

WATER INTAKE: TESTING PERIOD AND ANIMAL VARIATION

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Carbs

Protein

Fat

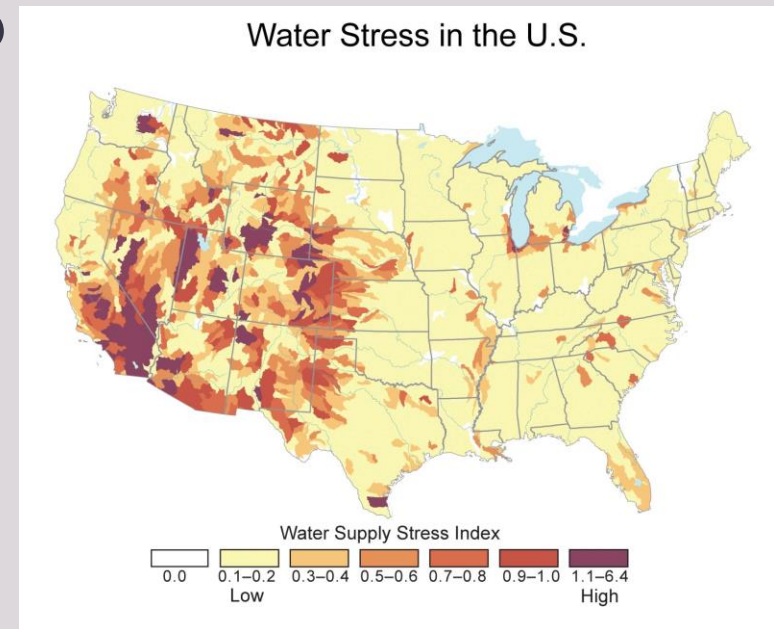
Vitamins

Minerals

Water

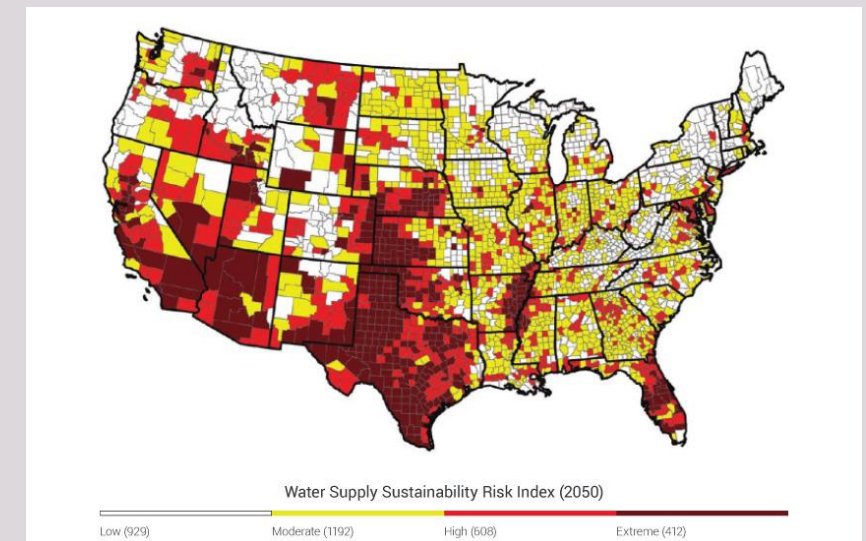
Why Water Intake?

- What are the 6 essential nutrients?
- Water shortages in some areas
 - *Importance can be variable*
 - Little rainfall
 - Water rights issues
 - Drought
 - Competition from other ag (irrigation, crop production)
 - Competition from wildlife
 - Competition from humans
- Has been tied to performance (weight gain and ability to deal with heat stress) in the literature
 - *Specific mechanisms are less well defined*
 - *Little exploration from a genetics standpoint outside of model organisms and some specific water conditions (i.e. high sulfur, Kessler et al. 2013)*



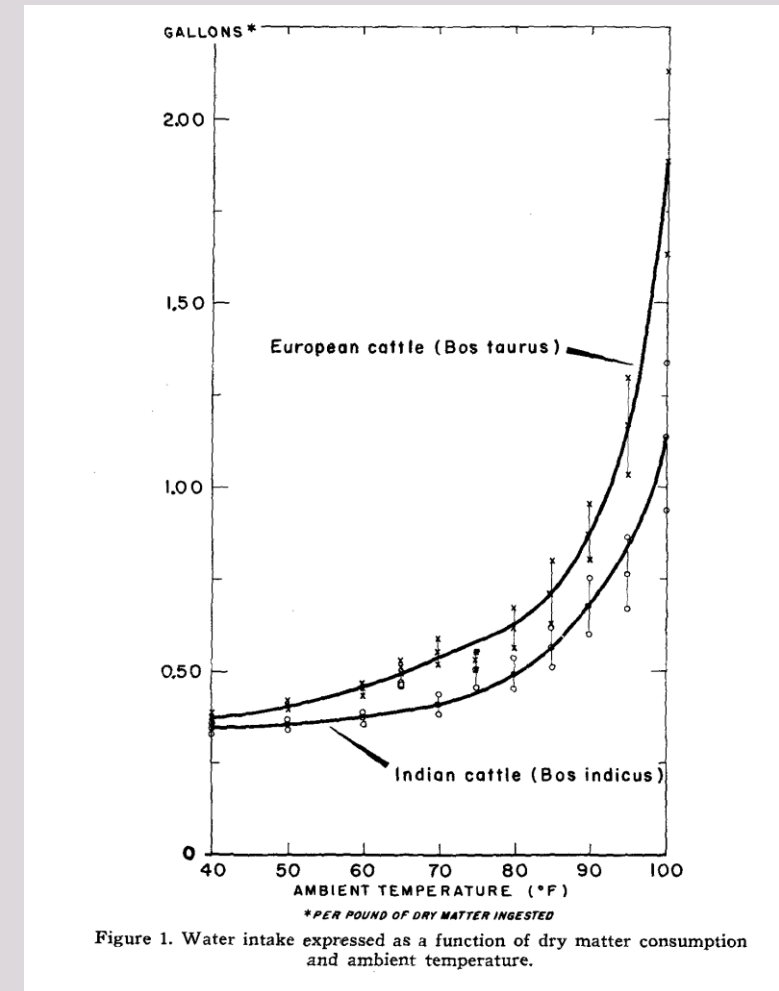
Demand from power, ag, and municipalities as a percentage of available water (globalchange.gov)

Projected decline in water supplies accounting for GHG emissions (globalchange.gov)



What do we know about water intake?

