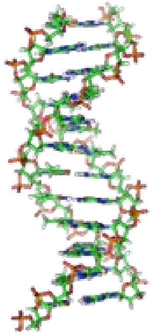
ICAR/Interbull Conference:

A recent research and development at International Genetic Solutions on discovery of novel functional variants affecting growth traits in beef cattle

Auckland, NZ
February, 2018



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IGS International Genetic Solutions

IOWA STATE UNIVERSITY OF SCIENCE AND TECHNOLOGY

ABS

International Genetic Solutions:

Today, **IGS** is a collaboration of 12 progressive breed associations that have put self-interest aside to focus on the needs of the commercial cattle producer.

Canadian Simmental Asso

SimGenetics PROFIT THROUGH SCIENCE

AMAA American Maine-Anjou Association

American Chianina Association

The Hybrid Advantage™ Chi Genetics to Unlock the Profit in YOUR Cattle

American Shorthorn Association

Canadian Shorthorn Association

World's largest multi-breed genetic evaluation
~17 million animals
400,000⁺ new/ year
100,000⁺ genotypes

Red Angus Association of America
4201 N I-35 • Denton, Texas 76207 • (940) 387-3502

Canadian Angus

American Gelbvieh Association

Canadian Gelbvieh Association
www.gelbvieh.ca

Limousin

LIMOUSIN NORTH AMERICAN LIMOUSIN FOUNDATION

Motivation to identify functional variants:

- Incorporation causative functional variants will improve the accuracies of **across-** and **multi-breed** genomic predictions.

Saatchi *et al. BMC Genomics* 2014, **15**:442
http://www.biomedcentral.com/1471-2164/15/442

BMC Genomics

RESEARCH ARTICLE **Open Access**

Large-effect pleiotropic or closely linked QTL segregate within and across ten US cattle breeds

Mahdi Saatchi[1], Robert D Schnabel[2], Jeremy F Taylor[2] and Dorian J Garrick[1,3*]

