

Beef Relationships using 50K Chip Information

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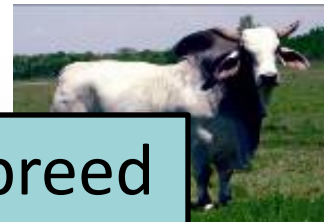


United States Department of Agriculture
Agricultural Research Service

What breed is it?



Not always easy to visually determine



Can we determine breed composition from genomic tools?



2000 Bull Project



- Collaborative Effort
 - Researchers
 - Breed Associations
- Breed associations provided semen for DNA on influential sires
- USMARC ran the Illumina BovineSNP50 (50K) chip on those 2,000 sires
- USMARC provides extensively phenotyped animals for use as training data set

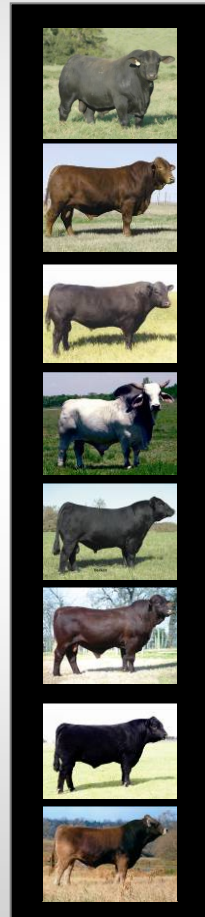
2,000 Bull Project

- Number of bulls from each breed somewhat proportionate to breed size
- Breed associations were responsible for selecting sires
 - High accuracy sires (verify the process)
 - Influential sires (greater gain from novel traits)

2,000 Bull Project: Number of Sires Sampled



- Angus 403
- Hereford 491
- Simmental 254
- Red Angus 175
- Gelbvieh 146
- Limousin 141
- Charolais 125
- Shorthorn 86

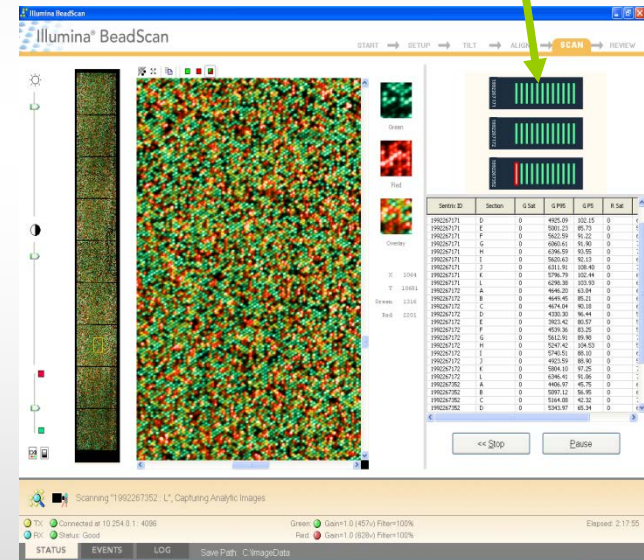
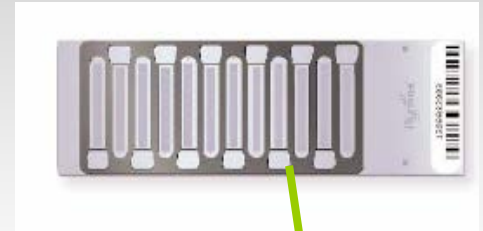


- Brangus 68
- Beefmaster 65
- Maine-Anjou 59
- Brahman 53
- Chiangus 47
- Santa Gertrudis 54
- Salers 41
- Braunvieh 27

