All images of mice from Charles River Laboratories http://www.criver.com

Mouse Genetics

(GSK Core Course: Experimental Biology - 09/12/2024)



Kat Hadjantonakis

9/12/25

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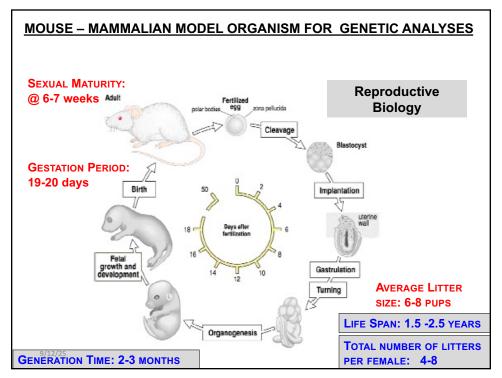
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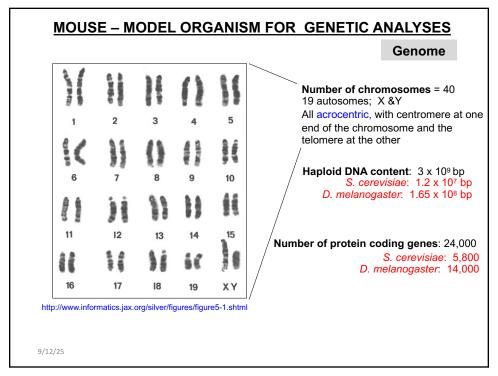
This **MORNING**

- 1. Overview of the mouse model:
 - 1. transgenic mouse models, embryonic stem cells and mouse chimeras.
- 2. Generation and analysis of genetically engineered mouse models (GEMMs):
 - 1. Nulls
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 - 3. Hypomorphs
 - 4. Conditionals
- 3. Genetic analyses in mice:
 - 1. Complementation tests
 - 2. Pathway analysis (are genes in the same pathway for the specific function)
 - 3. Autonomous/Non-autonomous functions of a gene (chimera analyses)
- **4. Genetic screens** (forward genetic approaches) **in mice:** dominant and recessive screens

This **AFTERNOON**

Yas Furuta's (Director, Mouse Genetics Core, MSK) lecture

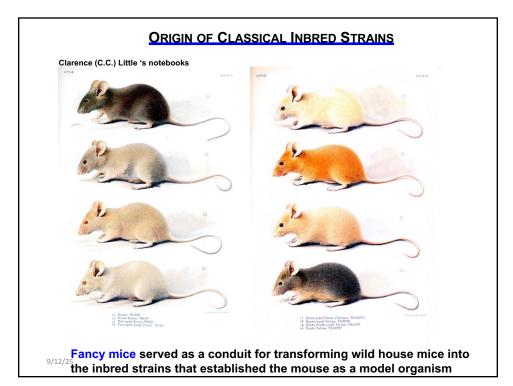




ORIGIN OF CLASSICAL INBRED STRAINS Laboratory mouse strains derive from subspecies of the Mus musculus group: domesticus, musculus, and castaneus Ancestral musculus subspecies musculus Eastern Europe Russia Northern China House mice: Commensal animals that depend molossinus Japan on human activity & shelter for Castaneus Western Asia Southeastern Asia Southern China survival domesticus Western Europe Approximate ~1,000,000 ~10,000 ~1,000 (Years) A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Frazer KA, Eskin E, Kang HM, Bogue MA, Hinds DA, Beilharz EJ, Gupta RV, Montgomery J, Morenzoni MM, Nilsen GB, Pethiyagoda CL, Stuve LL, Johnson 9/12/25 FM, Daly MJ, Wade CM, Cox DR. Nature. 2007 Aug 30;448(7157):1050-3. Epub 2007 Jul 29. PMID: 17660834

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ORIGIN OF CLASSICAL INBRED STRAINS Fancy mice provided a ready source of genetic variants for testing the applicability of Mendel's laws, rediscovered in 1900, to mammals. Ancestral musculus subspecies musculus Eastern Europe Russia Northern China East Asian 'fancy' mouse molossinus Japan European 'fancy'mouse castaneus Western Asia outheastern Asia Southern China domesticus Western Europe Approximate timeline ~1,000,000 ~10,000 ~1,000 (Years) 9/12/25 http://www.informatics.jax.org/silver/chapters/1-2.sht



INBRED STRAINS OF MICE

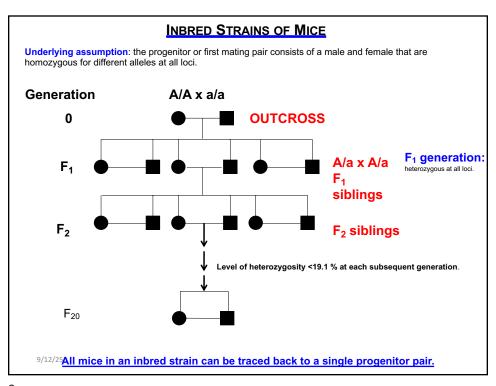
Strains that have been maintained by <u>brother-sister matings</u> for more than 20 consecutive generations.

