Genetics and Early Predictors of Resilience

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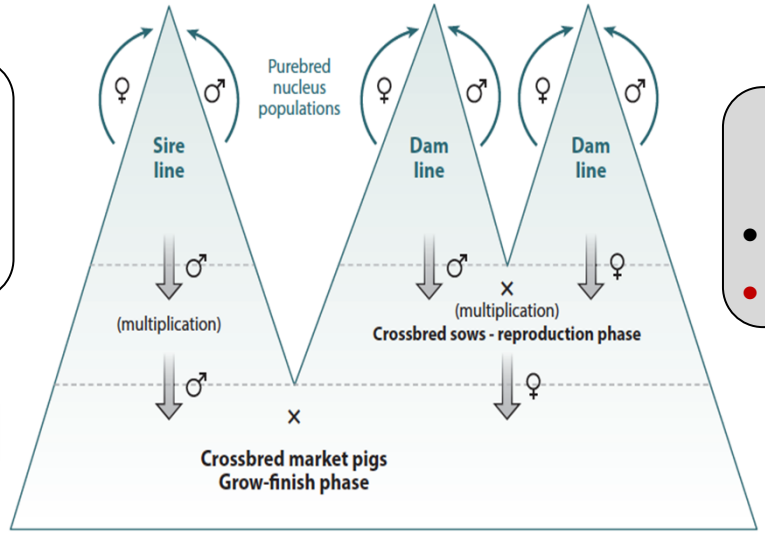
Application of Genomics to Improve Disease Resilience and Sustainability in Pork Production
PigGen Canada
USDA NIFA
The National Institute of Food and Agriculture
GenomeAlberta
GenomeCanada
GenomePrairie

Natural Disease Challenge Model (NDCM)

~3,500 weaned YxLR barrows from high health farms

Batches of 60-75 every 3 wks



Prediction of Resilience
- Phenotypic
- Genetic

Trait Genetics
- Parameters
- Architecture
- Mechanisms

Integrated statistical & bioinformatic analyses

Potential BIOMARKER data on young healthy pigs

- Immune response assays
- Blood transcriptome
- Blood metabolome
- Blood proteome
- Gut microbiome

