

# Concept for reproducible animal models for complex human disease: implications for personalized medicine

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# Acknowledgements

## The Jackson Laboratory

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Judy and Tony Evnin

**The Jackson Laboratory Scientific Services**  
**AMP-AD single-cell working group**  
**Resilience-AD Consortium**



Dorothy Dillon Eweson  
Lecture Series on the  
Advances in Aging Research

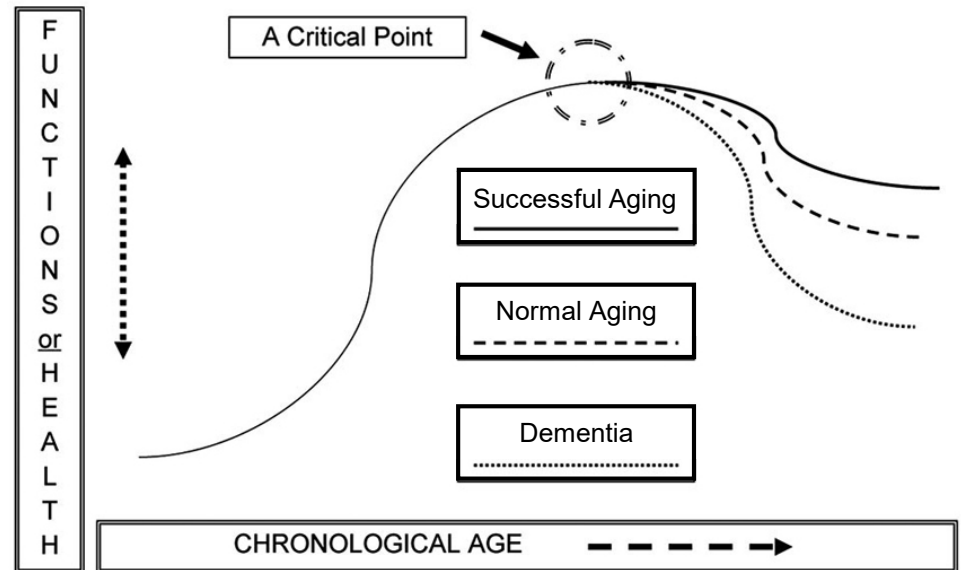


# Optimizing the relevance to human biology and disease

- Creation of a polygenic model of human aging and AD
  - Traditional models (single inbred strain) not well validated models of the human disease
- Characterization of cognitive and pathological variation
  - Optimal study design and application of statistical analyses
- Validation of the resource as a model of human late-onset AD
  - Genotype-phenotype validation of a complex disease: PRS
- The quantitation of genetic and environmental interactions
  - Reporting the residual unexplained variance

# Aging is complex and different for everyone

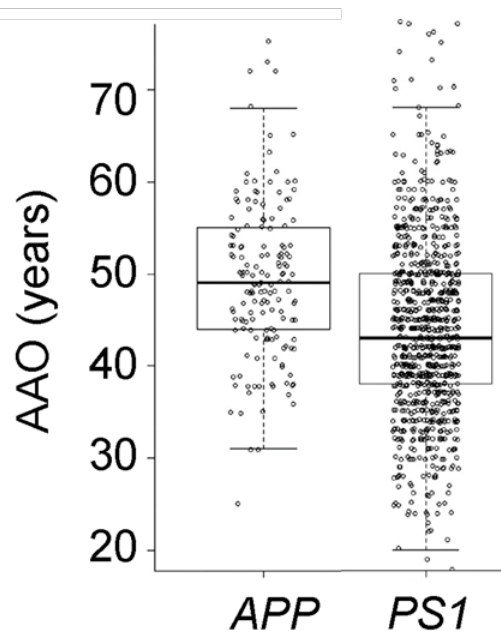
- Aging is a leading risk factor for many diseases, particularly dementia
- Genetic makeup plays an important role in determining susceptibility
- Identifying specific genes involved in regulating trajectory is critical for:
  - Understanding cause
  - Developing treatments



Cai et al, *Trends in Aging Neuroscience*, 2014

# Even among FAD patients, AAO varies widely

Human FAD  
Age at Symptom Onset by Mutation



Ryman et. al., *Neurology*, 2014

- Variation not explained by sex or *APOE* genotype
- Protective genetic factors exist in humans that delay onset of FAD
- Asymptomatic AD/resilience difficult to study in human populations



# The solution: Build a pre-clinical model of AD that better aligns with human disease



Human diversity

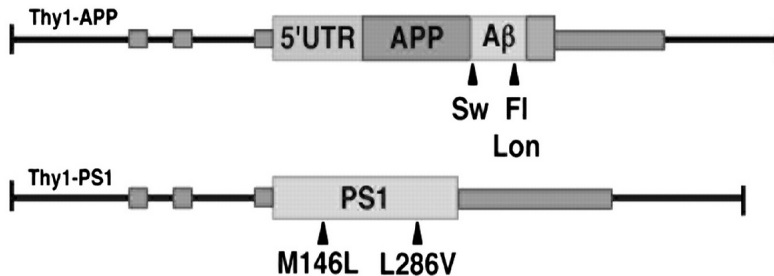


Mouse diversity

**Hypothesis:** The creation of a genetically diverse panel of mice that carry human mutations that cause AD would better model complex genetics in human AD, and enable identification of modifiers of AD dementia