At F₂₀ any randomly chosen (brother-sister) mating pair will be <u>homozygous for identical alleles</u> in 98.7% of their genom

Mating Type	Autosomal	X-Linked	Matings between	
	우 라	የ <i>የ</i>		
Incross	+/+ x +/+	+/+ x +/Y	Like homozygotes	
	r/r x r/r	r/r x r/Y		
Outcross	우 라	우 ♂		
	+/+ x r/r	+/+ x r/Y		
	r/r x +/+	r/r x +/Y	Unlike homozygotes	
<u>Backcross</u>	우 라	우 ♂		
	+/+ x r/+	1		
	r/+ x +/+		Homozygote	
	r/+ x r/r	r/+ x r/Y	- & Heterozygote	
	r/r x r/+	r/+ x +/Y		
Intercross	우 라			
	r/+ × r/+		Heterozygotes	

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INBRED STRAINS OF MICE

Individuals in an inbred strain are essentially identical genetically, i.e. ISOGENIC.

Spontaneous rate for deleterious mutations: ~ 10-5/locus/generation; each new mutation is either rapidly fixed or lost in further rounds of inbreeding.

Spontaneous mutation rate: 38 x 10^{-9} per nucleotide per generation

C57BL/6J

The most widely used strain and the 1st to have its genome sequenced (2nd mammalian species to have its genome published !). a.k.a. Black 6, B6, B6-J, C57 Black.

a bit of trivia: in 2013 Black 6 mice were flown into space aboard Bio-M No.1 & in 2015 Black 6 females were sent to the ISS on SpaceX CR-6!!

Generation: F226pF230; August 14, 2014

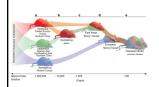
After 226 generations of brother-sister matings, embryos were <u>cryoPreserved</u> and then the strain has undergone another 230 generations of backcrossing.

Estimate of overall mutation rate

0.44 mutations /generation

1 mutation with phenotypic consequences per 2.3 generations.

3-5 years for new mutations to become fixed in a colony maintained by brother-sister matings.



INBRED STARINS WILL DIVERGE: C57BL/6J vs. C57BL/6N

1921: Clarence (C.C.) Little bought female mouse code-numbered 57 from Abbie Lathrop's farm and initiated construction the C57BL inbred strain.

1948: Starting with F24 C57BL mice Jackson Labs established the C57BL/6J inbred strain

1951: Starting with F32 C57BL mice NIH started production of the C57BL/6N inbred strain

2002: genome sequence completed and published in 2002; C57BL/6J

2011: ES cells used to construct the conditional knockout resource for the International Mouse Phenotyping Consortium (IMPC); C57BL/6N

Differences between these two C57BL/6 substrains:

51 coding variants

34 coding SNPs

2 indels

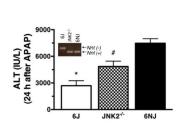
15 structural variants (SVs)

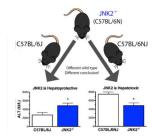
Identified/validated using deep sequencing data and comprehensive detection methods.

A comparative phenotypic, and genomic analysis of CS78L/6N mouse strains imm MM. Greenawy S, While JK, Fuch H, Gallus-Dume V, Wells S, Song T, Wong K, Bedu E, Carleright EJ, Dupour N, Ophalo S, Edebel J, Gür J, Hopkan M, Auditor J, Harver D, Harver D, Polar M, Alfaren A, Alfgrey B, Aggild, Bocker L, Blabe A, Brocker D, Caler M, Chumpy MF, Combe R, Danscok P, eli Fenza A, Garet M, Gerico K, Guite E, Brucock JM, Harver M, Wilson SM, Harver D, Marker D, M

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C57BL/6J vs. C57BL/6N





https://www.iax.org/news-and-insights/iax-blog/2016/june/there-is-no-such-thing-as-a-b6-mouse

Testing the effects of a Mapk9 (Jnk2) knockout on acetaminophen-induced liver injury model.

Using C57BL/6J vs. C57BL/6N as wild-type controls, the phenotype of the *Mapk9* knockouts fell in between the phenotype for these C57BL/6J and C57BL/6NJ controls.

The researchers found themselves in a situation where they could interpret their data in two opposing ways, depending on which control was used.

If they used C57BL/6J as controls, then the data indicated that MAPK9 was hepatoprotective.

If they used C57BL/6NJ as controls, then MAPK9 seemed to be hepatotoxic.

