*Talk*

# Genetic study for the potential improvement of spinal muscular atrophy


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## ABSTRACT

Spinal muscular atrophy (SMA) is a neuromuscular disease characterized by degeneration of the alpha motor neurons located in the spinal cord. The loss of these neurons gradually causes a loss of muscle strength (1). From a genetic point of view, SMA is an autosomal recessive disease related to the SMN1 gene mutation (2). Lack of SMN activity is lethal and reduced activity generates the disease with a decreased level in severity depending on the increasing level of expression.

The nematode Caenorhabditis elegans has a homologue of the SMN1 gene in humans. For this reason, it is used as a model in the study of the disease. The aim of our work is based on measuring the expression of target genes and compounds that increase SMN1 expression levels.

To study the disease in the nematode, a strain has been constructed in which the SMN1 gene, under its own promoter, is fused to the fluorescent protein mcherry. This strain will be studied under the two conditions with which we work, gene expression and exposure to compounds. In both cases, we expect to find candidates that increase the expression levels of SMN1 at the transcriptional, translational and post-translational levels.

The identification of compounds will be tested by exposing the nematode to them. The change in the expression of target genes is studied by RNA interfering technique. Smn1-mcherry expression changes and interfering RNA expression changes have been studied by confocal microscopy. However, this microscopy technique is complex to perform mass screening. Thus, a visualization protocol has been designed in a fluorescence stereoscopic loupe in order to perform such screening in a faster and easier way.

Currently, we work with two parameters used as controls. One of them is an empty plasmid and the other a candidate gene observed by RNA interference under the confocal microscope. After setting the parameters in the stereo magnifier, which allow observing expression changes, mass screening of genes and compounds that increase SMN-1 expression will be performed. The results of genes or compounds that increase or present changes in expression will be used in order to improve the treatment of SMA.

## REFERENCES

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