- Breed differences (Winchester and Morris 1956)
- Voluntary water restriction when quality is poor
 - *Some restriction even w/ chemically treated vs not* (Lardner et al. 2013)
 - *Up to 22% with high salt* (Lopez et al. 2016)
 - *Water restriction impacts body temperature regulation* (Finch 1986)
- NRC water intake values based off of Winchester and Morris paper from 1950s
 - *Need more contemporary data!*



Winchester and Morris, 1956

Water intake in the Literature

- Group-based Measurements
 - *Average intakes of 32.4-40 L/hd/day and 17.3 L/day in summer and winter, respectively* (Arias and Mader 2011, , Sexson et al. 2012, Parker et al. 2000)
- Now have the technology to collect large numbers of WI phenotypes on individual animals
 - *Meyer et al. 2004 (60 lactating dairy cows)*
 - WI range from 14-171 kg/day (Mean 81.5 kg/day)
 - *Meyer et al. 2006 (62 Holstein bulls on finishing ration)*
 - WI range 0 to 78.7 kg/day (mean 17.8 kg)
 - *Brew et al. 2011 (146 growing beef cattle)*
 - Mean WI of ~30 L/hd/day
 - Brahman and Romosinuano cattle drank less than British and Continental cattle
 - No difference between bulls, steers, and heifers
- No heritability estimates or genomic studies of water intake in beef cattle
 - *Heritable in mice (Bachmanov 2002), successful selection experiments*

Influence of breed composition on water intake of growing beef cattle (source: Brew et al. 2011)

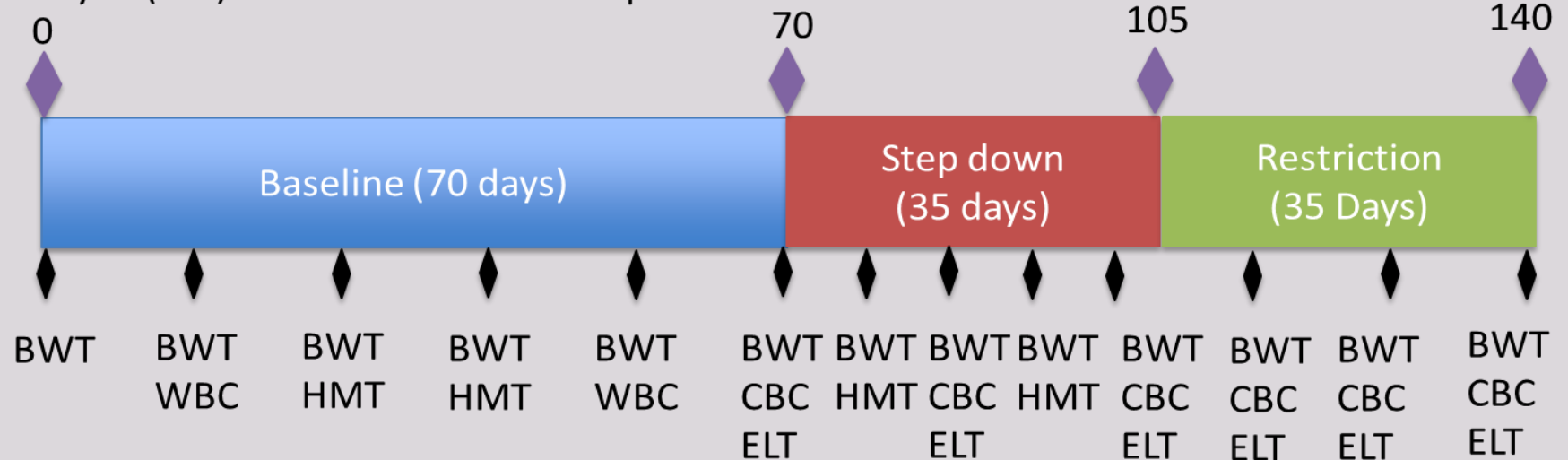
Breed Composition	Gross WI, L/head/d	WI/kg metabolic BW, L/head/d
Charolais X Angus	42.8 ^a	0.58 ^a
Angus X Brangus	30.8 ^b	0.42 ^b
Brangus	30.8 ^b	0.32 ^{c,d}
Charolais X Brangus	29.7 ^b	0.38 ^{c,b}
Brangus X Romosinuano	24.1 ^c	0.28 ^d
Charolais X Romosinuano	20.7 ^d	0.32 ^{c,d}

Study Design

- 579 crossbred steers
- Five groups (will be 7 total by project completion and ~800 animals)
 - *Group 1 (May 2014 to October 2014, Summer, n=117)*
 - *Group 2 (November 2014 to March 2015, Winter, n=116)*
 - *Group 3 (May 2015 to September 2015, Summer, n=118)*
 - *Group 4 (June 2016 to October 2016, Summer, n=105)*
 - *Group 5 (January 2017 to May 2017, Winter, n=123)*
- FI and WI collected using an Insentec System
 - *4 pens per group (~30 steers per pen)*
 - *6 feed bunks and 1 water bunk per pen*
 - *Access to shade under barn*
- All groups fed a growing diet
 - *15% corn, 51.36% sweet bran, 28.44% hay, 5.2% supplement*
- All groups access to *ab libitum* water
 - *Groups 1-3 managed using slick bunk feed call*
 - *Groups 4-5 access to ab libitum feed*

Material and Methods: Timeline

Figure 1: Study design. Body weight (BWT), white blood cells (WBC), hematocrit (HMT), complete blood cell counts including hematocrit (CBC), and serum samples for electrolyte analysis (ELT) were collected at the specified times.



