EAAP 2016
67th Annual Meeting of the European Federation of Animal Science
Belfast UK, 29 Aug – 2 Sept 2016

Universidade de São Paulo
Faculdade de Zootecnia e Engenharia de Alimentos

Núcleo de Apoio à Pesquisa
Melhoramento Animal, Biotecnologia e Transgenia

Copy number variations reveal metabolic pathways involved with feed conversion ratio in beef cattle

Miguel H.A. Santana, Gerson A. Oliveira Jr, Minos E. Carvalho, Lais Grigoletto, **José B.S. Ferraz**

Abstract number 24015

Session 27. Young scientists competition – Genetics Commission – part 2
Tuesday 30 August – 2016 - Belfast – UK

Motivation – Beef Production

Production*	**2011**	**2012**	**2013**	**2014**	**2015**
United States	11,983	11,848	11,752	11,078	10,868
Brazil	9,030	9,307	9,675	9,723	10,215
European Union	8,114	7,708	7,388	7,410	7,475
China	6,475	6,623	6,730	6,890	6,400
India	3,308	3,491	3,800	4,125	4,250
Argentina	2,530	2,620	2,850	2,700	2,850

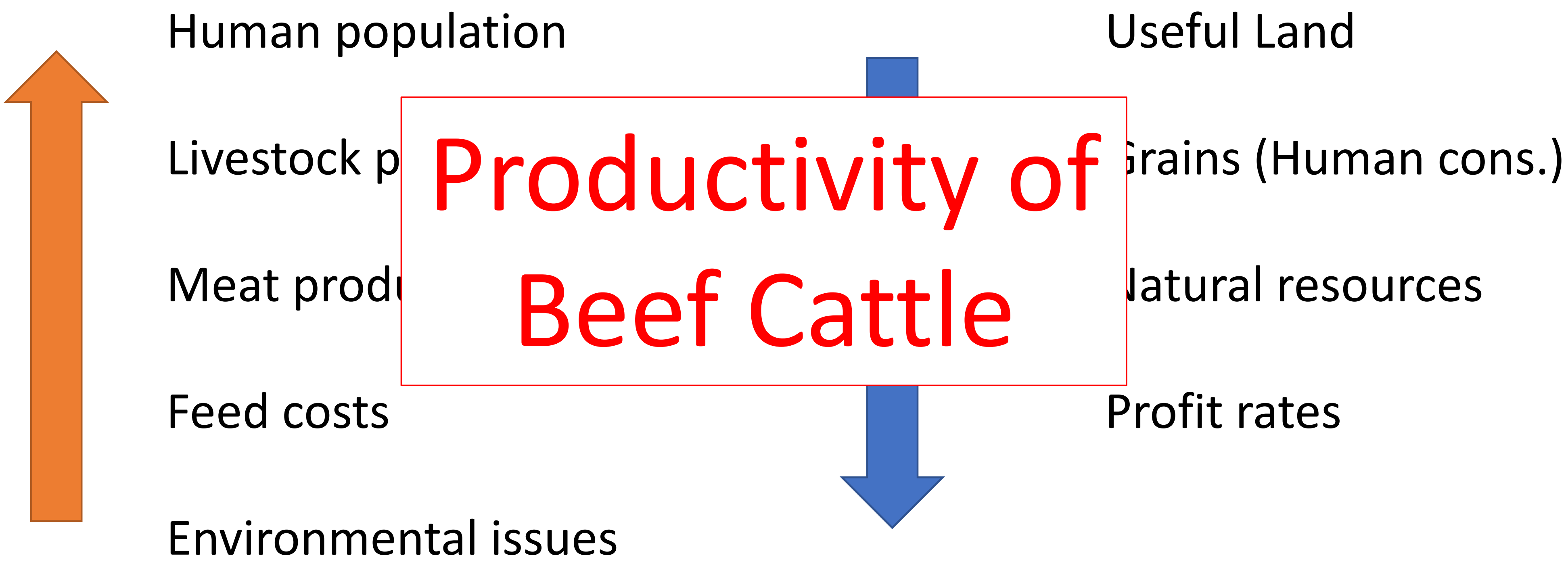
1,000 Metric Tons (Carcass Weight Equivalent)
Source: USDA 2015

