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Genomic evaluation systems in the dairy and beef industries have entered a phase of implementation and refinement, but their full potential will not be realized until all economically important traits in relevant production systems are incorporated. Many of the traits not yet incorporated, are either difficult or highly technical to measure. One example is individual animal feed intake for pasture-based production systems. Currently evaluation uses data from feedlot measurement using grain-based diets. The relevance of grain based feed intake data for predicting the merit of pasture fed animals must be questioned. The development of miniaturised wireless sensors and data capture systems now offers us the capability to study animals in their (various) production environment(s), and in a way that does not constrain them from expressing their full range of genetic drivers for the traits of interest. We describe an automated high throughput system for deep phenotyping of livestock maintained in environments that reflect commercial conditions, and present an early assessment of the system for more precise and relevant genetic/genomic evaluation.

Key Words: phenotyping, livestock, automation

P1029 A composite test to detect positive selection in cattle and sheep. Imtiaz A. S. Randhawa,* Mehar S. Khatkar, Peter C. Thomson, and Herman W. Raadsma, *REPROGEN Animal Bioscience group, Faculty of Veterinary Science, University of Sydney, Camden, NSW 2570, Australia.*

Rapidly emerging research in quantitative and qualitative genetics demands robust analytical tools to identify genetic loci involved in phenotypic appearance and underlying molecular mechanisms. Here we present a robust method for genome-wide selection scans (GWSS) using dense polymorphism data to map high-resolution signals by combining evidence from multiple selection tests. We investigated multi-breed data sets from 375 cattle and 2803 sheep for the presence or absence of either polledness or double muscling using 3 independent tests for selection signatures and a novel composite test. All cattle and sheep samples were genotyped with Illumina's BovineSNP50 and OvineSNP50 chip assays, respectively. Total of 38,610 SNPs for cattle and 47,502 SNPs for sheep were retained. For each trait, single (FST, ΔDAF or ΔAFD) and multiple (XP-EHH) marker based estimates for evidence of selection were computed. In addition, a novel composite signal was obtained by converting the fractional ranks of test statistics of each method into Z-statistics and combined in a composite score at each locus to detect a common selection signature. High-resolution peak scores were detected by GWSS in each analysis in the known candidate regions of cattle's autosome 1 (gene: SYNJ1) and 2 (MSTN), and sheep's autosome 10 (RXFP2) and 2 (GDF8), for the functional mutations which underpin polledness and double muscling, respectively. The strong association of the single and the combined signal at these loci confirms the robustness of composite signals for detecting selection signatures. This method can be used to identify the candidate regions harbouring functional SNPs in genes of complex networks, e.g., domestication, adaptation and production traits.

Key Words: genome-wide selection scans, composite signals, cattle and sheep

P1030 Multitrait composite interval mapping reveals pleiotropic QTL on chicken chromosome 1. Millor Rosario*[1,5], Rodrigo Gazaffi[2], Ana Moura[3], Monica Ledur[4], Katia Nones[1], Antonio Garcia[2], and Luiz Coutinho[1], *[1]Departamento de Zootecnia, USP/ESALQ, Piracicaba, 13418-900, Brazil, [2]Departamento de Genétcia, USP/ESALQ, Piracicaba, 13418-900, Brazil, [3]Universidade Estadual Paulista, UNESP/FMVZ, Botucatu, 18618-000, Brazil, [4]Embrapa Suinos e Aves, Concórdia, 89700-000, Brazil, [5]Departamento de Genética e Evolução, UFSCar/CCBS, São Carlos, 13565-905, Brazil.*

Genetic correlations between traits are caused by linkage or pleiotropy. Multivariate approaches are useful to help clarify this point. We implemented multitrait composite interval mapping to map pleiotropic QTL associated with performance, carcass, organs and physiological traits on chromosome 1 of a Brazilian chicken F2 population (broiler x layer). Genotypes from 453 F2 chickens were obtained using 26 microsatellite markers. Phenotypes for 24 traits were adjusted using family (5) and sex (2) as fixed effects and hatch (17) as a random effect in PROC MIXED. Conditional probabilities of QTL genotypes were obtained from GridQTL and cofactors were selected only if located outside of the chromosome 1, avoiding overparametrization. QTL analysis was carried out in R software and a significant threshold was defined as LOD > 17.0, considering Bonferroni correction. We mapped 4 pleiotropic QTL: at 173 cM (LOD = 20.5) associated with body weight 41 d (BW41), weights of heart and abdominal fat, and ash content in dry matter; at 203 cM (LOD = 20.4) associated with BW41, weights of wings, head, heart, gizzard and abdominal fat, and crude protein, ether extract and ash contents in dry matter; at 267 cM (LOD = 18.7) associated with BW41, weights of breast, shank, head, gizzard and crude protein content in dry matter; and at 436 cM (LOD = 22.9) associated with BW41, weights of breast, wings, shank, gizzard, intestinal length and cholesterol and triglycerides plus cholesterol levels. These 4 genomic regions will be useful to mine for SNP using 60k DNA chip to identify associations between SNP and poultry economical traits simultaneously.

Key Words: poultry, pleiotropy, multivariate analysis