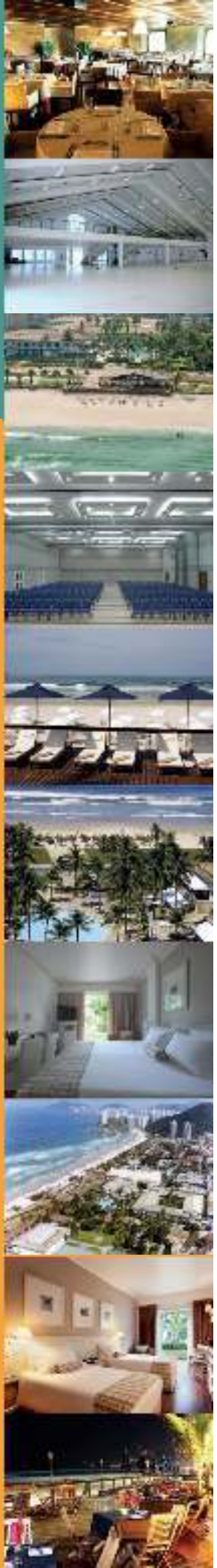
5th International Symposium on Animal Functional Genomics

September 9-11, Guaruja - SP, Brazil

PROGRAMME AND ABSTRACT BOOK



ISAFG 2013

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PROGRAMME

Understanding the function of genes, gene variants, gene expression modulators, and protein networks that underlie health and production of animal species is timely and needed. The purpose of ISAFG 2013 was to bring together academic researchers, industry representatives and policy makers who wished to exchange knowledge on the leading-edge developments about functional genomics and its application on animal health and production. The symposium themes included topics of importance in animal genomics, ranging from livestock to animal models of human diseases. The symposium venue was at the Casa Grande Hotel Resort & Spa, 70 km from the city of São Paulo, and just a few steps from the seashore of Guarujá island.

Sept. 8th (Sunday)

15:00 - 19:00 Registration

Sept. 9th (Monday)

8:00 - 8:30 Opening Ceremony - UNESP / USP / FAPESP / CNPq / CAPES / IAEA-FAO / USDA

Session 1: Keynote Speaker

8:30 - 9:30 James Womack - Center for Animal Biotechnology and Genomics at Texas A&M University) - United States

Title: A look at the brief history of livestock genomics and some thought to the future

Session 2: Genomics and Animal Health

Moderator: Cáris Maroni Nunes - FMVA - UNESP - Araçatuba - Brazil

10:00 - 10:45 Najib El-Sayed - University of Maryland - United States

Title: Improving knowledge on host-parasite interaction through genomics

10:45 - 11:30 Elinor Karlsson - Broad Institute Harvard – United States

Title: On the genetic interpretation of disease data

Session 3: Genomic Variation Impacting Phenotype Expression

Moderator: Fernando Cardoso - EMBRAPA - Pecuária Sul - Brazil

14:00 - 14:45 Olivier Hanotte - University of Nottingham - United Kingdom

Title: Times to tap the tropical livestock genome: the example of the East African Shorthorn Zebu

14:45 - 15:30 Johann Sölkner - University of Natural Resources and Life Sciences (BOKU) - Austria

Title: Pleiotropy at Work: Complex Inheritance of Melanoma and Pigmentation of Coat and Skin in Grey Horses

16:00 - 16:45 George Liu - Agricultural Research Service (ARS) - USDA - United States

Title: Structural and functional impacts of cattle copy number variations

Special Poster Session

17:00 - 19:30 Poster Session with Jazz, Wine & Cheese (Sponsors' Exhibition Session)

Sept. 10th (Tuesday)

Session 4: Above the Genes: Epigenomics

Moderator: Flavio Meirelles - FZEA - USP - Brazil

8:00 - 8:45 Lawrence Smith - University of Montreal - Canada and UNESP/Brazil

Title: Reprogramming the Epigenome of Domestic Animals

8:45 - 9:30 Daniel de Carvalho -Faculty of Medicine - University of Toronto - Canada

Title: Epigenomics and cancer: A model for gene function understanding

Session 5: Genomic Evolution Across Species Impacting Gene Function

Moderator: Paolo Ajmone-Marsan - UNICATT - Italy

10:00 - 10:45 Yana Kamberov - Harvard Medical School - United States

Title: Using genomes as an archaeological record to unravel patterns of natural selection

10:45 - 11:30 Jerry Taylor- University of Missouri - United States

Title: Dealing with entire cattle genomes: Lessons we've learned?

