

Genetics of Feedlot Cattle Health

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The economics behind genetic improvement of cattle health

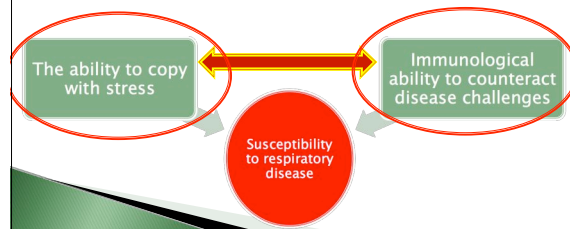
- Prevention and treatment of disease in the feedlot— >\$3 billion (Griffin, 1997)
- ~1.1 million cattle were lost to respiratory causes in 2005 @ > \$692 million (USDA, 2006).
- ~16 pounds reduction in HCW for animals treated in 1st 40 days (Snowder et al., 2007)
- Lung damage (yes/no) – 34 pounds of carcass weight (Engler, 2007)

Overview

- Project justification
- Project design
- Results relative to incidence of bovine respiratory disease
 - Characterization of "disease"
- Genetic component of BRD
- Influence of disease on carcass performance

The project and approach

- Funded by Pfizer, Inc. -Pfizer Animal Genetics
- The premise:
 - Susceptibility/resistance to disease is, in part, genetically controlled and that genetic control can be characterized by DNA markers.
- This genetic control is likely manifest through two mechanisms:



Data collected in the feedlot

- Phenotypes characterizing morbidity**
 - Sick (yes/no)
 - Time to recovery
 - Treatment records
 - drugs, temperatures, weight change
 - Mortality
 - Necropsy results
 - Bacteriology
 - FA tests
 - Lung lesion scores collected at harvest
 - BVD PI information
 - Respiration rates
 - Visual scores
 - Nasal discharge, Eye, Cough, Depression, rapid breathing
- Performance traits**
 - Weights--Arrival, re-implant
 - Carcass traits
 - HCW, MS, QG, REA, BF, YG
 - Ultrasound (3 times):
 - %IMF, REA, Backfat
 - Baseline stress and behavior characteristics**
 - Temperament-Flight speed, chute Score
 - Stress indicators
 - Baseline disease/immunological status measures**
 - Exposure in the feedlot
 - BVD I & II, PI3, IBR, BRSV
 - Tests for differences in immune response
 - Body temperature profiles

Study Background

- Steers were shipped to cooperating feedlot in Lamar, CO
- Split over 2 years
- No vaccination first year on arrival
- Vaccination on arrival second year
- Implants were used

Year	Number
1	1,551
2	1,319
Total No.	2,870

The Results

BRD Treatment Rates

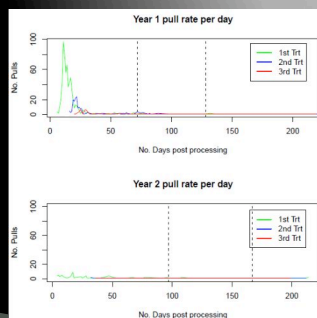
BRD Treatment Rates

- Year 1—45% treated
- Year 2—7.1% treated



Treatment and Death Summary--Year 1						Treatment and Death Summary--Year 2					
No Treatment	1 TRT	2 TRTS	3 TRTS	Died		No Treatment	1 TRT	2 TRTS	3 TRTS	Died	
55.00%	33.5%	7.5%	3.9%	6.2%		92.90%	6.4%	0.3%	0.4%	2.3%	

Treatment rates over time



Analysis of “disease” traits poses unique challenges

- Were animals treated truly “sick”?
 - Pen riders may pull deeper in an “outbreak”
- Exposure rate
 - Were all animal exposed?
 - Analogous to “did they have the opportunity to express genetic potential”?
- Were animals “sick” but never treated?
 - Lessons from the natural world
 - Some animals are likely exposed but never exhibit clinical signs (i.e. never pulled for treatment)

Goal

- To appropriately classify “sick” animals
 - better identification of sick animals will improve the probability of identifying genetic differences between animals.
- Improve identification will lead to better selection tools.
 - Ultimately leading to genetic progress

Literature suggests the use of lung lesion scores as a secondary method for determining incidence of BRD

Thomson, 2003 (unpublished)

