Advances on *Bos indicus* (Nellore) Genomics: Integrating Genomic Selection and GWAS Information

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**Cattle genomics beyond the perspective of a Holstein cow**

2007 First taurine reference genome draft assemblies
2008 Taurine 50K SNP chip commercially available
2008 US/Canada genomic selection in taurine dairy breeds

**What about the indicine “version” of the cattle (the *Bos indicus*)?**

**Indicine (or “zebu”) cattle gains the scene**
(particularly in Brazil)

**Beef statistics for Brazilian zebu:**
Largest world commercial herd (~150 M)
Major world beef exporter (ranks 1st)
> 80% is Nellore cattle (zebu)
~ 15% of international market
“Ongole” cattle expatriation from India to Brazil

Few and sparse importations from India from 1920-1960
> 100 years of introgression with local Creole taurine cows
~ 30 years of breeding programs and BLUP evaluations
Focus on carcass weight and size

Towards a Bos indicus reference genome (Nellore)

Bos indicus reference genome sequencing and assembly
140 X Illumina reads
10 X PacBio reads
20 Kb N50 contig
300 structural differences from taurine identified
Close to the end (???)

Overcoming SNP chip ascertainment bias

Re-sequencing of Bos indicus animals
30 individuals (~ 1 X coverage)
Development of the BovineHD chip (777 K)
Conclusions:

Predictive ability:

Compatible with findings in other breeds, using different methods and cross-validation strategies.
Genomic Selection project in Nellore

Our conclusions:

It works as in Holstein!

Did not have the same huge impact in the genetic progress (intrinsic reasons)

Did not reach sustainable cost/benefit ratio

Beef breeders are different from dairy breeders...

Genome-wide association studies (GWAS) and Runs of Homozigozity (ROH)

Conclusions:

Imputation to HD:

Feasible and practical and 15 K is the best
Bolormaa et al. (2014)'s method  
FDR = 4.81%

Stouffer method  
FDR = 4.46%

PC1  
FDR = 71.47%

Galvão et al. (2014) unpublished data

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Insulin-like Growth factor I and II
Growth Hormone-releasing hormone
Gonadotropin-releasing hormone
Chorionic Somatomammotropin
Prolactin-releasing hormone
Corticotropin-releasing hormone

WG
Cw
Pw
Mw
Nw
PWG
Cy
My
Ny
SCaw
BW
Conclusions:

Major QTLs for the majority of the traits (especially those with higher heritability)

PLAG1 case in birth weight, scrotal circumference and meta-analysis of carcass weight and size traits

Genome-wide association studies (GWAS) and Runs of Homozigozity (ROH)

Conclusions:

No signals of recent selection (no long common homozygote stretches)

Only short common ROH (< 4 Mb), consistent with remote selection (i.e., preceding the breeding program)

Signatures of adaptation/hardiness ???

The moderate to high heritability traits are in some sense “oligogenic”

Opportunity to map QTNs to improve accuracy of Genomic Selection

Some QTLs are common across traits – pleiotropic effect or are we measuring the same thing in different ways?

If these traits are “oligogenic”, additive selection should have promoted enough selection on these genes over the last 20 years, so we would not need GWAS information…

However, no “scars” left in the Nellore genome from additive selection for carcass weight and size...

What’s next?
We need novel phenotypes!!!

Go beyond beef quantity and achieve beef quality

GenoBeef project

Who we are?

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