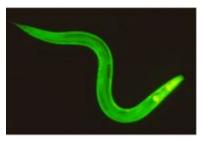
Models of ALS in zebrafish, flies and worms

MVIMG: Neuromuscular Biology and Disease

February 19, 2015

Each model system has its own strengths and weaknesses:



C. elegans

Strengths:

- Short life span (2-3 weeks), 4 day generation time.
- Breed at will
- Large numbers, easy to manipulate
- First multicellular organism to have its genome sequenced
- 302 neurons defined as is the connectome
- Ease of genetic manipulations
- Genetic screens

- Neural anatomy and neural circuitry different than in vertebrates (eg. no cortex, no spinal cord)
- Motoneurons are gaba-ergic (as opposed to cholinergic)
- Limited number of glia and no microglia
- Lack blood brain barrier



Drosophila

Strengths:

- Short life span (1 month), 7 day generation time.
- Breed at will
- Large numbers, easy to manipulate
- Strong genetic tools
- Ease of genetic manipulations
- Genetic screens

- Neural anatomy and neural circuitry different than in vertebrates (eg. no cortex, no spinal cord)
- Motoneurons are glutamatergic (as opposed to cholinergic)
- Limited number of glia and no microglia
- Lack blood brain barrier



zebrafish

Strengths:

- Vertebrate
- Longer lifespan (~2 yrs in the lab setting)
- Breed at will
- Large numbers, easy to manipulate
- Genetics. Genome sequenced, transgenics, knockouts
- Vertebrate genetic and chemical screens
- Vertebrate neuroanatomy
- Have robust glia and microglia
- Have a blood brain barrier
- Behavior

- ~3 month generation time
- No cortex
- Yes a vertebrate, but not a mammal



Strengths:

- Mammal
- Longer lifespan (~2 yrs in lab setting)
- Genetics. Genome sequenced, transgenics, knockouts
- Vertebrate genetic screen and chemical screens
- Vertebrate neuroanatomy and a cortex
- Microglia and a blood brain barrier
- Robust behavior

- 21 day gestation period and an ~2 month generation time
- Low numbers/small litters
- Not great for genetic or large drug screens
- Too inbred? Doesn't represent human population

Questions to ask when deciding on a model system

- Does your model system have the cells that are affected in the disease? *The entire system/circuit may not be present.*
- What are the genetics of the disease? In many cases it is not know whether ALS is caused by a lack of function or gain of function.
- How will you generate the model? If making a transgenic what promoter will be used?
- Is this an adult onset or embryonic/early disease? *Model organisms have shorter lifespans than humans.*
- What is your plan to assess the phenotype? The phenotype may look different in a model than in humans
- If your goal is to do a drug screen, do you have a readout?
- Does your plan play to the strengths of that model organism? *Genetics, imaging, cell biology, drug screens*

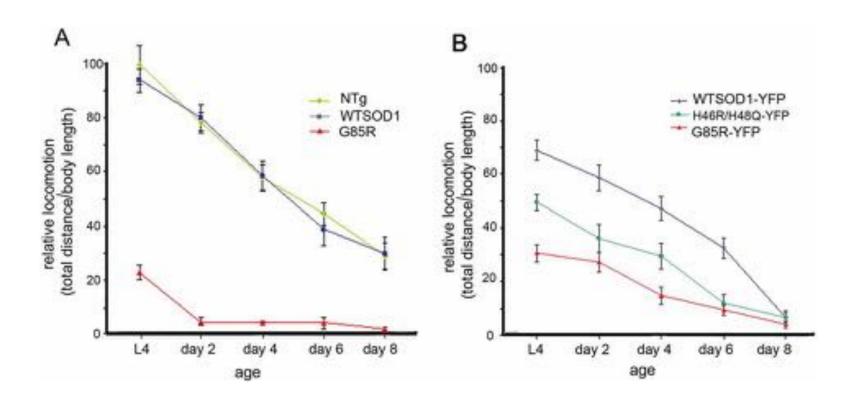
Look at SOD mutant over-expression in these 4 systems.

Look at phenotypes Compare across models What can we learn?