26% Pull rate	Lesions	No Lesions
Pulled	0.161	0.099
Not Pulled	0.318	0.422

Wittum, 1996

35% Pull rate	Lesions	No Lesions
Pulled	0.203	0.057
Not Pulled	0.503	0.237

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Pulled	0.203	0.057
Not Pulled	0.503	0.237
Year 1		
	Lesions	No Lesions
Pulled	.313	.126
Not Pulled	.394	.167
Year 2		
	Lesions	No Lesions
Pulled	.033	.030
Not Pulled	.438	.499

Approaches to lung scores

	Year 1 (2007)	Year 2 (2008)	Combined
	Disease classification percentage	Disease classification percentage	Disease classification percentage
Mean lung score			
0	9.7	3.3	6.4
0 < i ≤ 1	6.2	24.3	15.3
1 < i ≤ 2	31.6	56.1	44.1
2 < i ≤ 3	52.5	16.3	34.2
Lesions Present			
0	29.3	53.0	41.3
1	70.7	47.0	58.7

Is there genetic variability for these traits?

- ▶ Heritabilities
 - Lung Score = 0.0
 - Lesions present = .04
 - Treated (yes/no) = .15

Classifications for disease

- ▶ Treated versus not treated
- ▶ Number of BRD treatments
- ▶ "total BRD"
 - Animal was treated and/or animal had lung score >1.5

Are these traits heritable?

Classification	h ²
Trt	0.15 ± 0.06
NoTrt	0.04 ± 0.03
Total BRD	0.07 ± 0.06

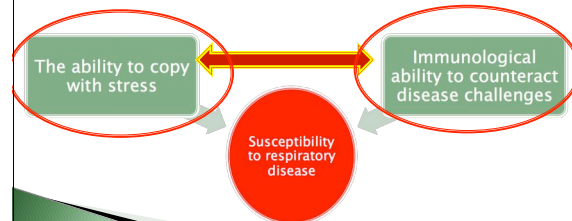
Approach to developing the tools

- ▶ Two questions:
 - Does the trait have a genetic component (non-zero heritability)?
 - Is it economically relevant?
 - Is it related to feedlot and/or carcass performance?

Effects on carcass performance (significant effects)

		Classification level			
		0	1	2	3
Trt	HCW	787	-9.7	-	-
	MS	407	-11.3	-	-
	Fat	.52	-0.03	-	-
NoTrt	HCW	787	-6.4	-9.7	-51
	LM area	12.8	.02	.12	-.87
	MS	407	-11.5	-14.8	-1.0
	Fat	.52	-.02	-.04	-.04
Total BRD					
	MS	407	-6.2		
	Fat	.52	-.02		

- This genetic control is likely manifest through two mechanisms:



The behavior traits

	Exit Velocity (arrival)	Exit Velocity (2 nd processing)	Chute Score (arrival)	Chute Score (2 nd processing)
Exit Velocity (arrival)	.17 ± .05	.74 ± .12	.57 ± .18	.27 ± .21
Exit Velocity (2 nd processing)	-	.27 ± .06	.21 ± .18	.26 ± .18
Chute Score (arrival)	-	-	.18 ± .05	.77 ± .16
Chute Score (2 nd processing)	-	-	-	.17 ± .05

¹HCW = hot carcass weight (kg), LM area = Longissimus muscle area (cm²), MS=marbling score, Fat = subcutaneous fat thickness (mm)

Proportion of variation explained through genome scans— NBCEC and Dr. Dorian Garrick

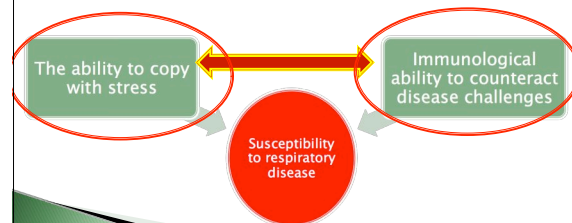
- Heritability
 - Treatment = .22
 - Mean lung score = .12
 - Exit velocity on arrival = .24
 - Chute Score on arrival = .22

Summary

- Appears to be genetic variation for susceptibility to BRD
 - Heritability = .15
 - Similar to heritability of heifer pregnancy
- Occurrence of BRD has a significant effect on carcass and feedlot performance


The next steps


- Begin to apply physiological outcomes to treatment information




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Questions?