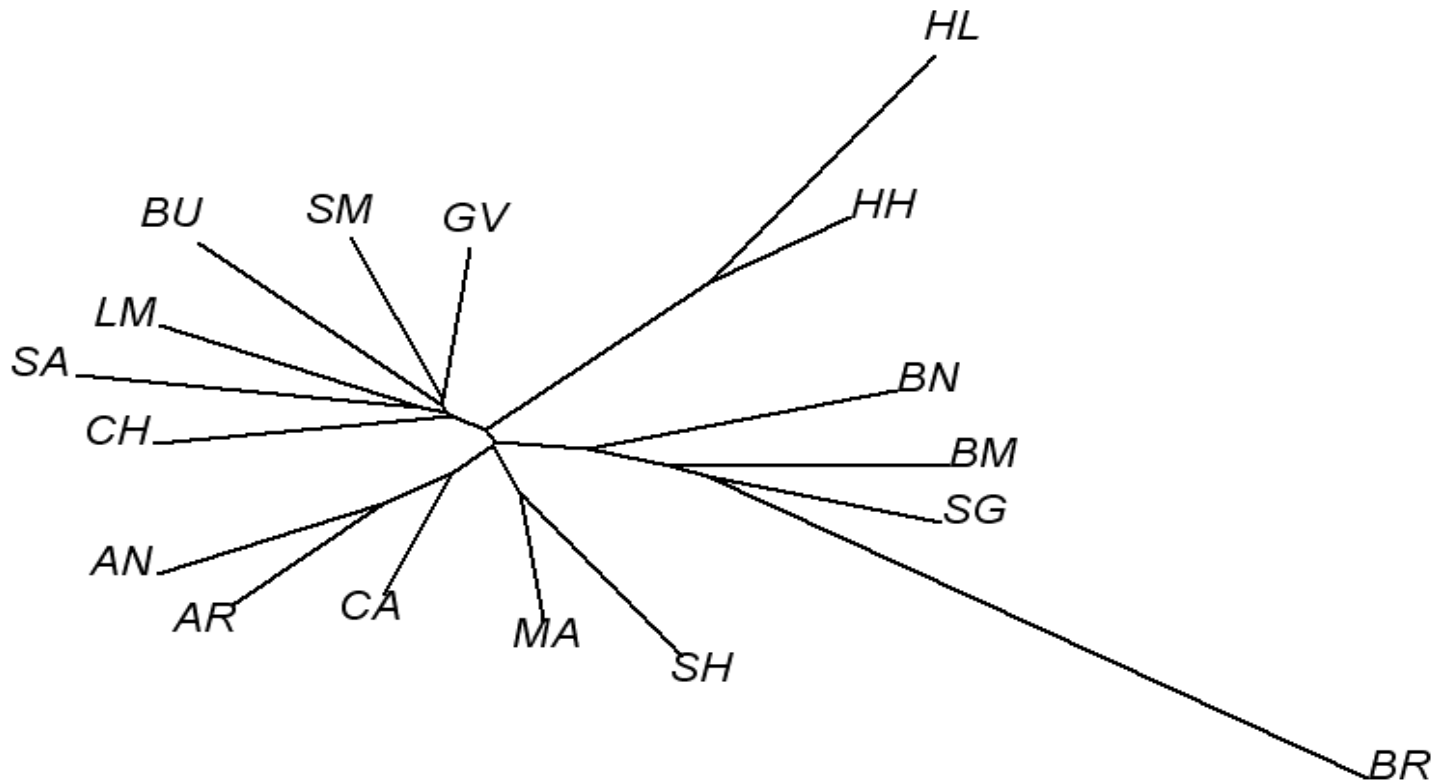
2,235

Illumina BovineSNP50 Beadchip

- Paradigm shift in beef cattle selection
- New opportunities for genomic selection
 - Dairy very successful
- Can be used to differentiate genomic differences among breeds



2,000 Bull - Breed Identification



Breed Composition Determination

- Several useful applications
 - Detection of breeds in pooled samples (marker assisted management)
 - Tracing individuals to herds of known breed composition
 - Prediction of heterosis/heterozygosity potential