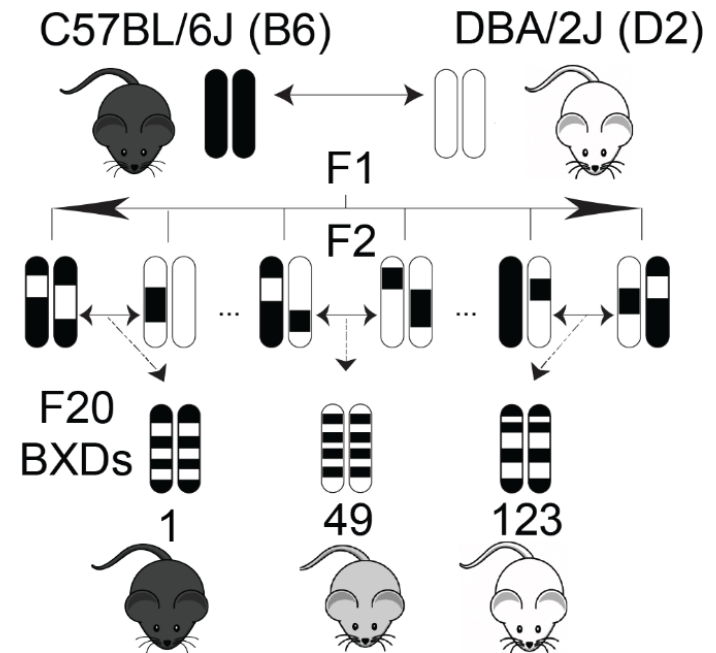
# AD-BXD panel to identify modifiers of AD

- Combines two well-established resources:
  - 5XFAD transgenic mouse
  - BXD genetic reference panel is a recombinant inbred (RI) strain

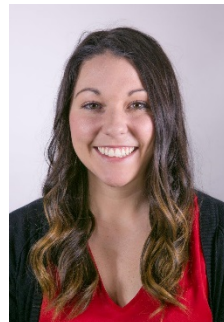


Oakley et al, 2006

X



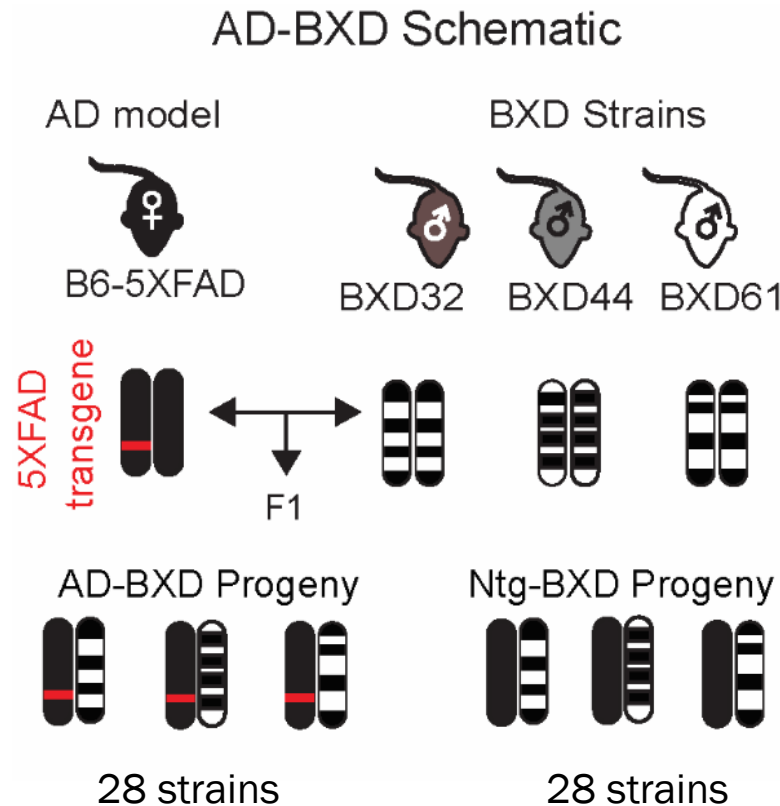
Peirce et al., 2004



Sarah Neuner, PhD  
(current, postdoc Goate lab)

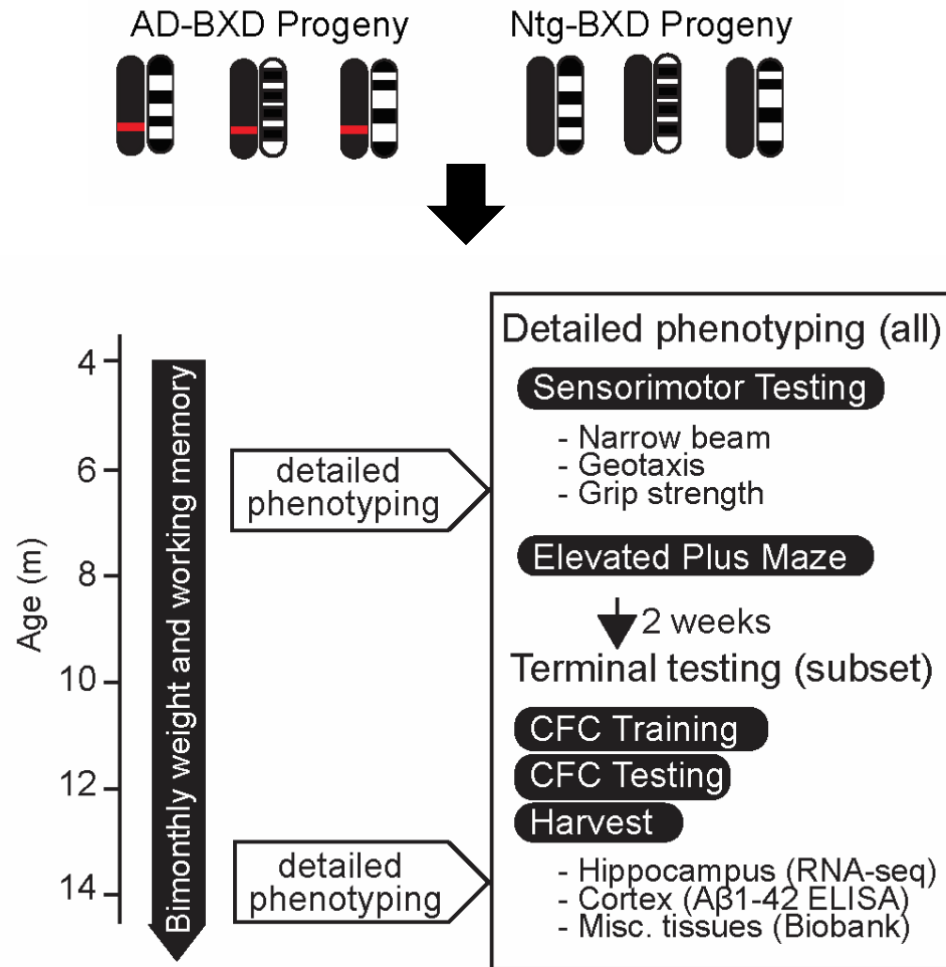
# AD-BXD panel to identify modifiers of AD