650K SNP genotypes

Nursery 2 **GrowFinish**

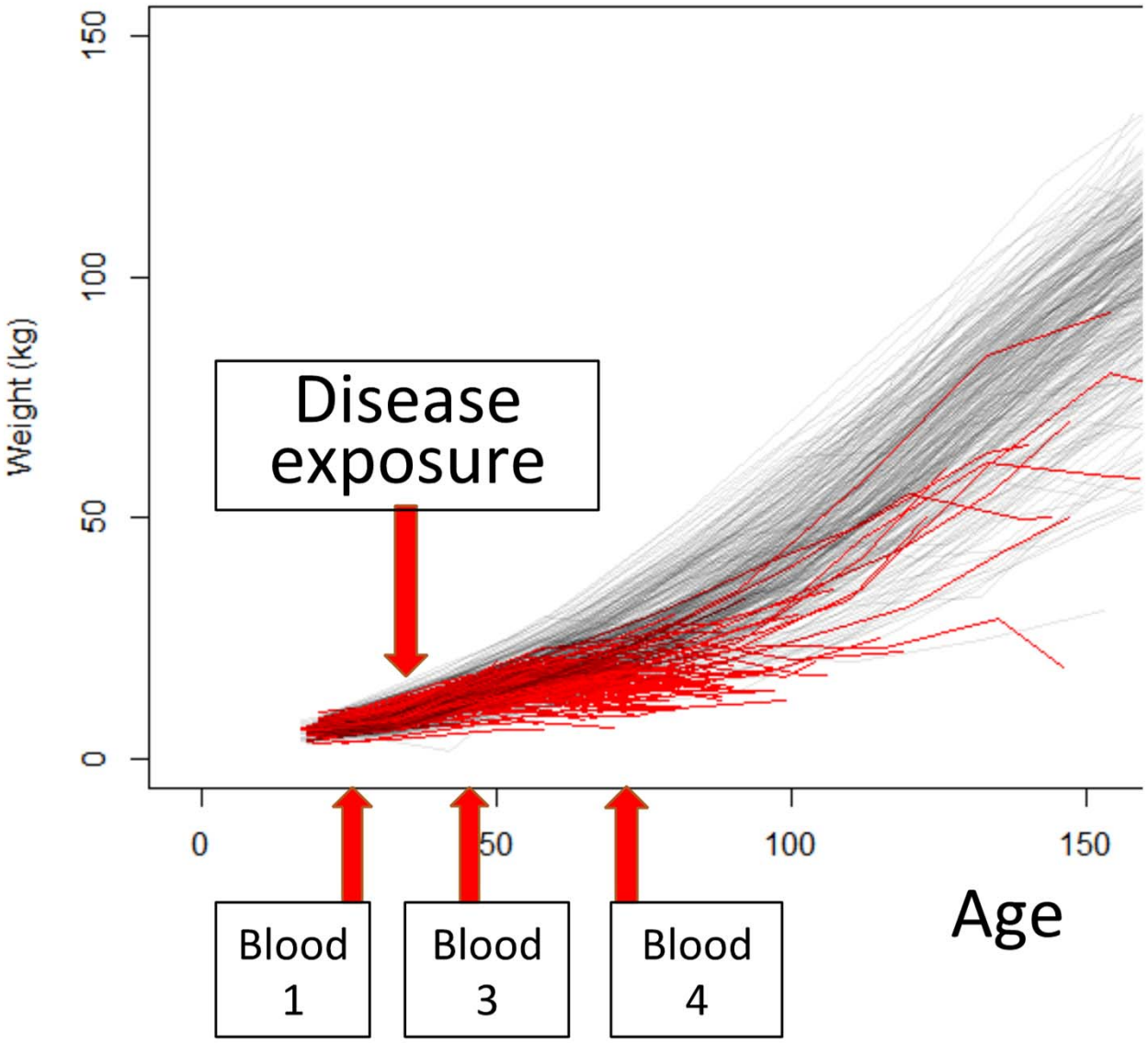
Phenotypes

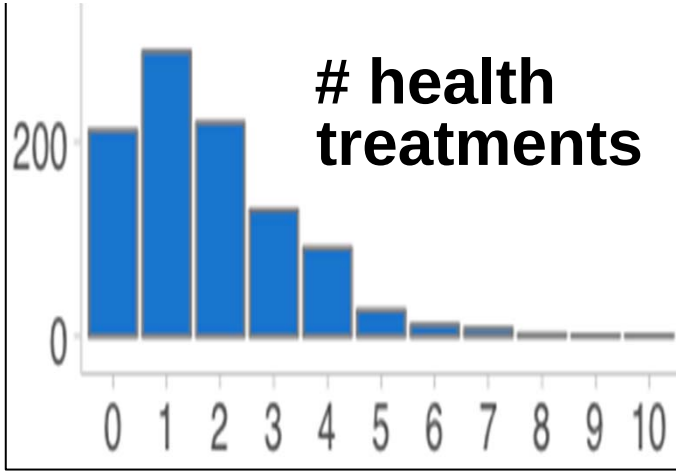
- Morbidity/mortality
- Growth performance
- Feed intake
- Water intake
- Carcass quality

Nursery Quarantine (19 days)

Natural Challenge Facility (~21 wks)

Example Growth Curves





Mortality Reasons %	
Lameness	10
Coughing	11
Unthrifty	5
Diarrhea red	1
grey/brown	19
yellow	7
Dermatitis	4
CNS	3
Respiratory	31
Arthritis	5
Inappetance	2
Cyanosis	2

Does the NDCM generate heritable data?

Putz et al.

ORIGINAL RESEARCH ARTICLE

Front. Genet., 08 January 2019 |

https://doi.org/10.3389/fgene.2018.00660

Trait		h^2
Growth	Nursery	**0.45** ± 0.07
	Finish	**0.26** ± 0.07
Feed Intake	Finish	**0.33** ± 0.07
Gain/Feed		**0.35** ± 0.07
RFI		**0.43** ± 0.07
# Treatments/day		**0.14** ± 0.07
Mortality	Liability	**0.26** ± 0.07
Carcass Wt		**0.31** ± 0.07
Destron BF		**0.52** ± 0.08
Destron LD		**0.40** ± 0.08
Lean Yield		**0.39** ± 0.09