Mispairing C57BL/6 substrains of genetically engineered mice and wild-type controls can lead to confounding results as it did in studies of JNK2 in acetaminophen and concanavalin A liver injury 9/12/25

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Chem Res Toxicol. 2011 Jun 20;24(6):794-6. doi: 10.1021/tx200143x. Epub 2011 May 24. PMID: 21557537

Genetic Background Can Modify Mutant Phenotypes

A null allele in the gene encoding the Epidermal Growth Factor Receptor (Egfr), *Egfr*^{m1Cwr}, was backcrossed onto 2 different outbred strains (CF-1 and CD-1), and one inbred strain (129/Sv) with each having a different defect.

- > Egfr^{m1Cwr/m1Cwr} on CF-1 background: peri-implantation death @ E4.5-6.5 with degeneration of the inner cell mass (ICM) of the blastocyst.
- ➤ Egfr^{m1Cwr/m1Cwr} on 129/Sv inbred background: developmental arrest @ mid-gestation (E12.5 - 13.5) with placental defects.
- > Egfr^{m1Cwr/m1Cwr} on CD-1 background: post-natal lethality. mutant pups live to 3 weeks and exhibit abnormalities in the skin, kidney, brain, liver, and GI tract.

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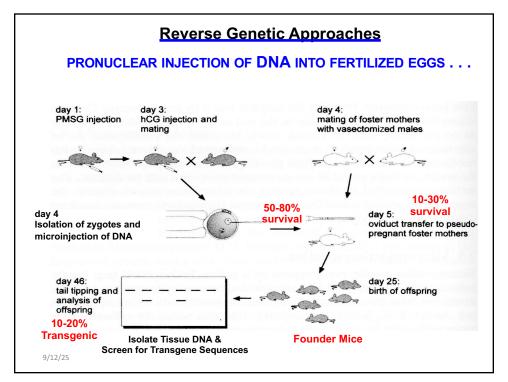
Targeted disruption of mouse EGF receptor: effect of genetic background on mutant bhenotype.

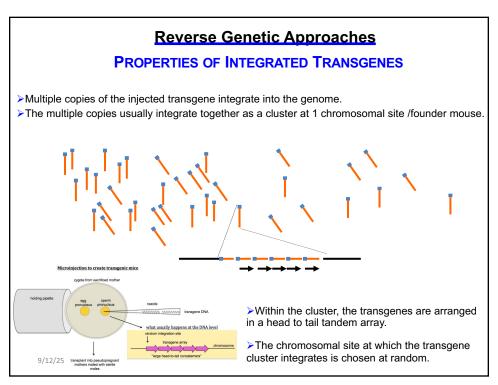
Threadgill DW, Dlugosz AA, Hansen LA, Tennenbaum T, Lichti U, Yee D, LaMantia C, Mourton T, Herrup K, Harris RC, et al.

Science. 1995 Jul 14;299(5221):230-4. PMID: 7618084

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Generating genetically Engineered Mouse Models (GEMMs): Reverse Genetic Approaches TRANSGENIC MICE Animals having acquired new genetic information in their germ line via manipulation of early the embryo Pronuclear DNA Injection Direct introduction into pre-implantation embryos Injected eggs surgically re-implanted for further development Fertilized eggs (oocytes) recovered for DNA injections





Reverse Genetic Approaches

Transgene Transmission

- The integrated cluster of transgenes is transmitted as a single Mendelian trait.
- >50% transmission from a founder: all cells contain the integrated transgene, i.e. transgene integration occurred early, possibly before cleavage to 2-cell stage.
- ><50% transmission: founder is mosaic, i.e. some cells contain the integrated transgene while other cells do not. Transgene likely integrated after the 2-cell stage.
- >>50% transmission: transgene integrated at more than one chromosomal site.
- >The site of transgene integration: chosen at random & integrations mediated by mechanisms of illegitimate recombination.
- >About 5-10% of transgenic lines carry recessive insertional mutations caused by the integration of the transgene. These mutations are usually gene disruptions.

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Reverse Genetic Approaches

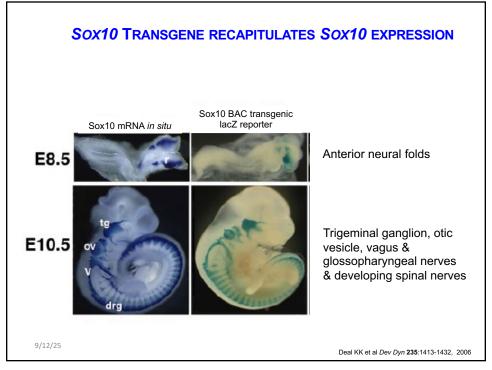
Transgene Expression

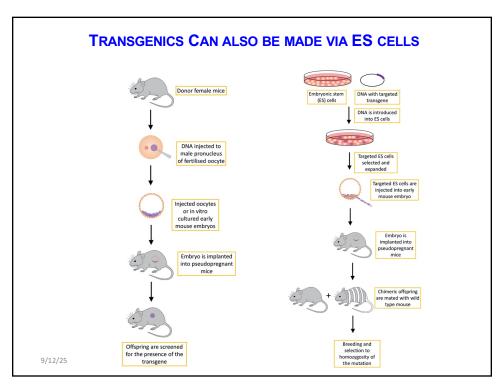
COMMON REQUIREMENT: transgene includes cis-acting transcriptional regulatory elements that function robustly and appropriately at a wide variety of chromosomal locations.

