Mouse Models of Friedreich's Ataxia

FARA has partnered with the Jackson Laboratories (JAX, https://www.jax.org/) to centralize and expedite sharing of existing FA mouse models and to characterize these models. Most mouse models are now available for purchase from JAX, and other are available by collaborating with the investigators that have developed them and characterized them. Three knock-out models are available from Helene Puccio and one through UCLA (Chandran et al Inducible and reversible phenotypes in a novel mouse model of Friedreich's Ataxia. Elife 2017). FARA is aware of several additional models that are being created and tested, including those described in Fil et al (Mitochondrial damage and senescence phenotype of cells derived from a novel frataxin G127V point mutation mouse model of Friedreich's ataxia. Dis Model Mech. 2020) and Salami et al 2020 (Stress-induced mouse model of the cardiac manifestations of Friedreich's ataxia corrected by AAV-mediated gene therapy. Human Gene Therapy, 2020).

These mouse models have been created by several different techniques and vary in degree of protein reduction, robustness of a phenotype, tissues involved and age of onset of any phenotype. Below is a table listing potential uses and suggestions on the *in vivo* models that might be best suited for each specific application, followed by a detailed description of each FA model.

Potential uses	Models	Name	Supplier/PI
Therapeutic approaches that upregulate FXN mRNA or protein, frataxin bypass interventions and other therapeutic approaches downstream of frataxin function	Mice with both Fxn alleles knocked out and transgenic for the human *FXN* gene with an expanded GAA repeat sequence	YG8R, YG22R, YG8sR YG8 800	JAX
	Mice with a repeat sequence inserted into the mouse gene	KIKO, KIKI	JAX
Gene therapy or frataxin replacement therapy, studies on frataxin loss in specific tissues	Conditional knock-out mouse models	MCK-Cre, NSE-Cre, PVALB-Cre	Helene Puccio (exon 4 deleted, MTA with INSERM)
		$Fxn^{flox/null}$:MCK-Cre, $Fxn^{flox/null}$::PV-Cre	JAX (exon 2 deletion)
		αMyhc-Cre	Stephen Kaminsky
	Point mutation models	G127V mouse	Jill and Marek Napierala
		I151F mouse	Jordi Tamarit

Temporal studies on FXN knock-down phenotype	Inducible knock-down	FRDAkd	UCLA – Vijay Chandran
I*n vivo* impact of the GAA repeats on silencing mechanisms	Mice with the mouse allele knocked out and transgenic for the human *FXN* gene with an expanded GAA repeat sequence Mice with a repeat sequence inserted into the mouse Fxn gene	YG8R, YG22R, YG8sR YG8 800 KIKO, KIKI	JAX JAX
Studies on repeat instability	Mice with the mouse allele knocked out and transgenic for the human *FXN* gene with an expanded GAA repeat sequence	YG8R, YG22R, YG8sR YG8 800	JAX

Mice with the human gene inserted (i.e. human gene with a GAA repeat sequence)

These mice are suitable for looking at frataxin upregulating compounds, and may be useful for compounds that act downstream of FXN and, possibly, for frataxin replacement strategies. Mark Pook (Brunel University, UK) created a humanized model containing a YAC carrying a human FXN gene with a repeat sequence ("Pook mice"), which is available on a background of a mouse where the mouse fxn gene has been deleted. The YG8-derived strains show repeat instability, but limited detectable phenotype. The three YAC transgenic mouse models (YG8R, YG22R and YG8sR) show a progressive decrease in the motor coordination. All three models exhibit GAA repeat somatic instability in the brain, cerebellum and liver, as well as exhibited glucose intolerance and insulin hypersensitivity. The greatest FXN deficiency of the three models tested was in YG8sR.