Session 6: Genomics, Animal Industries and Food Security

Moderator: José Fernando Garcia - FMVA - UNESP - Araçatuba - Brazil

14:50 - 15:05 John Cole - Animal Improvement Programs Laboratory - ARS - USDA - United States

Title: New applications of genomic technology in the US dairy industry

15:05 - 15:20 Curtis P. Van Tassell - Agricultural Research Service (ARS) - USDA - United States

Title: Critical analysis on the adoption of genomics in livestock industry in North America

15:20 - 15:35 Kathiravan Peryasami - Joint FAO/IAEA Division - Austria

Title: Advent of genomics to foster food production in developing countries: Challenges and Prospects

15:35 - 15:50 Scott Fahrenkrug - Department of Animal Science - University of Minnesota - United States

Title: Accelerating the genetic improvement of livestock with non-meiotic allele introgression

15:50 - 16:30 Round Table

Special Poster Session

16:30 - 19:30 Poster Session with Jazz, Wine & Cheese (Sponsors' Exhibition Session)

Sept. 11th (Wednesday)

Session 7a: Improving Genome Assembly Models and Revealing Variation Within Species

Moderator: Mario Binelli - FMVZ - USP - Brazil

9:00 - 9:45 David Schwartz - Departments of Genetics and Chemistry - University of Wisconsin-Madison - United States

Title: Single Molecule Approaches for Scalable Genomics

9:45 - 10:30 James Reecy - Iowa State University - United States

Title: Gene variant discovery by genome re-sequencing

Session 7b: Improving Genome Assembly Models and Revealing Variation Within Species

Moderator: José Buratini Jr. - IBB - UNESP - Botucatu - Brazil

11:00 - 11:45 John McEwan - Ag Research - New Zealand

Title: Genotyping by sequencing revealing new boundaries on genomic variation

11:45 - 12:30 Matt Settles - University of Idaho - United States

Title: Novel approaches to gene expression using RNAseq method

Session 8: Discussion, Final Remarks and Close of Meeting

Moderator: Tad Sonstegard - ARS - USDA

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Inbreeding effect and genotyping strategies for genomic selection in simulated data

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Abstract:

The conventional selection strategies have become more efficient with the use of the information of molecular markers into the statistical models (VANRADEN et al., 2009). The aim of this study was to estimate the direct genomic value in two populations with divergent levels of inbreeding and to evaluate the accuracy of prediction. Genomic and phenotypic data of a quantitative trait with heritability 0.30 and phenotypic variance equal to one, were simulated using the software QMSim of Sargolzaei and Schenkel (2009). Two divergent populations (P1 and P2) in relation to the mating system were selected for the highest estimated breeding values (EBV) for 10 non-overlapping generations. In P1, the aim was to maximize the inbreeding and in P2 was to minimize the it. The genome of animals consisted of 30 chromosomes of 100 cM each, with 1,666 equally space d SNP markers and 10 QTLs randomly assigned to each chromosome. The effect of allelic QTL was sampled from a gamma distribution with shape parameter of 0.40, as described by Hayes and Goddard (2001). The recurrent mutation rate for markers and QTL was 2.5x10-5 and the minimum allelic frequency (MAF) was 5%. The simulations were replicated 5 times. In P1 and P2, each training set was formed with 168 animals of the ninth generation. The choice of these animals followed 3 selection strategies: T1P1, 5% of the largest and lowest 5% of EBV; T2P1, 10% of the largest EBV; T3P1, 10 % of lowest EBV. Strategies T4P1 and T4P2 were formed by all the 1680 animals of the ninth generation. The validation set was composed by animals of the last generation 10th. The GEBVs were calculated using the package rrBLUP of software R with different training sets. The predictive power (PP) was estimated by Pearson correlation between GEBV of animals of validation set and TBV (True or simulated breedi ng values). The maximum values of inbreeding and linkage disequilibrium in 2 populations were respectively 0.3 and 0.31 for P1 and 0.02 and 0.28 for P2. Selection strategies in R1 (T1P1, T2P1, T3P1 and T4P1), had correlations and standard deviations of 0.20±0.002, -0.12±0.07, -0.09±0.05, 0.36±0.03, respectively, between GEBV and TBV in the validation sets. The correlations and standard deviations using P2 strategies (T1P2, T2P2, T3P2 and T4P2) were 0.26±0.01, -0.06±0.03, 0.07±0.04 and 0.36±0.05. It can be concluded that, for this simulation, the level of inbreeding does not affect the estimation of PP, however genotyping strategies are directly related to the power of prediction. Among the strategies analyzed, the strategy with the highest number of animals showed greater PP, but this strategy would result in a high cost of genotyping. Alternative strategies, which covered both ends of EBV have good predictions GEBV, since they need a few animals genotyped. In practice, sele ction strategies may have a greater influence over the choice of genotyped animals than the rates of inbreeding, enabling best accuracies with lower costs.