-Direct water consumption only, Water from feed not included in these data



- Data collected (baseline and restriction)
- WI, DMI, ADG
 - Respiration Rates
 - CBC and hematocrit
 - Electrolyte
 - Carcass (+ control)
 - Rumenocentesis
 - Entry and Chute Scores
 - Exit Velocity
 - Behavior Video (ind. animal)
 - Rectal Temp (chute)
 - Pedometer/accel (subset)
 - Fecal

Simple Statistics

Table 3. Means, standard deviations (Std), minimums (Min), maximums (Max), and CV% for daily water intake (DWI), dry matter intake (DMI), and starting weight within each group

Variables	Group	Mean	Standard deviation	Minimum	Maximum	CV%
DWI, kg	1	40.50	8.01	21.20	65.80	19.8
	2	28.23	5.63	15.60	44.70	19.9
	3	36.37	6.75	24.10	61.40	18.6
	4	49.46	13.07	32.00	101.40	26.4
	5	34.92	4.84	25.50	50.90	13.9
DMI, kg	1	10.12	1.39	6.36	13.69	13.7
	2	10.23	1.62	6.04	14.07	15.8
	3	10.24	1.52	7.16	14.76	14.8
	4	10.53	0.92	7.76	12.74	8.7
	5	11.67	1.23	8.96	16.17	10.5
Start weight, kg	1	327.81	24.75	253.64	388.18	7.6
	2	331.75	37.10	200.45	438.18	11.2
	3	366.93	29.02	283.64	445.45	7.9
	4	403.34	27.10	33.93	470.98	6.7
	5	341.30	37.27	262.73	434.55	10.2

Test Duration for Water Intake in Beef Cattle



Introduction: Test Day length

- Currently no guidelines for water intake
- Shortened test day length of 35 days feed intake (Wang et al. 2006 , Archer et al. 1997, Thallman 2018, Cassady et al. 2016,)
 - *Need 70 days only because of measuring gain*
- Collect feed and water intake at the same time with a shortened test?



The objective of this study was to determine the required test duration to accurately collect water intake phenotypes

Material and Methods: Test day length

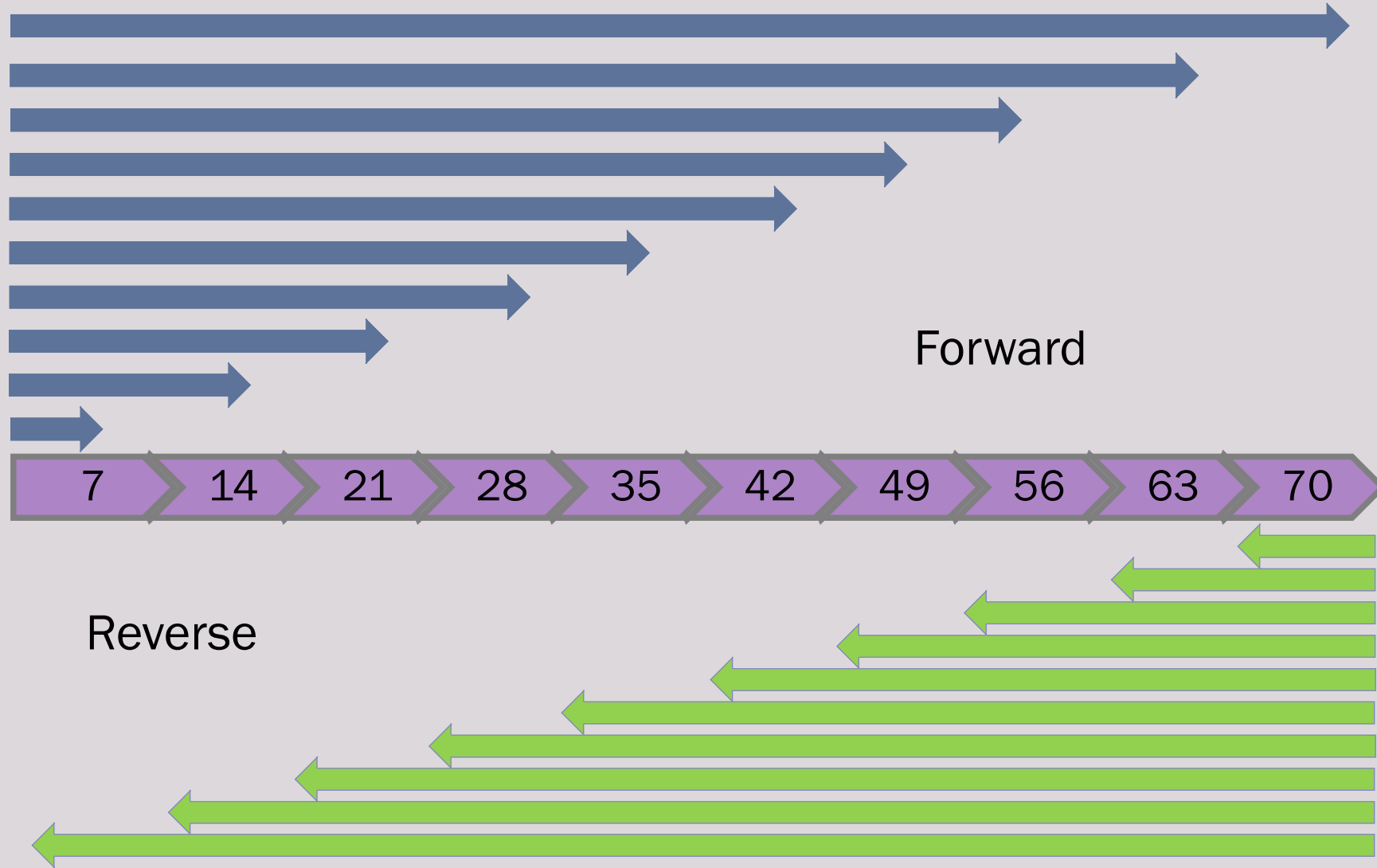


Table 7. Pearson and Spearman correlations for each shortened test duration and the full 70-d test period for water intake (WI, kg)

