

International Bovine Genetics Collaboration

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Collaborators involved with feed intake, carcass, and meat traits

- CRC for Beef Genetic Technologies (Australia)
- Universities of Guelph and Alberta (Canada)
- U.S. Meat Animal Research Center

Meta-analysis Objective

- To combine results of BovineSNP50 BeadChip associations from three groups to increase power of detecting SNP associations with production, carcass, and meat traits using meta-analysis

Collaborator Contributions

- Each has large populations of phenotyped animals with BovineSNP50 genotypes
- Traits include growth, feed intake, carcass traits, and meat quality
- Each collaborator retains and analyzes own data

Numbers of animals included

Trait group	U. S.	Australia	Canada	Total
Growth	2,550	500	600	3,650
Feed intake	1,150	500	600	2,250
Carcass	1,700	500	700	2,900

Initial Steps

- Common interpretation of chip genotype calls
- Common definition of traits by orienting and standardizing

Trait Groups

Growth (4)	Feed intake (2)	Carcass (7 age + 3 fat = 10)
Birth wt (2)	Intake	Carcass wt
Wean wt (2)	Adjusted intake	Rib fat depth
ADG		Marbling/IM fat %
Yearling wt	Tenderness (2)	Ribeye area
	WBS 2-7 d	KPH/body cav (2)
	WBS 14 d (2)	Retail/lean %
		Yield grade (2)

Calculations and test statistics

- Oriented regressions (standard deviation units) were weighted and averaged
- Compared to pooled SE (*t*-test)
- Heterogeneity of regressions tested by comparing between and within source variability (Q-test)

Example results:

- Fortifying (Feed intake)

Source	SNP b	SD	Prob	Prob Q
US MARC	0.20	0.05	0.00003	
Australia	0.15	0.10	0.13	
Canada	0.34	0.10	0.0004	
Combined	0.22	0.04	0.00000005	0.31

Example results:

- Diminishing (Feed intake)

Source	SNP b	SD	Prob	Prob Q
US MARC	0.19	0.05	0.0002	
Australia	0.09	0.08	0.29	
Canada	-0.06	0.10	0.58	
Combined	0.13	0.04	0.001	0.08

Example results:

- Heterogeneous (Feed intake)

Source	SNP b	SD	Prob	Prob Q
US MARC	-0.11	0.05	0.03	
Australia	0.35	0.08	0.00002	
Canada	0.04	0.09	0.68	
Combined	0.02	0.04	0.68	0.00001

Results presentation

Probability	≤0.01	≤0.001	≤0.0001	≤0.00001
Expected (50,000)	500	50	5	0.5
Example Actual	700	100	15	3
Reported	1.4	2	3	6

Meta-analysis results

Category (# traits)	Prob \leq 0.01	\leq 0.001	\leq 0.0001
Growth (4)	2.9	7.8	31.6
Feed Intake (2)	1.7	2.6	6.1
Carcass (10)	1.6	2.7	5.9
Tenderness (2)	1.2	1.5	1.9
Heterogeneity (18)	1.3	1.7	2.9

Results

- Proportions of SNP regressions are greater than random chance for most traits when probability ≤ 0.01 .
- Heterogeneity statistics slightly exceeded random values, especially for birth and yearling or mid-test weight.

Evaluating Increased Power

- If many SNP have similar associations across genetic backgrounds and environments, then more SNP are expected to have high P-values in the meta-analysis than in any of the contributing sources.

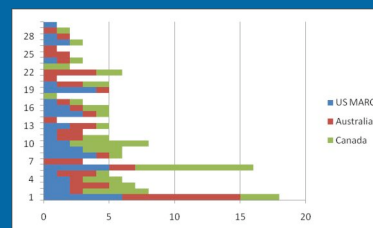
Meta-analysis results

Source (14 traits)	Prob \leq 0.001	\leq 0.0001	\leq 0.00001
US MARC	2.46	4.74	15.9
Australia	1.27	1.45	2.2
Canada	1.50	2.25	5.7
Average	1.74	2.81	7.9
Meta-analysis	2.50	5.37	19.8

Evidence of Increased Power

- Averaged across the 14 traits, meta-analysis identified more SNP than any individual source
- For the 4 growth traits (not shown), this was not true possibly due to higher heterogeneity of associations

Correspondence by chromosome



Conclusion

- Meta-analysis did increase power, identifying more associations
- Even more power (animals and markers) is needed for many traits

Future activities

- Reproductive traits
- Compare prediction equations vs single SNPs
 - Develop strategy to use HD panel on populations
- Select and sequence bulls of common interest
- Determine opportunities for addition of other 50k resources

Safe Travels