Motivation – Beef Exportation

Exportation*	2011	2012	2013	2014	2015
India	1,268	1,411	1,765	2,082	2,400
Brazil	1,340	1,524	1,849	1,909	2,235
Australia	1,410	1,407	1,593	1,851	1,590
United States	1,263	1,112	1,175	1,167	1,145
New Zealand	503	517	529	579	575
Paraguay	197	251	326	389	440

1,000 Metric Tons (Carcass Weight Equivalent)
Source: USDA 2015

Motivation – Global Perspective



Human population

Livestock p

Meat prod

Feed costs

Environmental issues

Useful Land

rains (Human cons.)

atural resources

Profit rates

Productivity of Beef Cattle

Feed Efficiency – Beef Cattle

Productivity = Production x Area

Production = Meat/Muscle/Body weight (gain)

Area = Resources used (Mainly food)

Feed Efficiency = Weight gain x Feed intake

Feed Efficiency = Productivity

Objective – Feed Efficiency

Detect copy number variations regions (CNVRs) and associate them with feed conversion ratio (FCR) in beef cattle

Identify candidate genes and putative pathways involved with FCR from CNVRs associations

Phenotypes

Phenotypic data from 1475 young bulls and steers (574±95-d old and 381±45 kg)

GrowSafe

CalanGates

Individual Pens

Phenotypes

- Average Daily Gain (kg/day)
- Dry Matter Intake (kg/day)
- Feed Conversion Ratio (kg/kg)

$$FCR = \frac{DMI}{ADG}$$

CNV and CNVRs detection

- We used 2253 animals genotyped in Illumina BovineHD

- CNVs were identified using LRR and BAF (PennCNV Wang et al. 2007)

Quality control = standard deviation of LRR (>0.30), the default for BAF drift (>0.01) and waviness factor (>0.05).

- The CNV regions (CNVRs) were determined by merging overlapping CNVs identified in two or more samples (CNVRuler, Kim et al., 2012)

- CNVRs with less than 5 % allele frequency were excluded.

Association Analysis, Genes and Pathways

- Linear regression was used to determine associations between CNVRs and the FCR
- The false discovery rate (FDR<0.05) method was used for multiple comparison correction
- Significant CNVR were considered as promising QTL
- Functional annotation was performed using DAVID v6.7 and pathway analyses using KEGG.

CNVs and CNVRs detection

- 139,089 CNVs were identified by PennCNV
- 32 % (44,558) were non-redundant, unique CNVs
- 2667 CNVRs were determined in autosomal chromosomes
- The pattern of the different types of CNVRs was specific for each segment with 1111 loss, 938 gain, and 617 mixed regions
- CNVRs were associated resulting in 16 non-fixed regions, where 12 (chromosomes 1, 5, 7, 10, and 12) had significant association.

CNVRs and FCR associations

Table 1. Copy number variation regions (CNVR) associated with feed conversion rate

CNVR	Chromosome	Start	End	Size	FDR
1	5	58386640	58441130	54491	<0.01*
2	12	74844575	74942860	98286	<0.01*
3	5	117356476	117639815	283340	<0.01*
4	5	59421039	59627471	206433	<0.01*
5	12	75016673	75141024	124352	<0.01*
6	7	44437375	44444959	7585	<0.01*
7	12	72748544	72882991	134448	<0.01*
8	10	22709100	22952910	243811	0.01*
9	1	93730576	93819471	88896	0.01*
10	12	73657824	73666963	9140	0.01*
11	12	72518489	72739627	221139	0.02*
12	7	42736530	43353211	616682	0.04*

Candidates genes and pathways

- These 12 significant regions resulted in 51 genes spread over four Chr (5, 7, 10, and 12)

- The metabolic pathways found in KEGG related with these genes were:

1. Endocytosis
2. Glycerophospholipid metabolism
3. Insulin signaling pathway
4. Histidine metabolism
5. Olfactory transduction
6. Oxidative phosphorylation
7. Retinol metabolism

Conclusions

- CNV approach found distinct genomic regions related to FCR
- Genes pointed here are part of the same biological processes (lipid, protein and energetic metabolism)
- These findings contribute to the knowledge of the genetic basis of feed efficiency

Thank for your attention

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More information about this research are published in Journal of Applied Genetics (2016) pp 1-10.
doi:10.1007/s13353-016-0344-7