Group ¹	Direction ²	Analysis	Day of test									
			7	14	21	28	35	42	49	56	63	70
1	Forward	Pearson	0.635	0.733	0.821	0.881	0.927	0.955	0.978	0.988	0.996	1.0
		Spearman	0.591	0.696	0.778	0.837	0.899	0.943	0.973	0.985	0.995	1.0
	Reverse	Pearson	0.831	0.888	0.913	0.922	0.935	0.954	0.973	0.984	0.996	1.0
		Spearman	0.848	0.883	0.903	0.917	0.936	0.955	0.970	0.982	0.994	1.0
2	Forward	Pearson	0.722	0.794	0.838	0.879	0.906	0.920	0.927	0.935	0.981	1.0
		Spearman	0.612	0.735	0.799	0.836	0.871	0.885	0.900	0.911	0.975	1.0
	Reverse	Pearson	0.448	0.462	0.652	0.783	0.889	0.932	0.964	0.984	0.995	1.0
		Spearman	0.452	0.461	0.647	0.777	0.871	0.916	0.957	0.981	0.994	1.0
3	Forward	Pearson	0.727	0.787	0.806	0.823	0.906	0.946	0.972	0.986	0.998	1.0
		Spearman	0.706	0.775	0.799	0.822	0.907	0.945	0.973	0.986	0.997	1.0
	Reverse	Pearson	0.766	0.850	0.905	0.935	0.942	0.953	0.978	0.989	0.997	1.0
		Spearman	0.795	0.851	0.915	0.938	0.950	0.957	0.977	0.988	0.997	1.0
4	Forward	Pearson	0.822	0.887	0.944	0.967	0.985	0.989	0.994	0.997	0.999	1.0
		Spearman	0.867	0.914	0.945	0.957	0.979	0.987	0.992	0.996	0.998	1.0
	Reverse	Pearson	0.879	0.940	0.967	0.973	0.982	0.988	0.992	0.996	0.999	1.0
		Spearman	0.845	0.927	0.956	0.961	0.971	0.978	0.989	0.996	0.999	1.0
5	Forward	Pearson	0.835	0.868	0.895	0.923	0.947	0.967	0.983	0.991	0.996	1.0
		Spearman	0.819	0.848	0.889	0.924	0.951	0.964	0.979	0.990	0.996	1.0
	Reverse	Pearson	0.694	0.863	0.910	0.919	0.940	0.966	0.982	0.992	0.997	1.0
		Spearman	0.634	0.833	0.886	0.907	0.935	0.962	0.979	0.989	0.995	1.0
Slick	Forward	Pearson	0.705	0.805	0.845	0.879	0.935	0.957	0.977	0.984	0.995	1.0
		Spearman	0.669	0.783	0.818	0.858	0.928	0.955	0.977	0.984	0.995	1.0
	Reverse	Pearson	0.686	0.818	0.902	0.931	0.945	0.958	0.980	0.991	0.998	1.0
		Spearman	0.638	0.800	0.904	0.936	0.953	0.963	0.982	0.991	0.998	1.0
Adlib	Forward	Pearson	0.894	0.930	0.960	0.975	0.986	0.991	0.995	0.997	0.999	1.0
		Spearman	0.932	0.947	0.960	0.970	0.980	0.987	0.993	0.996	0.998	1.0
	Reverse	Pearson	0.827	0.919	0.960	0.965	0.975	0.986	0.991	0.996	0.999	1.0
		Spearman	0.665	0.829	0.914	0.926	0.944	0.972	0.987	0.995	0.999	1.0
All	Forward	Pearson	0.830	0.892	0.921	0.941	0.966	0.977	0.988	0.992	0.997	1.0
		Spearman	0.793	0.858	0.876	0.903	0.947	0.966	0.983	0.989	0.997	1.0
	Reverse	Pearson	0.712	0.822	0.920	0.933	0.950	0.970	0.985	0.994	0.999	1.0
		Spearman	0.639	0.792	0.899	0.923	0.943	0.963	0.982	0.993	0.998	1.0

¹Slick-cattle managed with slick bunk feed protocol, adlib-cattle had access to ad libitum feed, all-all groups were combined.

²Forward-records were split into the first F7, F14, F21, F28, F35, F42, F49, F56, F63, and F70 d of the test and reverse-records were split into the last R7, R14, R21, R28, R35, R42, R49, R56, R63, and R70 d of the test.

Correlations for ADG and DMI were consistent with literature

ACCEPTED MANUSCRIPT

Test Duration for Water Intake, Average Daily Gain, and Dry Matter Intake in Beef Cattle ^{FREE}

C M Ahlberg, K Allwardt, A Brooks, K Bruno, L McPhillips, A Taylor, C R Krehbiel, M Calvo-Lorenzo, C J Richards, S E Place U DeSilva, D L VanOverbeke, R G Mateescu, L A Kuehn, R L Weaber, J M Bormann, M M Rolf ✉

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WI Correlations

- Pearson and Spearman correlations exceed 0.95
 - 35-42 d test duration for WI
- Can collect WI and DMI simultaneously, decouple gain

Side note: Environmental Effects on WI

Environmental effects on water intake and water intake prediction in growing beef cattle^{1,2}

Cashley M Ahlberg, Kristi Allwardt, Ashley Brooks, Kelsey Bruno, Levi McPhillips, Alexandra Taylor, Clint R Krehbiel, Michelle S Calvo-Lorenzo, Chris J Richards, Sara E Place, Udaya DeSilva, Deborah L VanOverbeke, Raluca G Mateescu, Larry A Kuehn, Robert L Weaver, Jennifer M Bormann, Megan M Rolf 

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A lot of individual-animal variation not tied to environmental parameters

Characterization of Water Intake in Beef Cattle



Water Intake Metrics

- WI and DMI collected through Insentec system
- ADG calculated from linear regression of body weights on time

- F/G and W/G calculated:

