International Collaboration on Genomics of Economically Relevant Traits

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Why Collaborate?

GENERAL SESSION SPEAKERS

- Goddard: More discovery data, validation

- Taylor: More discovery data, validation

- Garrick: More discovery data, validation, more environments

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How many animals???

Discovery animals = 14,000

$h^2 = 0.3$

Accuracy = 0.7

Why Collaborate?

- Expensive and limited genotypes and phenotypes

- Cross test predictions and methodology in other populations and environments

- Combine results for better predictions

Current Formal Collaborators

- CRC for Beef Genetic Technologies (Australia)

- Universities of Guelph and Alberta (Canada)

- New Mexico State University

- U.S. Meat Animal Research Center
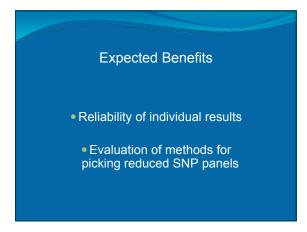
Met in January and December, 2008

Collaborator Contributions

- Each has large populations of phenotyped animals with BovineSNP50 genotypes

- Traits include growth, feed efficiency, carcass traits, meat quality, and female reproduction

- Each collaborator retains and analyzes own data

Share and Compare

- Individual SNP results

- Multiple SNP prediction equations

Weight traits

- Most combined data

- Use to develop strategies for other traits

Initial Steps

- Common interpretation of chip genotype calls

- Common definition of traits

Expected Benefits

- Reliability of individual results

- Evaluation of methods for picking reduced SNP panels

Future Interactions

- Others may have appropriate data

- Have discussed opportunities to share and compare results with commercial companies in a more limited way

Safe Travels