Pook YG8R model. This human FXN YAC transgenic mouse model has the mouse frataxin knockout allele (*Fxn*$^{-}$) and the human FXN YAC transgene from founder YG8, and carries two copies of the human FXN gene with ~82 and ~190 GAA repeats. Mice homozygous for the Fxn- knockout allele and hemizygous for the YG8 transgene, called YG8R mice, are rescued from knockout lethality and have transgene expression that results in an age-dependent, tissue-specific expansion of the GAA repeat, with expansion accumulation observed in the CNS (particularly cerebellum), similar to the human pathology of Friedreich's Ataxia. The GAA triplet repeats exhibit intergenerational instability. As this model recapitulates the epigenetic landscape, it is particularly useful to test molecules that act on the GAA repeat or the epigenetic modifications. This model has no overt ataxia phenotype and has overall limited phenotype before 6-12 months of age.
Note: At JAX this strain is maintained heterozygous for the Fxn deletion and hemizygous for the transgene. Mice singly homozygous for the FXN global null allele are embryonic lethal.
These mice are available on two genetic backgrounds:
Fxn^{tm1Mkn}Tg(FXN)YG8Pook/J (https://www.jax.org/strain/008398) original Pook mouse with mixed genetic background

B6.Cg-*Fxn*^{tm1Mkn} Tg(FXN)YG8Pook/J (https://www.jax.org/strain/012253) backcrossed to C57BL/6J for five generations
Description at:
https://www.ncbi.nlm.nih.gov/pmc/?term=PMC2842930
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4157886/

Pook YG22R model. This human FXN YAC transgenic mouse model has the mouse frataxin knockout allele (*Fxn*$^{-}$) and the FXN YAC transgene from founder YG22 (carrying a single copy of the human FXN gene with ~190 GAA trinucleotide sequence repeats). Mice homozygous for the knockout and hemizygous for the YG22 transgene, called YG22R mice, are rescued from knockout lethality and have transgene expression that models the phenotype of Friedreich's Ataxia (FRDA). Various phenotypes have been reported for these mice by different groups. These mice display an age dependent, tissue specific expansion of the GAA repeat, with expansion accumulation in the CNS (particularly cerebellum), similar to the human pathology of Friedreich ataxia. These strains are maintained heterozygous for the targeted mutation and hemizygous for the transgene and are available on two genetic backgrounds:
B6.Cg-Fxn^{tm1Mkn}Tg(FXN)YG22Pook/J (http://jaxmice.jax.org/strain/012910)
Fxn^{tm1Mkn}Tg(FXN)YG22Pook/J (https://www.jax.org/strain/010963)
Description at: https://www.ncbi.nlm.nih.gov/pubmed/?term=PMC2842930
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4157886/

Pook YG8sR model. This human FXN YAC transgenic mouse model has the mouse frataxin knockout allele (*Fxn*$^{--}$) and the human FXN YAC transgene single repeat YG8s, in which one of the two copies of the human FXN gene was lost. GAA repeat size in this mouse is ~250-300. Mice homozygous for the knockout are rescued from lethality by the expression of the YG8s transgene are called YG8sR mice. Compared to YG8R, the YG8sR model is characterized by lower level of frataxin. The YG8s transgene exhibits somatic GAA repeat instability.
Description at: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4348561/
Fxn^{tm1Mkn}Tg(FXN)YG8Pook/2J (https://www.jax.org/strain/024113)

Pook YG8 800 Fxn^{null}::YG8s(GAA)$_{>800}$. Fxn^{null}::YG8s(GAA)$_{>800}$ mice are a human FXN YAC transgenic mouse model harboring a global null allele of mouse frataxin (Fxn^{null}) and the human FXN YAC transgene single repeat YG8s with a GAA repeat size of >800 . As of December 2017, the GAA repeat values were in the 800-899 range - please inquire with JAX about the current GAA repeat size. As of November 2018, JAX breeding of hemizygous mice with noncarrier mice results in 58% of offspring that are hemizygous, and 80% of those hemizygotes stay in the 775-900 range. The phenotype characterization of Fxn^{null}::YG8s(GAA)$_{>800}$ has not been completed to date. However, they may be expected to have a phenotype similar to that of YG8sR mice (Stock No. 024113). Of note, The Jackson Laboratory Stock No. 030395 colony reports the majority of Fxn^{null}::YG8s(GAA)$_{>800}$ mice exhibit hair loss, even when singly housed. A control strain is available with the same Fxn^{null} allele and a single copy integration of the Y47 human FXN YAC transgene encoding human frataxin with normal-sized (GAA)$_9$ repeats: Fxn^{null}::Y47. Note that the Fxn KO allele in this strain was created in house by JAX (exon 2 deletion Fxnem2.1Lutzy) and is different from the YG8R and YG8sR (exon 4 deletion)
Description at: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4348561/
Fxn$^{em2.1Lutzy}$ Tg(FXN)YG8Pook/800J (https://www.jax.org/strain/030395)

Summary of recent workshop on YG8 models.