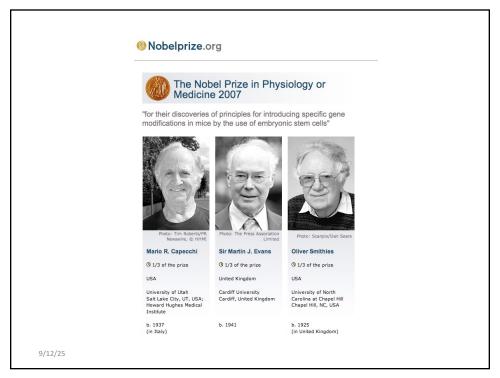
TRANSGENE: cell/tissue-specific regulatory elements direct ectopic expression of heterologous gene & one or more introns

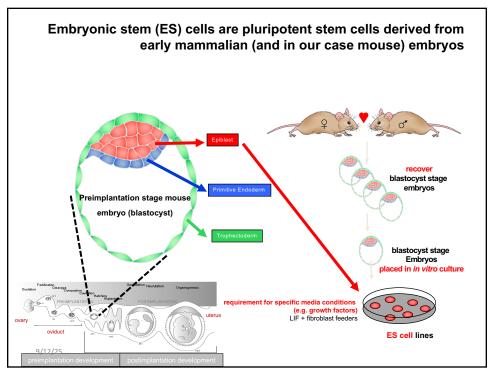


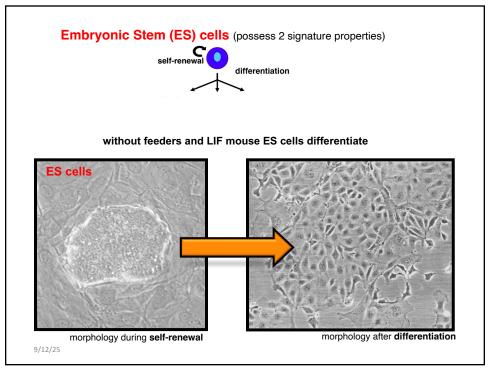
- · cDNA/cDNA-genomic hybrid
- Histological/fluorescent reporters (LacZ, GFP, RFP etc)
- · Modulators of activity of transgene or endogenous reporters/alleles
- Enzymes (Cre/FLP recombinases)
- · Transcriptional regulatory factors (inducers & repressors)

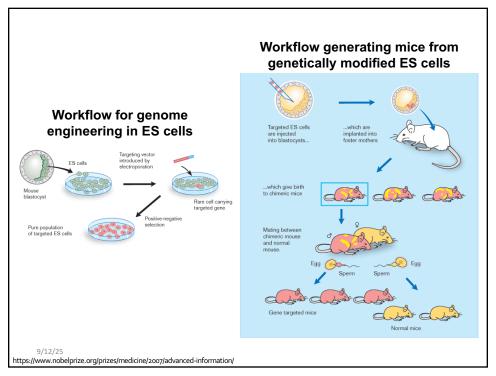


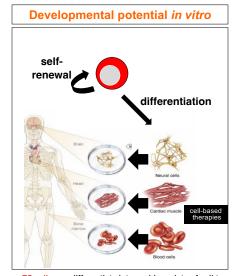


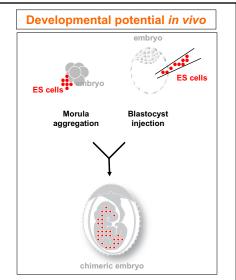




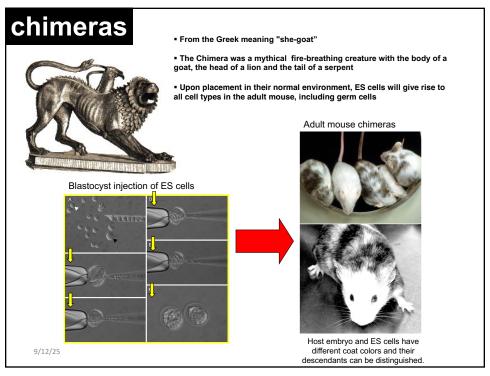








- ES cells can differentiate into a wide variety of cell types in culture (developmental potential *in vitro*)
- ES cells can participate in normal development when incorporated into a pre-implantation embryo and produce tumors (called teratomas) containing many differentiated cell types if injected subcutaneously (developmental potential in vivo)





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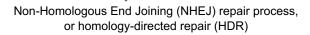
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CRISPR-Cas9 as a method to induce more efficient homologous recombination by creating double strand breaks at specific DNA sequences

but creates insertions/deletions (indels) at a higher efficiency...