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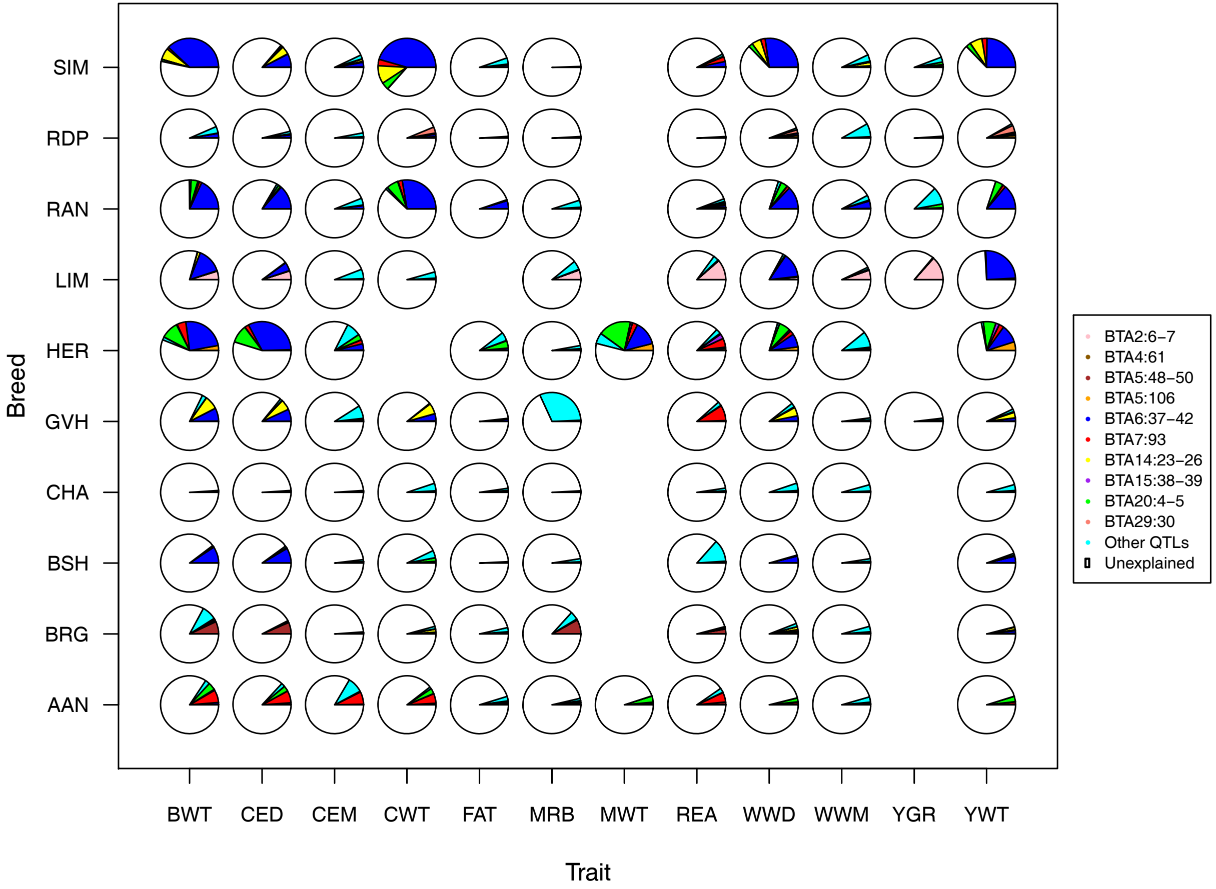
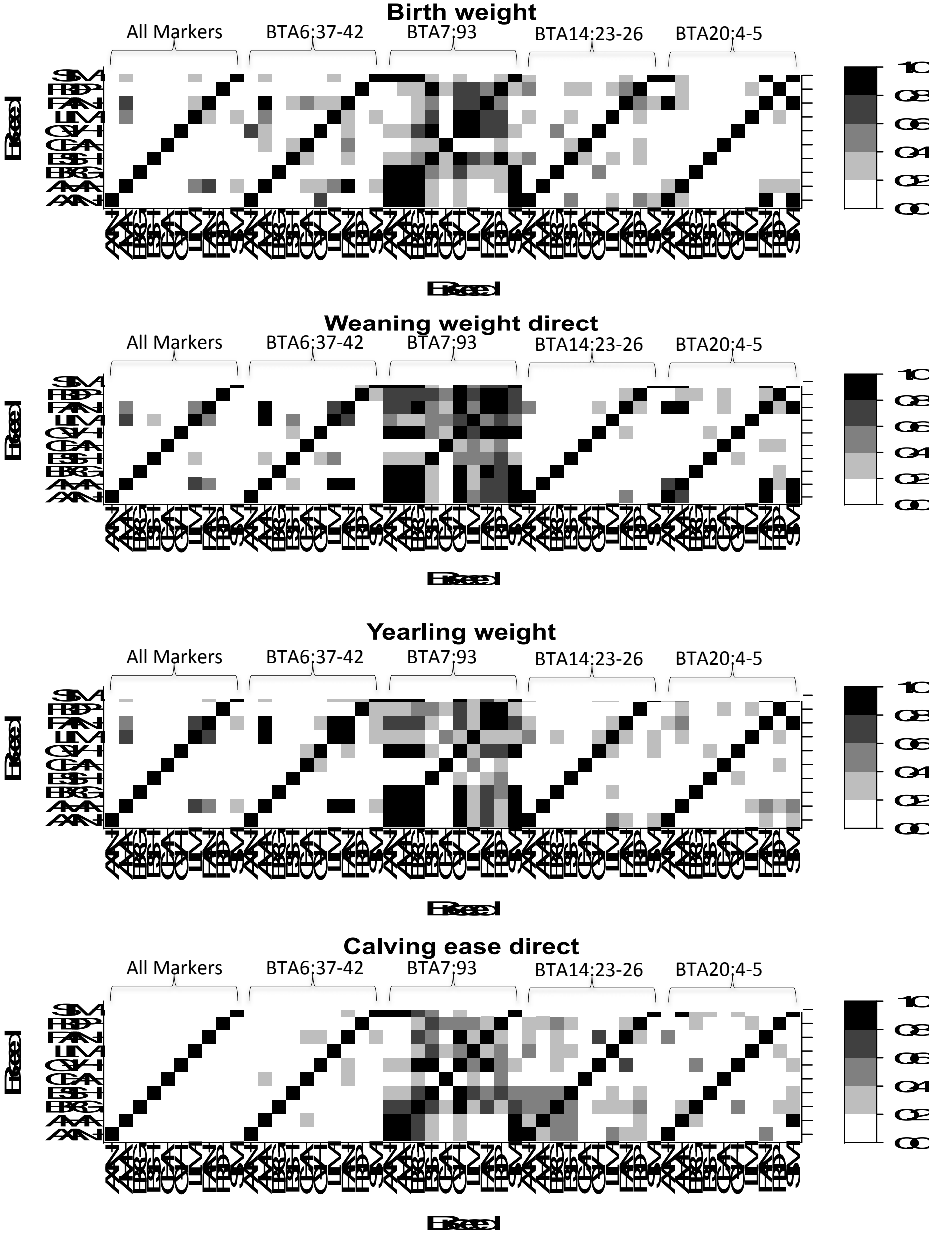


Across-breed genomic predictions:

Simple correlations between marker estimates obtained in ten different beef cattle breeds for all or subset of markers.