- Panel of ‘high-risk’ carriers and nontransgenic (Ntg) age-matched littermates
- Replicable across time and laboratories





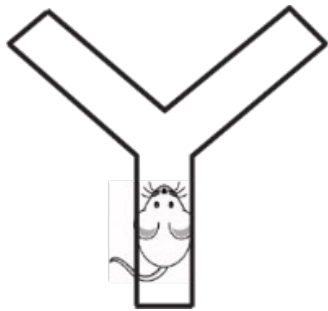
# Phenotyping pipeline to identify modifiers of AD



Heritability ( $h^2$ ) range from 0.5-0.8

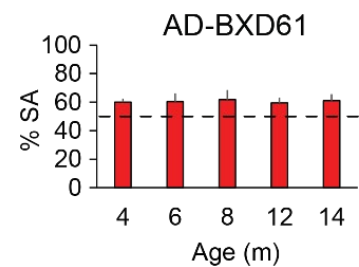
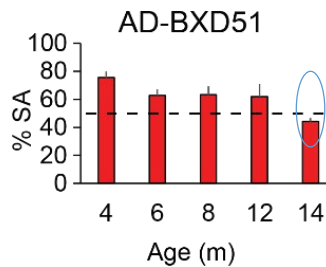
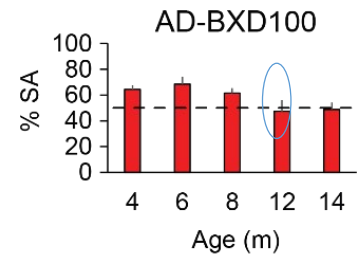
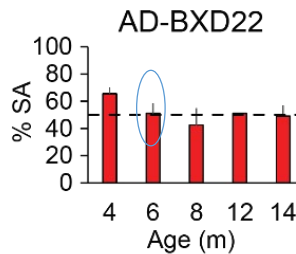
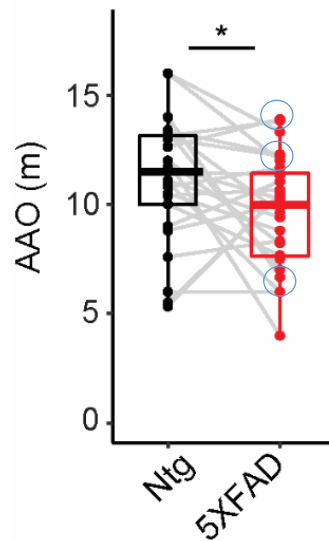
# Genetic background modifies age at onset (AAO) of working memory deficits

Y-maze test

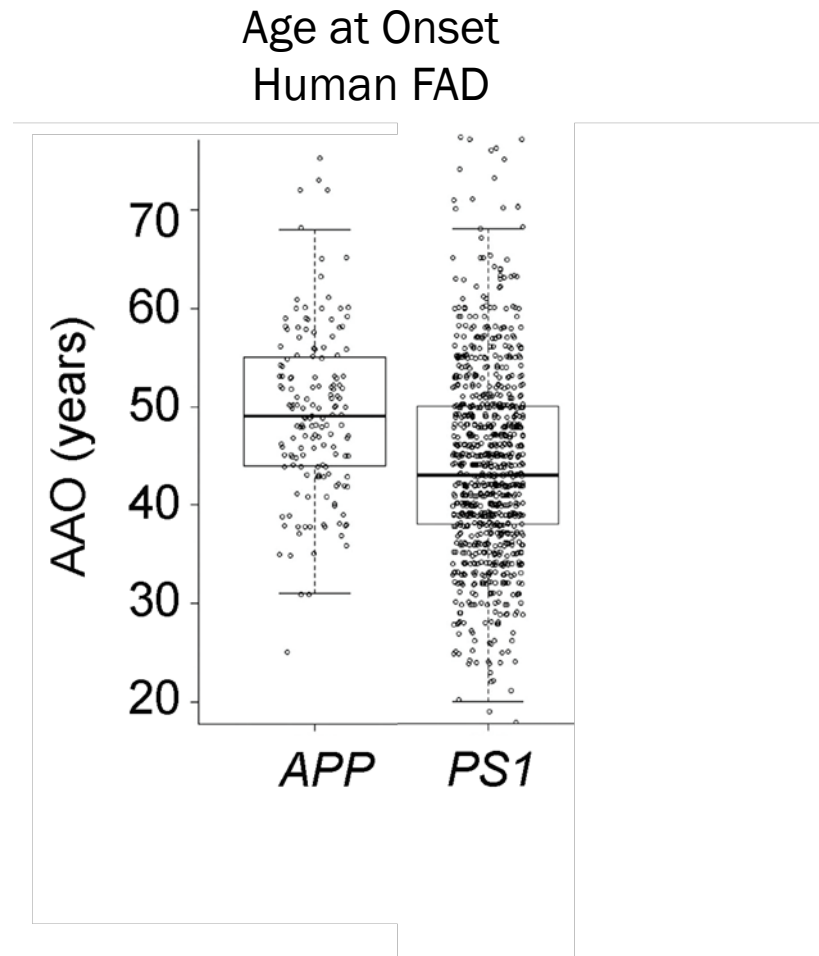
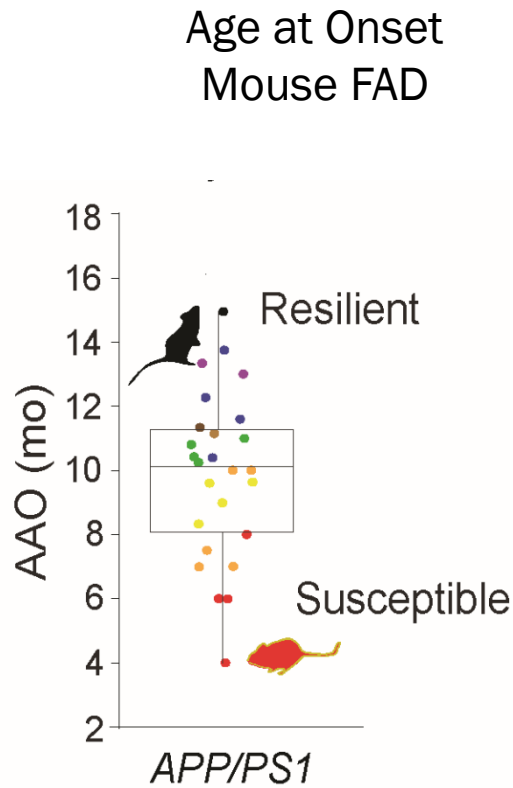


