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Avian *TAP* genes: detection of nucleotide polymorphisms and comparative analysis across species

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The nucleotide sequence data reported in this paper have been submitted to the EMBL Nucleotide Sequence Database (European Bioinformatics Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK), and have been assigned the following accession numbers: from AM420706 to AM420797, and from AM420901 to AM420999.

ABSTRACT. *TAP1* and *TAP2* genes code for the two subunits of the transporter associated with antigen processing (TAP), and in chicken they are located between the two MHC class I genes. Using primers based on chicken sequences, the genomic regions corresponding to chicken *TAP1* exons 6 to 7 and *TAP2* exons 4 to 6 (which encode portions of the chicken TAP1 and TAP2 molecules corresponding to the human peptide-binding regions) were amplified and sequenced from chicken (70 birds), turkey (24), pheasant (6), and guinea fowl (7). A total of 80 within-species single nucleotide polymorphisms (SNPs) were identified. None of the chicken SNPs detected here was present in public databases. The SNP frequencies in chicken were 9.57 SNP/kb in *TAP1* and 19.16 SNP/kb in *TAP2*, while turkey showed similar SNP frequencies in the two genes. Putative amino acid sequences were inferred to identify non-synonymous substitutions.

The alignment of the consensus polypeptide sequences showed that most of the amino acid variations were conserved or semi-conserved substitutions. In conclusion, a high variability in the level of nucleotide polymorphism was observed within the two genes, with chicken showing the highest polymorphism rate in both genes. Most of the SNPs identified were within introns, and a general conservation of both amino acid numbers and characteristics of residues among and within the species was found. These data underline the functional importance of these molecules, but also suggest their capacity to bind different antigenic peptides.

Key words: Poultry; Single nucleotide polymorphisms; Major histocompatibility complex; *TAP1*; *TAP2*

