## A multi-breed, multi-association **Database**

1 genetic evaluation database 13 associations/organizations supplying data Standardization

**Contemporary Groups** International ID Same Parent multiple IDs Same Animal multiple IDs Matching to Genomic Record Common Interface (Data Record) **IGS** Database **Automated Weekly Evaluations** 

### Standardization

- Breed Associations keep the same data
- BIF provides framework for data and codes
- Breed Codes multiple birth code
- International data some units
- Field data

## **Contemporary Groups**

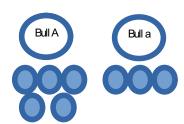
- Contemporary groups are the primary unit used to identify genetic differences
- Evaluation system was designed for the data to determine comtemporary groups

  - BW: breeder id, herd, sex, birth date Wwt: breeder id, herd, sex, age, weigh date, management
- . Association defined contemporary groups
- Understanding is critical cg change more between evaluation then data

#### International Animal ID

- BBBCCCSnnnnnnnnnnn
- BBB breed code (3)
- . CCC country codè (3)
- . S sex code (1)
- . nnnnnnnnnn system/registration nbr (12)
- LIMUSAM000001394641
- . AANUSAM000016243248
- . Animal, sire, dam, recip dam

#### Same Parent multiple IDs



The same parent can have different international ids in different datasets (Associations)

#### Same Parent multiple IDs







- The same parent can have different international ids in different datasets (Associations)
  Cross reference table of all known IDs for an animal
- 9 different IDs for the same animal

#### Same Animal multple IDs

- . Same data reported to more than 1 association
- Use the best record most data, largest cg
- Difficult to merge records
- Coordinate dam and sire IDs

#### Matching to Genomic Record

- . The genomic id can be a registration number or barcode, lab id, breeder-tatto, association id
- . In order to use genomics in the 1 step model the genomic information must match up with a record in the pedigree file
- . Create and maintain a genomic id cross reference

### Common Interface -Data Record

- 1 Common Record layout with all information
- Must be data requirements
- Text delimited file
- · Upload portal/process anytime
- Automatic processing
- Immediate notifications of errors
- Good records updated in database immediately

## **IGS** Database

Canadian Angus	757,245	US Red Angus	1 157 298
Australian Shorthorn	232,407	US Maine-Anjou	1,157,298 664,719
US Shorthorn	979,086	Canadian Simmental	1,457,984
US Chianina	588,099	Chinese Simmental	13,730
Canadian Gelbvieh	153,075	US Simmental	5,609,230
US Gelbvieh	1,627,427	Miscellaneous	72,939
Canadian Limousin	477,397		
US Limousin	2,387,043	Total	17,177,679

- Adding 350,000 records/year7.2 million purebreds

## **IGS Phenotypes**

Birth Weights	11,136,533	Carcass Marbling	103,145
Calving Ease Scores	10,475,137	Carcass rea	101,684
Weaning Wts	10,433,748	Carcass bfat	97,837
Yearling Wts	3,932,813	Carcass Weight	111,844
Scanimf	663,959	Weaning Docility	634,004
Scan bfat	669,022	Yearling Docility	57,121
Scan rea	650,870	Heifer Preg	

- 132,584 genomic records165,000 breeders

# **IGS Sire Usage**

Number of Sires	Number of Associations with Progeny
6	12
8	11
29	10
63	9
139	8
227	7
421	6
728	5
1453	4
3844	3
23857	2

### **Automated Evaluation**

- 1. 12:01 am every Tuesday pedigree, performance and other support files are generated from extracts of the IGS database notification set if successful
- 2. When successful extract notification is set data prep is started
- (adjustments, contemporary grps) notification set if successful 3. When successful notification set genomic data prep is started notification set if successful
- 4. When successful notification set evaluation the evaluation is started – growth, calving ease, carcass1, carcass2, stayability, docility - notification set if successful
- 5. When successful notification set post processing is started resulting in epd and other output files generated for each associations (Friday)
- 6. Emails and web status reports 7. Many advantages to frequent genetic evaluations