C. Elegans

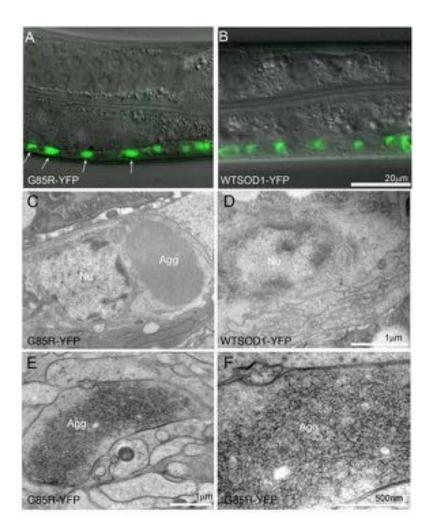
Drove mutant human SOD pan-neuronally (worm synaptobrevin promoter)

See movement defects

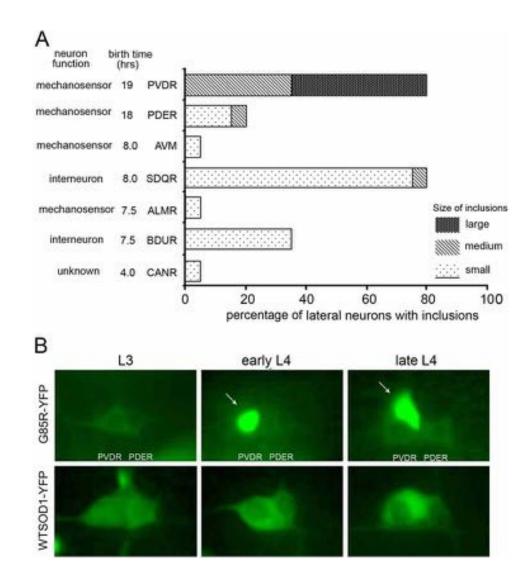


Wang et al (2009) PLoS Genetics: 5, e1000350

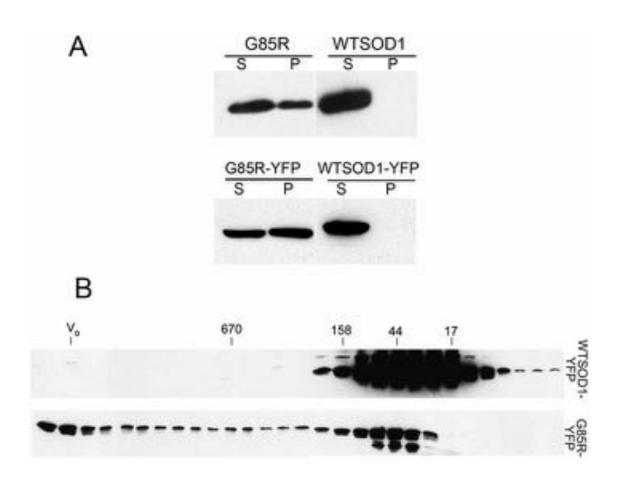
Neuronal aggregates form in transgenics expressing mutant SOD



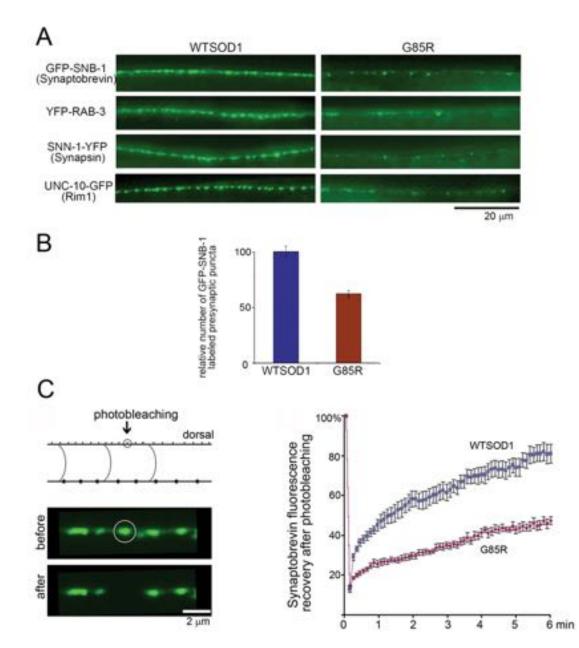
Neuronal birthdate and type do not correlate with aggregates