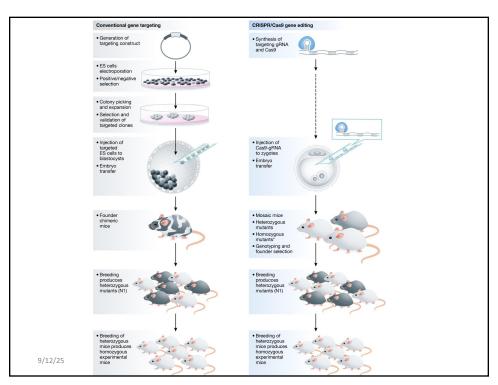
Double stranded break in DNA is created at site of single stranded RNA (guide RNA - sgRNA) binding to DNA



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Wiles et al., CRISPR-Cas9-mediated genome editing and guide RNA design, Mammalian Genome (2015)

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The percentage cost savings and the timelines using the CRISPR/Cas9 method compared with traditional homologous recombination technology in mouse ES cells

These estimates include project initiation through the N1 stage, at which germline transmission has been achieved and a genetically modified mouse strain has been established. The major difference between the costs and timelines reflects the necessity of performing electroporation, selection, clone picking, and the subsequent screening in mES cells for traditional gene targeting. Downstream phases (injections and subsequent breeding) are similar with respect to the timelines. Note that for conventional targeting for which there are no murine ES cells for the desired background strain, the project timeline will increase by an additional 6–18 months, depending on the extent of backcrossing required to move the mutation to the desired background strain.

	mES cells	CRISPR (in zygotes)					
	conventional gene targeting	indel (small deletion/ins ertion)	deletion	precise editing (SNP)	conditional KO (LoxP, FRT)	KI (reporter)	
% cost savings	baseline	81%	68%	59%	38%	41%	
avg. timelines	12 months	6.5 months	7 months	7 months	8 months	8 months	

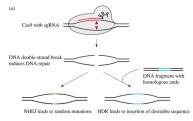
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Lui et al., EMBO Rep 2017

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Applications of CRISPR-Cas9 in cells of mice

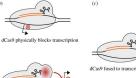
Indel (insertion/deletion) that can cause a null mutation, hypomorph or make a dominantnegative acting protein

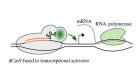


Insertion can be a reporter gene, produce a tagged fusion protein, a point mutation, WT gene copy to repair an endogenous mutation (DNA repair)

Other

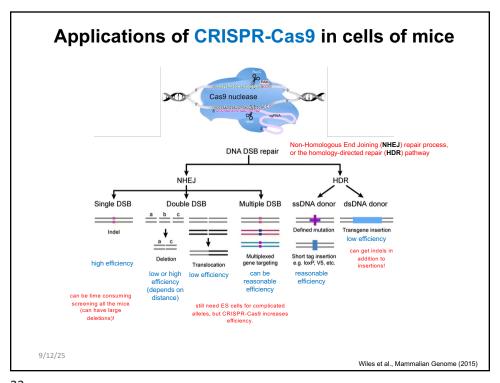
nuclease activity of Cas9 is inactivated and new activities created via fusion proteins