In general, the correlations were higher in large-effect QTL regions than those obtained from all markers especially for markers within QTL on BTA 7 at 93 Mb.

Saatchi & Garrick. 2014, WCGALP.



Materials & Methods:

Some 96 new functional variants of candidate genes within these QTL regions were selected from the public sequence databases (dbSNP & Ensembl).

- Candidate genes: LAP3 (BTA6), NCAPG (BTA6), LCORL (BTA6), ARRDC3 (BTA7), PLAG1 (BTA14), ERGIC1 (BTA20) and SH3PXD2B (BTA20) and some others on BTA2, 5, 6, 7, 10 and 24.

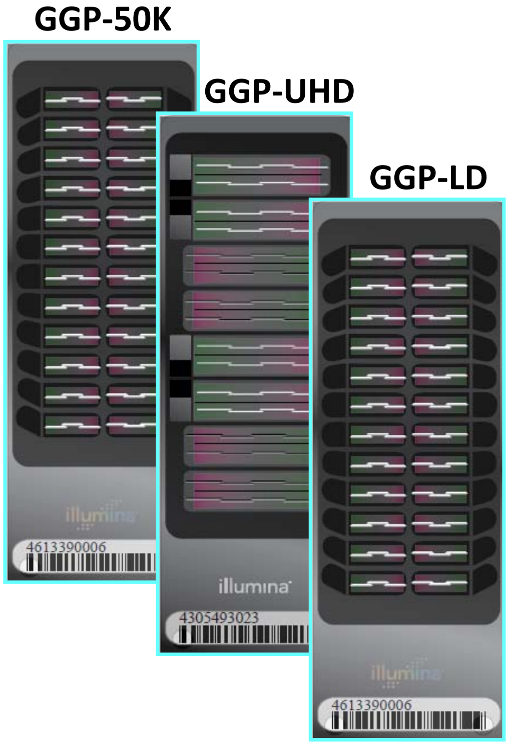
Materials & Methods:

Criteria:

- Predicted variation effects on protein function (SIFT value).
- Multiple observation.

Materials & Methods:

The 96 candidate functional variants assayed into the new versions of GeneSeek Genomic Profilers (GGP-LD, GGP-UHD and GGP-50K). They named as MS-rs#.



Materials & Methods:

- Some 5,964 Simmental, 2,982 Gelbvieh and 2,871 Red Angus animals were genotyped with one of these assays.
- The animals recorded for birth, weaning and yearling weights.

Association study:

- Using linear mixed model in GEMMA software (numerator relationship matrix was used to account for population structure).

Results & Discussion:

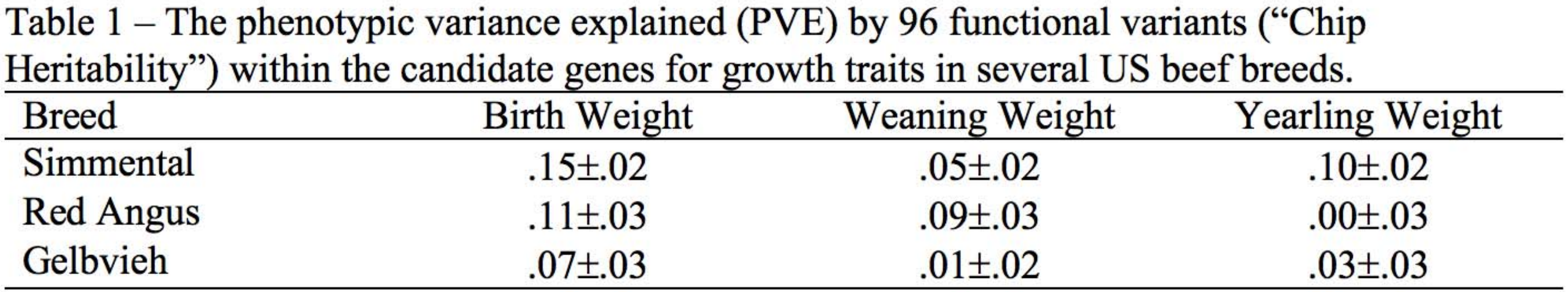


Table 1 – The phenotypic variance explained (PVE) by 96 functional variants ("Chip Heritability") within the candidate genes for growth traits in several US beef breeds.

