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Report of new alleles at BG loci in Camperos chickens

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ABSTRACT

Camperos are meat-type chickens developed in Argentina that are under study for their response to disease. Nine new alleles were found in Campero chickens (from INTA EEA Pergamino) at the highly polymorphic BG loci within the Major Histocompatibility Complex (MHC), and were later reported to the GenBank (Accession numbers: DQ17443, DQ174444, DQ176443-DQ6449). All of them vary from previously reported BG alleles obtained from white Leghorn chickens and the Red Jungle Fowl from the Chicken Genome Project. Animals were selected from line-crossing among Plymouth Rock Red, Rhode Island Red and Cornish Red. Sequences reported add further evidence about the extreme diversity of these highly polymorphic, rapidly-evolving MHC genes.

Key Words: MHC. BG genes. Alleles. Camperos chickens

RESUMEN

Se han hallado nueve nuevos alelos de los genes B-G del Complejo Mayor de Histocompatiblidad en Pollos Camperos (pollos para carne) desarrollados en Argentina. Estos nuevos alelos han sido registrados también en el GenBank o Banco de Secuencias Mundial donde se les asignaron números de acceso y representan variantes de secuencias anteriormente publicadas, provenientes trabajo.

Palabras claves: maíz, alelos letales, heterosis, cadenas de Markov, QTL.

Introduction

Chicken BG genes located within the major histocompatibility complex (MHC) encode highly polymorphic membrane-associated proteins. BG molecules are apparently limited to some avian species and may evolve rapidly. Distant BG relatives found in mammals include myelin oligodendrocyte glycoprotein, butyrophilin, and other members of the TRIM family, many of which are encoded within the vicinity of the MHC. BG molecules bear immunoglobulin-like extracellular domains. Hence BG genes are members of the large immunoglobulin gene superfamily (IgSF). Although similar to MHC class I and class II molecules

in their polymorphism, BG molecules (sometimes called class IV molecules) have a distinct structure and form disulfide-linked dimers. Each BG monomer bears a single IgV-like extracellular domain (exon 2), a single transmembrane domain (exon 3), and a series of small (heptad) domains that are predicted to form, in dimers, alpha-helical coiled-coils in the cytosol. The number of exons devoted to the coiled-coil region varies among BG alleles, some have as few as four exons and others as many as 25. With an estimate of 14 to 16 BG loci within MHC B region, alleles form tightly linked haplotypes. The highly polymorphic nature of BG molecules suggests that they have a role in immunity. Although their function is not thoroughly understood, they have been shown to have an adjuvant effect in alloimmunizations and to possibly enhance the response to disease.

In poultry, MHC haplotype contributes to disease resistance and susceptibility. We are interested in the contribution of MHC variability to the hardiness of Campero chickens, line selected at INTA EEA Pergamino, Argentina, as adequate for local free-range production. The aim of this work was to examine BG allelic variability in Campero chickens. We cloned and sequenced BG alleles present within Camperos and compared these with BG alleles reported to the GenBank. Most of them derive from Red Jungle Fowl and experimental strains originated from white Leghorn lines. Campero chickens were selected from crosses between male and female broiler lines. The female parental line is a hybrid originated from a Cornish Red and Rhode Island Red cross.The male line is also a hybrid line derived from a cross between Plymouth Rock Red stock introduced in Argentina during the 60's and a more recent Plymouth Rock Red commercial line.

Material and Methods

We performed PCR reactions in order to amplify the 3'-portion of Exon 1, intron 1 and the whole of Exon 2 from Camperos BG genes. A significant fraction of BG gene polymorphism resides in exon 2; this region provides a suitable means for defining BG allelic variability in chickens. PCR products were cloned into pGEM-T Easy vector (Promega, WI, USA) and introduced into E. Coli XL1 Blue. In order to avoid cloning heteroduplex PCR products and obtain hybrid sequences derived from different members of the BG gene family, we treated PCR products with T7 endonuclease prior to cloning.

Results and Discussion

All nine sequences obtained were different from the BG sequences previously reported to the GenBank and represent new BG alleles. Sequences were reported to the GenBank and accession numbers were assigned: DQ174443, DQ174444, and DQ176443-DQ176449. These plus other four alleles already reported (GenBank No. AF388369 -AF388372) (Iglesias et al, 2003) define 13 new BG alleles of the BG gene family. A phylogenetic analysis, currently under study, will contribute to the understanding of these complex genes.

References

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