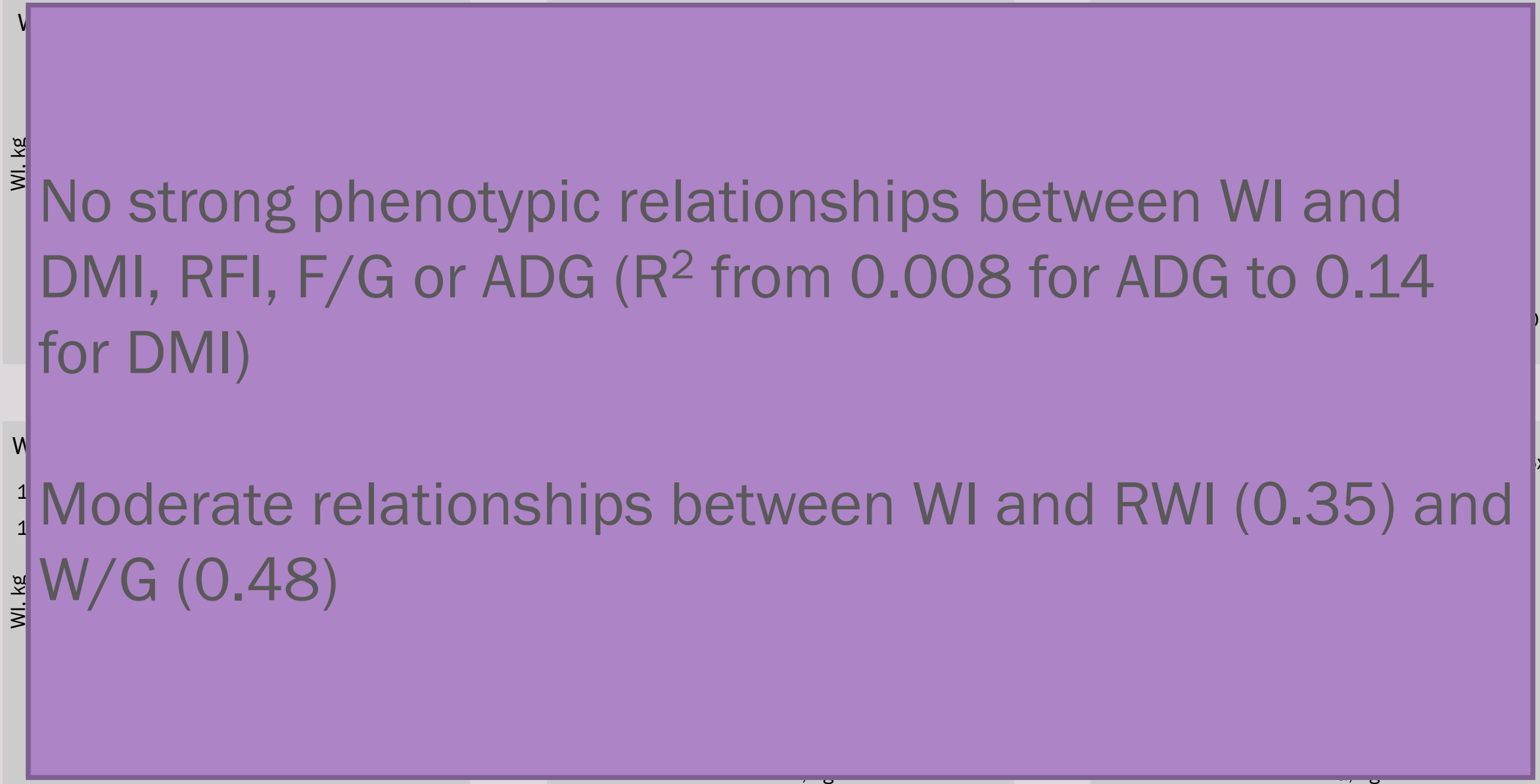
$$\frac{F}{G} = \frac{DMI(kg)}{ADG(kg)} \quad \frac{W}{G} = \frac{WI(kg)}{ADG(kg)}$$

- RFI and RWI calculated:

$$RFI = DMI - eDMI$$
$$eDMI = b_0 + b_1ADG + b_2MMWT$$

$$RWI = WI - eWI$$
$$eWI = b_0 + b_1DMI + b_2MMWT$$

Phenotypic Relationships With WI



Estimation of Genetic parameters

- GBLUP (BLUPF90 software package)

- The numerator relationship matrix A^{-1} is replaced with H^{-1} , which is defined as follows:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - A_{22}^{-1} \end{bmatrix}$$

- Where G^{-1} is the inverse of the genomic relationship matrix for genotyped animals, and A_{22}^{-1} is the inverse of the numerator relationship matrix for genotyped animals
- Genomic relationship matrix was calculated as $G=ZZ'/k$ as presented in VanRaden (2008).
 - Where Z is a matrix of SNP markers centered based on allele frequency estimated from genotyped animals, and k is $2 \cdot \sum(p \cdot (1-p))$.

- We did not have pedigree so H^{-1} was essentially G^{-1}

- Bivariate linear animal models

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix} = \begin{bmatrix} X_1 b_1 \\ X_2 b_2 \end{bmatrix} + \begin{bmatrix} Z_1 u_1 \\ Z_2 u_2 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \end{bmatrix}$$

- Fixed effects of group and feed management (slick or adlib)

- Covariates included start weight, percent British, percent continental, percent *Bos indicus*, and percent dairy

- Standard deviations were calculated for heritability and genetic correlations by repeated sampling of parameters estimates from the asymptotic multivariate normal distribution, based on methodology presented by Meyer and Houle (2013)

Estimation of Breed composition

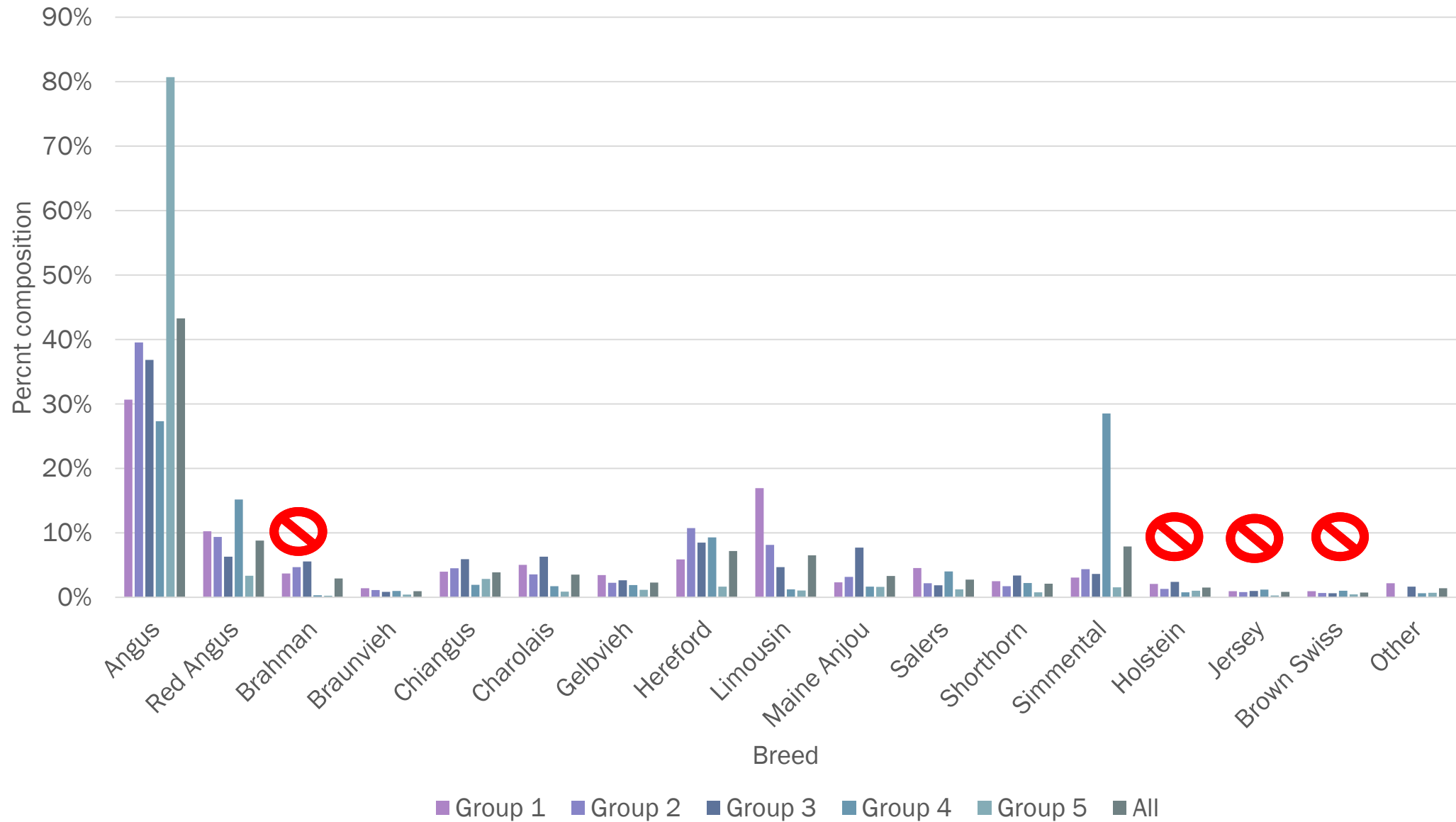
- No defined pedigree, lots of admixture in this population of steers
- Genotyped using the GeneSeek[®] Genomic Profiler[™]High-Density genotyping array (GGP HD150K).
 - *Approximately 150,000 single nucleotide polymorphisms (SNPs)*
- *Use for formation of G as well as estimation of breed composition using multiple regression-based methodology (Kuehn et al. 2011)*

