



Analysis of genetic diversity of the heat shock protein 70 gene on the basis of abundant sequence polymorphisms in chicken breeds

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ABSTRACT. This study was designed to detect the sequence variation of the chicken heat shock protein 70 (*HSP70*) gene. A total of 102 individuals from 8 native Chinese breeds together with Dwarf White Chicken and Red Junglefowl were used to detect sequence variations. The coding regions of the chicken *HSP70* gene from 102 individuals were cloned and sequenced. Thirty-six variations were identified, which included 34 single nucleotide polymorphisms and 2 indel mutations. Fifty-seven haplotypes were observed, of which, 43 were breed-specific and 14 were shared. There were 7 Red Junglefowl-specific haplotypes, while Haidong and Silkie only had 2 specific haplotypes. Eleven and 3 haplotypes were shared between and within species, respectively. The variation in nucleotide diversity (P_i) and average number of nucleotide

differences (K) among species were consistent. The total Pi of *HSP70* was 0.0016, and the total K was 4.1998. The Pi value of Red Junglefowl was the highest (0.0018) and K was 4.8000, while the Pi of Silkie was the lowest (0.0010) and K was 2.5000. These results demonstrated that variation in chicken *HSP70* was abundant between and within species.

Key words: Chicken; *HSP70*; Single nucleotide polymorphism; Haplotype