INTERNATIONAL JOURNAL OF HEALTH & ANIMAL SCIENCE FOOD SAFETY

Keywords

Copy Number Variant, Chicken, Genetic variability

CORRESPONDING AUTHOR

Erica Gorla
erica.gorla@unimi.it

JOURNAL HOME PAGE

riviste.unimi.it/index.php/haf

UNIVERSITÀ DEGLI STUDI DI MILANO
DIPARTIMENTO DI SCIENZE VETERINARIE PER LA SALUTE, LA PRODUZIONE ANIMALE E LA SICUREZZA ALIMENTARE

Genomic variability in Mexican chicken population using Copy Number Variation

Erica Gorla[1*], Maria C. Cozzi[1], Sergio I. Roman-Ponce[2], Felipe de Jesus Ruiz-Lopez[2], Vicente E. Vega-Murillo[2], Silvia Cerolini[1], Alessandro Bagnato[1], Maria G. Strillacci[1]

[1] *University of Milan, Department of Veterinary Medicine, Italy*

[2] *Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias, Mexico*

Abstract

Copy number variants (CNVs) are polymorphisms which influence phenotypic variation and are an important source of genetic variability (Mills *et al*., 2011). In Mexico the backyard poultry population is a unique widespread *Creole chicken* (Gallus gallus domesticus) population, an undefined cross among different breeds brought to Mexico from Europe and under natural selection for almost 500 years (Segura-Correa *et al*.2004, Rodriguez *et al*., 1996). The aim of this study was to investigate genomic variation in the Mexican chicken population using CNVs.

A total of 256 DNA samples genotyped with Axiom® Genome-Wide Chicken Genotyping Array were used in the analyses. The individual CNV calling, based on log-R ratio and B-allele frequency values, was performed using the Hidden Markov Model (HMM) of PennCNV software on the autosomes (Wang *et al*., 2007; Peiffer *et al*., 2006). CNVs were summarized to CNV regions (CNVRs) at a population level (i.e. overlapping CNVs), using BEDTools.

The HMM detected a total of 1924 CNVs in the genome of 256 samples resulting, at population level, in 1216 CNV regions, of which 959 gains, 226 losses and 31 complex CNVRs (i.e. containing both losses and gains), covering a total of 47 Mb of sequence length corresponding to 5,12 % of the chicken galGal4 assembly autosome. A comparison among this study and 7 previous reports about CNVs in chicken was performed, finding that the 1,216 CNVRs detected in this study overlap with 617 regions (51%) mapped by others studies.

This study allowed a deep insight into the structural variation in the genome of unselected Mexican chicken population, which up to now has not been never genetically characterized with SNP markers. Based on a cluster analysis (pvclust – R package) on CNV markers the population, even if presenting extreme morphological variation, does not resulted divided in differentiated genetic subpopulations. Finally this study provides a CNV map based on the 600K SNP chip array jointly with a genome-wide gene copy number estimates in Mexican chicken population.

ISSN: 2283-3927

References

Mills R.E., Walter K., Stewart C., Handsaker R.E., Chen K., Alkan C. et al., 2011. Mapping copy number variation by population-scale genome sequencing. Nature. 470, 59-65.

Segura-Correa J.C., Sarmiento-Franco L., Magaña-Monforte J.G., Santos-Ricalde R., 2004. Productive performance of Creole chickens and their crosses raised under semi-intensive management conditions in Yucatan, Mexico, Br Poult Sci. 45(3), 342-345.

Rodriguez J.C., Allaway C.E., Wassink, G.J., Segura J.C., Rivera T., 1996. Estudio de la Avicultura de traspatio en el municipio de Dzununcàn, Yucatàn. Vet Mex. 27(3), 215-219.

Wang K., Li M., Hadley D., Liu R., Glessner J., Grant S., Hakonarson H., Bucan M., 2007. PennCNV: an integrated hidden Markov model designed for high- resolution copy number variation detection in whole-genome SNP genotyping data. Genome Res.17, (11):1665–1674.

Peiffer D.A., Le J.M., Steemers F.J., Chang W., Jenniges T., Garcia F., et al., 2006. High-resolution genomic profiling of chromosomal aberrations using Infinium whole-genome genotyping. Genome Res.16, 1136–1148.

ISSN: 2283-3927