Animal classified as 'impaired' when alternation % reached chance levels (50%)

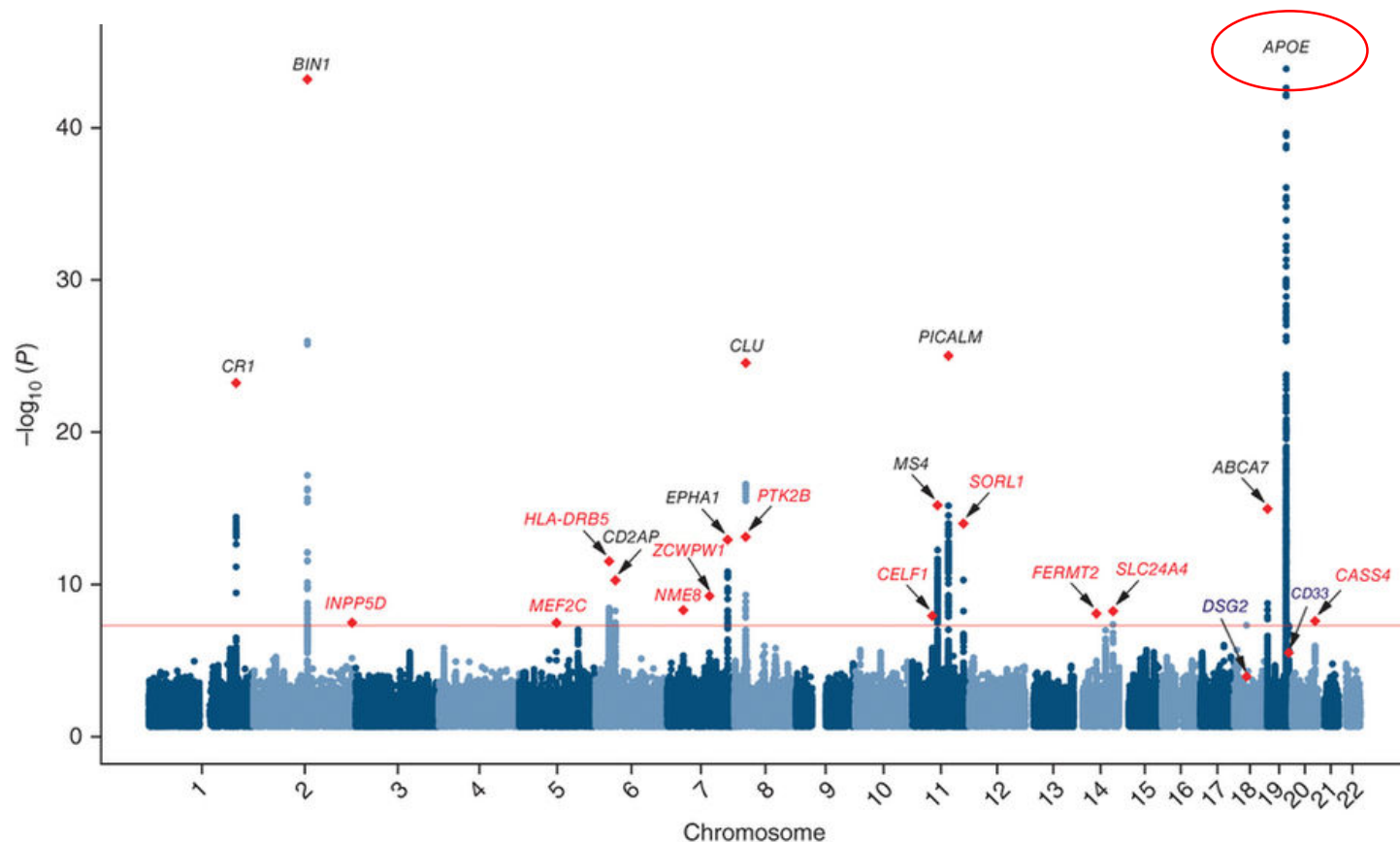
Age at Onset



# Genetic background modifies age at onset (AAO) of working memory deficits

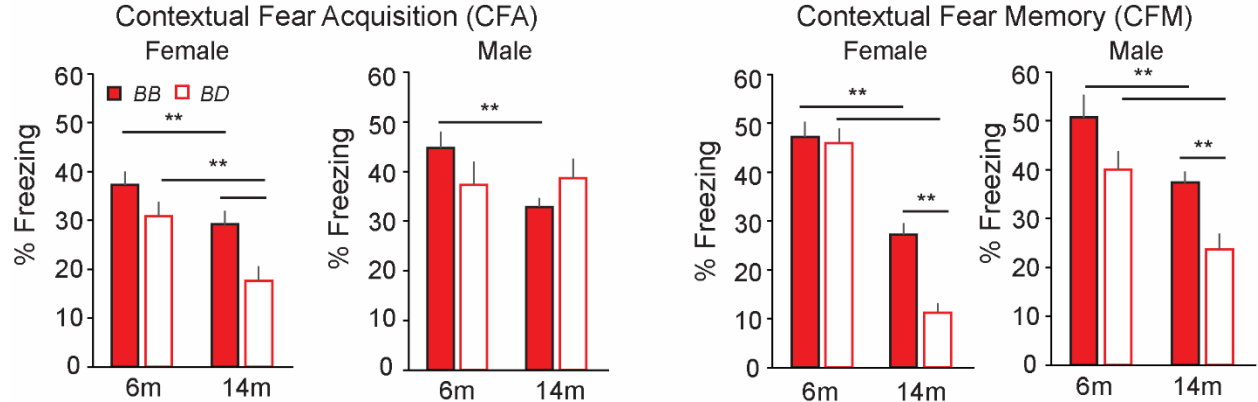
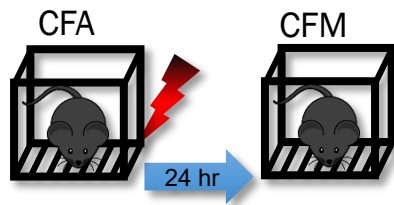


# Is susceptibility to AD across our panel sensitive to variation in known human AD risk loci?



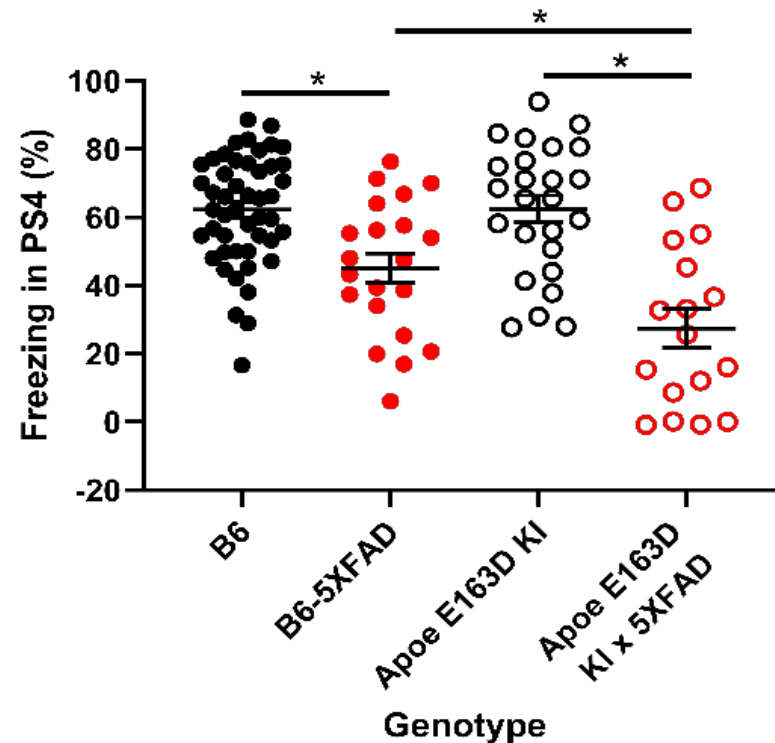
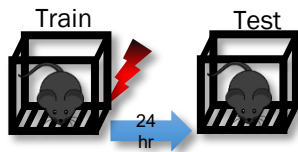
# Cognitive function in AD-BXD is sensitive to variation in *Apoe*

human position		118		153	158	
<i>Apoe</i> $\epsilon$ 2	RLGADMEDV	C	GRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDA	DDLQK	C	LAVY
<i>Apoe</i> $\epsilon$ 3	RLGADMEDV	C	GRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDA	DDLQK	R	LAVY
<i>Apoe</i> $\epsilon$ 4	RLGADMEDV	R	GRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDA	DDLQK	R	LAVY
<i>Apoe</i> B6	RLGADMEDL	R	NRLGQYRNEVHTMLGQSTEEIRARLSTHLRKMRLMRDA	EDLQK	R	LAVY
<i>Apoe</i> D2	RLGADMEDL	R	NRLGQYRNEVHTMLGQSTEEIRARLSTHLRKMRLMRDA	DDLQK	R	LAVY
mouse position		122		163	168	



# Naturally occurring genetic variants at *ApoE* locus in mice protect against cognitive decline in FAD mutation carriers