There is consensus that the YG8sR models with long repeats (>800 GAA) have lower body weight than matched controls and hair loss.

Performance in several neurobehavioral assessments varies from lab to lab. Tests that are suggested include beam walk test and spontaneous wheel running. Rotarod tests show lab-to-lab variability. The earliest phenotypes are detected at 6-9 months. In performing behavioral assessments, it is important to consider and correct by lower size and body weight. The choice of behavioral tests depends on the neuroanatomical site of intervention/expected benefit of treatment.

An n of 10 per genotype and sex is recommended. Some sex differences have been described; therefore, it is important to separate males and females.

Cardiac assessments: No consensus on reproduceable functional or structural/histological assessments.

There is no consensus on the control lines to use as a comparator for this model. Two are proposed: C57BL/6J (B6) WT mice or the Y47 mouse developed in Mark Pook's lab. The Y47 mouse is a FXN YAC transgenic mouse model with mouse frataxin knockout alleles (Fxn--) and the human FXN YAC transgene with normal GAA repeat size. The YAC transgene in the Y47 model integrated randomly in a different locus from the YG8R model. The Y47 mice weigh more that B6 mice and tend to perform worse than B6 mice. A proper control mouse obtained by CRISPR-Cas9 excision of the GAA repeats in the YG8sR 800 mouse will be available at JAX soon.

Most researchers recommend using an ELISA to assess frataxin levels. Frataxin levels in this model have generally inverse correlation with repeat size. As far as choosing the control mouse, Y47 and C57BL/6 have different frataxin levels in different tissues, so this is an important consideration to take into account.

Animal husbandry may impact phenotype in these mice. Given that FA is a mitochondrial disease, protein and carb composition of chow is important.

These lines of mice display intergenerational instability, with both expansions and contractions, and GAA repeat lengths should be assessed in all offsprings.

Exon 2 vs exon 4 KO do not differ in the amount of functional mouse frataxin that is made; both are full knock outs.

The suggested breeding strategy (from JAX) is

[i] breeding mice heterozygous FXN KO and hemizygous YG8s with mice heterozygous FXN KO and wildtype (noncarrier) YG8s

[ii] breeding mice heterozygous FXN KO and wildtype (noncarrier) YG8s with mice homozygous FXN KO and hemizygous YG8s

Sarsero model. Joseph Sarsero (Murdoch Children's Research Institute, Australia) created a humanized model by inserting the FXN human sequence with 500 interrupted GAA repeats on a bacterial artificial chromosome (BAC) in the mouse genome. These Tg(FXN);Fxn- mice harbor the the FXN*500GAA transgene (Tg(FXN)1Sars) and frataxin knockout allele (*Fxn*^{tm1Mkn}). The FXN*500GAA transgene was found to have an interrupted 500 GAA trinucleotide repeat inserted into intron 1. This transgene was

injected into C57BL/6J donor eggs. FISH and karyotyping of mice from founder line 1 shows one copy of the transgene inserted on Chromosome 5. These mice have much lower frataxin levels than control mice (~10% expression of wild type frataxin), but no overt behavioral phenotype has been identified. These mice might not be suited for gene reactivation studies because the GAA repeat is interrupted, unlike the human condition, and the mechanism of silencing is unclear.
Description at https://www.cell.com/molecular-therapy-family/molecular-therapy/pdf/S1525-0016(05)01223-2.pdf
B6.Cg-Tg(FXN)1Sars *Fxntm1Mkn*/J (http://jaxmice.jax.org/strain/008586).

Mice with a repeat sequence inserted into the mouse gene

Massimo Pandolfo (Erasme University, Belgium) was able to insert GAA repeats into the endogenous mouse Fxn gene. Mice heterozygous for the GAA insertion and harboring a Fxn knockout allele (KIKO) are suitable for looking at compounds that act downstream of FXN, or compounds that replace FXN. Subtle behavioral phenotypes have been observed in the KIKO mice at about 1 year of age, and biochemical and physiological changes can be detected much earlier.