$$y = Xb + e$$

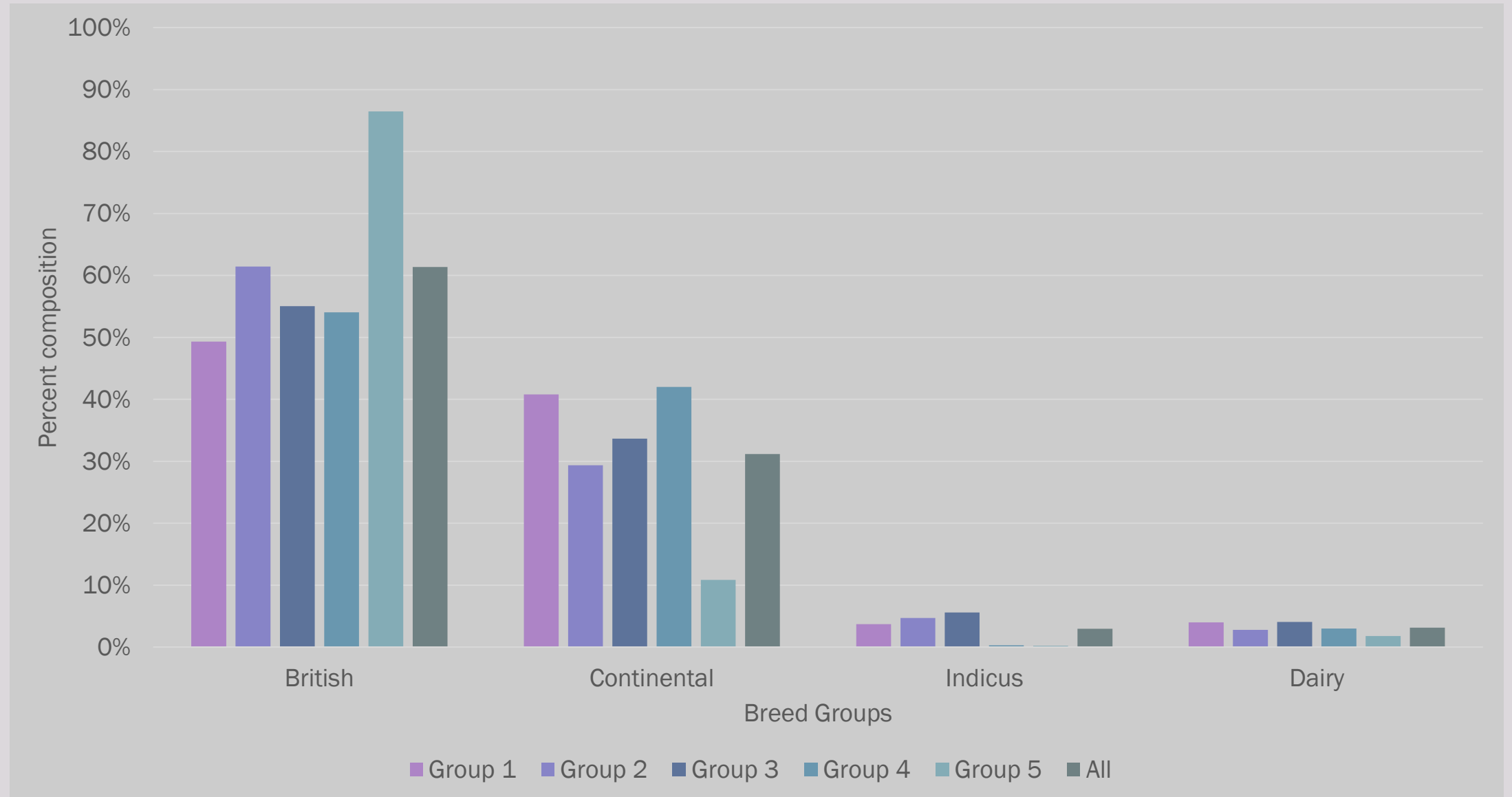
- Y is a matrix of individual “allele frequencies” for each animal (n x m)
- X is a 36,403 by 16 (m x b) matrix of frequencies for Illumina-defined allele B
- b is a vector (16 x 1) of regression coefficients that represents the percentage of each breed for each individual animal in y
- e is a vector of random residuals.