Breed	Birth Weight	Weaning Weight	Yearling Weight
Simmental	.15±.02	.05±.02	.10±.02
Red Angus	.11±.03	.09±.03	.00±.03
Gelbvieh	.07±.03	.01±.02	.03±.03

Results & Discussion:

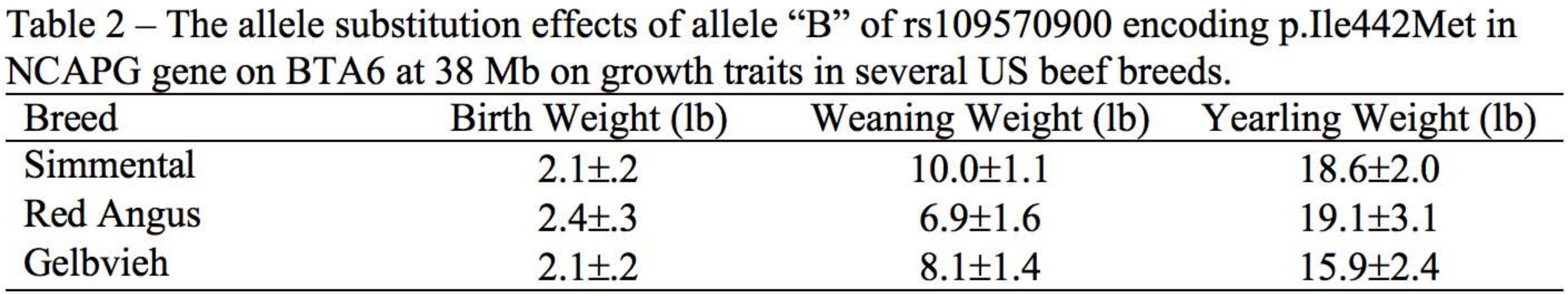


Table 2 – The allele substitution effects of allele "B" of rs109570900 encoding p.Ile442Met in NCAPG gene on BTA6 at 38 Mb on growth traits in several US beef breeds.

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	2.1±.2	10.0±1.1	18.6±2.0
Red Angus	2.4±.3	6.9±1.6	19.1±3.1
Gelbvieh	2.1±.2	8.1±1.4	15.9±2.4

Results & Discussion:

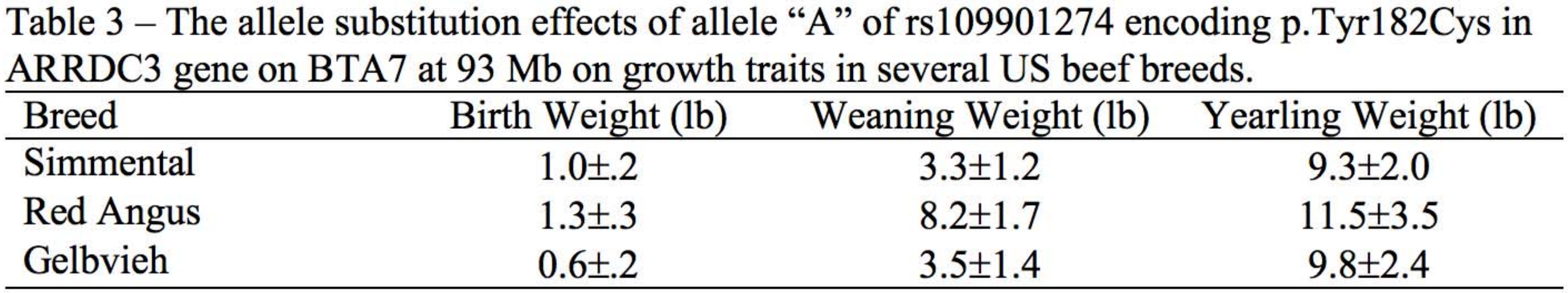


Table 3 – The allele substitution effects of allele “A” of rs109901274 encoding p.Tyr182Cys in ARRDC3 gene on BTA7 at 93 Mb on growth traits in several US beef breeds.