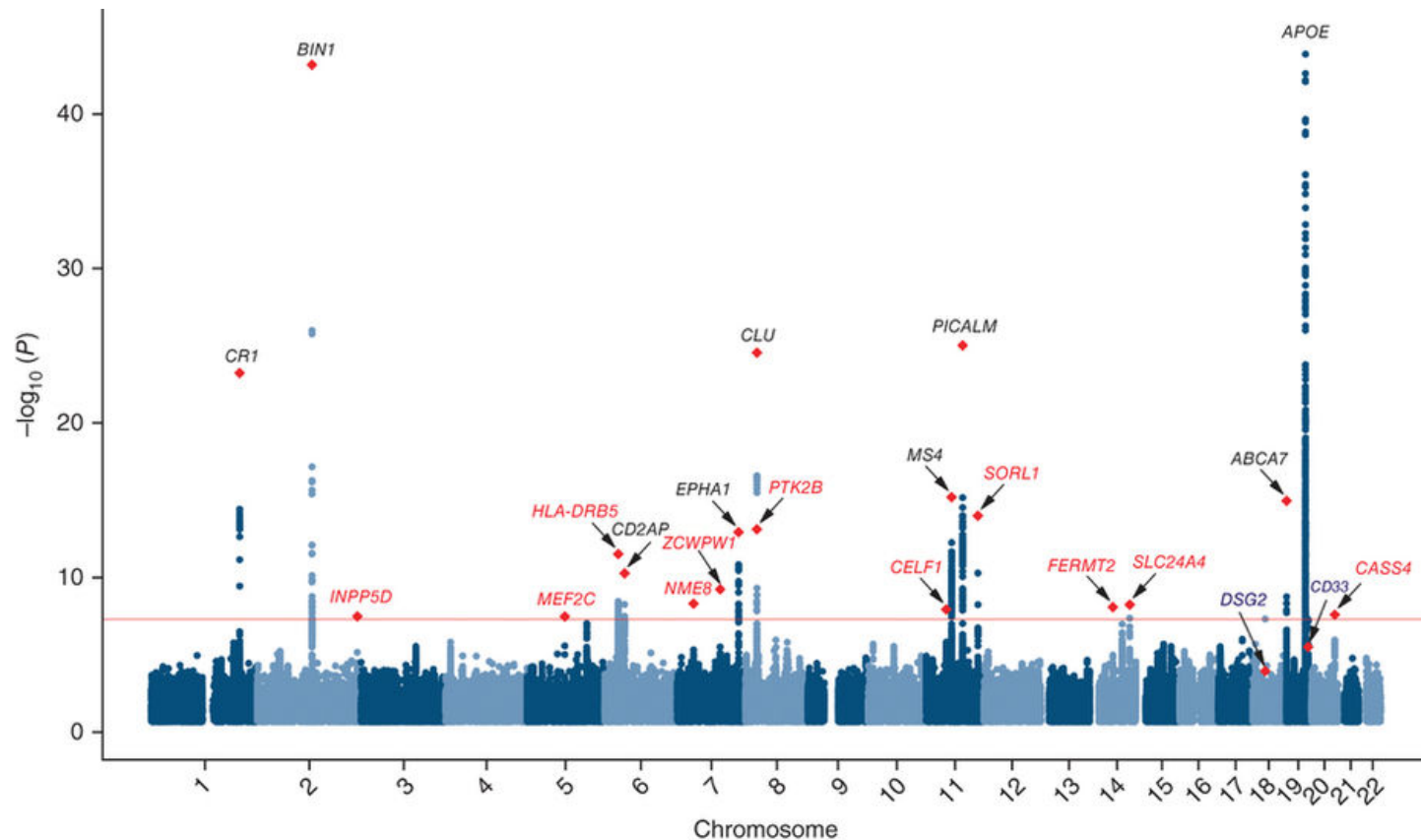
<i>Apoe</i> B6	RLGADMEDL <b>R</b> NRLGQYRNEVHTMLGQSTEEIRARLSTHLRKMRKRLMRDA <b>E</b> DLQK <b>R</b> LAVY
<i>Apoe</i> D2	RLGADMEDL <b>R</b> NRLGQYRNEVHTMLGQSTEEIRARLSTHLRKMRKRLMRDA <b>D</b> DLQK <b>R</b> LAVY
mouse position	122 163 168



**David Anderson, unpublished data**

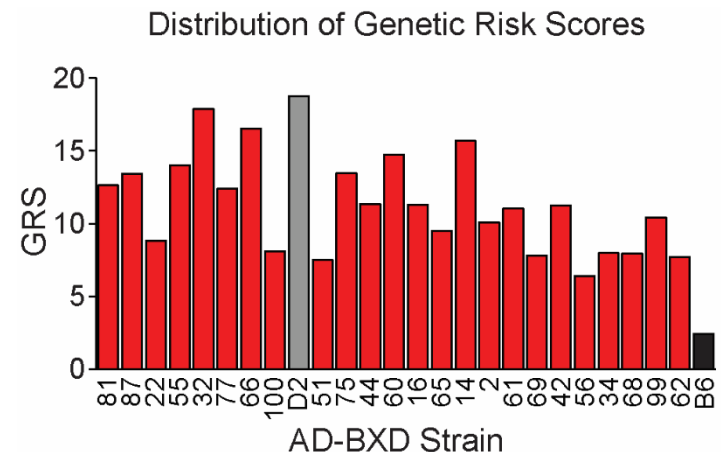
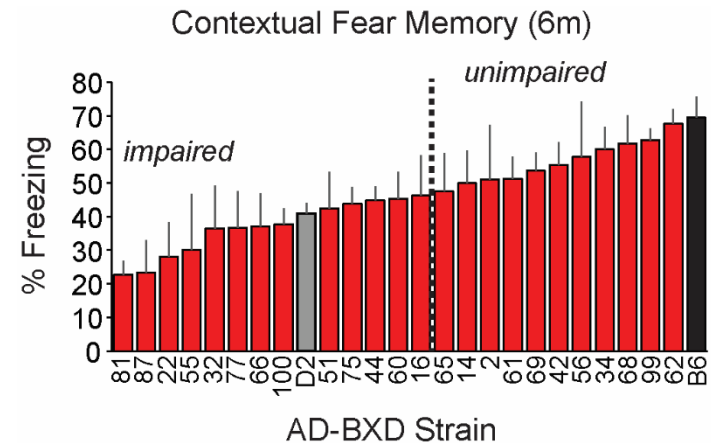