All observations were scaled to sum to 1 if necessary

Results: Breed Composition



Results: Biological types

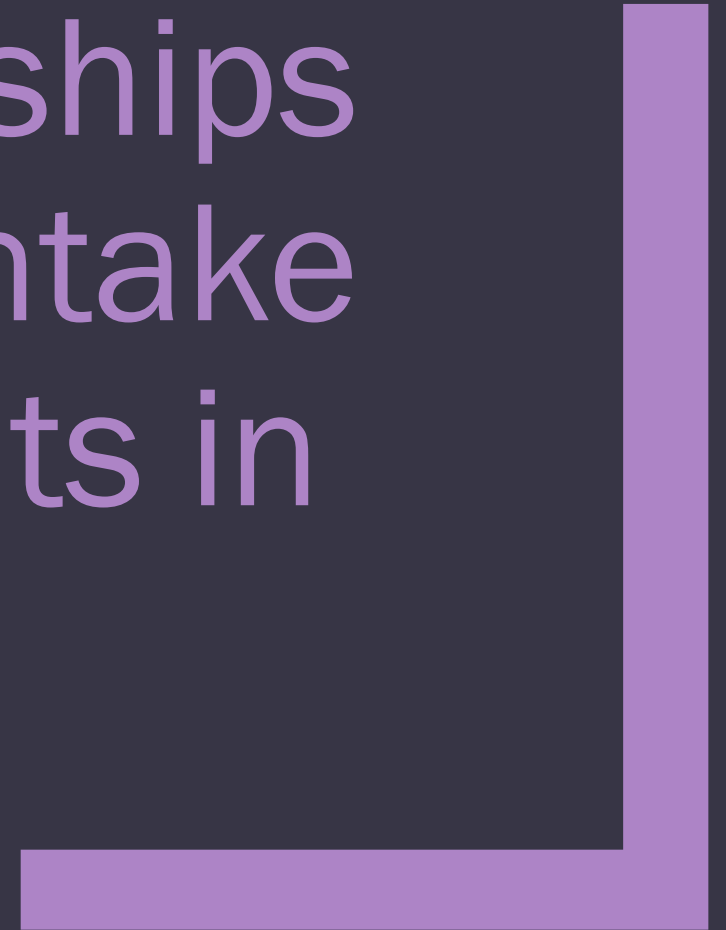


Results: Genetic Parameters

- WI and water efficiency traits are moderately heritable
- No strong antagonistic genetic relationships between WI and DMI, RFI, or F/G
 - Relationship with F/G is strong???, DMI and RFI moderate
- No relationship with ADG

Other traits?

Phenotypic and Genetic Relationships between Water Intake and Carcass Traits in Beef Cattle



Material and Methods: Models

- 70 day baseline and 70 day water restriction period
- Cattle were transitioned to finishing diet over 28 days
- Carcass data collected using cameras
 - *HCW, REA, BFAT, MARB, and YG*
- Final body weight measured within 24 hours of harvest

Materials and Methods: Harvest Plants

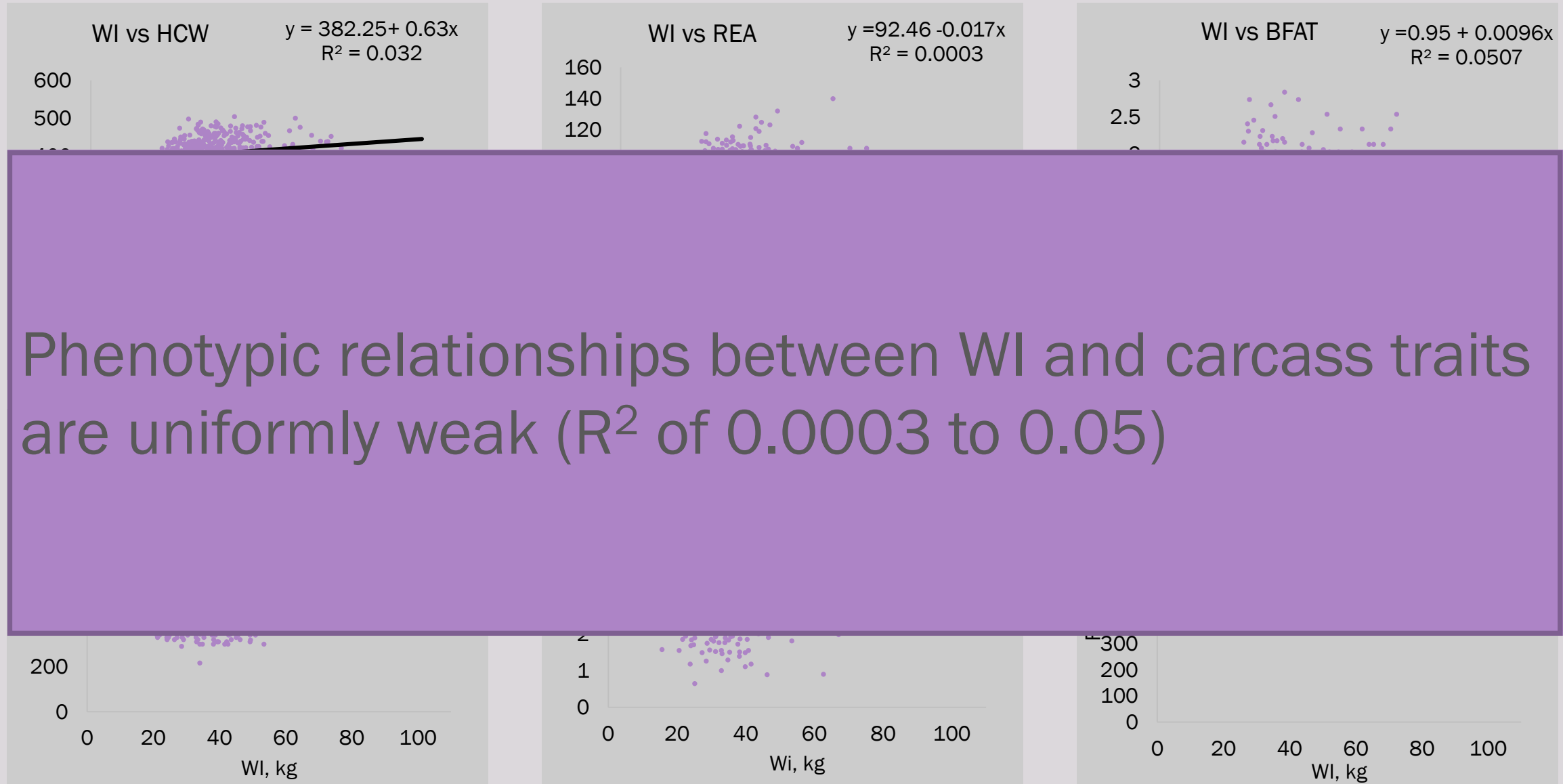
Group	Plant	n	DOF ^a	Location
1	FAPC ^b	5	85	Stillwater, OK
	Creekstone Farms	48	106	Arkansas City, KS
	Tyson Fresh Meats	8	106	Amarillo, TX,
	FAPC ^b	6	115	Stillwater, OK
	Tyson Fresh Meats	42	127	Amarillo, TX,
	FAPC ^b	3	130	Stillwater, OK
2	Tyson Fresh Meats	28	70	Garden City, KS
	Tyson Fresh Meats	26	91	Amarillo, TX,
	Creekstone Farms	57	93	Arkansas City, KS
3	Creekstone Farms	45	79	Arkansas City, KS
	Tyson Fresh Meats	27	130	Amarillo, TX,
	Creekstone Farms	32	133	Arkansas City, KS
4	Cargill Meat Solutions	105	37	Dodge City, KS
5	Creekstone Farms	123	45	Arkansas City, KS