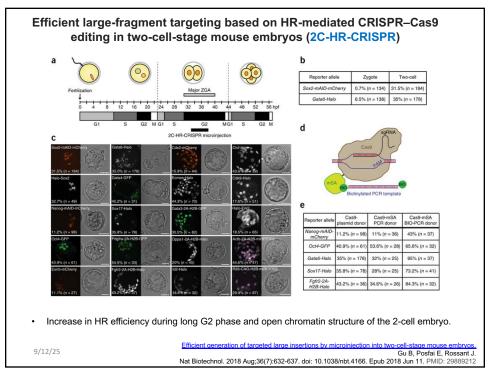


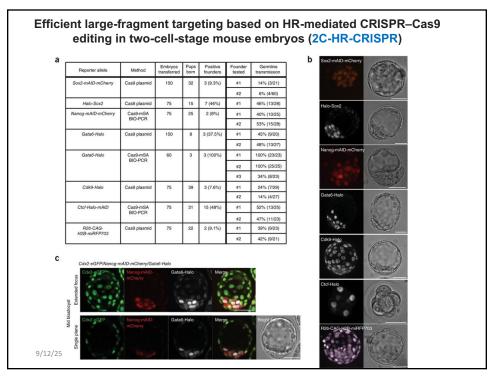


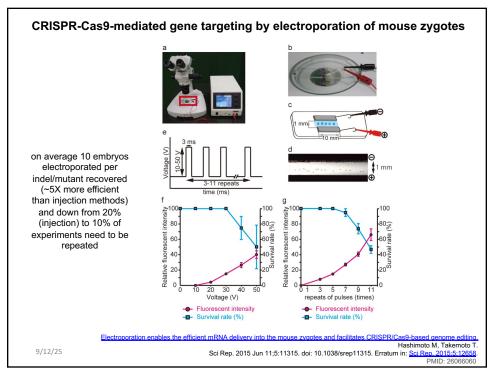
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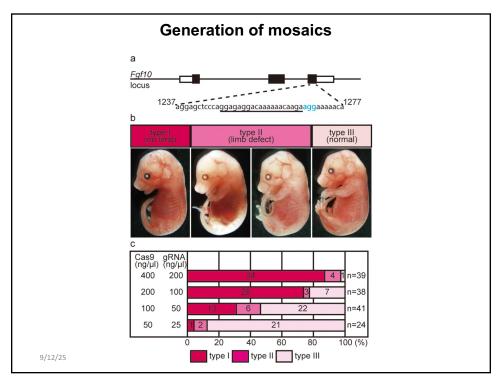
Hille and Charpentier, Philos Trans R Soc Lond B Biol Sci (2016)