Pandolfo KIKO model. These frataxin knock-in/knockout (KIKO) mice harbor one allele of the frataxin $(GAA)_{230}$ expansion mutation (*Fxn*^{tm1Pand}) on one chromosome, and one allele of the frataxin exon 4-deleted mutation (*Fxn*^{tm1Mk}) on the homologous chromosome. KIKO mice are viable and fertile. Analysis of frataxin levels in tissues from KIKO mice demonstrate a reduction of frataxin to 25-36% of wildtype controls. KIKO animals up to 1 year of age perform equivalent to wildtype controls on rotarod test. Total iron concentrations were similar in all tested tissues of KIKO and wildtype mice except in pancreas: KIKO mice demonstrate lower iron levels in pancreatic tissues. No iron deposits and only mild collagen staining around the vessels of the heart were observed in both year old KIKO mice and wildtype controls. In contrast to Friedreich's Ataxia patients, no detectable change in GAA repeat size was found over six studied generations. Moreover, no evidence of somatic cell instability was noted as GAA repeat expansion size was the same in all analyzed tissues. However, characterization of KIKO mice performed at The Jackson Laboratory revealed that starting at 6 months of age, these animals exhibit an abnormal "weaving" gait when subjected to a forced treadmill walk. This phenotype occurs with increasing penetrance as the mice age.
JAX distributes two versions of this model, with and without the neomycin selection cassette
B6.Cg-*Fxn*^{tm1Mkn}*Fxn*^{Tm1Pand}/J (https://www.jax.org/strain/014162)
B6.Cg-*Fxn*^{tm1Mk}*Fxn*^{tm1Pand}/J (https://www.jax.org/strain/012329)
Description at: https://pubmed.ncbi.nlm.nih.gov/11852098/
Phenotype described in: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5719255, https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5051948/, https://pubmed.ncbi.nlm.nih.gov/29259026/, https://pubmed.ncbi.nlm.nih.gov/32269244/, https://pubmed.ncbi.nlm.nih.gov/31974344/

Pandolfo frda$^{230GAA/230GAA}$ or "KIKI" (knockin/knockin) model. These mice express a $(GAA)_{230}$ expansion repeat from the endogenous *Fxn* locus. Homozygotes produce an average of 75% of wild-type levels of frataxin protein, as assayed by Western blot densitometry analysis. The GAA repeat size was found to be stable over the 6 generations studied. Mice that are homozygous for the targeted mutation are viable, fertile, normal in size and do not display any gross physical or behavioral abnormalities.

JAX distributes two versions of this model, with and without the neomycin selection cassette
B6.129-*Fxn*^{tm1Pand}/J (http://jaxmice.jax.org/strain/008470)
B6.129-*Fxn*$^{tm1.1Pand}$/J (http://jaxmice.jax.org/strain/011113)
Description at: https://febs.onlinelibrary.wiley.com/doi/abs/10.1016/S0014-5793%2802%2902251-2

Frataxin knock-out mouse models

Conditional knock-out mouse models are perhaps best for gene and protein replacement strategies and to understand tissue-specific downstream events of frataxin deficiency. This is because the endogenous gene is ablated to recapitulate an FRDA-like phenotype, although to a more severe extent, since there is a complete absence of frataxin in the tissues of interest. Exon 2 vs exon 4 KO do not differ in the amount of functional mouse frataxin that is made; both are full knock outs.

Puccio FXN conditional knockout models. The Puccio team has shown that full frataxin knockout is embryonic lethal at E6.5 days, demonstrating that frataxin is an essential protein. In these conditional knockout mice, frataxin may be knocked out in specific tissues when the Cre recombinase is expressed. Mice have severe cardiac or neuronal phenotypes. The cre-loxP recombination system was used to make a conditional allele of the mouse *Fxn* exon 4 from (Fxn^{L3}). The exon 4 deleted allele is denoted Fxn^{L-}. To obtain the conditional knockout (cKO), mice heterozygous for the deleted allele Fxn$^{+/L-}$ and carrying a tissue-specific Cre transgene is crossed with a mouse homozygous for the conditional allele (Fxn$^{L3/L3}$). The conditional mutant animals bear the following genotype: Fxn$^{L3/L-}$; TgCre^{+}. Cardiac-specific (MCK-Cre) and neuronal (NSE-Cre, Prp-CreERT) models of FRDA are available (Puccio et al., 2001; Simon et al., 2004). More, recently a Parvalbumin cKO which has more of the CNS specific phenotype associated with FA was also generated (Piguet et al. 2018). Beta-cell and liver specific conditional knockout have also been generated.
Review: http://www.ncbi.nlm.nih.gov/pubmed/17203663;
Neuronal mouse model: http://www.ncbi.nlm.nih.gov/pubmed/14985441;
https://www.ncbi.nlm.nih.gov/pubmed/29853274
Cardiac mouse model: http://www.ncbi.nlm.nih.gov/pubmed/11175786

Parental lines to obtain Frda $^{L3/D;}$ MCK-Cre+ (MCK-CRE) and Frda $^{L3/D}$; NSE39-Cre+ (NSE-CRE) are available from Helene Puccio. An MTA needs to be signed with INSERM.

