The "Weight Trait Project"

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Consortium

EJP at BIF 2008: The Transition

"We are in process of a very important, yet troubling transition in the beef industry."

What has the year seen since Calgary?

This Past Year

Large SNP panel discovery.

Very large number of animals genotyped with the 50K panel.

This Past Year

Analysis of phenotypic (or EPD) information in the populations genotyped.

Dorian Garrick: "*Yet to commercialize a SNP from this process*"

This Past Year

Identification and clarification of many issues needing to be addressed in the realm of discovery.

Dorian Garrick:
We hope to see an annual trend in the correlations we achieve from the associations studies over coming years

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Discovery Issues

Goddard - "*Therefore we need to estimate the prediction equation from very large reference populations….*"

ISSUE – How many animals?

"If we use the phenotype of animals in the discovery population for a trait with h^2 = 0.3, we will need 4,000 animals to achieve an accuracy of 0.5."

Discovery

ISSUE – How to handle breeds?

Goddard – *"We have often found that a prediction that works in one breed or herd does not work in other breeds and herds."*

Taylor – *"LD does not extend far across breeds and so pooling animals across breeds may not provide a solution."*

Discovery

ISSUE – Phenotypes versus EPDs?

Dairy has focused on large numbers of well proven sires for traits using their genetics predictors comparable to our EPDs.

With a few notable exceptions (Taylor, Angus) beef research have focused on using phenotypes.

We need to do more of the former:
Build Repositories!!!!

Avoid Duplication!

Discovery

ISSUE – How to reduce the 50K results to an "affordable" panel?

Garrick – *".... can a much smaller and cheaper subsample of no more than a few hundred markers be used without substantially eroding predictive ability?"*

Status

So in the last year we have learned:

We DO NOT have enough animals or enough SNPs

We need to continue to build our animal resources and we need to share resources.

We need more SNPs for within breed discovery but maybe more importantly for across breed robustness of discovery.

Status

So in the last year we have learned:

We DO HAVE some very appealing results.

We need to do something THIS YEAR with those results.

Dorian Garrick: *"Yet to commercialize a SNP from this process"*

Question from the floor:

"It is fine to say we are going to move DNA information into genetic evaluation, but are we preparing for that?"

Cowboys Lament:

"There does not seem to be any organization to what we are doing or where we are going."

So the Next Step

We NOW need to be developing projects that fosters collaboration on problems at every phase of technology transfer, and do so by integrating resources from other projects and grants.

I view the WTP is an organized effort to facilitate DNA technology transfer and while at the same time providing a national focus for integration.

Academics

Research (US MARC, NBCEC and UNL)

SNP discovery / validation (US MARC)

Field implementation (NBCEC)

Data Analysis (UNL, WGEAS grant)

Academics

Extension (UC Davis[1] and NBCEC)

Educational material

Workshops

[1] USDA Integrated Grant – Alison Van Eenennaam

Integrating DNA information into Beef Cattle Production Systems

Breed Associations

Breeds were selected as those represented in the proposed discovery data set:

Cycle Seven

Breed Associations

LIMOUSIN **HEREFORD**

AMERICAN Simmental ASSOCIATION
406-587-4531

American Gelbvieh Association

Identified collaborating producers

Provide data and EPDs for analysis

Database MBVs (genotypes)

Building Better Beef...
Red Angus

Genetic Testing Company

Facilitate the creation of the "reduced panel" chip and provide genotyping services to the project.

igenity

Seedstock Producers

Collect DNA samples (hair) on 2009 born calves and their dams.

**18 Seedstock providers
4 university herds
~6000 Cows
~6000 Calves**

Seedstock Producers

Collection and genotypes was to be on the calves and cows in the herd representing the nominating breed.

However, virtually all collaborators have volunteered to collect cattle from their other breeds and any crossbred (eg. Balancers).

North Dakota

2 Collaborators

South Dakota

4 Collaborators

Iowa

Nebraska

1 Collaborator

6 Collaborators

Colorado

1 Collaborator

Kansas

5 Collaborators

Target Traits: Early Growth

Rationale:

Abundant data in discovery populations

Non-threatening to commercialization

Seedstock collaborators can evaluate success of the panel in their own herds

trait(s) will depend on the level of association
         - one trait: weaning weight
         - two traits: WW + YW
         - three traits: WW + YW + restricted BW

Discovery

US MARC discovery populations

International Collaboration (Australia, US and Canada)

Validation

This first phase of the weight trait project is focused on validation issues.

Alison Van Eenennaam: *".... validation has focused on whether a product worked or not."*

Internal validation: done on resources within the company.

External validation: done by an independent third party.

Validation

Moving to *"proportion of additive genetic variation accounted by a test". Thallman et. al.*

The populations like the one we are developing in the weight trait project will allow for us to study estimating this proportion for weights
and
to do so within breed and across breed.

Integration of MBVs and EPDs

Goddard – *"Therefore the MBV should be combined with the traditional EBV to give a prediction of breeding value that is more accurate than either source of information alone."*

This can be done in several ways to include:

Blending the MBVs and EPDs (Garrick, USDA)

Integration of DNA information into GE programs (WGEAS grant)

Integration of MBVs and EPDs

In the weight trait project we will do genetic evaluations for the weight traits with DNA information (MBVs or genotypes) and without that information included to examine the impact on accuracy of yearling bulls.

Allows the breed associations to address how they would capture and organize DNA information in their databases and for genetic evaluation.

Integration of MBVs and EPDs

In addition, we can examine:

Nebraska
UNIVERSITY OF
Lincoln

Combinations of fitting large panel results (50K) on bulls and reduced panels on calves and dams. (Portfolio of panel sizes)

Integration both within breed versus multiple breed.

Including multiple sources of MBVs as they occur.

ON animals the industry can relate to.

Timing

Plan to capture DNA on all calves and cows spring and 2009.

Genotype during the fall and winter.

"Validation analysis" winter.

Genetic evaluation analyses research 2010.

Further Assessment (if successful)

Replicate across several environments.

So don't be surprised if I come knocking on your door next year for DNA!

MBV x environment interaction (x Breed)

Comparisons across regions using Angus as the reference breed in each region.

Involve other breeds.

Summary

Year 1: Avery good year for analytical investigation of the application of the 50K to populations and very encouraging results from those analyses for some cases.

But, as always, the more we learn the more we discover we need to learn….

This year: Build DNA repositories, focus on collaborations (international and national), develop outreach materials to support the momentum gained this year.