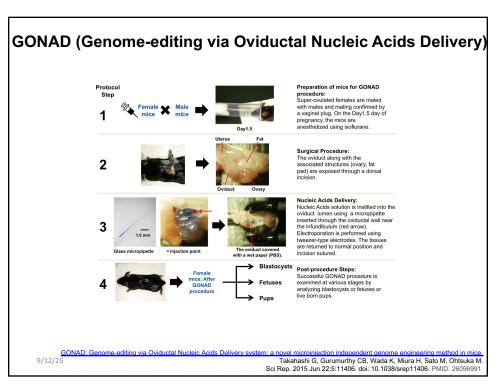


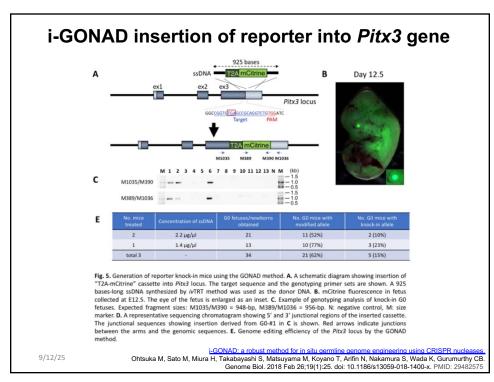


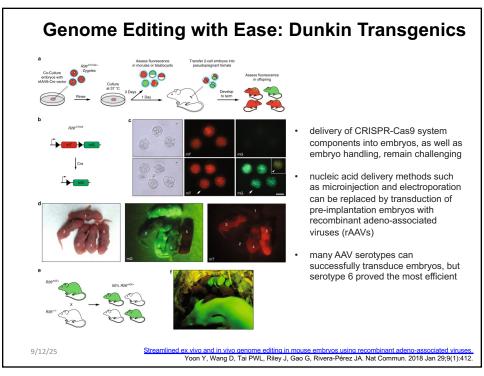


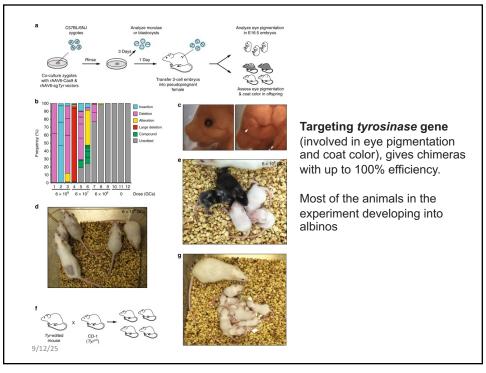


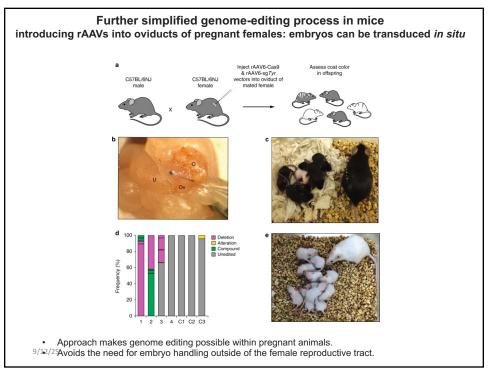


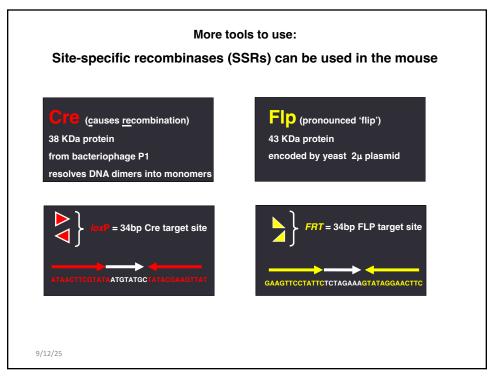


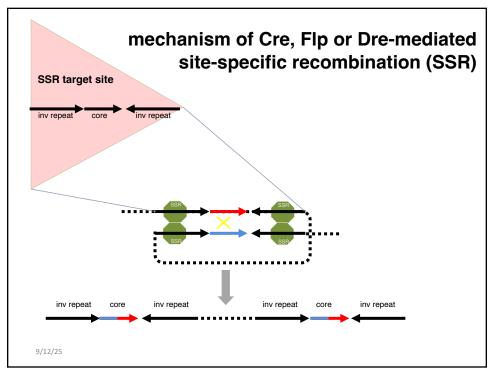


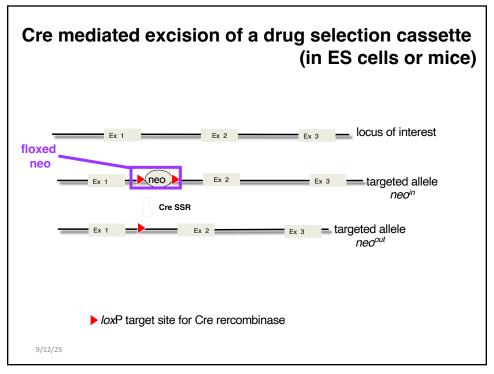


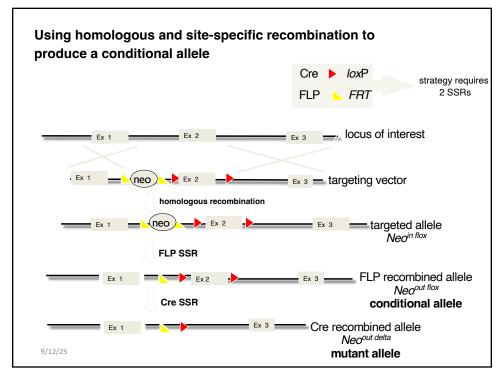


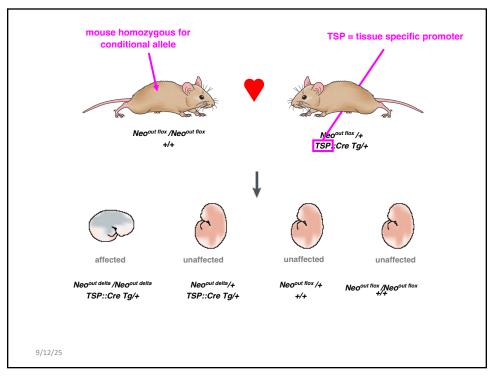


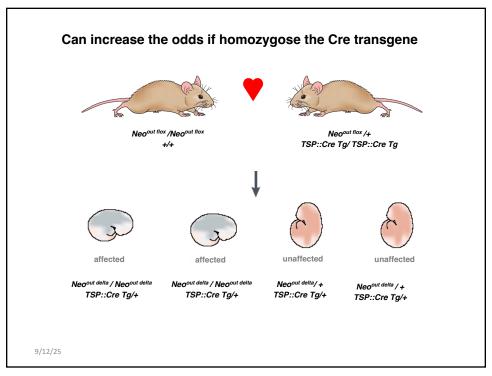


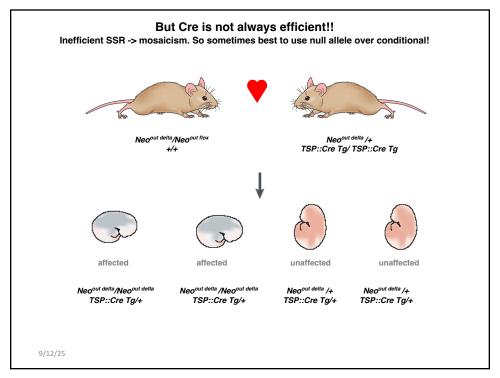


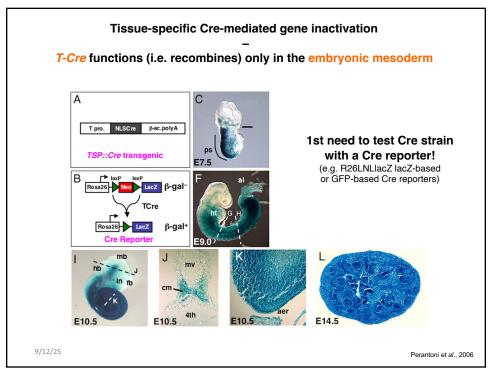


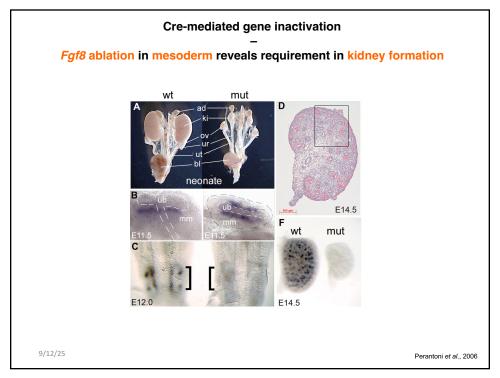


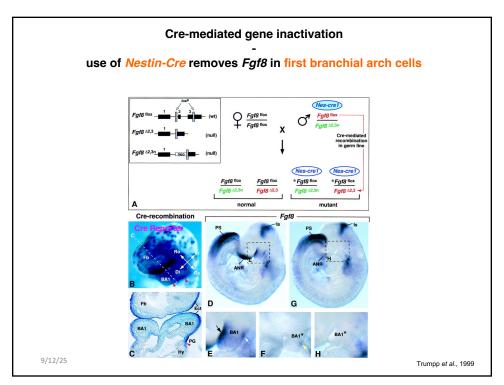












Cre-mediated gene inactivation Fgf8 ablation in first branchial arches (BAs) reveals requirement in craniofacial development wt mut yt pormal Fgf8.Wes-cre mutant mut wt mut Trumpp et al., 1999

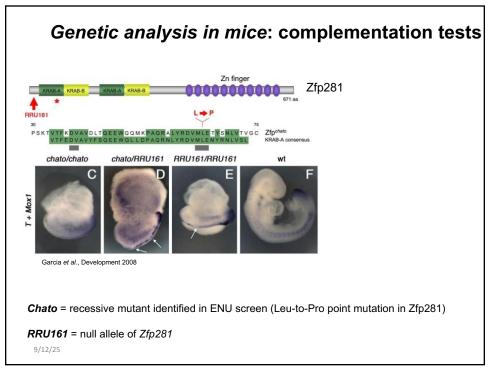
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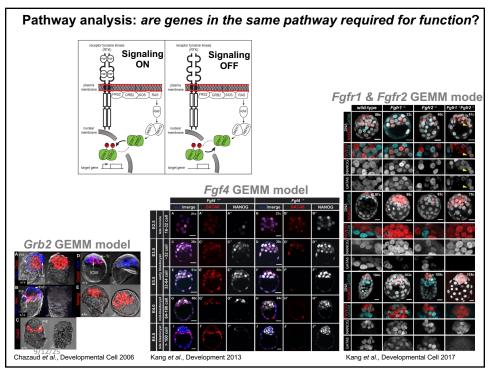
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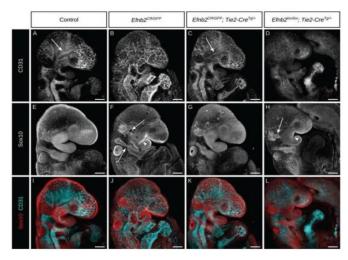
This **AFTERNOON**

- 5. The International Mouse Phenotyping Consortium (IMPC)
- 1. 9/07/biased comprehensive catalog of mammalian gene function





Cell autonomous vs. Cell non-autonomous functions of a gene



Neural crest defects in ephrin-B2 mutant mice are non-autonomous and originate from defects in the vasculature

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Lewis et al., Developmental Biology 2015

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FORWARD GENETIC APPROACHES

CHEMICAL MUTAGENESIS FOR GENOME-WIDE SCREENS