Biochemical analysis revealed insoluble SOD protein in Tgs

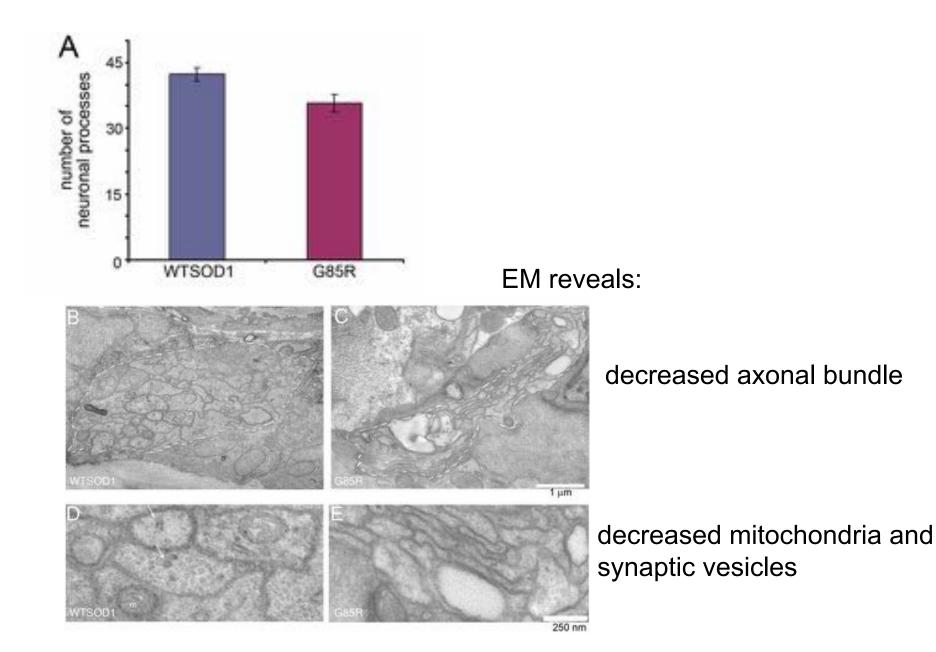


Tg animals have reduced presynaptic puncta and indicate less vesicle content



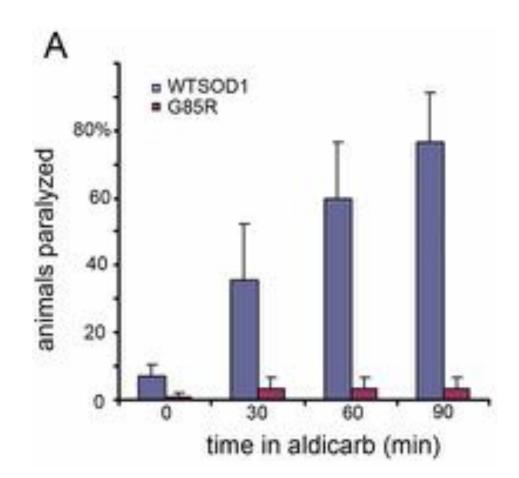
Decreased recovery after photobleaching suggests defects in axonal transport.

The number of neuronal processes is mildly reduced



To assess synaptic function, put embryos in a cholinesterase inhibitor (aldicarb) which paralyzes wt worms.

Had no effect in Tg worms suggesting loss of cholinergic synaptic transmission.



Did an RNAi screen to look for genetic modifiers of aggregation

Just feed the worms bacteria expressing RNAi constructs (!) Look 3-6 days later for changes in the number/intensity of the aggregates

Table 1. Summary of 81 RNA interference hits that worsenedaggregation.

Protein chaperones, turnover, and modification	22	27.2%
Redox	3	3.7%
Signal transduction	7	8.6%
Transcription, RNA processing	6	7.4%
Metabolism	6	7.4%
DNA replication and repair	4	4.9%
Extracellular matrix	2	2.5%
Translation	2	2.5%
Intracellular trafficking	2	2.5%
Uncategorized	27	33.3%

Took candidate genes from RNAi screen and tested them genetically

Table 2. Selected genes whose inactivation strongly aggravates formation of SOD-YFP neuronal inclusions¹.

CATEGORY	GENE	FUNCTION	² RNAI SCORE	³ ALLELE SCORE
Chaperone/quality control	hsf-1 (Y53C10A.12)	Heat shock transcription factor	5	sy441 ++
	C30C11.4	homolog to human apg-1 (a heat shock 110 kDa protein)	3	gk533 ++
	dnj-19 (T05C3.5)	homolog to DnaJ subfamily A member 2	3	gk649 ++
	F08H9.4	neuron-specific HSP16	3	ok1976 ++
	stc-1 (F54C9.2)	member of HSP70 superfamily (microsome associated)	3	
Protein turnover	sel-10 (F55B12.3)	member of the CDC4/CUL-1 family of ubiquitin ligases	3	
	rbx-1 (ZK287.5)	RING box protein RBX1, a subunit of the SCF ubiquitin-ligase complex	2	ok782 +
	W07G4.4	Predicted aminopeptidase	4	
Protein modification	uba-2 (W02A11.4)	sumo activating enzyme	5	
	ubc-9 (F29B9.6)	sumo conjugating enzyme	4	
	gei-17 (W10D5.3)	Homologous to E3 SUMO-protein ligase PIAS1	3	
Redox	bli-3 (F56C11.1)	dual oxidase	3	e767 ++
	pdi-2 (C07A12.4)	Protein disulfide isomerase	2	gk375 ++
	C30H7.2	thioredoxin domain-containing protein precursor	2	
Signal transduction	dbl-1 (T25F10.2)	member of the TGF β superfamily	3	nk3 +
Dopamine metabolism	dat-1 (T23G5.5)	plasma membrane dopamine transporter	3	tm903 +
Dna replication & repair	top-1 (M01E5.5)	DNA topoisomerase I	5	
	div-1 (R01H10.1)	homolog of the B subunit of the DNA polymerase alpha-primase complex	3	or148 ++
Transcription	H43I07.2	RNA polymerase I and III, subunit RPA40/PRC40	3	
Longevity factor	pha-4 (F38A6.1)	FoxA transcription factor	4	