Jackson Labs has created an in-house exon 2 FXN knockout model (Fxn$^{em2.1Lutzy}$) different from Dr. Koenig and Dr. Puccio's FXN exon 4 knockout to create the following conditional KO models:

Fxn$^{flox/null}$:MCK-Cre. These mice harbor a Cre- conditional frataxin allele, a frataxin global knockout allele and a cardiac/skeletal muscle-specific Cre recombinase transgene. These mice show a strong cardiac phenotype. Due to early-onset cardiomyopathy, Fxn$^{flox/null}$::MCK-Cre are distributed at 4-5 weeks old. JAX distributes phenotypically-normal parental lines:

C57BL/6J-Fxnem2Lutzy/J (https://www.jax.org/strain/028520)
Fxn^{flox} homozygous frataxin floxed exon 2
B6.Cg-Fxn$^{em2.1Lutzy}$ Tg(Ckmm-cre)5Khn/J (https://www.jax.org/strain/029100)

Fxn^{null}::MCK-Cre. These mice harbor a frataxin global knock-out allele and a cardiac/skeletal muscle specific Cre recombinase transgene. These double mutant mice are "phenotypically normal"

B6.Cg-$Fxn^{em2Lutzy}Fxn^{em2.1Lutzy}$Tg(Ckmm-cre)5Khn/J (https://www.jax.org/strain/029720)

$Fxn^{flox/null}$::PV-Cre These mice have a Cre-conditional frataxin allele, a global knockout frataxin allele and a parvalbumin neuron-specific Cre recombinase knockin allele. Due to early-onset ataxia, Fxnflox/null::PV-Cre are distributed at 4-7 weeks of age. JAX distributes the phenotypically-normal parental lines:

C57BL/6J-Fxnem2Lutzy/J (https://www.jax.org/strain/028520)

Fxn^{flox} homozygous frataxin floxed exon 2

B6.Cg-$Pvalb^{tm1(cre)Arbr}$ $Fxn^{em2.1Lutzy}$/J (https://www.jax.org/strain/030218)

Fxn^{null}::PV-Cre These mice harbor a frataxin global knockout allele and a Pvalb knock-in allele directing Cre recombinase expression to parvalbumin-expressing neurons. These mice are phenotypically normal and are a parental control used to generate the progressive ataxia mouse line $Fxn^{flox/null}$::PV-Cre.

B6.Cg-$Pvalb^{tm1(cre)Arbr}$ $Fxn^{em2Lutzy}$ $Fxn^{em2.1Lutzy}$/J (https://www.jax.org/strain/029721)

αMyhc-Cre This is a mouse model of FA cardiomyopathy less severe than the MCK-Cre. The cardiac promoter αMyhc drives the CRE recombinase cardiac-specific excision of FXN exon 4. This FA model is normal at rest, but exhibits the cardiac phenotype with stress. This model was developed by Dr Stephen Kaminsky and Dr Ronald Crystal at Weill Cornell Medical College.
https://pubmed.ncbi.nlm.nih.gov/32646255/

Frataxin inducible knock-down mouse model

These animals were created by Vijay Chandran in Daniel Geschwind's laboratory at UCLA and could be used for therapeutic strategies that do not involve increasing endogenous frataxin. This is because an inducible shRNA knocks down *Fxn* mRNA to recapitulate an FRDA-like phenotype. The endogenous gene in this model does not have GAA repeats. They are available through UCLA, https://techtransfer.universityofcalifornia.edu/NCD/24493.html.