N-ethyl-N-nitrosourea (ENU):

powerful alkylating agen't that transfers its ethyl group to nucleophilic nitrogen or oxygen sites in DNA; if unrepaired, the mis-pairing caused by the ENU-induced DNA adducts will result in mutations during DNA replication in spermatogonial stem cells.

ENU-induced mutations

single base-pair substitutions: A-T to T-A transversions (44%) or A-T to G-C transitions (38%)

Missense mutations (46%); splicing (26%); nonsense (10%)

Frequency of ENU-induced mutations

Sequence based studies: 1 mutation every 1-to-2.7 Mb \rightarrow 1,000 mutations per male gamete; with ~20 with the potential to generate a phenotype

Enable unbiased genome-wide screens that yield in discovery of novel gene functions

Random mutagenesis of the mouse genome; a strategy for discovering gene function and the molecular basis of disease

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Nguyen N, Judd LM, Kalantzis A, Whittle B, Giraud AS, van Driel IR.

Am J Physiol Gastrointest Liver Physiol. 2011 Jan;300(1):G1-11. doi: 10.1152/ajpgi.00343.2010. Epub 2010 Oct 14. PMID: 20947703

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FORWARD GENETIC APPROACHES ENU MUTAGENESIS FOR RECESSIVE EMBRYONIC MUTATIONS G0 G1 THE PROACHES ENU H/H (CH3) THE PROACHES ENU H/H (CH3) F1 H/M (B6:C3H) G2 H/H H/H H/M H/M H/M H/M H/M H/M M/M

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Essential genes

Genes that are critical to the survival of an organism

- Survive in a dish
- Survive to birth/weaning
- Survive until a reasonable life expectancy as an adult

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