilling on ice and decapitation. LAL (from the back of the neck) (28) muscles were dissected in oxygenated mammalian physiological saline. For proteomic and quantitative western blotting experiments, LAL muscles were separated into rostral and caudal bands and quickly frozen on dry ice. The muscles were stored in −80°C freezers until enough tissue was collected for analysis. C56Bl6/J mice subjected to sciatic nerve lesion were sacrificed and the FDB and deep lumbrical muscles were isolated. Muscles were either processed for immunohistochemistry or rapidly frozen on dry ice for subsequent western blotting. Neonatal Taiwanese-SMA mice and littermate controls were sacrificed and the gastrocnemius muscles were isolated. Muscles from each biobank were processed for immunohistochemistry or rapidly frozen on dry ice for subsequent western blotting. Quadriceps femoris biopsy samples were obtained from two different biobanks. Proteins from muscle biopsies were extracted in RIPA buffer with 10% protease inhibitor cocktail (Sigma) for quantitative western blotting. Neonatal Taiwanese-SMA mice and littermate controls were sacrificed and the gastrocnemius muscles were isolated. Muscles were either processed for immunohistochemistry or rapidly frozen on dry ice for subsequent western blotting. Quadriceps femoris biopsy samples were obtained from two different biobanks. Proteins from muscle biopsies were extracted in RIPA buffer with 10% protease inhibitor cocktail (Sigma) for quantitative western blotting.

**Label-free proteomics**

Protein was extracted in MEBC buffer [50 mM TRIS, 100 mM NaCl, 5 mM NaEDTA, 5 mM NaEGTA, 40 mM β-glycerophosphate, 100 mM sodium fluoride, 100 mM sodium orthovanadate, 0.25% NP-40, 1 Roche ‘complete’ protease inhibitor tablet, pH 7.4]. Protein concentration was determined by BCA assay according to manufacturers’ instructions on solubilized muscle (WT-Rostral and KO-Rostral). Then 10 μg of aliquots of each muscle type were reduced with 10 mM DTT and alkylated with 50 mM iodoacetamide prior to digestion with trypsin (Roche, sequencing grade) overnight at 30°C. Technical replicates (3 × 2.5 μg) of each digested muscle type were injected onto an nLC-MS/MS system [Ultimate 3000 (Dionex) coupled to an LTQ Orbitrap XL (Thermo Scientific)]. The peptides from each digest were separated over a 65 min linear gradient from 5–35% acetonitrile in 0.1% formic acid. The LTQ Orbitrap XL was configured with a TOP 5 methodology comprising a 60K resolution FT-MS full scan followed by IT-MS/MS scans for the five most intense peptide ions. The raw data were then imported into Progenesis LCMS for label-free differential analysis and subsequent identification and quantitation of relative ion abundance ratios, both upregulated and downregulated. Individual peptide sequences generated by the proteomic analysis were submitted to MASCOT for protein identification. A stringent selection criteria was used before a protein was included; identification of at least two peptides was needed, and a minimum cut-off of 20% change against the littermate controls was used (P < 0.05) (60,61).

**Quantitative fluorescent western blotting**

Protein was extracted from both human and mouse muscle samples. Quantitative western blots were performed as described previously (60,62), using primary antibodies against SMN (BD Transduction Laboratories or Santa Cruz), VDAC-2 (Abcam), parvalbumin (Abcam), phospho-histone H2AX (Upstate) and beta-V-tubulin (Abcam). Odyssey secondary antibodies were added according to manufacturers’ instructions (goat anti-rabbit IRDye 680 or 800 and goat anti-mouse IRDye 680 or 800 depending on required combinations). Blots were imaged using an Odyssey Infrared Imaging System (Li-COR, Biosciences) at a resolution of 169 μm. Where possible, each sample was independently run and measured multiple times to minimize user variability.

**In silico protein network and functional pathway analysis**

To obtain further insights into functional pathways modified as a result of low-SMN levels in muscle, the Ingenuity Pathways Analysis (IPA) application (Ingenuity Systems) was used to analyse our proteomic data. IPA dynamically generates network of gene, protein, small molecule, drug and disease associations on the basis of ‘hand-curated’ data held in a proprietary database. Of the submitted protein candidate list (97 proteins in total), 83 proteins were recognized by the software and therefore eligible for pathway analysis.

**NMJ immunohistochemistry and muscle fibre diameter measurements**

LALs from Smm−/−;SMN2 and littermate controls (P1 or P5) or FDB and deep lumbrical muscles from C56Bl6/J mice were fixed in 0.1 m PBS containing 4% paraformaldehyde (Electron Microscopy Services) for 10 min and then exposed to α-BTX conjugated to tetramethyl-rhodamin isothiocyanate (TRITC-α-BTX; 5 mg/ml, Molecular Probes) to label post-synaptic acetylcholine receptors. Muscles were then processed for immunohistochemistry as previously described (29). Primary antibodies against either neurofilament (2H3, Developmental Studies Hybridoma Bank) or phospho-histone H2AX (Upstate) were used. Before mounting in Mowiol, the
dissections were incubated in TOPRO3 (Molecular probes) for 10 min. Fluorescence images were captured using a laser scanning confocal microscope (40× objective; ZEISS LSM 510) with 488, 543 and 633 nm laser lines used for excitation. Confocal Z-series were merged using Zeiss software. Reconstructions of FITC-labelled muscle preparations were produced using Adobe Photoshop software by layering and combining multiple micrographs covering the entire muscle. All images were prepared for publication using Adobe Photoshop. For muscle fibre diameter measurements, individual muscle fibre diameters were imaged using phase contrast optics on an inverted microscope equipped with a chilled CCD camera (20×/0.40 objective; Olympus IX71 microscope; Hamamatsu C4742–96–12G04) and measurements were made using ImageJ.

Statistical analysis
All data were collected into Microsoft Excel spreadsheets and then analysed using GraphPad Prism software. For all statistical analyses, \( P < 0.05 \) was considered to be significant. Individual statistical tests used are detailed in the results section or figure legends.

SUPPLEMENTARY MATERIAL
Supplementary Material is available at HMG online.

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Conflict of Interest statement. None declared.

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