Measures of Resilience based on feed intake patterns

Putz et al.

frontiers in Genetics

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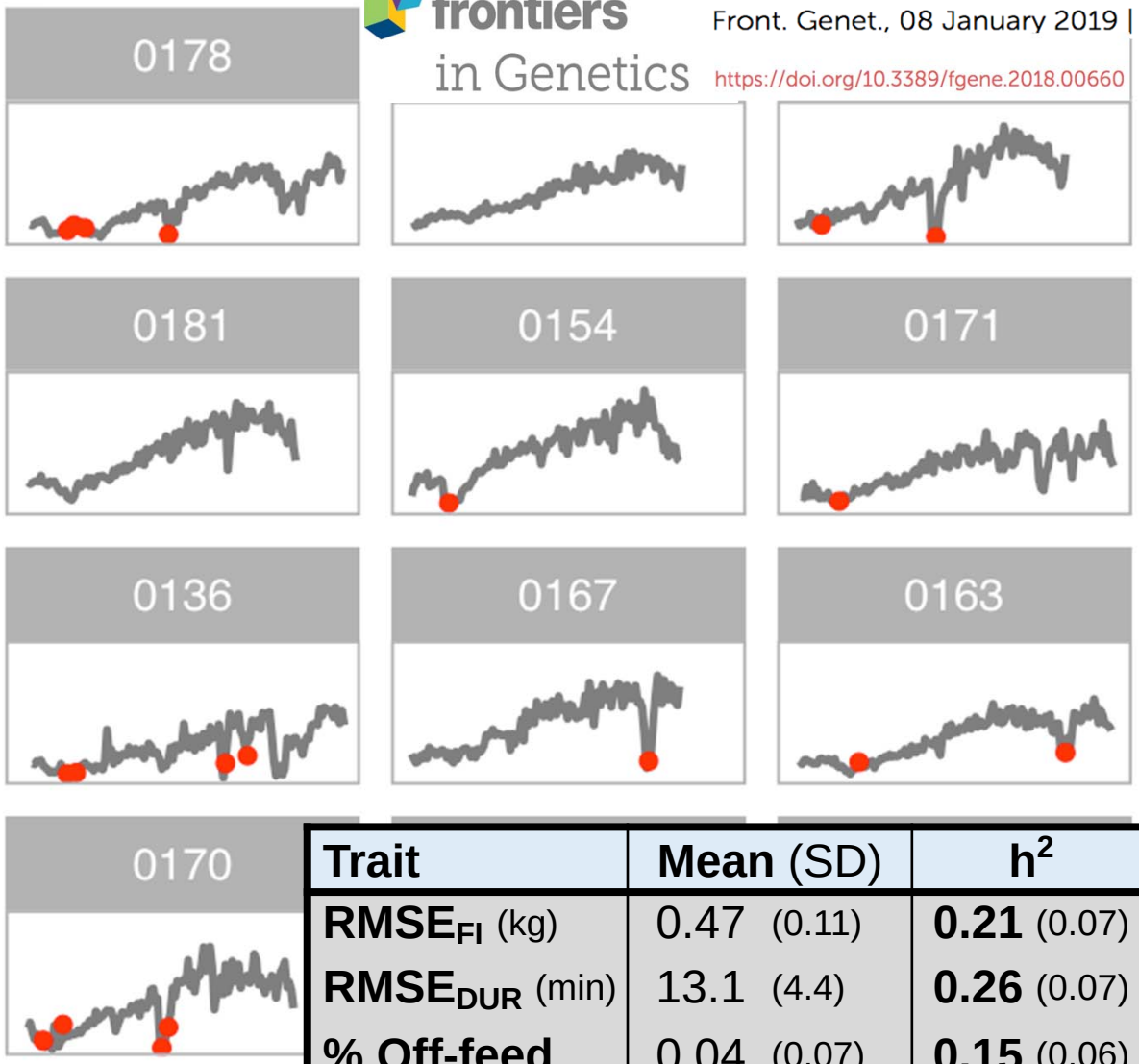
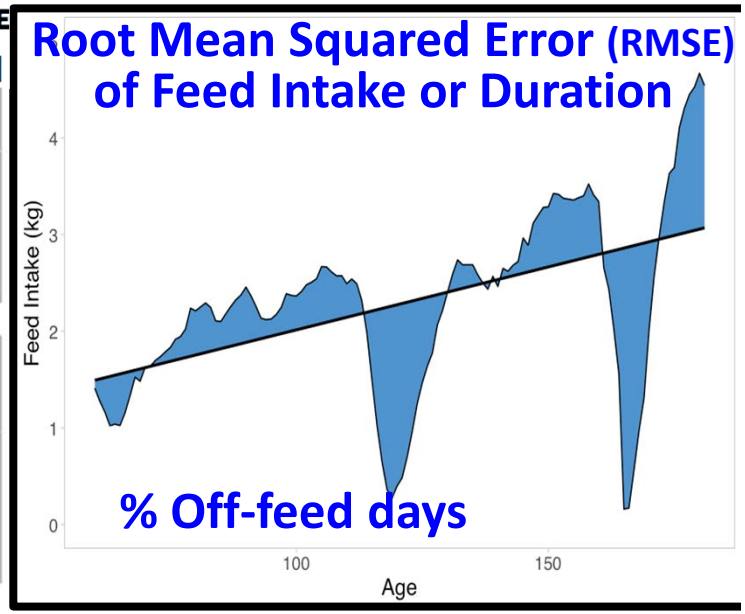