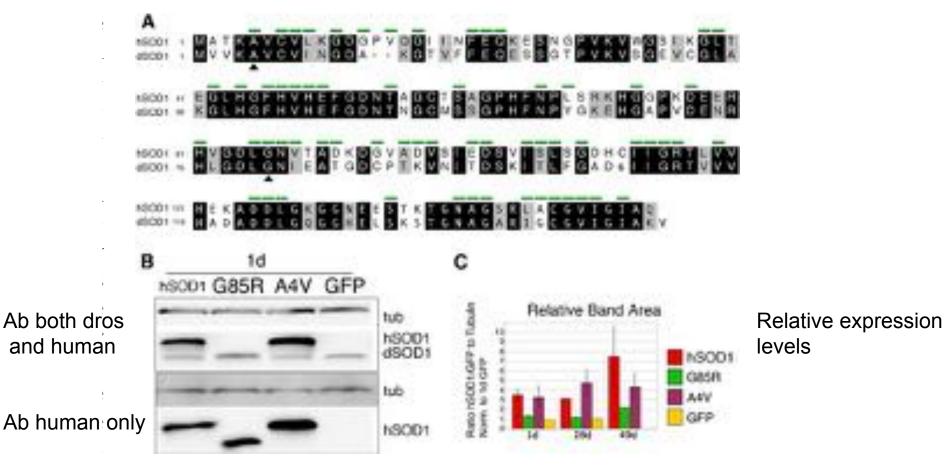
Summary of worm model:

Neuronal aggregates Movement defect Synapse defect (find link to aggregates- ie lines with more aggregates had a stronger presynaptic defect) Ability to do a large scale RNA interference screen (16,757 RNAi clones screened)

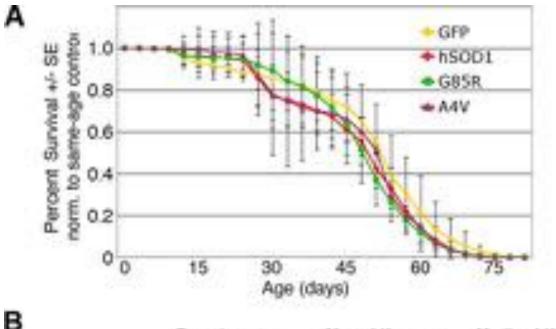
Model only expressed mutant SOD in neurons Did not see any evidence of neuronal cell death

Drosophila:

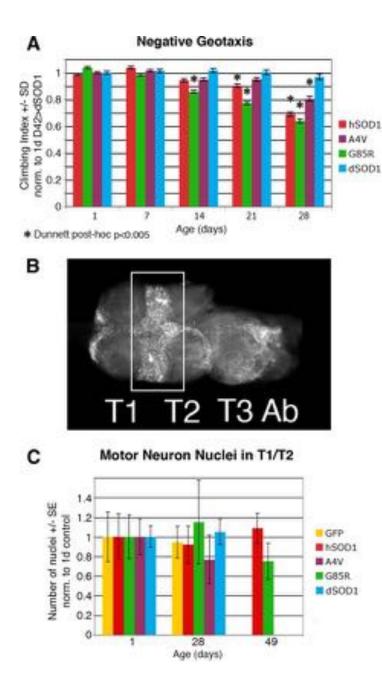
Used Gal4:UAS system to drive human SOD wt and mut in motoneurons (D42-larval-adult) and eye hSOD and dSOD differ in 49/153 residues so also used dSOD