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	1.0±.2	3.3±1.2	9.3±2.0
Red Angus	1.3±.3	8.2±1.7	11.5±3.5
Gelbvieh	0.6±.2	3.5±1.4	9.8±2.4

Results & Discussion:

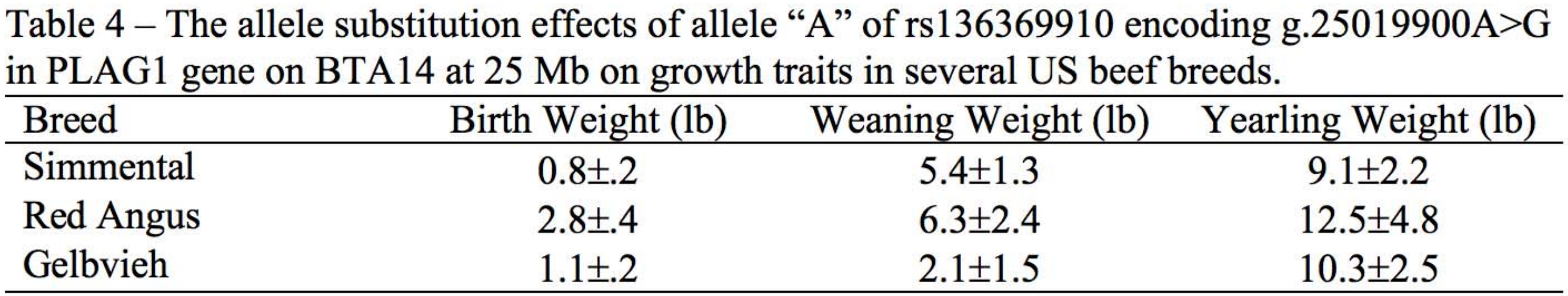


Table 4 – The allele substitution effects of allele “A” of rs136369910 encoding g.25019900A>G in PLAG1 gene on BTA14 at 25 Mb on growth traits in several US beef breeds.

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	0.8±.2	5.4±1.3	9.1±2.2
Red Angus	2.8±.4	6.3±2.4	12.5±4.8
Gelbvieh	1.1±.2	2.1±1.5	10.3±2.5

Results & Discussion:

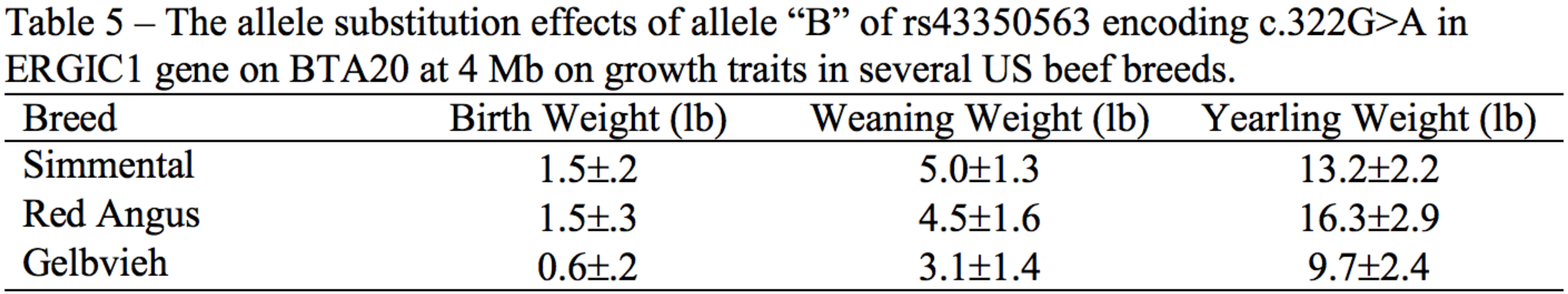


Table 5 – The allele substitution effects of allele "B" of rs43350563 encoding c.322G>A in ERGIC1 gene on BTA20 at 4 Mb on growth traits in several US beef breeds.

Breed	Birth Weight (lb)	Weaning Weight (lb)	Yearling Weight (lb)
Simmental	1.5±.2	5.0±1.3	13.2±2.2
Red Angus	1.5±.3	4.5±1.6	16.3±2.9
Gelbvieh	0.6±.2	3.1±1.4	9.7±2.4

Summary:

- This study identified some putative functional variants which are remarkably associated with growth traits in beef cattle.
- Once confirmed in validation studies, these new functional variants will be included into the future genetic evaluations of the International Genetic Solutions (IGS).
- Using the chip assays to discover/validate some candidate functional variants seems to be a good strategy (reliability, affordability).

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Acknowledgments:

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Thank you!

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