Sparse Genome Scan

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Sparse Genome Scan (SGS) Genotyping

- Roughly 1,000-10,000 highly informative markers spread evenly across the genome to allow tracking inheritance throughout the genome of a pedigreed population.
- Sufficiently inexpensive to be used on entire population.
- I believe it is just a matter of time before the required genotyping technology becomes a reality.
- Will the beef industry be positioned to take advantage?

The Primary Distinction from Many Other Genotyping Approaches:

- We are not trying to genotype specific markers that predict specific traits.
- Instead, we are trying to track inheritance patterns of a pedigreed population throughout the entire genome and use that to infer genomic states throughout the genome.
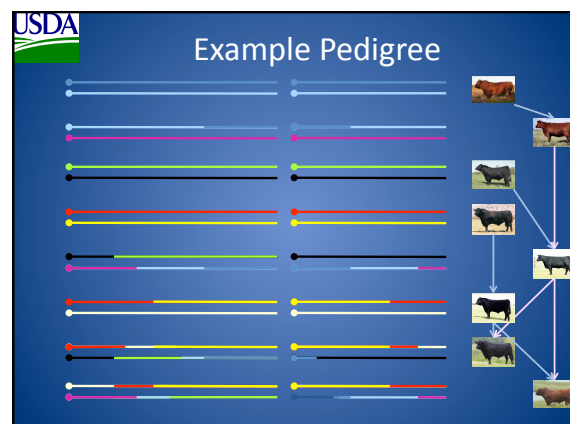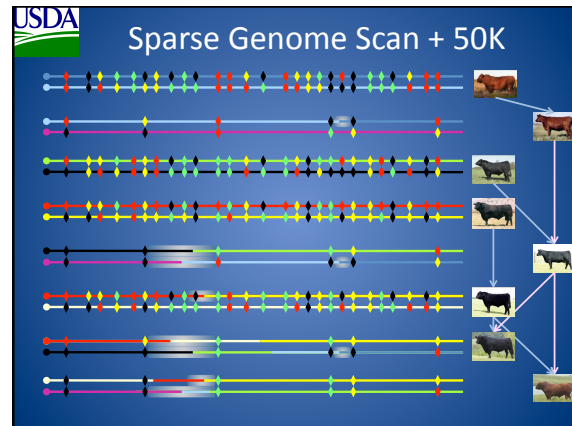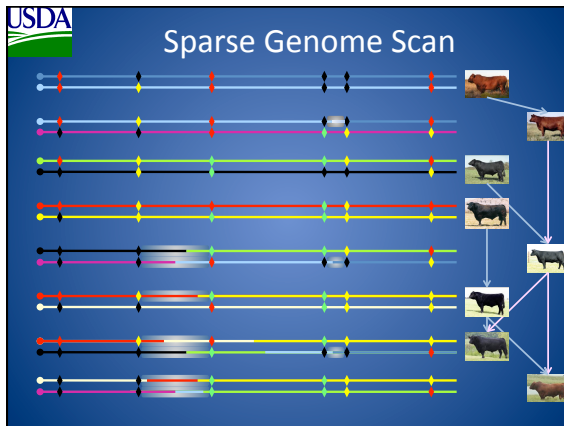

Objective of Sparse Genome Scan

- To provide an inexpensive replacement to most other DNA testing that might be done on seedstock cattle.
  - But, to be effective, it needs to be applied to the whole population.

Sparse Genome Scan as Part of a Complete Pedigree Genotyping and Imputation System

- Run sparse genome scan on most or all of the individuals in the population.
- Run the 50K chip on most or all AI sires.
- Individually sequence as many of the highly influential ancestors in the population as is feasible.

Example Pedigree

Sparse Genome Scan

Sparse Genome Scan + 50K

Fundamental Objective of Sparse Genome Scan

- Impute as much sequence as possible to entire populations at a cost per animal that is lower than most current genomic testing.
- The imputed sequence will not be perfect or perfect complete, but it will be orders of magnitude more complete than we now have.

Information Derived from Sparse Genome Scan Genotyping

- Parentage verification
  - Could improve accuracy of conventional EPDs
- Paternity determination
  - Greater power than conventional tests
  - Extend genetic evaluation into commercial herds
- Genetic defect testing
- Prediction of quantitative traits
  - Through imputation of 50K SNP or sequence
- Testing for single gene traits
  - Color, polledness, F94L, etc.

Impact of Sparse Genome Scan on Discovery

- Imagine a phenotyped population of a million animals.
- Assume that, for any given location in the genome, we could determine the sequence for half of those animals.
- The fact that the sequence is ambiguous in the other half of the million becomes irrelevant.
- We still would have a far more powerful training resource than has ever been available in cattle.

Applications of Sparse Genome Scan Genotyping in Other Species

- Currently being used in swine and poultry breeding
- A variation on SGS is currently being used in Holsteins at a price of about $40/animal to provide parentage and imputed genomic PTAs (using 9K chip)

Take-Home Messages

- The current approach to incorporating genomic information into EPDs is a great start, but not the final answer.
- Investment in chip genotypes today should have value for years to come.
- The delivery mechanism (GE-EPDs) will remain essentially the same, but the boost in accuracy will improve.

Take-Home Messages

- For breeders currently using genomics aggressively (parentage, genetic defects, black, polled, quantitative traits), the investment in genomics should remain similar but be distributed over the entire herd and yield much more information.
- Breeders not currently using genomics will find that the increased information produced will make it economically viable.

Questions?

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