UCLA mouse model. Chandran created an FRDA mouse model, by genomic integration of a single copy of an Fxn-targeting shRNA transgene (doxycycline-inducible) under the control of H1 promoter in the rosa26 genomic locus. These mice can be induced to conditionally knock down frataxin to low levels using doxycycline to induce the expression of the Fxn-targeted shRNA. This mouse model displays a phenotype similar to FRDA patients, including cardiac hypertrophy, elevated iron-responsive proteins, neurodegeneration, motor neuropathy, scoliosis, and ataxia. On removal of dox (and increased levels of frataxin) mice can recover most functions. The physiology and molecular characterization of this recovery is still under investigation and not fully understood.
Description of the model: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5736353/

Summary of recent workshop on FRDA kd model

Number of animals necessary to power tests for each phenotype: 15 animals. There may be sex differences in phenotypes (https://pubmed.ncbi.nlm.nih.gov/39171530/). Separating males and females is suggested.

Best dosing regimen for doxycycline (DOX) treatment: in chow 200ppm

Neurobehavioral and cardiac phenotypes are robust (https://pubmed.ncbi.nlm.nih.gov/39171530/) and timeline is similar in different labs: Differences are generally seen after 10-12 weeks of doxycycline (DOX) treatment (and up to 20 weeks). There is no consensus on what the amount of residual frataxin is at these time points in different tissues. Use caution when interpreting differences between tissues, as DOX does not distribute the same across all tissue.

Best control: Ideally using 3 controls: WT, WT + DOX and FRDA kd -DOX.

Reversibility of phenotypes after cessation of DOX: Both dose and time of removal are critical to see reversal of phenotype. Reversibility of any phenotype may be confounded by the tissue distribution and clearance of DOX. Also the relative contribution of cell death vs cell dysfunction determines reversibility.

Given the half-life of mitochondrial proteins (especially membrane proteins) choosing the right time points is important. Timing of phenotype and frataxin expression might not correlate because of the stability of FeS cluster proteins in heart and brain.

It is important to remember that this is an acute reduction of frataxin in a system that does not have time to compensate, unlike the human disease. This model misses the development component of the human disease. No data is available on whether DOX can be administered to pregnant animals and with what regimen.

The possibility of promoter leakage cannot be excluded and some expression of shRNA without DOX could be present. However transcriptomics analysis suggests that this produces minimal effects.

Point mutation mouse models

G127V. CRISPR/Cas9 was used to introduce the G127V missense mutation (equivalent to the human G130V mutation) in the Fxn coding sequence and a homozygous mice (FxnG127V/G127V) was generated. In this mouse, the endogenous Fxn G127V protein is detected at much lower levels in all tissues analyzed from FxnG127V/G127V mice compared to age and sex-matched WT mice without differences in Fxn transcript levels. FxnG127V/G127V mice are significantly smaller than WT counterparts, but perform similarly in most neurobehavioral tasks. A further characterization of this model is underway.
https://pubmed.ncbi.nlm.nih.gov/36638893/

I151F. Mouse models homozygous for the FXN I151F mutation (equivalent to the human mutation I154F) present low frataxin levels in all tissues. They display neurological deficits resembling those observed in FA patients. Biochemical analysis of heart, cerebrum and cerebellum have revealed decreased content of components from OXPHOS complexes I and II, decreased aconitase activity, and alterations in antioxidant defenses. https://pubmed.ncbi.nlm.nih.gov/35038030/

Conditional G127V/knockout mouse.

This novel mouse model of severe FXN depletion in the nervous system, developed in the lab of Dr Jordi Magrane, reproduces important neurobehavioral phenotypes of FRDA over a distinctive timescale, while presenting residual FXN levels. The model provides the research community with a fast progressive neuropathology *in vivo* FRDA model, but still with a long enough window for therapeutic interventions. Dr Magrane generated a nervous system-specific FXN depletion mouse model using the Cre/*loxP*-recombination system and the FXN G127V missense mutation in the mouse *FXN* gene. He used the *Nestin* promoter to achieve low levels of mature FXN in neurons and glia of both peripheral and central nervous systems *in vivo* from perinatal stages through adulthood. G127V/KO mice are viable and display progressive neurobehavioral deficits, which affect coordination and balance, as demonstrated by wire-hanging, notched bar, accelerating rotating rod, and footprint tests. Based on these abnormalities, an early disease onset of 8.5 weeks (60 days) is defined. Dr Magrane is currently assessing tissue and biochemical disease features at both pre-symptomatic and late stages of the disease (26.5 weeks, 186 days).