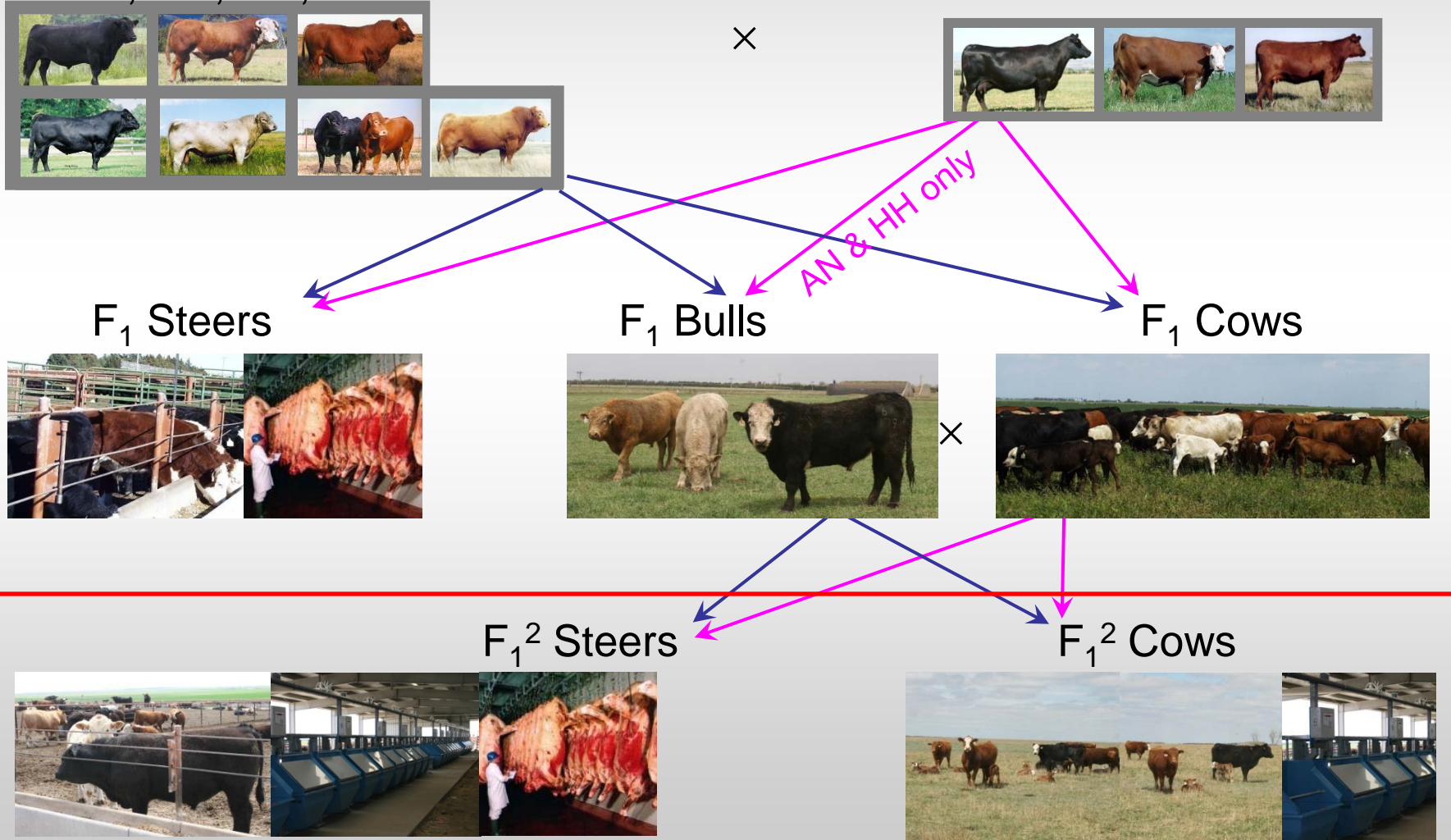
Breed Composition

- Can exploit breed distance to determine breed composition in animals with unknown origin/pedigree
- Relatively simple procedure using individual breed frequencies
- Our objective was to evaluate the accuracy of estimated breed composition of crossbreeds based on their BovineSNP50 genotypes and allele frequencies from the 2,000 bull project