Trait	Mean (SD)	h^2	Genetic correlation (SE) with $RMSE_{FI}$	$RMSE_{DUR}$	% Off-feed
$RMSE_{FI}$ (kg)	0.47 (0.11)	**0.21** (0.07)	-	0.47 (0.26)	0.50 (0.31)
$RMSE_{DUR}$ (min)	13.1 (4.4)	**0.26** (0.07)		-	0.67 (0.28)
% Off-feed	0.04 (0.07)	**0.15** (0.06)			-
Mortality (%)			**0.37** (0.34)	**0.60** (0.26)	**0.75** (0.27)
Treatments/day			**0.56** (0.18)	**0.62** (0.13)	**0.85** (0.16)

High Immune Response Technology for Dairy Cattle

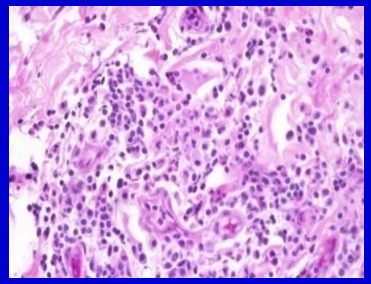
Bonnie Mallard et al.,
University of Guelph

Two Tests to Capture Broad-based Disease Resistance

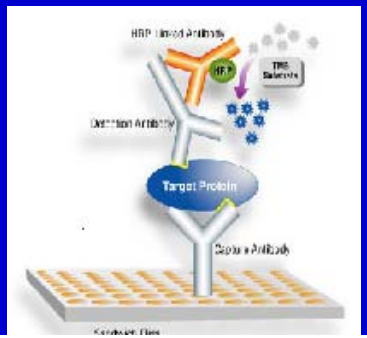
CELL-MEDIATED IMMUNE RESPONSE

+

ANTIBODY- MEDIATED IMMUNE RESPONSE

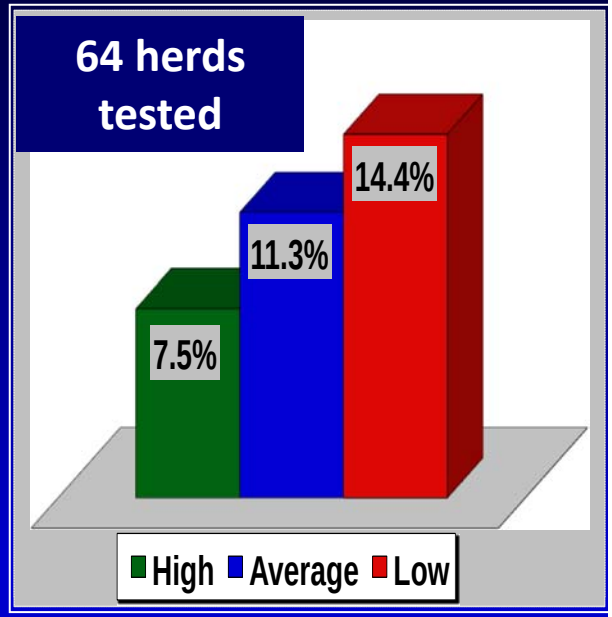


h^2 ~ 30%



Photos and figures courtesy of Dr. B. Mallard

High Immune Response Cows have less disease



Disease data from: Wagter, et al. 2000 J. Dairy Sci. 83:488-498; Thompson-Crispi, et al. 2012. J. Dairy Sci. 95:3888-3893; Thompson-Crispi, et al. 2013. Clin Vacc Immuno. 20:106-112.

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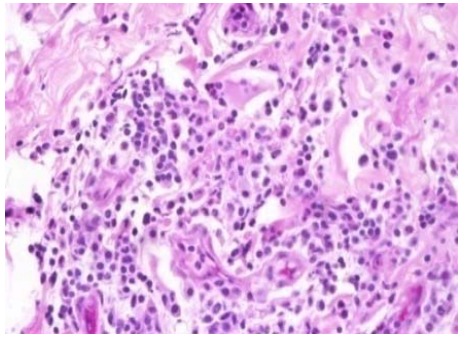
From the University of Guelph

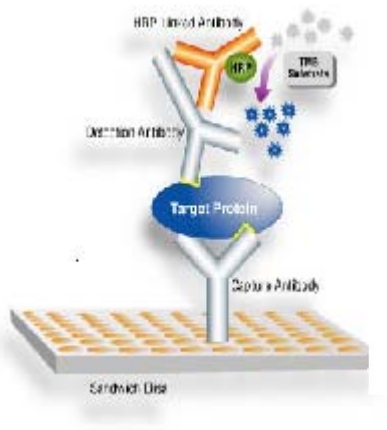
High Immune Response Technology in pigs

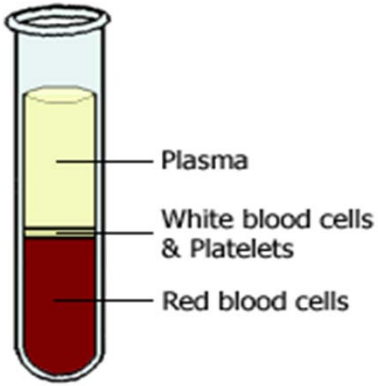
Julie Schmied, Bonnie Mallard
University of Guelph

CELL-MEDIATED IMMUNE RESPONSE

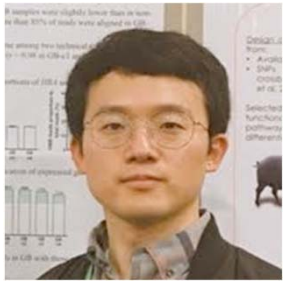


ANTIBODY- MEDIATED IMMUNE RESPONSE





Blood transcriptome of young healthy pigs as a biomarker to improve disease resilience



