



## **QTL detection for coccidiosis resistance using SNPs**

Nicola Bacciu, Olivier Demeure, Bertrand Bed'Hom, D. Zelenika, Frederique Pitel, Pascale Le Roy, Marie-Hélène Pinard-van Der Laan

### **► To cite this version:**

Nicola Bacciu, Olivier Demeure, Bertrand Bed'Hom, D. Zelenika, Frederique Pitel, et al.. QTL detection for coccidiosis resistance using SNPs. Animal Genomics for Animal Health International Symposium, May 2010, Paris, France. hal-01193711

**HAL Id: hal-01193711**

**<https://hal.science/hal-01193711>**

Submitted on 6 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

## POSTER ABSTRACTS

2-PA02

### PIONEERING ANIMAL GENETICS AT QUANTITATIVE CYTOGENETIC AND MOLECULAR LEVELS

A. ALI

Department of Livestock Production, University of Veterinary and Animal Sciences, Outfall Road – 54000, Pakistan

Email : ahmadali@uvas.edu.pk

Pakistan is a land enriched with the world's finest Animal Genetic Resources. Nili, Ravi, Nili Ravi, Kundi and Azakheli breeds constitute 60% of the dairy and beef market whereas Sahiwal, Red Sindhi, Cholistani and Crossbred cattle are feeding 40% of the national food market. Similarly, Pakistan holds 25 goat and 28 sheep breeds stretching across the country from the north to the south. With the advancements in breeding, selection and livestock biotechnologies, the drive to enhance and develop superior genetic potentials is taking a big pace. With increasing government commitment to come up to the challenges of rising demands of food of animal origin and management/conservation of valuable animal genetic resources of Pakistan, institutions like the National Buffalo Research Institute and the Research Centre for Conservation of Sahiwal cattle have been established. On the innovation and research side, the dedicated team of the University of Veterinary and Animal Sciences, is undertaking high profile molecular cytogenetic, genomic and quantitative genetic studies focusing on the identification, characterization and evaluation of genes of economic importance such as milk production, disease resistance, reproductive efficiency, feed efficiency. An elaborate set up to undertake genome studies through QPCR, Illumina Bead Express microarray system and the development of Bioinformatics and quantitative genetic labs are providing services to the whole public and private dairy and meat sectors. Finally the field application of reproductive biotechnologies is expected to bring about a revolution in the country.

2-PA03

### QTL DETECTION FOR COCCIDIOSIS RESISTANCE USING SNPS

N. BACCIU<sup>1,2</sup>, O. DEMEURE<sup>1,2</sup>, B. BED'HOM<sup>3</sup>, D. ZELENKA<sup>4</sup>, F. PITEL<sup>5</sup>, P. LE ROY<sup>1,2</sup> AND M.H. PINARD<sup>3</sup>

<sup>1</sup>INRA, UMR 598 Génétique animale, 35000 Rennes, France. <sup>2</sup>Agrocampus Ouest, UMR 598 Génétique animale, F-35000 Rennes, France. <sup>3</sup>INRA, UMR 1313 Génétique animale et Biologie intégrative, 78352 Jouy-en-Josas Cedex, France. <sup>4</sup>Centre National de Génotypage, 2 rue Gaston Crémieux, CP 5721, 91057 Evry Cedex, France. <sup>5</sup>INRA, UMR 0444 Génétique cellulaire, BP 52627, 31326 Castanet-Tolosan Cedex, France

Corresponding Author: nicola.bacciu@rennes.inra.fr

Avian coccidiosis is a major parasitic disease responsible for substantial economical discomforts to poultry production. The biggest problems regard growth and feed efficiency in affected birds. Since drugs and vaccination prove to be not an effective solution an alternative approach is needed. Genetic resistance would allow a decrease of important costs associated to coccidiosis. A genome scan in an F2 cross issued from a resistant Fayoumi line and a susceptible Leghorn line was performed to detect QTL for disease resistance traits to *Eimeria tenella* in chicken. Animals were genotyped for 1536 SNP and 157 microsatellites panel across the whole genome and different traits related to disease resistance (body weight growth, plasma coloration, hematocrit, rectal temperature and lesion) were measured. A Factor Analysis was performed and a new variable was obtained as a linear combination of the original traits. QTL detection analyses were performed by using QTLMAP software. The single QTL analysis detected 20 chromosome-wide significant QTL for the different traits. Out of these, a very significant (< 1%) QTL was detected on *GGA18* and three more co-located and very significant QTLs on *GGA16*. Several significant QTLs (<5%) were also detected on *GGA3*, *GGA5*, *GGA7*, *GGA10*, *GGA11*, *GGA14*, *GGA15* and *GGA17*. Using an F2 cross from resistant and susceptible chicken lines proved to be a successful strategy to detect QTL for genetic resistance to coccidiosis in chicken. Obtained results could be of help to develop and eventually implement new breeding strategies in poultry industry.