GPE Cycle VII Population Used to Verify Process

AI Sires: AN, HH, AR,
SM, CH, LM, GV

Base Cows:
AN, HH, MARC III



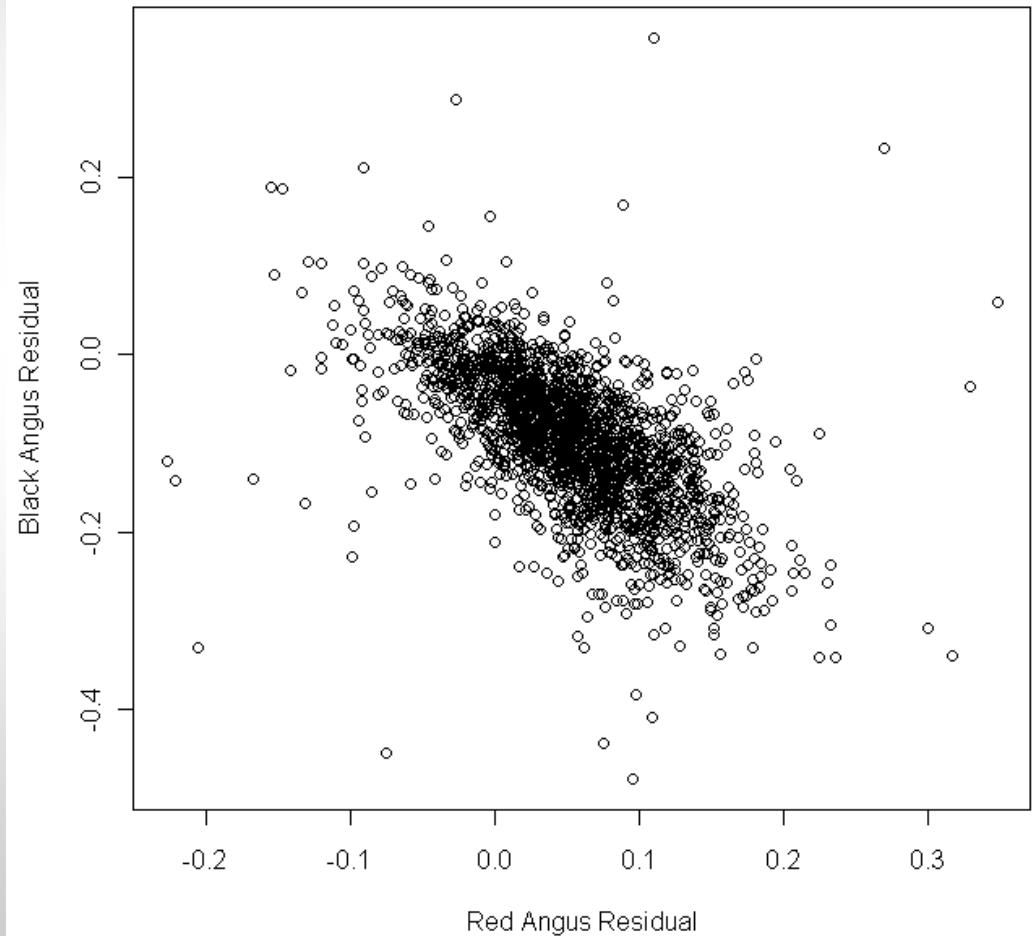
Results – SNP Predicted Breed Frequency Relative to Pedigree

Breed	Regression (SNP % on Pedigree %)	R ²
Angus	0.737 ± 0.008	0.789
Red Angus	0.883 ± 0.011	0.772
Hereford	0.981 ± 0.006	0.920
Limousin	0.925 ± 0.008	0.880
Charolais	0.873 ± 0.007	0.879
Gelbvieh	0.922 ± 0.007	0.898
Simmental	0.882 ± 0.006	0.905

Generally under-predicted Accuracy reasonable in all breed percentages but Angus and Red Angus