Differences in plants and DOF are in response to changing market conditions

Material and Methods: Genetic parameters

- Methods were identical to previous study with WI and FE traits except:
 - *Fixed effects*
 - WI: Same as before (Group and feed management)
 - Carcass traits: group
- Covariates included start weight (WI), days on finishing ration (carcass), percent British, percent continental, percent *Bos indicus*, and percent dairy

Results: Water Intake vs Carcass Traits



Phenotypic relationships between WI and carcass traits are uniformly weak (R^2 of 0.0003 to 0.05)

Genetic Correlations with Carcass Traits

Genetic correlations between WI and carcass traits are zero to slightly positive

- Potentially slight antagonisms with HCW, MARB, and FBW (large std dev)

Future Work

- Analysis of data from last 2 groups of animals (n~240) as well as adaptability to water restriction and some sequencing data on kidney samples
 - *Jessica Neal*



- Analysis of mRNA sequencing data on liver samples
 - *Devin Jacobs*



- Additional analysis of phenotypic data from all animals as well as additional analyses on sequencing data on liver samples
 - *Layna Bond*



- A variety of other analyses on metagenomic sequencing data and other phenotypic data at OSU

Conclusions:

- Test length needed is compatible with decoupled feed intake and gain tests
 - *2 phenotypes for the price of 1, if facility has technology*
- WI is moderately heritable
- Antagonistic relationships with feed efficiency related traits and carcass traits are generally low to moderate and should not seriously hinder selection efforts
 - *Index is still likely the best method*
 - *Importance of trait likely varies substantially by region and may require personalization*

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- *Dr. Larry Kuehn*

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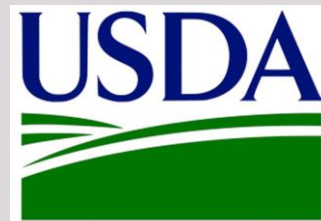
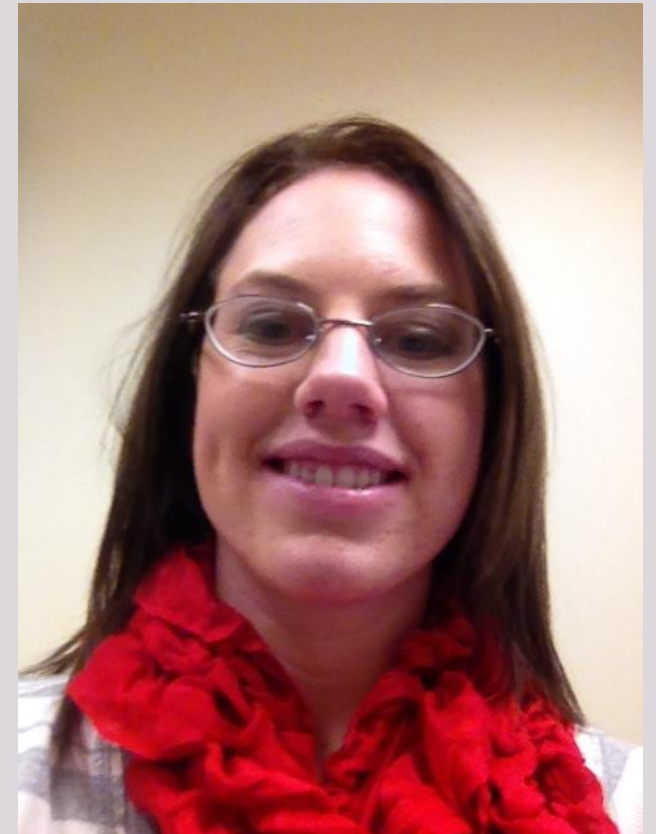
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- *Dr. Krehbiel*
- *Dr. Calvo-Lorenzo*
- *Dr. Richards*
- *Dr. Place*
- *Dr. DeSilva*
- *Dr. VanOverbeke*
- *Dr. Mateescu*

- OSU Graduate Students

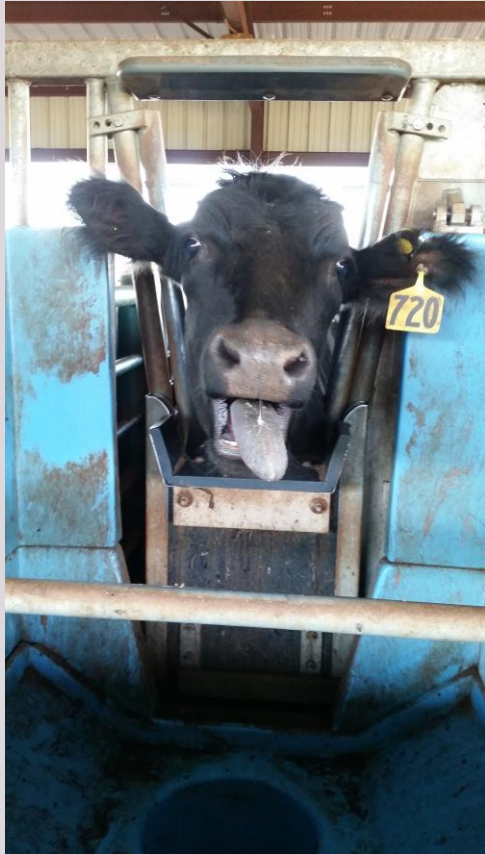
- *Kristi Allwardt*
- *Ashley Broocks*
- *Kelsey Bruno*
- *Alex Taylor*
- *Levi McPhillips*

- KSU Graduate Students

- ***Cashley Ahlberg***



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Questions?

