Genome Wide Association for Udder Traits in Beef Cows
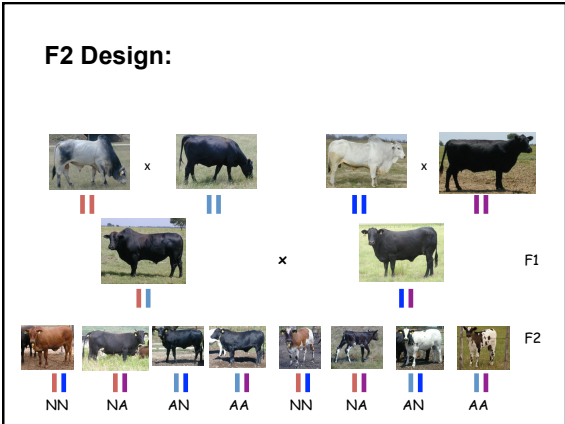
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Udder Dimensions

- **Dairy production traits**
- **Weaning weights in beef cattle**
- **Reasons for removal in beef cows**
- **Heritable trait (Bradford et al., 2016)**
- **Next logical step: Responsible genes**

GWAS Udder

- **Dairy: many, particularly Cole et al., 2011**
- **Beef cows**
  - **Vallée et al. (2016) –Charolais**
  - **Pausch et al. (2016)—Fleckvieh**
  - **Michenet et al. (2016)—Blonde D'Aquitaine; Limousin**
    - **"Udder Swelling"**

Objective

- **Identify genomic regions associated with udder characters**

Experimental Population

- **Full-sibling F2 Nellore-Angus females (187 cows) produced by embryo transfer: 4 bulls and 14 cows with progeny**
- **Half-sibling families by natural mating: same 4 bulls; F1 or F2 Brahman-Angus or Brahman Hereford dams (108 cows)**
- **Born 2003 through 2007; records: 2005-2014**
- **First exposed to bulls as yearlings**

F2 Design:

Traits

- **Teat length and diameter**
- **Udder support score: 1 to 9**
- **Repeated measures**

295 Cows

Trait	N	Mean	SD	Minimum	Maximum
Udder support score	1,746	5.89	1.11	2	9
Diameter	1,749	2.79	1.43	0.48	12.86
Length	1,749	4.89	1.81	1.51	11.91

Methodology

- **Generated residuals from a repeated measures model including cow age**
- **Contemporary groups: year-season of birth**
- **JMP Genomics**
- **Genomic Relatedness modeled**
- **Fixed regression on number of minor alleles**

Genotypes

- **Bovine SNP50**
- **Quality editing: 34,980 SNP for analyses**
  - MAF 0.05
  - HW proportions rejected
  - 90% animals genotyped

Correlation Coefficients

Trait	US	Length	Diameter
Udder support		−0.44	−0.56
Teat length	−0.22		0.64
Diameter	−0.42	0.55	

High and Low Family US

Fam.	n	US	Length					Diameter				
			Mean	RF	LF	RR	LR	Mean	RF	LF	RR	LR
95	27	5.36[b]	5.53	6.06	6.23[a]	4.83	4.90	3.51	3.71[a]	3.93[a]	3.15[a]	3.20
83	20	6.61[a]	4.57	5.02	4.95[b]	4.13	4.16	2.27	2.43[b]	2.37[b]	2.12[b]	2.12
SE		0.21	0.35	0.42	0.42	0.34	0.34	0.30	0.35	0.37	0.29	0.30

Mb	Candidate	Distance (bp)
21.6	SPCS3	98,926
22.7		56,441
32.6	VDR	within
39.0		104,837
39.9		11,249
43.0	PTPRR	within
43.6		59,452
43.7		9,882
45.7	IL22	within
46.3	DYRK2	39,671
46.4	DYRK2	30,159
46.5	DYRK2	119,742
46.5	DYRK2	163,137
46.5	DYRK2	192,136
48.1		45,909

Results

- **Strong r² for 12 most distal markers (0.27 to 0.85)**
- **Average proportion of phenotypic variance explained by marker 0.075 ± 0.028**
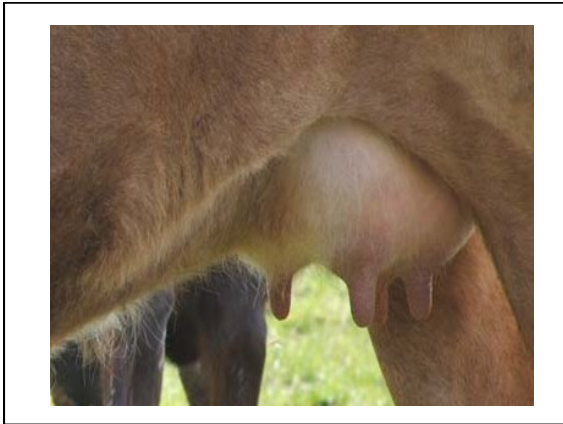
Comparison to Other Work

- **Dairy**
  - Udder attachment (Boichard et al., 2003; Ashwell et al., 2005)
  - "Udder texture score", and "Mammary System" (Kolbedhari et al., 2008)
  - Cole et al. (2011)
- **Beef**
  - Teat length in Charolais (Vallée et al., 2016)

Candidate Genes

- *Vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR)*
  - *Development, regulation, dynamics across life cycles*
  - *Infection response (somatic cell score associatons on BTA 5: Heyen et al., 1999; Ashwell et al., 2004; Lund et al., 2008; Cole et al., 2011)*
- *Interleukin 22 (IL22)*
  - *Infection response*
  - *Pathway interaction VDR*

Candidate Genes

- *Protein tyrosine phosphatase, receptor type, R (PTPRR)*
  - *Dynamics of udder across life stages*
  - *Eye-udder (Michot et al., 2016; RP1 BTA 14)*
- *Dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2 (DYRK2)*
  - *Mammary gland development*
  - *Eye development in Drosophila*

Remarks

- Very good udders in this population
- Other *Bos indicus* populations may have more variability
- Proximal contamination (Listgarten et al., 2012) may have underpowered this study
- F3, F4, F5 populations for refinement
- Brahman: longitudinal study of udders (TAMU, UF, LSU, MSU, NMSU).

Thank you!!

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