

basis to inform the development of the dairy sector in Eastern Africa.

P1064: Genome Mapping, Tagging & Characterization: Cattle

Genome-Wide Scan for Selection Signatures in Zebu and Taurine Cattle Reveals Regions Associated with Adaptive and Production Traits

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Over the course of their evolutionary history, modern cattle breeds have been exposed to a wider range of ecological stressors and human guided selective breeding. Natural environmental selective pressures have likely shaped the genome of African cattle populations adapted to marginal and heterogeneous landscapes. On the other hand, temperate *Bos taurus* cattle breeds have been continuously selected for economically importance traits. To identify genomic regions under divergent selection for ecological and production traits, we performed a genome-level scan using 68,007 autosomal SNPs derived from indicine breeds in Ethiopian cattle populations (n = 272), Nellore (n = 99), Bangladeshi zebu (n = 52), taurine reference populations, Holstein, (n = 21) and Hanwoo, (n = 22) based on a population differentiation (F_{ST}) test. We identified potential candidate genes involved in thermo-tolerance (*DNAJB5/Hsp40*, *DNAJB6*, and *HSPA13*), parasite loads and resistance (*BBS9*, *FAM177A1*, *SRP54*, *PSMA6*, *PLD4*, and *CDCA4*), fertility (*INHBC*, *STAT6*, *ID3*, and *MSRB3*), disease/immune response (*ARG2*, *AKIRIN2* and *TRIM24*), body stature (*LYN*, *CHCHD7*, and *SDR16C5*, and *POLR2*), and growth and meat traits (*TG*, *ASAPI*, *MEF2A*, and *HERC3*). The identified genes are involved in different pathways (vasopressive-regulated water reabsorption, metabolism, melanogenesis, and thyroid and hormone synthesis). The results from the present study can be used as a basis for further understanding and exploitation of the molecular basis of adaptive and production traits.

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Tracking Zebu Introgression in Mediterranean Cattle Breeds

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A recent work investigating genetic origin, admixture and population history of primitive European cattle highlighted, by using genome-wide single nucleotide polymorphisms, zebu gene flow in the Balkan and Italian Podolic cattle populations. Haemoglobin protein polymorphism analysis in Italian breeds highlighted the presence of zebuine markers in both Italian Podolic and Alpine Grey cattle. Based on the above evidences, we here specifically look for genomic regions of zebuine ancestry in a different dataset of 50K genotypes from Mediterranean breeds including 29 Marismena (Spain); 30 Bazadaise and 30 Gasconne (France); 24 Alpine Grey, 97 Piemontese, 51 Chianina, 5 Marchigiana, 121 Romagnola, 24 Podolica, 24 Modenese, 30 Reggiana, 30 Cinisara and 30 Modicana (Italy); 24 Guelmoise (Algeria); 24 Cika (Slovenia), 43 Illyrian Mountain Buša (Albania). Additional taurine and zebuine breeds from previously published studies are also included in the analyses. Special emphasis in genetic analyses is also given to the identification of genomic regions potentially associated with a phenotypic trait observed in several taurine breeds as well as in some zebuine breeds, characterized by calves having a fawn coat at birth, while turning to various shades of grey in adult animals. The obtained results contribute to a better characterization of history and genetic structure of Mediterranean cattle breeds.

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Identification of cis-eQTLs Associated with Feed Efficiency in Nellore Cattle

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The search for genomic regions associated with feed efficiency (FE) in beef cattle has been the focus of many researches in the past years by trying to associate SNPs in the DNA with the phenotypic trait. Recently, a new approach called “functional genomic selection” seeks to identify variants most likely to be the cause of phenotypic change, to improve the portability of genomic predictions between breeds and across populations. With this aim, we combined data from liver gene expression (RNAseq) and 80k genotype (GeneSeek GGP Bos Indicus HD[®], Illumina) of 14 Nellore bulls identified as extremes of FE, on a cis-eQTL analysis. Only SNPs with MAF>0.4 and at least 3 samples in at least 2 genotypes were tested, considering a 2Mb window surrounding 100 candidate genes for FE that were identified in our previous work. Gene expression was estimated by HTseq counts, using *Bos taurus* UMD3.1 as reference genome, and then normalized by library size. Data were analyzed considering a standard additive linear model and an ANOVA model that account for both additive and dominance effects, using Matrix