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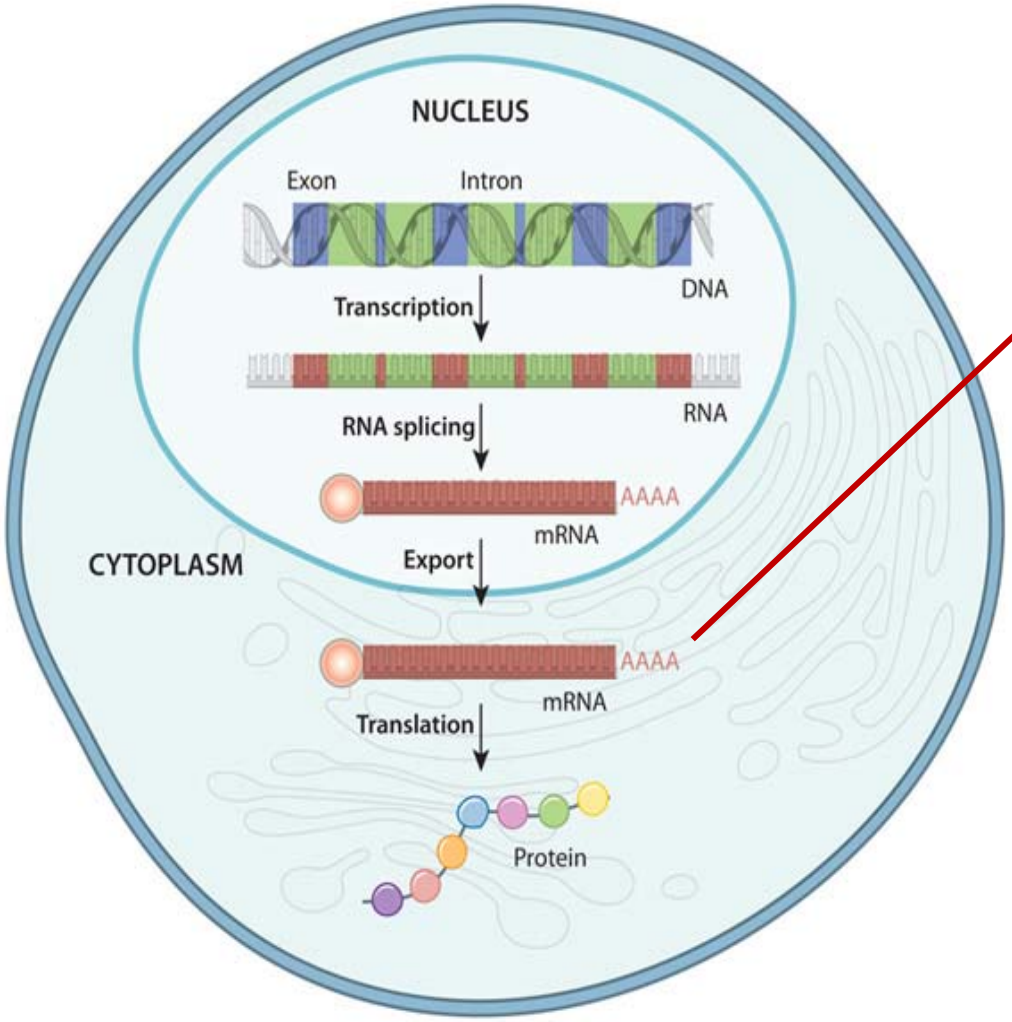

Level of expression of **>14,000 genes** measured in blood sample of 950 young healthy piglets