Watson et al., (2008) JBC 283: 24972-24981



Genotype	Experiments (n per Experiment)	Mean Lifespan +/- SE (days)	Median Lifespan 95% CI (daya)
0425GFP	3 (399, 231, 399)	48.3 +/-0.52	51 51-51
D42-wthSCD1	(199, 361, 400)	42.6 +/- 0.49	48 45-48
D42-G85R	(394, 221, 281)	46.9 ±/- 0.47	48 48-48
D42>A4V	(241, 1980	45.1 +/- 0.67	51 48-51



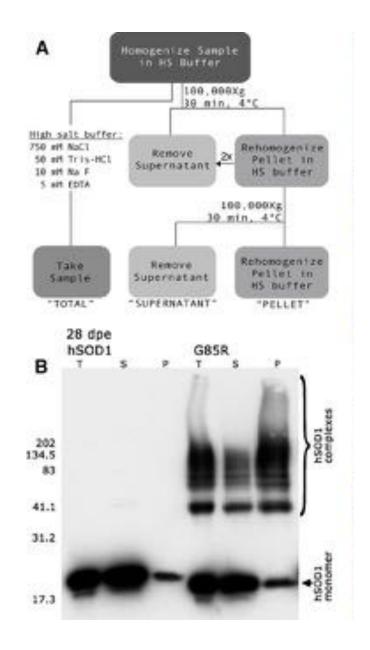
Flies expressing WT or mutant hSOD1 showed progressive loss of climbing when compared with dSOD1 controls, starting at 14 days (G85R) or 21 days (WT)

Counted nuclei in the T1/T2 thoracic ganglia

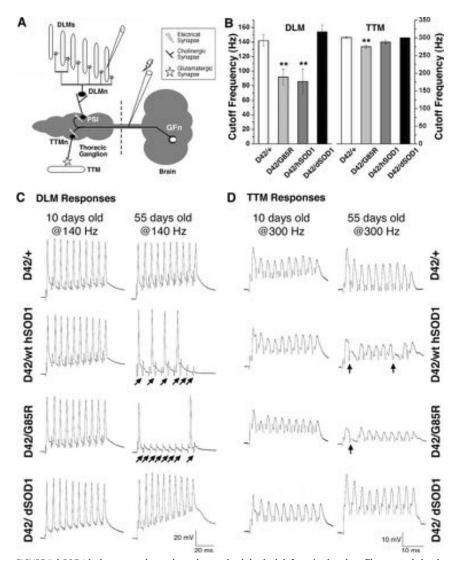
Large scale motor neuron loss did not occur

Climbing loss may reflect motor dysfunction.

Large MW forms of mutant SOD present when driven in the eye



U U SUPI



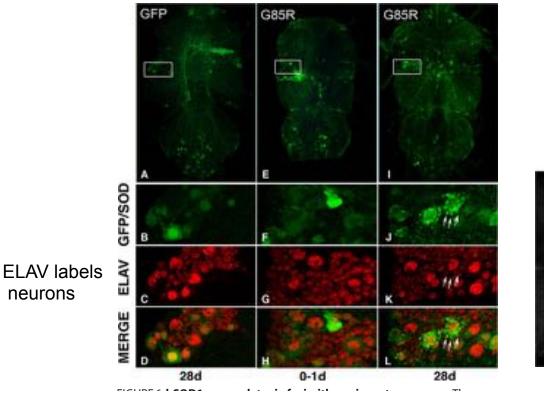
Flies expressing hSOD1 and dSOD1 in motor neurons were assessed for reduced or abnormal signaling at the neuromuscular junctions of the giant fiber system.

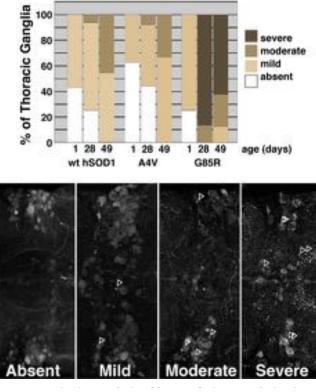
Looked at synaptic physiology of indirect flight muscles.