# Is susceptibility to AD across our panel sensitive to variation in known human AD risk loci?

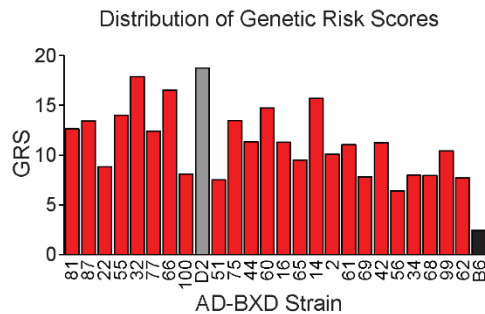


# Definition of a genetic risk score to assess sensitivity to variation in AD risk loci

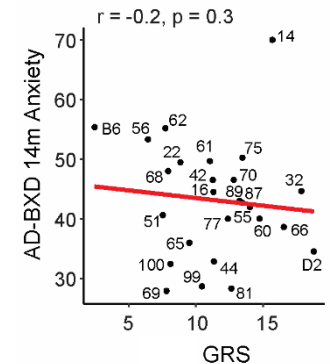
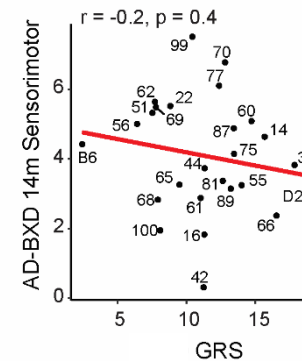
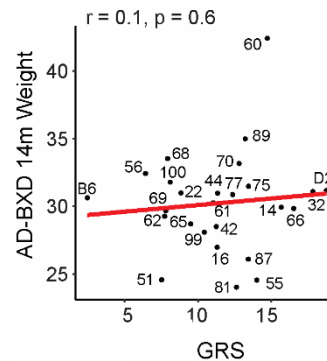
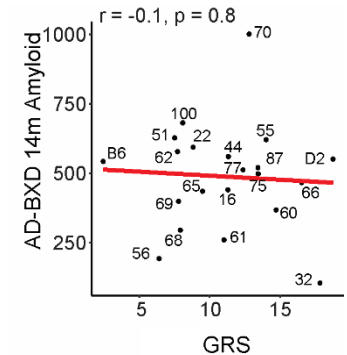
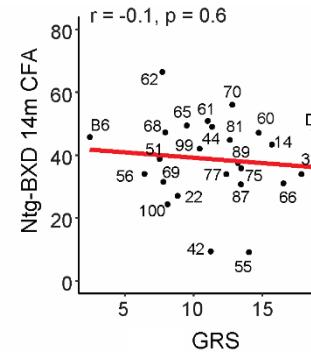
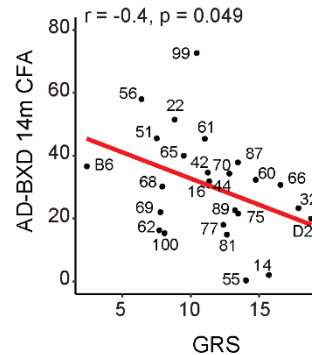
- Stratify 'impaired' vs 'unimpaired' based on 6m CFM
- Determine each strain's genotype at 21 loci known to confer risk for LOAD
- Designate risk allele & calculate odds ratio
- Combine into overall genetic risk score



# Genetic risk score predicts AD-related cognitive decline



- No association with Ntg-BXD CFA
- Association specific to cognitive traits



# Conclusions

- Naturally occurring mouse genetic diversity can be utilized to understand susceptibility to age- and AD-related cognitive decline.
- Use of genetic diversity across model systems is likely to greatly enhance translational relevance of preclinical findings
- Reproducible nature of the BXDs and CCs (with or without the 5XFAD transgene) facilitates future studies to investigate hypotheses regarding mechanism
- Wide array of mouse models of polygenetic diseases will likely be improved by inclusion of genetic diversity and translationally relevant environmental exposures.

