Amyotrophic lateral sclerosis (ALS) progression: searching for predictive microRNAs in SOD1G93A mice
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Abstract
Evaluation of muscle and plasma miRNA expression in SOD1G93A mice in order to identify potential biomarkers for ALS, aiming at new targets for therapeutic approaches.
Key words: ALS, miRNA, biomarker

Introduction
Amyotrophic lateral sclerosis (ALS) is a lethal motoneuron disease that progressively debilitates sick individuals. The diagnostic process relies on a series of examinations to rule out alternative disorders with a similar presentation. There is no cure for ALS and the only approved disease-modifying drug, Riluzole, only modestly slows the evolution to death. Therefore, biomarkers are greatly needed to facilitate ALS diagnosis and prognosis, indicating the potential success of new therapy trials. As a potential candidate as biomarkers, microRNAs (miRNAs), small posttranscriptional modifiers of gene expression, are frequently altered in disease conditions. Besides their important regulatory role in a variety of biological processes, miRNAs can also be upregulated in the plasma due to pathological disorders. In order to find biomarkers for ALS, we have studied miRNA alterations (miR-206, miR-9, miR-424, miR-886-5p) at skeletal muscle and plasma of male and female SOD1-G93A mice.

Results and Discussion
The samples were obtained from SOD1-G93A strain, from presymptomatic (70days), symptomatic (100days) and terminal stage mice (=140days). Blood was extracted through the left ventricle, and plasma was collected. Immediately after the blood extraction, the muscles were dissected out (right and left tibialis anterior) and the samples were stored at -80°C. The total RNA from plasma was extracted using miRVana (Ambion, Life Technologies) according to kit instructions. Trizol was used for muscle RNA extraction. The quantity and quality of each extraction was obtained through NanoPhotometer (Implen), and the integrity was assessed through agarose gel 1%. The cDNA was synthesized using Taqman miRNA Reverse Transcription for cDNA synthesis.

<table>
<thead>
<tr>
<th>Samples</th>
<th>ng/μL</th>
<th>260/280</th>
<th>260/230</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>294</td>
<td>1.83</td>
<td>2.27</td>
</tr>
<tr>
<td>2</td>
<td>288</td>
<td>1.83</td>
<td>2.20</td>
</tr>
<tr>
<td>3</td>
<td>210</td>
<td>1.80</td>
<td>2.25</td>
</tr>
<tr>
<td>7</td>
<td>265</td>
<td>1.79</td>
<td>2.19</td>
</tr>
</tbody>
</table>

Samples were considered valid when values of concentration were above 100ng/μL and ratios between 1.7 and 2.5.

Conclusions
We expect that the quantification of the mentioned miRNAs will be used as a tool for diagnosis and prognosis in patients with ALS.

Acknowledgement
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References