DLM motoneurons mediate wing depression during the escape response

TTM motoneurons initiate leg extension

Both wt hSOD and mutant SOD show protein accumulations in motoneurons





hSOD1 accumulation in motor neurons

Expression of SOD in motoneurons is associated with a stress response in glia

49d D42>G85R Е Glial chaperone response Α 100 % of Thoracic Ganglia Strong 80 i Moderate 60 H Low Hsp70 Absent 408 в 20 28 49 Age (days) 28 28 1 49 GFP A4V G85R wt hSOD1 hSOD1 C G 49d D42>G85R ELAV Merge Hsp7

HSP70 expressing cells are not neurons

Repo=glial cell marker

Summary of fly model:

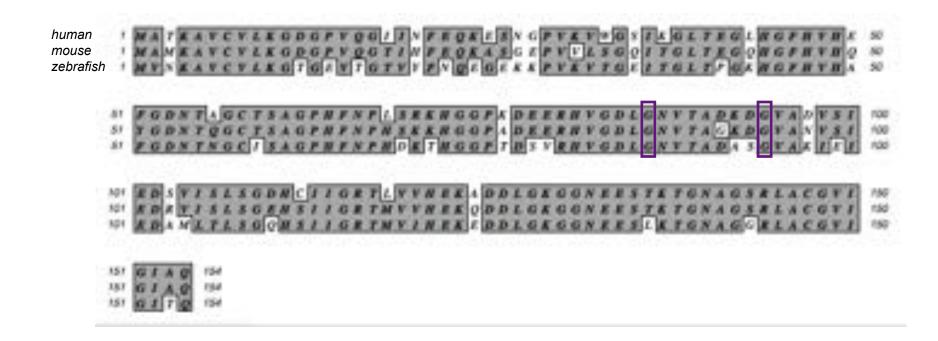
Motor dysfunction Failure of high frequency synaptic transmission Neuronal aggregates Non-cell autonomous stress response in glia

Model only expressed mutant SOD in motoneurons Did not see any evidence of neuronal cell death

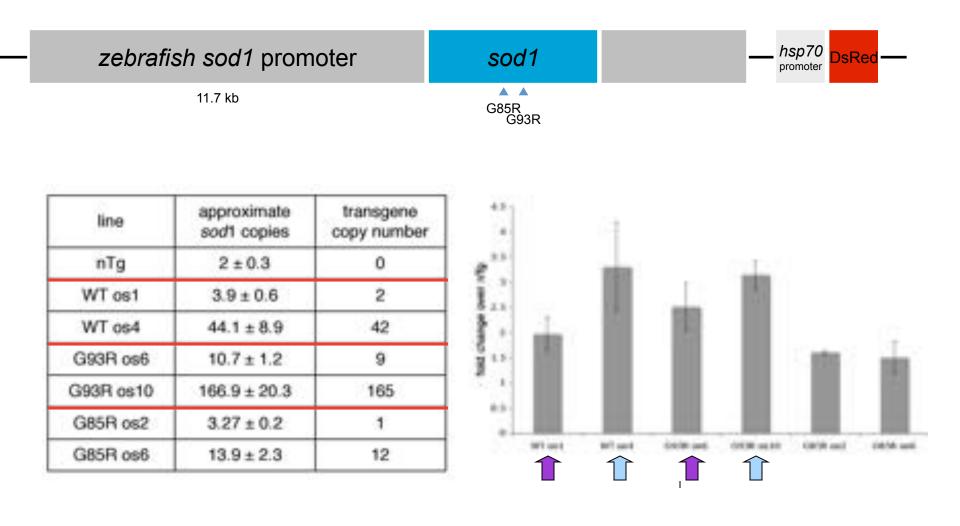
Zebrafish

Conservation of SOD1

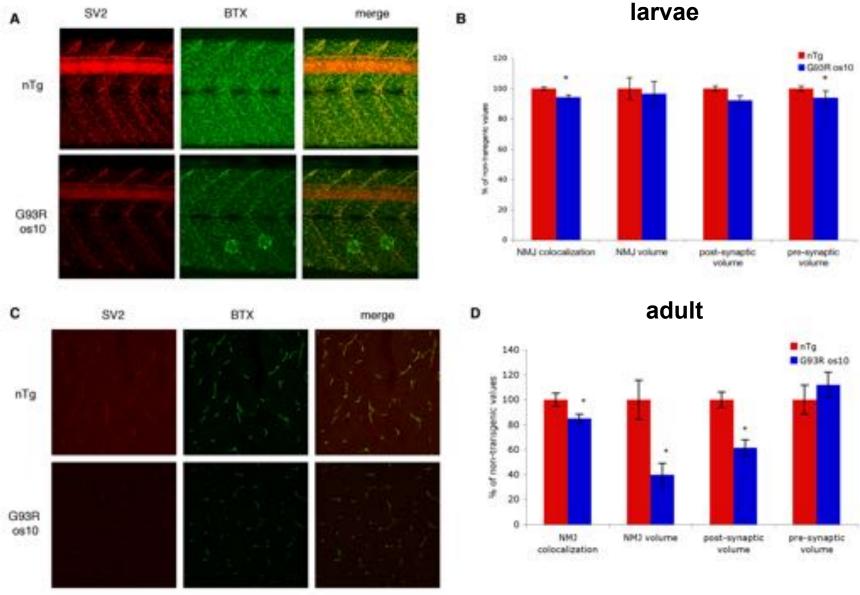
- Human & mouse sod1: 83% identical, 88% similar
- Human & fish sod1: 71% identical, 81% similar



