

Genetic Diversity of the Antiviral Mx Gene in 14 Chicken Lines

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Summary and Implications

Genetic resistance to avian influenza has previously been associated with a Ser631Asn mutation of the chicken Mx gene. A portion of the Mx gene from 14 genetically diverse chicken lines were PCR amplified and sequenced. The Ser631Asn mutation showed genetic variation among the Iowa State University chicken lines, with some lines having the resistant allele while other lines had the susceptible allele. The diversity in the Mx gene warrants future studies into contrasting host resistance after viral infection in these Iowa State University lines.

Introduction

Avian influenza (high pathogenicity) is a major concern to the global poultry industry. Also, human health concerns are mounting over the highly virulent H5N1 influenza strain. To date, the H5N1 virus strain has not been detected in the USA but much effort is devoted to being prepared. The Mx gene exists in a wide variety of species, from yeast to most animals. It has been documented that in chickens, certain Mx alleles have more antiviral function, including resistance to Influenza A. Additionally, commercial traits such as egg and meat production, as well as immune functions, have been reportedly linked to the Mx gene in chickens. Exon 13 of the chicken Mx gene (Figure 1) has been described as the region where a single nucleotide polymorphism (SNP) causes a single amino acid substitution from Serine (Ser) to Asparagine (Asn) at position 631. The Asn allele confers viral resistance to avian influenza. The objective of this study was to assess the Iowa State University chicken lines for the Ser631Asn SNP genotypes in the Mx gene.

Materials and Methods

An outbred broiler line originating from commercial broiler breeder male line and 13 lines of inbred chickens (estimated inbreeding > 99%) originated between 1925 and 1964 were used in the study. The inbred lines consist of 2 Fayoumi (Egyptian), 1 Spanish, and 10 Leghorn lines. The DNA from 3 samples from each inbred line and 6 from the broiler line were PCR amplified for the Mx gene from the 12th intron to the 3' UTR and submitted to the Iowa State University DNA facility for sequencing. Red jungle fowl sequences were found on Ensembl (<http://www.ensembl.org>). Amplicons were digested with restriction enzyme Hpy8I to confirm SNP genotyping.

Results and Discussion

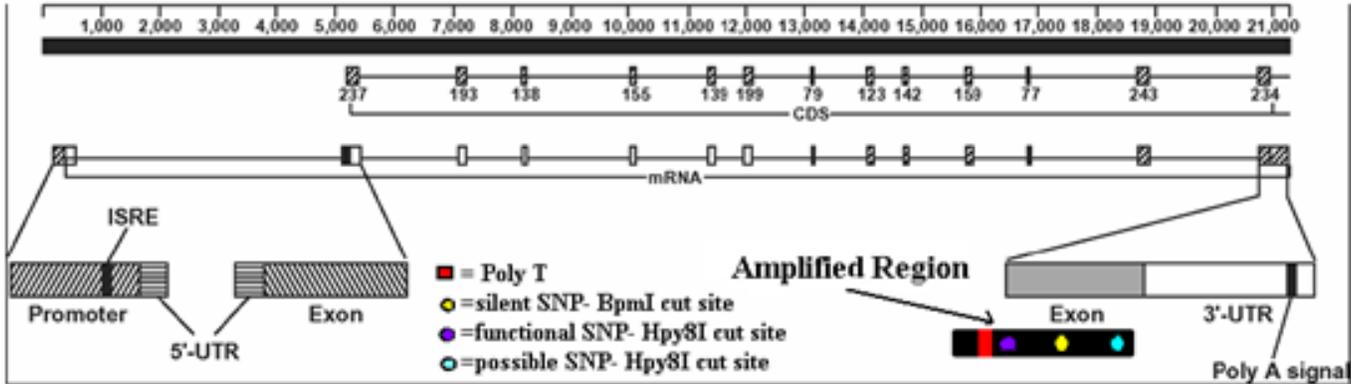
Based on the reports of resistant and susceptible Mx alleles to viral infections, 6 lines possess the G allele coding for the amino acid Serine at position 631 and would be expected to be more susceptible to Influenza A, while seven lines with the 631Asn (SNP A) allele presumably are more resistant to viral infection (Table 1). One inbred line, HN (12,12), appeared to be heterozygous for the Ser631Asn SNP, and this unexpected variation in an inbred line should be further investigated.

It is important for the poultry industry to protect their birds from pathogenic infection. However, it has been reported that virus resistance can negatively affect commercial productivity. Careful evaluation of the allelic effects should be conducted prior to commercial application of the Mx genotyping for genetic selection. The genetic diversity among the Iowa State University lines serves as a basis to further evaluate host resistance to viral infection and interaction of background genes with the Mx gene.

Acknowledgments

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Figure 1. Genomic organization of the chicken Mx gene.



CDS = coding sequence; the number of CDS = the length of each exon; ISRE = interferon stimulated response element; UTR = untranslated region

Modified from Li, X.Y., L.J. Qu, Z.C. Hou, J.F. Yao, G.Y. Xu, and N. Yang. 2007. Genomic Structure and Diversity of the Chicken Mx gene. *Poult. Sci.* 86:786-789.

Table 1: Chicken lines genotypes for Mx gene exon 13 SNP; where at position 631 G codes for the amino acid serine (susceptible) or A codes for asparagine (resistance).

Genetic Line	Functional SNP Ser631Asn
Red Jungle Fowl	CAAG G TAA
Broiler	CAAG G TAA
GHs (13,13)	CAA A TAA
GHs (6,6)	CAA A TAA
M (15.2,15.2)	CAAG G TAA
M (5.1,5.1)	CAAG G TAA
19 (15.1,15.1)	CAAG G TAA
19 (13,13)	CAAG G TAA
Sp (21.1,21.1)	CAA A TAA
GH (1,1)	CAA A TAA
GH (15.1,15.1)	CAA A TAA
GH (13,13)	CAA A TAA
HN (15,15)	CAAG G TAA
HN (12,12)	CAAR T TAA
8 (15.1,15.1)	CAA A TAA