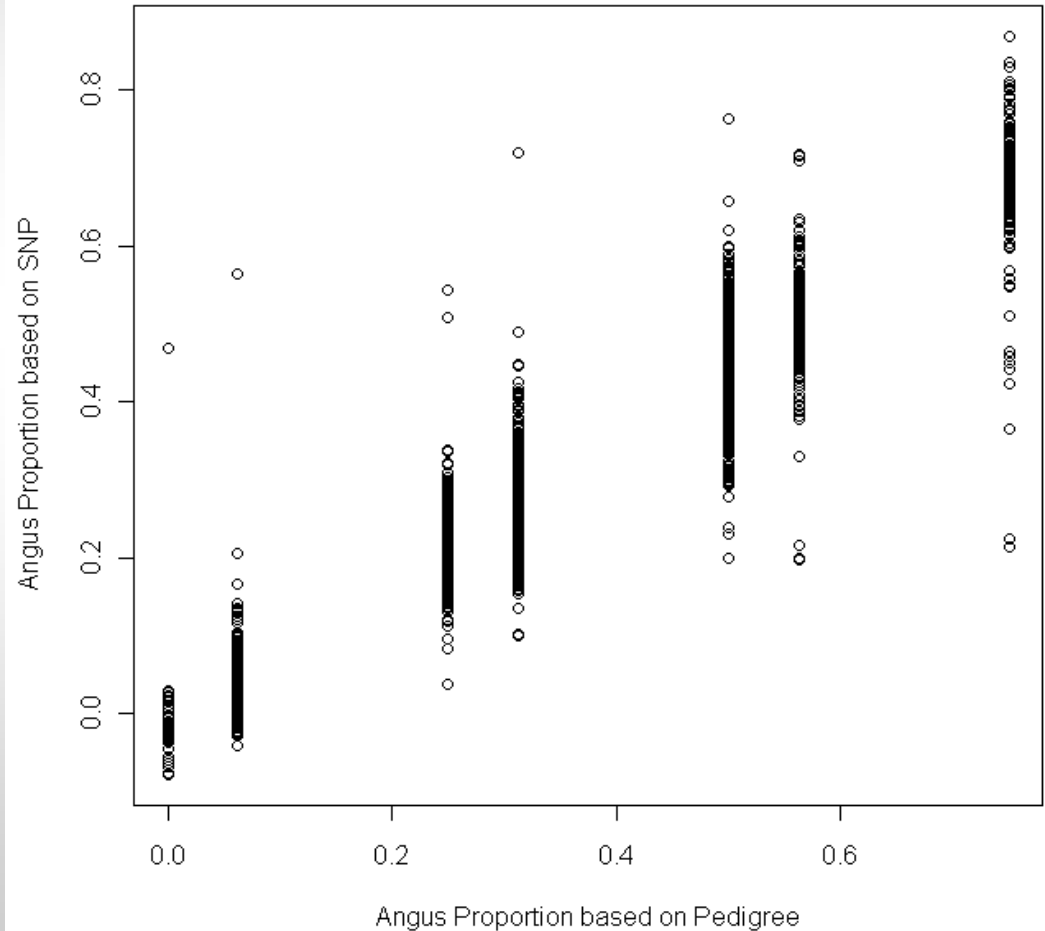
Angus Relative to Red Angus

- Residuals from prediction of SNP breed percentage using pedigree breed percentage
- Strong tendency to interchange Angus/Red Angus
- $r = -0.61$



Angus and Red Angus Combined

- Gain ~10% in percentage of variance explained
- $R^2 = 0.882$
- $b = 0.917$
- Plot representative of other breeds



Variation in Breed Composition

- Partially due to chromosomal inheritance:
 - 4-way cross (red, purple, blue, yellow)
 - Pedigree estimate: 1/4 for each breed



- Chromosomal estimate is:

6/18 red 3/18 purple

1/18 blue 8/18 yellow

- Average across chromosomes closer to pedigree

Summary

- Breed compositions are generally predicted in a reasonable interval (i.e. R^2) but not perfectly
- From analyses with reduced sets of markers, increasing the number of markers does not seem to help after a certain point
 - ~15,000 randomly sampled markers
 - 3K actually achieves ~83% R^2

Conclusions

- We can do a good job of identifying breeds using large marker panels
 - Already being applied in animal traceback scenarios
 - Some breeds hard to differentiate
- Need a representative sample of breeds in order for them to be predicted
 - For instance, Longhorn composition could not be predicted from our current 2,000 bull resource

Questions

