Standardization of Reporting DNA Test Results?

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Current

DNA tests for several traits are now made up of panels of multiple markers.

Reporting genotypes (CC, CG or GG) or summaries of genotypes (# of stars) is giving way to numeric representation of test results.

Current

We currently have three providers of DNA diagnostic tests for tenderness.

We currently have three different reporting schemes.

Reporting schemes

Quantitative score for DNA panel results

- Igentity => 1 to 10
- Bovigen => additive effects
- MMI => MGVs (total genetic merit)

Igentity

Constructed a 1 to 10 score based on haplotype effects (with modifications) for poorly estimated haplotypes.

The scale is not in units of the trait.

Decision on expanding the range or keeping it constant.

Bovigen = GPDs

Publish the breeding value associated with a genotype. For shear force range is from 0 to -2.2 lbs.

The scale is units of the trait.

Range will expand with additional markers.

MMI = MGVs

Large panel of SNPs go into the assessment of MGV's.

GV = additive + dominance + epistatic

Non-additive

Genetic Value

GV = additive + dominance + epistatic

Selection

Genetic Value

GV = additive + dominance + epistatic

Mating Strategies

Genetic Value

GV = additive + dominance + epistatic

Phenotypic Prediction

So what?

Sire (Igentity = 7)

Dam (Bovigen = -0.5)

Progeny = ?

Future

Where are we headed relative to providing information to our customers (seedstock and commercial producers)

Trends in DNA Information

QTL Identification:
Candidate genes
Unknown mutations
Expanding panels

Large Panels:
Mostly unknown genes
Unknown mutations
Numeric scores

QTL Identification:
Identifying genes
and casual mutation

Mixture of marked regions, known mutations and residual "marker" and polygenic effects.

DNA and Phenotype Information: continued phenotypic data collection?

Scale of variation (or accuracy)

Threshold

Zero

The termination of routine data collection for GE is a simple ROI issue. At what point does the investment exceed the return?

One

Trends in Data

1. In reality, likely continue to collect routine data
2. Likely not to collect expensive data, although technology for some observations will evolve (instrument grading).
3. Likely to collect targeted data "post discovery" for periodic reassessment of panels.

Evaluations

DNA / Phenotypes	YES	NO
YES	MA-EPDs Should we Should we not	Current systems EPDs
NO	Molecular-EPDs	Trait development

How do we accommodate given this is a transition solution.

Results

1. EPDs (phenotypes and pedigrees)
2. MA-EPDs (markers, phenotypes and pedigrees)
3. M-EPDs (markers)

Make Sense?

Probably not.

So what do we want?

Additive prediction (just one per trait)