# Acknowledgements

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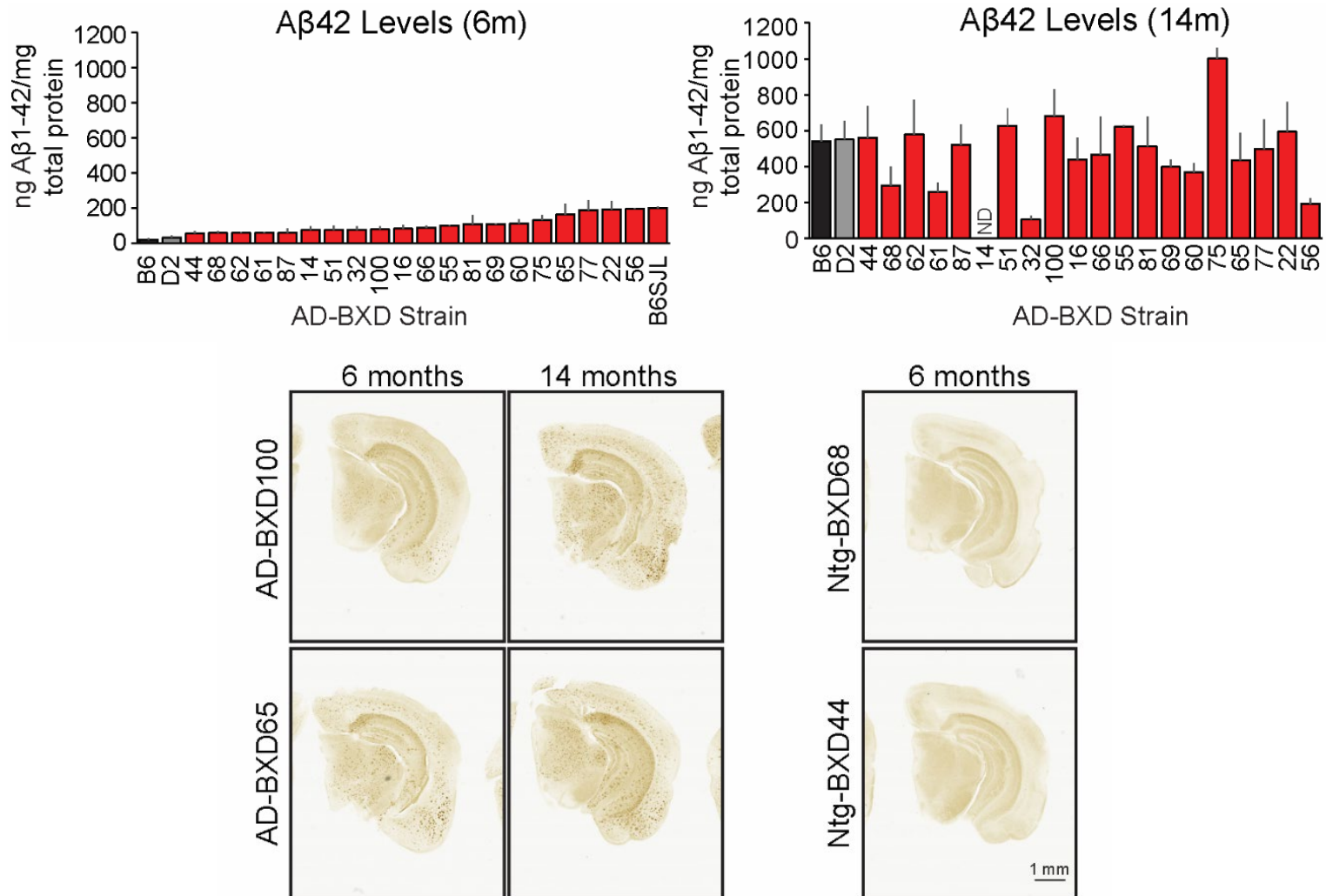
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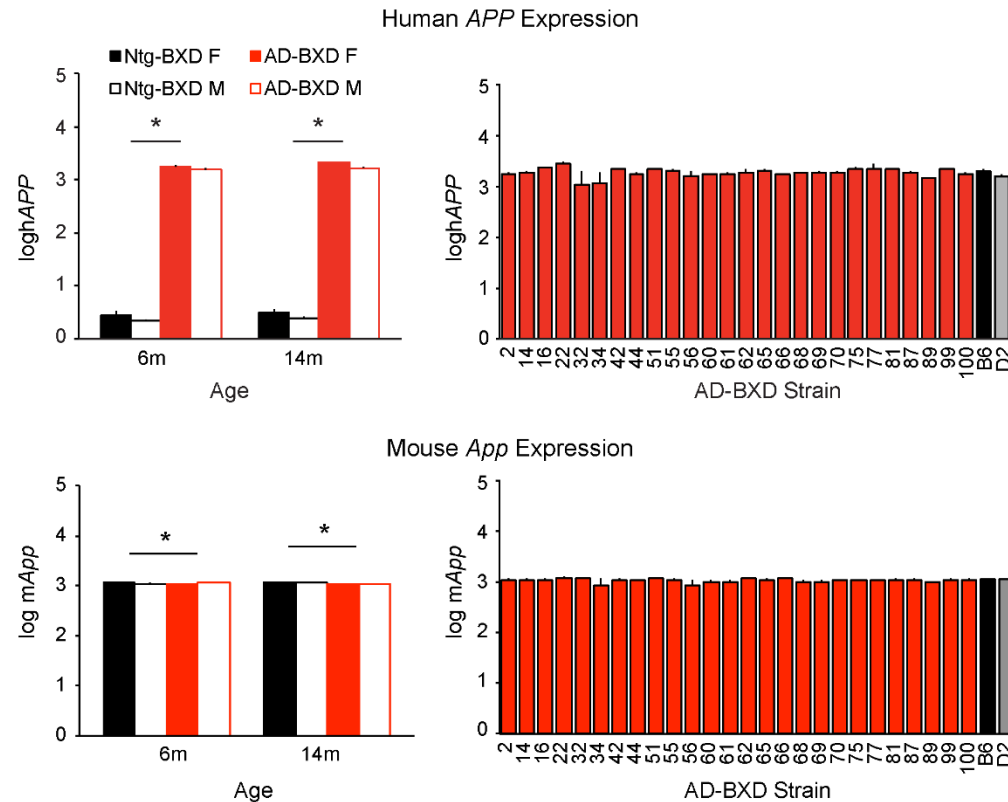


# Genetic background modifies human amyloid-beta 1-42 accumulation



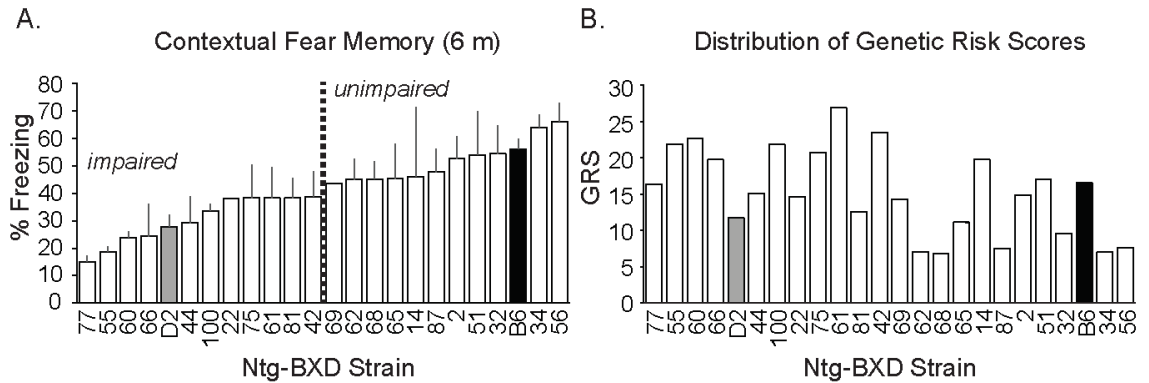


# Genetic background does not modify the expression of human or endogenous mouse *APP* mRNA (or *Psen1*, \*not shown)



# Ntg-based GRS is not associated with cognitive outcomes

- Hypothesized repeating the process using Ntg-BXDs as baseline would produce uninformative GRS



# Ntg-based GRS is not associated with cognitive outcomes

- Hypothesized repeating the process using Ntg-BXD as baseline would produce uninformative GRS
- No correlation with cognitive or non-cognitive outcomes