Generation of transgenic mutant sod1 zebrafish

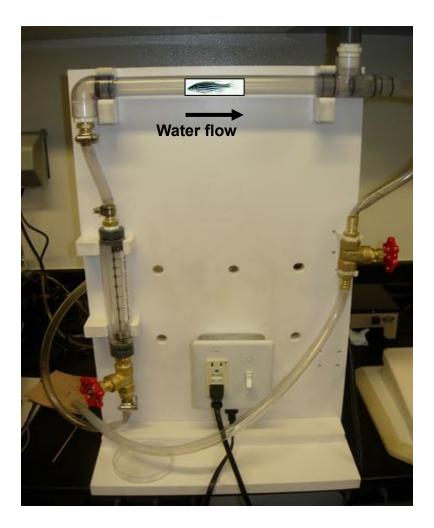


Progressive pre-synaptic defects



Analysis using Image J

Testing swimming strength in zebrafish

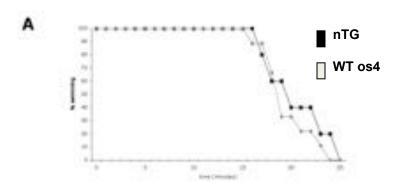


Fish swim against the water current

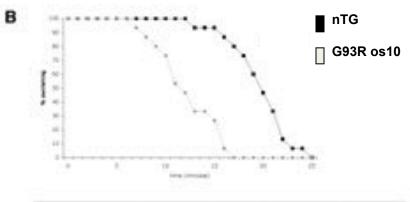
Flow rate is low initially and rate is increased by 3.25 cm/sec every 5 min

Fish drop out at specific flow rates

Critical swimming speed (U^{crit}) is calculated

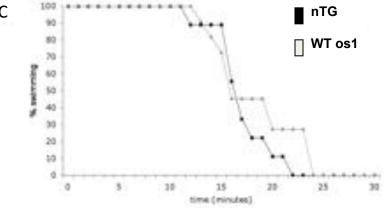


	nTg	WT os 4
10 months	16.2 ± 2.8	15.6 ± 2.1

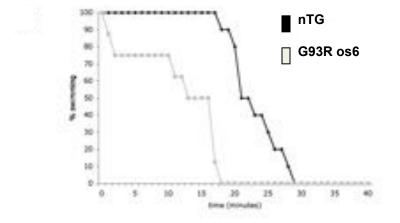


	nTg	G93R os10
12 months	15.7 ± 2.5	9.6±2.6

D

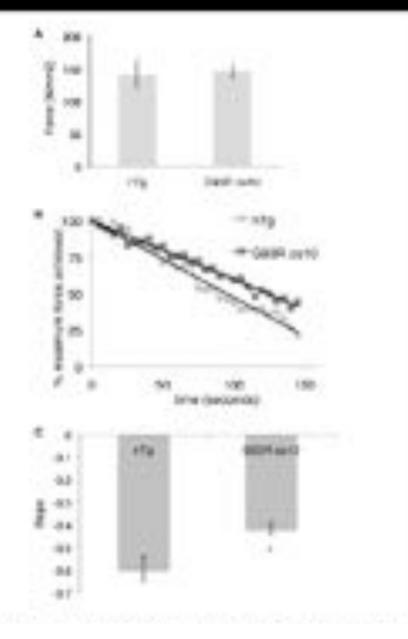


	nTg	WT 061
24 months	13.0 ± 2.1	142 ± 3.1



nTg	G93R 066
16 months 14.7 + 2	2 72+44

Muscle physiology



No difference in maximal twitch force. Indicates that muscle contractile properties are intact.