>14k new "phenotypes"

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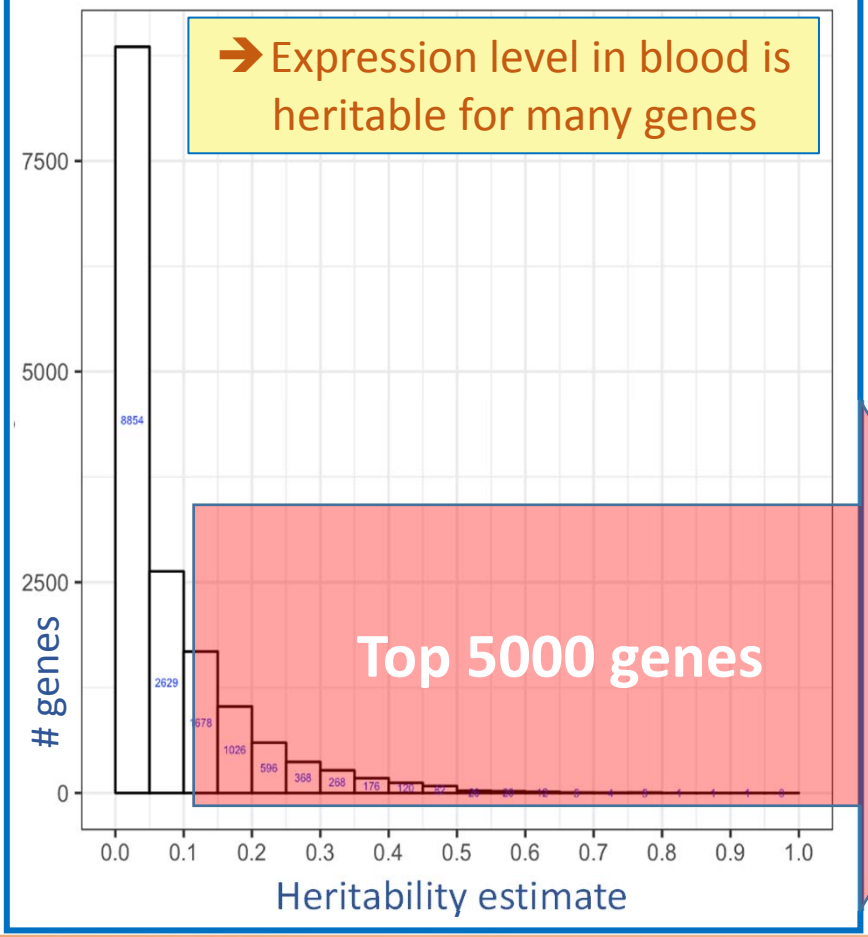
Blood gene expression data generated on ~14,000 genes on 950 pigs and used for genetic analyses