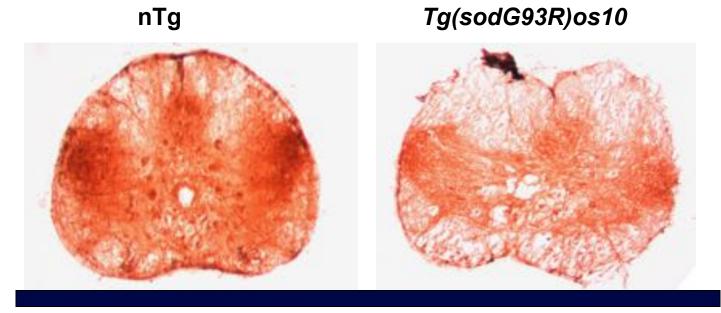
Was a difference in response to fatigue due to repeated stimulations (4 ms at 0.2 htz)

Sod mut had better fatigue resistance (this was also found in SOD mut mice)

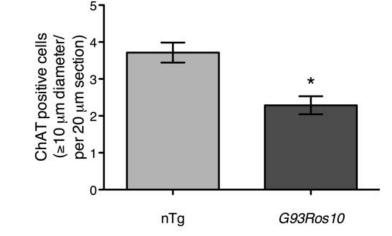
Late/end stage behavior in adult *Tg(sodG93R)os10*



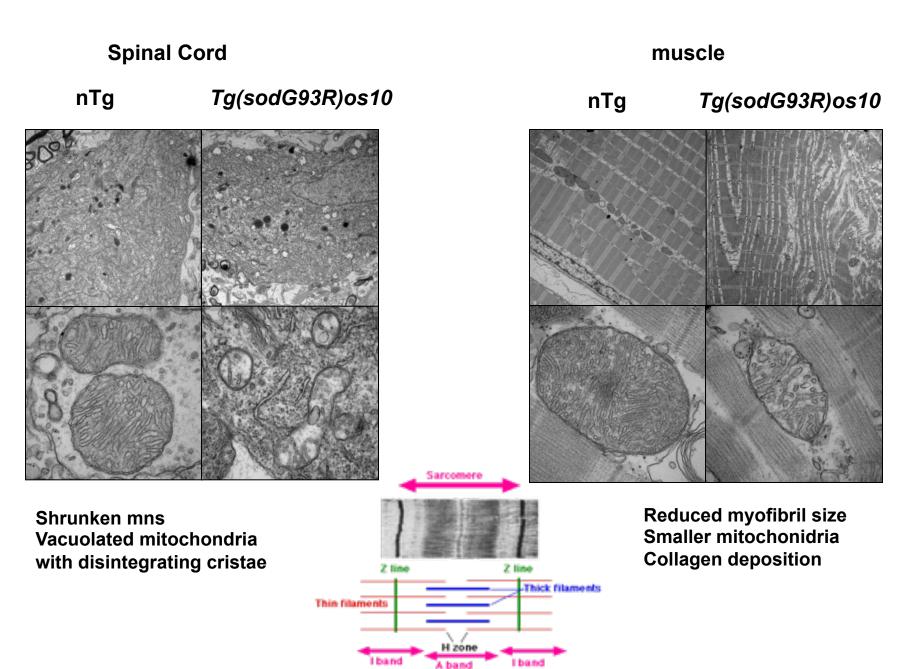
Endstage fish overexpressing mutant Sod1 show motoneuron loss



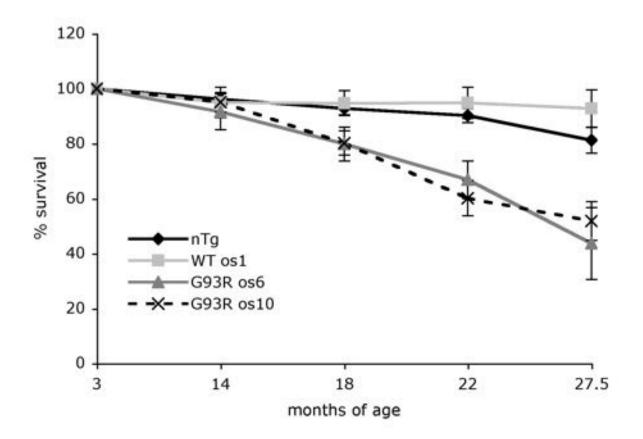
ChAT antibody labeling



EM reveals spinal cord and muscle degeneration in endstage fish



Premature death in fish expressing mutant Sod



Summary of zebrafish model:

Presynaptic defects Movement defect Motoneuron cell loss Premature death

No aggregates found

Mouse model:

Used endogenous promoter Neuronal aggregates Loss of motoneurons Decreased movement followed by paralysis Axon sprouting and reinnervation

A commonly used model has 17-20X protein expression Inbreed lines- will small changes translate to outbreed systems? Sick animals make drug/genetic screens difficult

Discussion points:

What are the common themes? Is this telling us something?

Is it relevant to express mutant protein in only selected cell types?

The strength of non-mammalian models for genetic and drug screens

Is it useful to have non-mammalian models?