>14,000 estimates of heritability

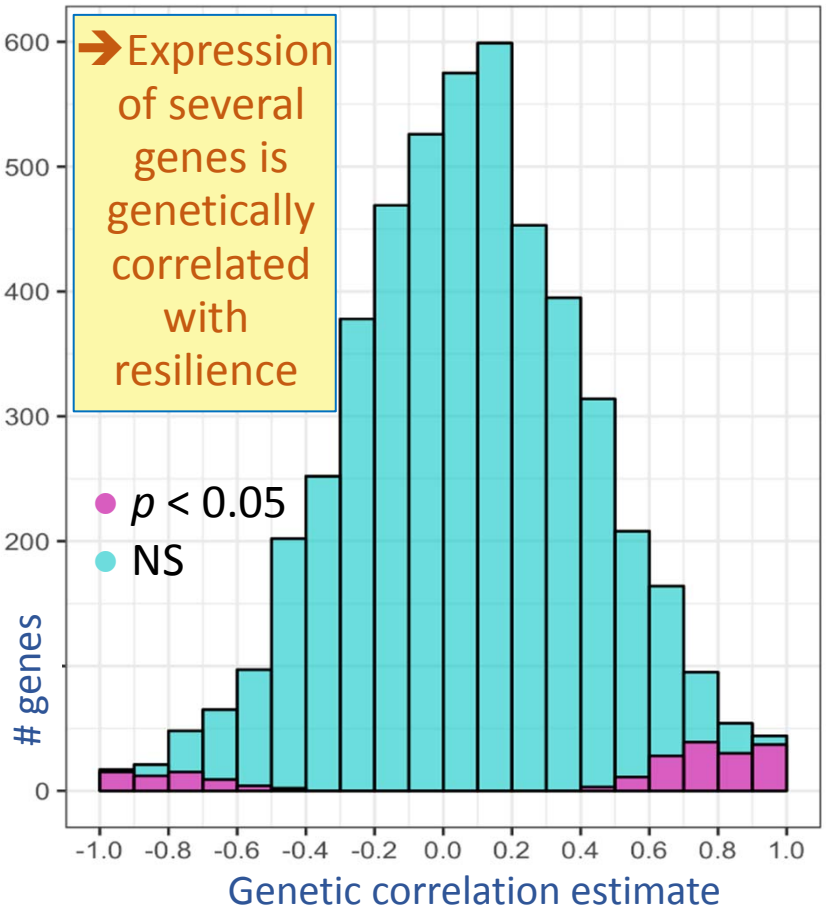
➔ Expression level in blood is heritable for many genes



Top 5000 genes

5,000 estimates of genetic correlations of expression with mortality

➔ Expression of several genes is genetically correlated with resilience



Conclusions

- A natural challenge model to characterize disease resilience in pigs has been established successfully.

  → Heritable variation in growth, feed intake curves, mortality, morbidity

- Phenotypes derived from day-to-day fluctuations in feed intake under disease are heritable measures of resilience.

- Immune assays conducted on young healthy pigs show promise as heritable indicator traits to select for resilience.

- Transcriptome and other –omics data obtained from blood of young healthy pigs provides a wealth of information that can be used to identify early indicator traits for disease resilience

Acknowledgements & collaborators

Project Team

Michael Dyck, U of Alberta, Project Lead

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